16th DSBS

Deep-Sea Biology Symposium

Brest, 12-17 September 2021

Abstracts

Version 11th of September 2021

Monday 13th September

08:30 - 09:00

Keynote Sabine Gollner Deep-seabed mining: Integrating knowledge on resilience of benthic communities to management and governance

Deep-sea minerals are seen as an upcoming potential resource for critical metals to support growing populations and the development of a green energy economy. At the same time, mineral exploitation may severely threaten future integrity of deep-sea ecosystems. Policy makers currently develop governance frameworks for the management of mineral resources, whilst scientists make at high pace new discoveries on e.g. biodiversity and resilience. The mitigation of any future deep-seabed mining impacts will need the integration of science, management and governance. In this talk I will present preliminary results on biodiversity of nodule infauna and on restoration experiments in impacted polymetallic nodule areas and what these results imply for mitigation strategies. At hydrothermal vents with polymetallic sulfides, we investigate the uniqueness of active vents, as well as ecological connectivity of active vents with their surrounding areas and how this knowledge can be applied for area-based management tools.

Special 1g/1h: Deep-sea mining

09:35 – 09:50

Malcolm Clark, Scott Nodder, Joe O'Callaghan, Daniel Leduc, Vonda Cummings, Chris Hickey, Jenny Beaumont, Charine Collins, Chris Eager, Rachel Hale, Valeria Mobilia, Campbell Murray, Lee Rauhina-August, Ashley Rowden, Rob Stewart, Di Tracey and the rest of the ROBES team The effects of sedimentation in the deep sea: emerging results from New Zealand on the impacts of potential seabed mining

Interest in seabed mining is continuing to increase. However, potential impacts on deep-sea ecosystems remain poorly understood, especially those resulting from sediment suspension and deposition associated with mining vehicles or discharge waters. In 2016 NIWA initiated research into the effects of sedimentation from such seabed disturbance ("ROBES"-Resilience Of deep-sea Benthic communities to the Effects of Sedimentation) using a combination of field disturbance and monitoring surveys, and laboratory experiments. The field work consisted of three surveys in a region with potential for phosphorite nodule mining, at depths of 300-500m on the Chatham Rise, New Zealand. The programme involved a baseline survey in 2018, after which parts of the site were disturbed - in 2018 with NOAAs Benthic Disturber, and in 2019 with a modified tyne-harrow plough. Monitoring surveys were repeated immediately after each disturbance, and again in 2020. Oceanographic data were collected from vessel ADCP, an ocean glider, moorings deployed over two year-long periods, CTD casts, and multibeam and acoustic echosounder surveys. Sediment data were gathered from benthic landers, moorings with sediment traps, and from an extensive multicore grid which also supported onboard sedimentation experiments. Seabed imagery (video and stills) and further environmental data were collected from a towed underwater camera frame. Live sponges and corals were returned to the laboratory for experimental exposure to a range of suspended sediment concentrations and frequencies over time. Here we present some highlights of this multidisciplinary research programme, including data on the dynamic nature of natural environmental conditions, plume effects on water column turbidity and chemistry, effects of sediment capping, direct and indirect sediment effects on benthic faunal abundance, biomass and community respiration, physiological responses of key habitat-forming species to suspended sediments, and importantly, indications of the time period of recovery of benthic communities.

09:35 - 09:50

Travis Washburn et al. Benthic Responses to One of the First Excavation Tests Targeting Deep-Sea Seafloor Massive Sulfides

The Japan Oil, Gas and Metals National Corporation (JOGMEC) has undertaken first-of-their-kind mining experiments in order to test new deep-sea mining technologies and explore impacts of future mining activities on unique deep-sea habitats. In January of 2017, an excavator was used to displace a total of 20 m2 of ore and sediment at a seafloor massive sulfide (SMS) in the Okinawa trough off of Japan. A total of six stations within the disturbance vicinity were sampled before and/or different time points after the disturbance out to December, 2019. Analyses included many sediment characteristics such as different concentrations of metals as well as bacteria, meiofauna, and macrofauna. Since all sampled stations were in close proximity to the disturbance site, elevated levels of metals expected to be impacted by mining combined with measurements of resedimentation and current information were used to determine the level of impact at each station. All components of the infaunal community appeared to change due to the excavation test; however, there was evidence that the spatial extent and time of initial impact were different for bacteria, meiofauna, and macrofauna. Data also suggest that different size classes of organisms recovered at different time scales. This study provides a possible way to assess the level of impacts from mining of SMS deposits at nearby seafloor locations. It also shows how different components of the infaunal community may respond to deep-sea mining in this habitat. While this experiment of course takes place over a much smaller spatial and temporal extent than industrial mining activities will occur, and extrapolation of conclusions should be done with caution, it nonetheless represents an important step in understanding and hopefully mitigating the impacts of deep-sea mining to the surrounding ecosystem.

10:05 – 10:20

Rachel Boschen-Rose, Malcolm Clark, Ashley

Rowden, Jonathan Gardner Integrated environmental management for deep-sea mining: Perspectives from the Kermadec Volcanic Arc, New Zealand

Deep-sea mining is rapidly becoming a reality, yet there are considerable gaps in our knowledge of the seabed assemblages that could be affected by mining activities. Conducting comprehensive environmental baseline studies is a key step towards determining environmental management strategies that can effectively mitigate the impacts from mining activities. Environmental baseline studies were conducted along the Kermadec Volcanic Arc to determine biological seafloor assemblage structure at multiple spatial scales, the connectivity of assemblages at different sites, and the functional sensitivity of assemblages to Seafloor Massive Sulfide (SMS) mining. The combined findings of these studies highlight that a network of highly connected protected seabed areas could be the best approach to mitigating the impacts of any future SMS mining activities. Synthesing and integrating information on assemblage structure, connectivity, and functional sensitivity into a systematic conservation planning framework supports the identification of the most appropriate sites for inclusion within such a network. The lessons learned from this process are also used to highlight the additional knowledge that is required to conduct a full Ecological Risk Assessment for the region and to support Environmental Impact Assessments. Perspectives gained through the integrated approach applied to the New Zealand situation are presented in the broader context of SMS exploration in other regions.

10:20 - 10:35

Jeffrey Drazen, Brian Popp, Erica Goetze, Erik Thuesen, Dhugal Lindsay, Angel White,Sara Ferrón, Jessica Fitzsimmons, Mariko Hatta, Glenn Carter, Victoria Assad, Tiffany Bachtel, Leah Ann Bergman, Alexus Cazares, Michael Dowd, Jesse van der Grient, Nathan Lanning, Elizabeth Miller, Javier Montenegro, Jessica Perelman, Andres Salazar-Estrada, Gina Selig, Gabrielle Stedman, Brent Summers Designing environmental baseline surveys to detect midwater impacts of nodule mining in the eastern CCZ

Midwater ecosystems have been studied very little in the CCZ region, in part due to a focus on mining-specific effects on the seafloor. However, deep-sea mining activities will have a variety of potential effects on biological communities in the ocean's midwaters including sediment plumes from midwater discharge, noise and release of dissolved metals. The International Seabed Authority has modifed their recommendations for baseline ecosystem research to include midwater ecosystems, and a few contractors, including Deep Green Metals (now The Metals Company), have now contracted with scientists to conduct this research. We have begun a comprehensive midwater ecosytem baseline assessment in the eastern CCZ, within in the NORI-D license block. Our goals are to characterize the abundance, biomass, composition and diversity of the microbial, zooplankton, gelatinous zooplankton, and micronekton communities from the sea surface to near the seafloor in advance of mining impacts. This research is being accomplished with a diversity of tools including eDNA sequencing, nets, ROV sampling, and bioacoustics. Further, we are assessing food web connections between dominant taxa and between particle food resources and biota using stable isotope approaches. Environmental conditions are being characterized through water column chemistry, including trace metals, macronutrients, and particle profiles. The first field expedition was conducted in March/April of 2021. The upper water column is strongly stratified with a pronounced and shallow oxygen minimum zone with the planned sediment discharge depth for a 2022 nodule collector test (~1200m) located below the lower oxycline. The design of the pelagic sampling program and preliminary results will be discussed.

10:35 -10:50

Daniel O. B. Jones, Erik Simon-Lledó, Jennifer Durden, Andrew Sweetman, Adrian Glover Seabed Mining and Resilience to Experimental Impact

Mining for deep-see polymetallic nodules has the potential to have far-reaching impacts on abyssal ecosystems. Information on resistance and resilience of nodule ecosystems to mining disturbance as well as on the ecosystems themselves is rapidly increasing with extensive recent research. Here we present the results of a new systematic evidence review on the ecological effects of deep-sea mining. Evidence continues to build that impacts are often severe immediately after mining, with major negative changes in density and diversity of most groups occurring. In some cases, the mobile fauna and small-sized organisms appear more resilient over the longer term. We find more evidence that suggests that the relatively quick recovery observed in some earlier studies is rare in modern assessments. Recent assessments of baseline conditions show greater heterogeneity than older studies, which has some important implications for ecological assessments and management. There have also been improvements in sampling and sampling strategies that will help ensure robust surveys that can reliably detect impacts. The weight of evidence supports the hypothesis that resistance and resilience of abyssal systems is extremely low, albeit variable and depending on the subject of investigations and extent of impact. This work was done to launch a new large UK-funded research project, Seabed Mining And Resilience To EXperimental impact (SMARTEX), which will be introduced to highlight some future research directions.

10:50 - 11:05

Jessica Perelman, Eric Firing, Jesse M.A. van der Grient, Benjamin A. Jones, Jeffrey C. Drazen Mesopelagic scattering layer behaviors across the Clarion-Clipperton Zone: Implications for deep-sea mining

The Clarion-Clipperton Zone (CCZ) is a 4 million km2 region in the eastern Central Pacific Ocean exhibiting large variability in oceanographic parameters, particularly oxygen and primary production, that is being targeted for deep-sea polymetallic nodule mining. The remote region's pelagic biology is very poorly sampled, including for micronekton and zooplankton that provide essential ecosystem services such as carbon flux and support for commercial fisheries. We built a baseline of deep scattering layer (DSL) depths and vertical migration behaviors, proxies for mesopelagic micronekton and zooplankton communities, using shipboard acoustic Doppler current profiler datasets. Acoustic data were compiled from research cruises passing near or through the CCZ from 2004-2019, and environmental data including midwater oxygen, surface chlorophyll-a, and sea surface height anomaly were assembled from climatological and satellite oceanographic datasets. Our results suggest that midwater oxygen, which is associated with the Eastern Tropical Pacific Oxygen Minimum Zone (OMZ), is the strongest predictor of daytime DSL depths and vertical migration strength in this region. We used these relationships to predict micronekton and zooplankton behaviors across the CCZ, including licensed mining exploration areas and no-mining reserves. While most licensed exploration areas lie within the OMZ, the current network of reserves lies outside of the core OMZ and ultimately may not represent or protect the pelagic OMZ fauna at highest risk from mining impacts. We will further present preliminary acoustic and oceanographic data collected by Saildrone USVs at several targeted sites within the CCZ, highlighting the behavioral variability of scattering layers across the region. This research will assist in developing resource exploitation regulations by the International Seabed Authority and will provide mesopelagic baseline information for monitoring changes that may occur in the CCZ once industrial-scale mining begins.

General & Special Sessions 2 Biodiversity and ecosystem functioning from microbes to megafauna (biodiversity patterns, species distribution, function, food webs)

09:35 -09:50

Charles von der Meden, Paula Pattrick, Grant van der Heever, Donia Wozniak, Francesca Porri, Lara Atkinson, Zoleka Filander, Prideel Madjit, Lisa Levin, Kerry Sink

Prime Primnoid real estate: Quantifying complex surface area of biogenic habitat and incidence of use

Deep-sea epifauna such as octocorals are known to offer complex biogenic structures that provide habitat, refugia, elevated feeding platforms and nurseries for the attachment of eggs and larvae of a variety of species. How much additional habitable area these biogenic structures create, and how consistent the use of these features is, are not well known. We examined the incidence of benthic species attached to commonly occurring primnoid octocoral, Thouarella sp., along South Africa's Agulhas Bank, and at the Southern Ocean Prince Edward Islands. Direct measurements of the complex surface area of Thouarella colonies showed that at natural densities, established by visual field surveys, between 14 % and 46 % additional habitat per square meter of seafloor is added. Results also showed a remarkable consistency in the use of these biogenic structures. Approximately 76% of the colonies examined hosted scale worms, 69% hosted bivalves and 46% were inhabited by ophiuroids. Less commonly, but of significance, colonies were demonstrated to be nursery habitat supporting nests of fish eggs and associated larvae. These eggs and larvae were barcoded, identifying a Paraliparis sp. Results give a unique quantitative perspective of biogenic habitat provision and inter-species ecology of the Agulha.

09:50 - 10:05

Bhavani E Narayanaswamy, Ivan Cautain, Natalia Serpetti, Kim S. Last, Colin Abernethy

Spatial changes in benthic megafaunal community composition in the Barents Sea across Atlantic

The Arctic marine ecosystem, especially the shelves, are experiencing considerable changes in the extent ofsea ice and as a result the seasonal ice zone is replacing multi-year ice. This change may lead to increased levels of primary and secondary productivity which in turn impacts the faunal communities found here, including the benthos. In particular the ice-edge is considered to be a biological productivity hotspot and questions arise as to whether similar hotspots will be observed in the benthic communities. The megafaunal community was investigated at set stations at a depth of 200 – 400 m, along a longitudinal (30°E)transectin the Barents Sea using a towed camera. The stationsspanned the Atlantic and Arctic-influence water masses, as well as the seasonal ice zone. Using BIIGLE, the next generation image annotation programme, the photographs were analysed by identifying fauna to the lowest possible taxonomic level and counts made of the fauna present. Our first results indicate that there are noticeable changes in the faunal community, particularly with regards to the ophiuroids, Porifera and decapods. The Porifera showed an increased abundance at the northern end of the transect, with the highest number of Porifera found in Arctic waters, whilst the decapods showed the converse to this, with greater numbers observed at the southern end of the transect, situated in Atlantic waters. The ophiuroids were found in greatest numbers in the middle of the transect located near Hopen Bank, a potential abundance hotspot and which also shows some similarities to other work undertaken in this region. Overall ophiuroids were observed much more frequently than any other group seen in the images. Placing these results into context of the oceanographic polar front and results from the wider Arctic PRIZE programme may help explain some of our findings.

10:05 - 10:20

Heidi Meyer, Emyr Martyn Roberts, Andrew Davies, Joana Xavier, Hans Tore Rapp The Secrets of the Schulz Bank - Exploring the community structure of deep-sea sponge grounds on an Arctic Seamount

The Schulz Bank is a large seamount situated on the Arctic Mid-Ocean Ridge and rises from 3000 m depth at the base to 560 m at the summit. The seamount is subjected to a complex oceanographic setting which allows a plethora of diverse sponge communities to thrive along its slopes. Previous studies have only just shown a glimpse into these distinct communities, mostly focusing on the summit of the seamount. Yet the Schulz Bank has much more to offer. In this study, remotely operated vehicle (ROV) footage was used to explore the megafaunal communities along bathymetric gradients all the way from the soft bottom basin to the tip of the spicule mat-covered summit. We uncover the changes in community types, explore the distribution of the characterizing fauna, and investigate the factors driving these patterns. We found distinct communities on the Schulz Bank: from sponges (Geodia hentscheli, Caulophacus arcticus, and axenillids) and crinoids covering the exposed bedrock in the basin to the slopes dominated by glass sponges (Schaudinnia rosea and Asconema foliata) and soft coral (Gersemia rubiformis) to the dense summit community characterized by large demosponges (Geodia parva and Stelletta rhaphidiophora), ascidians, and anemones. Species richness and diversity increased with decreasing depth, where the upper slopes and summit were most diverse. Environmental variables such as substrate type and water mass properties likely influence the patterns observed. With this knowledge, we can improve our understanding of how these rich and pristine Arctic communities may be affected by anthropogenic impacts, and support management actions towards their preservation.

10:20 - 10:35

Marie-Anne Cambon-Bonavita, Johanne Aubé, Valérie Cueff-Gauchard, Julie Reveillaud Niche partitioning in the *Rimicaris exoculata* holobiont: the case of the first symbiotic Zetaproteobacteria

The hydrothermal vent shrimp Rimicaris exoculata, which dominates animal communities along the Mid-Atlantic Ridge, houses a complex bacterial community in its enlarged cephalothorax, including Campylobacteria, Desulfobulbia, Alphaproteobacteria, Gammaproteobacteria and some recently discovered iron oxyhydroxide-coated Zetaproteobacteria. This epibiotic consortium uses iron, sulfide, methane, and hydrogen as energy sources. Long debated, shrimp nutrition has been proven to occur through the cephalothorax integument, where small organic molecules produced by the symbionts pass in the circulatoty system, rather than through the digestive system. The phylogenetic and metabolic diversity of this epibiotic community suggests a high flexibility adapted to the chemically contrasting environments inhabited by the shrimp. We have collected specimens in three geochemically contrasted vent fields, TAG, Rainbow, and Snake Pit, to unravel the specificity, variability, and adaptation of Rimicaris–microbe associations. We reconstruct 49 metagenome-assembled genomes (MAGs) from the TAG and Rainbow vent fields, including 16 with more than 90% completion and less than 5% contamination based on single copy core genes. These MAGs belonged to the dominant Campylobacteria, Desulfobulbia, Thiotrichaceae as well as some novel candidate phyla radiation (CPR) lineages. Most importantly, two MAGs in our collection were affiliated to Zetaproteobacteria. Genes for CBB carbon fixation, iron, and sulfur oxidation, as well as nitrate reduction, occurred in both MAGs. However, genes for hydrogen oxidation and multicopper oxidases occurred in one MAG only, suggesting shared and specific potential functions for these two novel Zetaproteobacteria symbiotic lineages. Overall, we observed highly similar symbionts co-existing in a single shrimp at both the basaltic TAG and ultramafic Rainbow vent sites. Nevertheless, further examination of the seeming functional redundancy among these epibionts revealed important differences. These data highlight microniche partitioning in the Rimicaris holobiont and support recent studies showing that functional diversity enables multiple symbiont strains to coexist and cooperate in/with animals colonizing hydrothermal vents.

10:35 -10:50

Miguel Guerreiro, Véronique Merten, Fleur Visser, Kim Heimberg, Fernando Á Fernández-Álvarez, Roger Villanueva, Henk-Jan Hoving Applying 3D models to study Deep-Sea Cephalopod Distribution in the North East Atlantic

Oceanic cephalopods are widely distributed, abundant and diverse predators of the ocean, as well as prey of many marine top predators. Furthermore, due to their post-spawning mass death events, they provide carbon and food pulses to the seabed, feeding benthic communities, contributing to the carbon pump. However, due to their remote habitat and active avoidance of trawling equipment, deep-sea and open ocean species observations are relatively few, highlighting the need to use alternatives to characterize their distribution. In this study we develop a 3D (Longitude, Latitude plus Depth) model to determine the distribution of cephalopods in the deep sea of Northeast Atlantic with the aim of identifying the main environmental variables limiting their ecological niche and locating the cephalopod biodiversity hotspots within the Atlantic. For this, we used depth resolved environmental variables datasets collected from Copernicus Marine Service and GEBCO to characterize the habitat of cephalopods physically (pressure, distance from seabed, temperature and salinity), chemically (Oxygen concentration) and biologically (Zooplankton biomass), at the sites where animals were previously registered on eDNA sampling campaigns (POS-532, PE-456), captured by scientific trawls (WH383, Mafia-2015, Bathypelagic-2018) or in the literature (10 cruises of the NW African coast from 2004 to 2012). This data was conveyed to an ensemble of Species Distribution Models, designed to calculate the habitat suitability of the NE Atlantic Ocean to each of the cephalopod species. Preliminary analysis shows that the distribution of cephalopods is centered around regions of high productivity, close to islands and seamounts, which is in line with the literature. With the results of this study, we aim to identify regions of increased cephalopod diversity and hotspots of cephalopod carcass deposition.

10:50 - 11:05

Julien Marticorena, Jozée Sarrazin, Loic N. Michel, Gauthier Schaal, Marjolaine Matabos

Hydrothermal food web recovery after a small-scale disturbance on the Lucky Strike vent field (MAR)

Our knowledge of the natural dynamics of hydrothermal ecosystems is still scarce and limits our ability to predict their resilience to natural and anthropogenic disturbances. Understanding colonization processes is essential to assess the natural regeneration capacity of vent communities in response to modification of their habitats. However, the natural recovery of vent communities is difficult to assess in place where natural disturbance are extremely rare, like in the Mid-Atlantic Ridge. In this study, we applied an innovative approach for the deep sea, by removing all faunal communities from a series of 8 quadrats deployed on the active Montségur edifice using a claw and suction sampler from a submersible. During 2 years, we followed the recolonization dynamics of the macrofauna associated with a Bathymodiolus azoricus mussel assemblage in terms of functional diversity and food web structure, together with environmental conditions. One year after the disturbance, predator/scavenger species (such as Mirocaris fortunata) were biomassdominant, instead of deposit feeders in pre-disturbed assemblages. Our results suggest that during the first step of recolonisation, these species may play an important role in the food web structure by reducing the trophic diversity and complexity through a top-down control. However, two years after the disturbance, we observed a fair recovery of the overall food web structure despite differences in taxonomic diversity and community structure, with notably a higher proportion of grazers. This study provides relevant insights on the resilience of vent communities in response to disturbance and represents one of the first to use biomass and community-wide isotopic metrics to assess functional recovery in vent ecosystems.

Special 1g/1h: Deep-sea mining

11:25 - 11:40

Matthias Haeckel, Annemiek Vink

Impacts of deep seabed mining – Initial results from the trial of a pre-prototype manganese nodule collector Impacts of deep seabed mining – Initial results from the trial of a pre-prototype manganese nodule collector

Interest of various states and companies in the mining of metal ores (polymetallic nodules, massive sulphides, and cobalt-rich crusts) from the abyssal seabed has been sparked by the projected future demands of metals for the transition to a low-carbon energy system and the increasing consumption of high-tech products in conjunction with global population growth. While extracting metals from deep-sea ores may contribute to the desired overall reduction of our CO2 emissions, it will certainly introduce a new environmental threat to our oceans. Abyssal ecosystems show unrivalled high biodiversity in combination with high spatial and temporal variability of faunal populations and environmental variables. Recent research results of the European MiningImpact project on potential impactsfrom future deep-sea mining operationsindicate that these will be at least locally severe and last for centuries to millennia. Currently designed mining technology will not only remove the metal ore, which forms the habitat for rich and specific benthic fauna, but the entire biologically active surface layer of the seafloor, which forms the basis of the abyssal food web. In addition, suspended particle plumes will also blanket the benthic ecosystem outside the mined areas. Larger-scale consequences are still uncertain due to the largely unknown species connectivity and our limited understanding of ecosystem structure and functions. At the anticipated scale of impact of several hundreds of square kilometres per year for each nodule mining operation, careful and adaptive spatial planning of mining operations on regional and even global scale is required. Conservation areas must be set aside that closely match ecosystem characteristics in mined areas, and ecological indicators and threshold values indicative for harmful effects need to be defined. Here, we present the design and initial results of the independent scientific monitoring of the first industrial trial of a pre-prototype nodule collector vehicle, which took place in the CCZ in April to May 2021.

11:40 - 11:55

Nancy F. Mercado-Salas, Sahar Khodami, de Pedro Martínez Arbizu

On the importance of reference libraries in deep-sea monitoring at the Clarion Clipperton Fracture Zone

The Clarion Clipperton Fracture Zone in the central Northeast Pacific has been recognized as one of the most economically important regions of the world because its polymetallic nodules represent a major source of manganese, iron, copper, nickel, cobalt and other minerals on earth. Commercial deep-sea mining of polymetallic nodules might potentially take place in near future and it is commonly agreed that mining activities will have severe impacts in deep-sea ecosystems. However precise predictions on the impacts and risks of deep-sea mining are difficult to assess because of the many gaps of knowledge on deep-sea biodiversity, especially in the extraordinarily diverse meiobenthic communities. New methodologies -such as metabarcoding- are seen as revolutionary, standardized, cost-effective and rapid tools to assess and monitor diversity. Nevertheless, it is commonly overlooked that this approach relies on the availability of reference libraries to assign a taxonomic identity to each particular sequence. It has been stressed the critical importance of maintaining the expertise and capacity in morphological taxonomic identification in order to validate the metabarcoding data, especially in those areas of the world that are considered under studied or ongoing under direct anthropogenic changes. Herein, we characterize the meiobenthic copepod community in the test trial area at the German License Area (CCZ) following an integrative approach. Our reference library includes 572 copepod species from which morphological (vouchers) and molecular data (mtCOI and V1V2) is available. In order to provide a more reliable species estimation, we performed and compared five different species delimitation analyses using exploratory methods including distance (ABGD, ASAP, BINs) and tree-based (GMYC, mPTP) approaches for each molecular marker. Finally, we analyzed the genetic distance for each molecular marker at order, family, genus and species level and define similarity thresholds for group discrimination at each taxonomic category that will serve as reference to metabarcoding studies.

11:55 - 12:10

Lénaïck Menot, Alexandre Bourdon, Loïc N. Michel, Lucie Pastor Macrofaunal assemblages in iSMS-associated metalliferous sediments of the mid-Atlantic Ridge: community structure and trophic ecology

Seafloor Massive Sulfides (SMS) are mineral deposits of mining interest, which are formed by hydrothermal activity. Since mining active hydrothermal vents may prove challenging for technological and environmental reasons, inactive SMS (iSMS) are priority targets for future deep-sea mining. Large iSMS are older deposits, which have undergone weathering and accumulated pelagic sediments. As a result, iSMS are more likely to be surrounded and draped by soft sediments that should be removed during the mining process. These iSMS-associated sediments might host novel macrofaunal assemblages, of which hardly anything is known. Developing integrative knowledge of these communities' ecology is highly desirable to support the environmental management of resource exploitation. During the BICOSE2 cruise on the Mid-Atlantic Ridge, sediments were sampled in the older TAG and the younger Snake Pit vent fields at about 3500 m depth. Snake Pit sediments were anoxic, rich in metal sulfides and mostly of hydrothermal origin. The macrofauna was abundant and dominated by polychaetes, such as ampharetids and hesionids, known from chemosynthetic environments. C, N and S stable isotope ratios showed that the dominant species depended on chemosynthetic organic matter for their nutrition. TAG sediments, on the contrary, were oxic, rich in iron hydroxide and of mix hydrothermal and pelagic origins. Macrofaunal abundances were very low, even by abyssal standards. Our study suggests that iSMS-associated macrofauna resemble abyssal rather than hydrothermal fauna. The hypothesis however remains to be fully tested, which may prove difficult considering the low densities, high diversity and commonness of the rare that characterise abyssal communities.

12:10 - 12:25

Muriel Rabone, Adrian Glover A deep dive into DeepData: taxonomic records in the ISA biological data holdings and the published literature for the CCZ

Although exploration activities for polymetallic nodule mining have been underway in the Central Pacific's Clarion-Clipperton Zone (CCZ) since the 1970s, there is a well-documented lack of biodiversity knowledge for the region. These knowledge gaps urgently need addressing, especially given potential exploitation of the polymetallic nodule fields. Systematic efforts are finally underway and have resulted in remarkable recent gains in biodiversity knowledge of the CCZ. Another recent development is the launch of the International Seabed Authority (ISA) database DeepData, the key repository of contractor data, including biological, oceanographic and geological datasets. With a large body of data already collected, it is timely to review the baseline taxonomic data currently available for the CCZ. To help address this need, metazoan taxonomic records published in DeepData and in pre-processed contractor data from all faunal size classes have been analysed and compared with records available in global data aggregators (Ocean Biodiversity Information System, OBIS and Global Biodiversity Information Facility, GBIF) and the published literature. The project will provide the foundational work for a systematic review on taxonomic studies done in the CCZ and contribute recommendations and priorities for further taxonomic work in the region.

12:25 - 12:40

Elin Thomas, Aoife Molloy, Nova Hanson, Monika Böhm, Mary Seddon, Julia Sigwart Deep-sea mining and the global extinction risk to vent-endemic species

Hydrothermal vents are host to an incredible array of life in the deep sea, however, as the accelerating deep-sea mining industry threatens these habitats and their unique taxa, we face an increasing conservation dilemma of how to protect the remote and often understudied species in the deep sea. As a well-established and globally recognised conservation tool, The International Union for the Conservation of Nature (IUCN) Red List of Threatened Species is uniquely placed to shine a light on these threatened species to industry, policy makers, and the general public, alike. We therefore applied the Red List Criteria to all vent-endemic molluscs to produce the first global assessment of extinction risk for an entire taxonomic group under the threat of deep-sea mining at hydrothermal vents. In doing so, we demonstrate the robust applicability of universal conservation tools like the IUCN Red

List to even the most data-limited deep-sea species. Of the 184 vent-endemic mollusc species assessed, 62% are listed as threatened: 39 are Critically Endangered, 32 are Endangered, and 43 are Vulnerable. In contrast, the 25 species that are fully protected from deepsea mining by local conservation measures are assessed as Least Concern, and a further 45 species are listed as Near Threatened, with some subpopulations under mining threat and others lying within protected areas. This set of molluscs and their Red List status not only serves as a proxy for the uniqueness of each hydrothermal vent site but also provides a comprehensive illustration of the geographic spread of mining threat to all vent-endemic species. This study exemplifies how taxonomy-driven tools can be utilised to cultivate deep-sea conservation and sets the precedence for the application of the Red List criteria to all taxa from the deep sea's diverse range of habitats.

12:40 - 12:55

Katja Uhlenkott, Annemiek Vink, Thomas Kuhn, Benjamin Gillard, Erik Simon-Lledo, Martínez Arbizu Distribution modelling with random forest in a potential deep-sea mining area

The Clarion Clipperton Fracture Zone is well-known for its high abundance of polymetallic nodules on the seafloor. At the same time, the polymetallic nodule fields are known to harbour a highly diverse benthic fauna that is endangered by potential future mining activities. Therefore, the designation of preservation zones with comparable communities is vital before the onset of exploitation, to enable the efficient monitoring of nearby impacted sites and also to later enable the resettlement of fauna into mined areas. Predicted distributions of different taxa and diversity indices can be used to find spots with similar faunal attributes. Also, distribution models can be used to investigate the fauna according to different environmental predictors. One of the main difficulties of distribution modelling in the deep sea is the scarce availability of environmental predictors on a suitable scale for predictions. Hence, bathymetry and backscatter data have to serve as the basis of faunal predictions on the scale of several hundreds of kilometers. On a smaller scale, spatial prediction of environmental data, e.g. on sediment characteristics, can act as an additional source for the spatial investigation of faunal distributions. The random forest algorithm has been used to compute faunal distribution models. Although spatial variability is high, model performance remains acceptable for several meio- and megafaunal taxa. Generally, meiofauna abundance is predicted to be lower in areas with high nodule abundance compared to areas with lower nodule abundance. The distribution of a high number of megafaunal taxa varies comparing seamount and hill sites to the abyssal plain.

12:55 - 13:10

Jesse van der Grient, Jeffrey Drazen What can shallow-water animal sensitivity thresholds to increased suspended sediments teach us about the effects of deep-sea mining plumes?

Interest in the mining of polymetallic nodules, sulfide deposits, and ferromanganese crusts in the deep sea is growing. The mining process, from the seafloor collection of deposit materials to the discharge of unwanted sediments, can potentially cause a host of impacts. There is, however, little to no empirical data on the responses of deep-sea animals to discharge and collector-vehicle plumes. Yet, this information is necessary to evaluate the spatial and temporal scales of sediment plume effects and evaluate and manage wider environmental risks. While empirical data is needed, obtaining these data will take time. Here, we present the results of a meta-analysis investigating suspended sediment effects in shallow-water animals from several taxa and feeding guilds across different habitats (e.g., marine, estuarine, and freshwater habitats) to understand how animal responses to increased suspended sediments differ between habitats. We find that responses to increased suspended sediments are shared between habitats, and that relative sediment concentration increases (compared to natural background conditions) are negatively correlated with animal performance in various response types, including behavior, feeding, growth, physiology, respiration, reproduction, and survival. There are habitat-specific differences in the strength of these responses, indicating that natural background conditions are important in determining the effect of increased suspended sediment concentrations. We derive sensitivity thresholds based on the proportion of species affected by different sediment concentrations. These different sensitivity threshold values were used to derive placeholder values for deep-sea animal sensitivities. In addition, we show some initial results of applying the general response functions obtained from this work to a North-Pacific midwater food-web model to understand wider ecosystem effects in response to increased suspended sediments caused by discharge plumes.

General 2: Biodiversity

11:25 - 11:40

Clara Diaz, University of Plymouth, Kerry Howell, Martin Atrill, Nicola Foster

Environmental drivers of the Mesophotic Coral Ecosystems community structure over the depth gradient in the Chagos Archipelago, Indian Ocean.

Mesophotic coral ecosystems (MCEs) are light-dependent communities occurring in deeper waters, typically between 30 m and 150 m deep. Despite the exponential growth in research on MCEs in recent years, their study is still at its infancy. This is mostly due to the logistical difficulties and safety issues with conventional scuba diving encountered at these depths and the expense of using deepdiving technologies in these 'too shallow' coral environments. In addition, geographical disparities are observed among MCE research, with the Indian Ocean remaining relatively unexplored, with only 1% of global studies based in this region. The Chagos Archipelago, considered a biodiversity hotspot in the middle of the Indian Ocean, is a relatively unperturbed ecosystem due to its protected status – one of the largest no-take Marine Protected Areas – and its remote location. Here, we present results on the variation in species diversity and community structure of MCEs along the depth gradient and their environmental drivers around Egmont Atoll, based on the most extensive survey of MCEs in this area to date. Using a Remotely Operated Vehicle (ROV), video transects were collected at multiple depths from shallow reefs (15 m) to the lower mesophotic zone (160 m). In addition, numerous environmental data were collected (e.g. temperature, salinity, pressure, topography, substratum type). We firstly observed a decrease in species diversity along the depth gradient and secondly a variation in benthic communities with a shift from scleractinian corals to octocorals and hydrozoans, which may have implications for the potential biological connectivity of mesophotic benthic species. This study provides detailed description of the entire depth range of MCEs within the Chagos Archipelago providing critical knowledge on the diversity and potential distribution of MCEs in the region, with the environmental factors that may drive it, contributing to conservation and local management plans within the Archipelago.

11:40 - 11:55

Andreas Kelch, Davide Di Franco, Angelika Brandt Biodiversity assessment of the isopod family Paramunnidae Vanhöffen, 1914 (Crustacea, Malacostraca) from the Weddell Sea, Southern Ocean

The long evolutionary history and isolation through geologic and climatic events over the last 30 Ma resulted in a unique and high benthic biodiversity in the Southern Ocean. Nevertheless, many species are still unknown. The present study aims to improve the knowledge on isopod diversity of the family Paramunnidae Vanhöffen, 1914 and investigates the influence of environmental variables of this environment on their species composition and richness. Paramunnids are asellote isopods and due to their size between 0.4-3 mm, their inability to swim and reduced gene flow (as peracarids are brooders), they are interesting to study regarding their occurrences and range sizes. Samples were collected during four expeditions in various areas of the Atlantic sector of the Southern Ocean. Sampling areas were characterised by different regimes of ice coverage: the seasonally ice-covered Filchner Trough (JR275) and Eastern Antarctic Peninsula (PS118), as well as the Prince Gustav Channel (JR17003a) which was formerly covered by an ice shelf and the South Orkney Islands (JR15005) with very low sea-ice concentrations or ice free. With about 2494 of 17293 total isopod individuals the Paramunnidae was the second most abundant isopod family of the sampled material. The family was characterised by a high diversity, with 30 species from eleven genera. Approximately 23 species are unknown. Abundances and number of paramunnid species varied between sampling areas. Statistical analyses revealed that ice coverage was the main environmental variable driving Paramunnidae assemblage structure and species richness. Our results showed that the knowledge on Southern Ocean isopod diversity is still far from understood and investigated as many species are still discovered. Climate change is rapidly changing the Southern Ocean environment, it is therefore very likely that the consequent loss of sea ice will highly threaten future Southern Ocean isopod diversity.

11:55 - 12:10

G. Luongo, C. Corinaldesi, A. Dell'Anno, A. Pusceddu, E. Rastelli, M. Tangherlini, R. Danovaro Benthic prokaryotic assemblages and virus-host interactions in deep-sea sediments of the Ross Sea (Antarctic Ocean)

In the Ross Sea, the patterns of primary production and related organic matter (OM) downward fluxes to the seafloor are highly dynamic in time and space, with possible effects on deep-sea benthic prokaryotic abundance, activity and diversity, as well as viral abundance and virus-prokaryote interactions. In this study, we investigated such processes by comparing two deep-sea macro-areas (B, 586m, and C, 432m, at 200-km relative distance), also assessing the temporal and the spatial variability by sampling over two weeks two sub-areas within each macro-area. Most of the analyzed variables differed markedly between macro-areas, being otherwise quite consistent between sub-areas within each macro-area and between sampling times. Macro-area B showed higher sedimentary OM and phytopigment concentrations, higher prokaryotic and viral abundances and heterotrophic C production rates, and higher viral production rates than C. Nevertheless, the virus-induced prokaryotic mortality was 10 times higher in area C and positively correlated with aminopeptidase activity and protein turnover, suggesting that higher food limitation in C could trigger more efficient OM turnover and nutrient cycling, enhanced by viral lysis. At the Family level, the prokaryotic assemblages showed significant differences between macro-areas, but not between sub-areas nor between different sampling times. Conversely, at the ASV level, we identified significant differences also between sub-areas and between sampling times, indicating high strain-level spatial and temporal turnover diversity within prokaryotic families. Consistent with the higher OM contents, area B showed higher abundances of taxa related to phytodetritus degradation and breakdown of labile organic molecules, while area C displayed higher relevance of taxa involved in refractory substrates utilization and in nutrient regeneration via ammonia oxidation. Overall, these results provide new insights on the spatial and temporal variability of the prokaryotic and viral assemblages in the Ross Sea, advancing our understanding of the benthic Antarctic deep-sea ecosystem functioning.

12:10 - 12:25

Elisa Baldrighi, Marco Basili, Donato Giovannelli, Grazia Marina Quero, Massimo Cafarella, Elena Manini Different benthic size classes shed light on deep-sea fauna smallscale spatial patterns

Deep-sea investigations on spatial scales are often conducted on broad scales (100skm) with loss of resolution of smaller spatial scale, and focused on a single benthic component rather than considering different benthic communities. Critical to gain insights in different benthic component dynamics is identifying the scale at which the important processes occur. To test whether significant changes in structure, diversity, function and standing stock occur at local-scale (ca. 7km), we used a hierarchical sampling design to assess spatial patterns of three different benthic components: micro-, meio-, and macrofauna and related environmental variables. Sediment samples were collected along the Nurra slope (Sardinia), from 600m to 2400 m with intervals of 300 m among sampling depths and from three stations at each depth located along a 1 km-length horizontal transect. Results indicated that the spatial scale we considered was not effective to catch clear significant differences in the prokaryotic community composition. Meiofaunal diversity, functional and standing stock variability was evident along the bathymetric gradient and even between stations at same depth, while changes in macrofauna were mainly associated to the bathymetric gradient. However, a high beta diversity has been reported for both meio- and macrofauna communities at different depths and between stations along the 1-km transect, indicating substantial changes in the metazoan benthic communities inhabiting the Nurra slope. These findings imply that a multiple scale analysis is necessary to unravel which spatial scale is important in determining the variability of different benthic communities and indeed to understand the processes driving their structure, diversity, function and standing stock in the deep-sea.

12:25 - 12:40

Harriet Baldwin, Ella Treloar, Craig M. Robertson, Furu Meinis, Gerard C.A. Duineveld, Marc Lavaleye Andrew J. Davies

Benthic functional biodiversity across a habitat complexity gradient within the Deep-Sea coral reefs of the Rockall Bank, NE Atlantic

There is a growing need for ecological indicators, such as measures of functional diversity (FD), to inform marine ecological understanding. Although baseline studies provide valuable biodiversity information, there is a need to understand the nuance of functional services provided by resident benthic fauna in an ecosystem. The use of functional indices is essential to understanding the relationships between anthropogenic impacts, benthic ecosystem functioning and community biodiversity. This study aimed to address knowledge gaps in benthic FD and use FD indices to better understand benthic community assemblages associated with Desmophyllum pertusum cold-water coral reefs in the Logachev Mound Province, of the Rockall Bank (UK). Specifically, trends in the FD of benthic communities across a habitat complexity gradient will be examined. The study utilised boxcore benthic samples collected from two-cross mound transects from the Haas Mound, to draw comparisons between habitat heterogeneity and FD of benthic assemblages. FD was assessed through biological trait analysis, using a selection of biological traits assigned to taxa families to calculate FD indices. Spearman's rank correlation analysis will be conducted to verify the relationship between FD and habitat heterogeneity. Samples were obtained from four biotopes: coral rubble, low coral framework, dead coral framework and live coral framework. The following hypotheses were answered (1) FD (FRic, FEve, FDiv, and Rao'sQ) positively corresponded with increased habitat heterogeneity and (2) FD had a significantly greater association with habitat heterogeneity in comparison to species taxonomic diversity. Our findings will be available to present at the symposium, addressing knowledge gaps within deep-sea benthic biology. The findings highlight the usefulness in using BTA as a tool for assessing biodiversity ecosystem function and is a step forward in our understanding of the details of ecosystem services in a deep –sea coral habitat.

12:40 - 12:55

Jaime Ríos-Osorio, Patricia Puerta, Dierk Hebbeln, Covadonga Orejas, Claudia Wienberg, André Freiwald

Spatial patterns of benthic mega-fauna associated to Cold-water coral reefs on the continental margin off Angola

Cold-water coral (CWC) reefs provide habitat to multiple deep-sea species, including commercial ones, creating valuable and unique ecosystems in the deep sea. The CWC reefs and their associated fauna have been widely studied in several locations of the North Atlantic Ocean and Mediterranean Sea, but very scarce information is currently available on these deep-sea communities from the South Atlantic. A recent expedition to the continental margin off Angola in 2016 (R/V METEOR expedition M122) discovered a benthic biodiversity hot-spot area, which is characterized by the presence of CWC reefs dominated by Lophelia pertusa thriving under extreme hypoxic conditions with dissolved oxygen concentrations as low as 0.5 mL· L -1 . We aimed to investigate the distribution of the mega-fauna assemblages associated to these CWC reefs based on video footage recorded by a Remotely Operated Vehicle (ROV Squid). For this purpose, we produced quantitative standardized data for occurrences and abundance, showing more than 91 mega-faunal taxa found along four video transects. In addition, we used these data to perform species distribution models (SDMs) and build habitat suitability maps of the biodiversity and total abundance of the CWC reef associated fauna. Based on the bathymetry, terrain variables and oceanographic parameters of the area, we provided a comprehensive overview of the spatial patterns of the deep-sea mega-benthic biodiversity. Data showed that although biodiversity seems to be lower if compared to other Atlantic counterpart sites, the observed biodiversity and population density in several of these deep-sea species was remarkably high despite the hypoxic conditions. This work contributes to characterize these vulnerable marine ecosystems and allows to better understand their communities associated thriving under very low oxygen conditions. Therefore, it highlights the importance of the study area in terms of biodiversity and the adaptation capability of deep-sea vulnerable taxa to face the future scenarios of climate change.

12:55 - 13:10

Verena Tunnicliffe, Thomas Giguère

Beta-Diversity Metrics Assess Biodiversity Distribution in Hydrothermal Vent (and Other) Deep-sea Ecosystems

The arrangement of species in discrete habitats over large ocean areas may form one of many patterns best assessed through beta-diversity metrics. Such pattern analyses can contribute fundamental insight to management of vulnerable marine ecosystems. The first requirement is good data on both habitat distribution and alpha diversity. We test the hypothesis that diversity distribution is similar among hot vent systems using new data from the Mariana back-arc, the Mariana volcanic arc and the Juan de Fuca mid-ocean ridge. Species overlap, species replacement and richness differences create different diversity distribution patterns within the three systems in which the volcanic arc shows the largest vent to vent differences with deterministic assembly processes likely. Each system would require a different management strategy to meet biodiversity protection objectives. We then update species presence data in biogeographic areas across the western Pacific by verifying every published record and adding new collection data. We find that there is a high species replacement not only from southwest to central to northwest Pacific, emphasizing faunal separation among these regions. Species replacement was also evident between each arc and its corresponding back-arc hot vent faunae. Models of connectivity that may predict recolonization after natural or anthropogenic disturbances cannot assume all interchanges with neighbouring vent systems are possible.

Special 1g/1h: Deep-sea mining

14:50 - 15:05

Craig R. Smith, Malcolm R. Clark, The 45 Other Participating Scientists of the Deep CCZ biodiversity Synthesis Workshop Patterns of Seafloor Biodiversity and Ecosystem Function in the Clarion Clipperton Zone: Are No-Mining Areas Representative of Regional Patterns?

The Clarion Clipperton Zone (CCZ) is a vast region of abyssal plains and seamounts targeted for potential mining of polymetallic nodules. To safeguard biodiversity and ecosystem functions across the region in the face of mining, the International Seabed Authority (ISA) in 2012 provisionally designated nine 400x400 km no-mining areas, called Areas of Particular Environmental Interest (APEIs). The APEIs were designed, using environmental correlates of biodiversity and ecosystem function, to be representative of the full range of habitats and seafloor communities potentially impacted by nodule-mining activities. Since 2012, substantially more biodiversity data have been collected within the CCZ, providing a new opportunity to assess regional patterns. We convened 47 scientific experts at the Deep CCZ Biodiversity Synthesis Workshop (Oct 1-4, 2019 at Friday Harbor, USA) to (a) collect and review available biodiversity and ecosystem function data from the CCZ, (b) synthesize patterns of seafloor and benthic-boundary-layer biodiversity, community structure, species ranges, genetic connectivity, ecosystem function, and habitat heterogeneity along and across the CCZ; and (c) evaluate the representivity of the APEIs relative to licensed mining exploration areas. Fifteen peer-reviewed papers derived from the workshop are published or in press in a special volume of Frontiers in Marine Science. Here we synthesize and summarize the results of the workshop and special volume, and conclude: (1) Biodiversity is high, variable, and still poorly sampled across the CCZ, with likely thousands of new species to be collected and described. (2) Key biodiversity drivers in the CCZ include POC flux, nodule abundance, and bottom topography. (3) Connectivity patterns are variable across the CCZ and across taxa, with some species occurring widely while many others have been collected only at single sites. (4) The current APEI network captures substantial habitat variability, but nodule-rich habitats are poorly represented and should be prioriyized for placement into additional APEIs.

15:05 - 15:20

Erik Simon-Lledó, Diva Amon, Daphne Cuvelier, Sofia P. Ramalho Katja Uhlenkott, Pedro Martinez Arbizu, Anemiek Vink, Jennifer M. Durden, Craig R. Smith, Tammy Horton, G. Bribiesca-Contreras, Ellen Pape, Chailinn Park, Se-Jong Ju, Kirsty McQuaid, Daniel O. B. Jones Regional patterns in biodiversity of abyssal benthic megafauna at the Clarion Clipperton Zone

The abyssal seafloor of the Clarion Clipperton Zone (CCZ) in the central Pacific has the largest known deposits of polymetallic nodules and associated faunal communities with high biodiversity. Benthic megafauna (animals > 1 cm) richness estimations obtained from seabed image data can exceed 200 taxa in local assessments, which makes the CCZ one of the most species-rich abyssal plain areas in the world. However, the ecology and connectivity of these remote habitats is still poorly understood and little is known of the environmental factors that drive biodiversity nor the scales at which these operate, because comprehensive analyses of biogeographic distributions are lacking. Here, we collate and standardise megafaunal distribution data from imagery surveys from across the CCZ to investigate patterns of benthic biodiversity across this region. We found clear variations in faunal density, increasing from west to east in most taxonomic groups, particularly in suspension-feeding fauna. Community compositions were clearly distinct across many of the areas studied. Betadiversity patterns were characterised by a predominance of balanced variations in the abundance (e.g., replacement) of dominant taxon groups rather than by differences in richness. Even relatively close areas had distinct assemblages, for example the central easternmost exploration claim areas were significantly different from the nearest protected area ~500 km away (APEI 6). Results of this regional assessment show that abyssal plain areas, despite the lack of clear physical barriers, can harbour much higher levels of benthic community heterogeneity than was previously hypothesised. Our study provides important information to ensure the efficiency of regional environmental management plans.

15:20 - 15:35

Tanja Stratmann Regional differences in carbon cycling in a prospective deep-seabed

mining area in the eastern Clarion-Clipperton Fracture Zone (Pacific)

The seafloor of abyssal plains between 3,500 and 6,000 m water depth is often covered with mineralrich polymetallic nodules (also called manganese nodules) that contain metals, such as cobalt, nickel, and copper. As land-based mines for these metals are either located in politically instable countries and/ or are more and more depleted, polymetallic nodules are considered a prospective future resource for these metals. However, the extraction of these nodules will likely have severe consequences for the ecosystem, such as habitat removal and compaction and sediment-plume creation. To understand these impacts and to assess the potential recovery of the ecosystem from these disturbances, biological baseline information about biodiversity and ecosystem functioning is required. For this study, the first carbon-based food-web models for an area in the Clarion-Clipperton Fracture Zone (CCZ, North-East Pacific) were developed. The license area of Belgium and Global Sea mineral Resources (GSR), respectively, is in the northeastern part of the CCZ and consists of three not-connected subzones (west: B2, central: B4, east: B6) that are approximately 60 to 270 km apart. I will present one food-web model developed for station B4SO3 in B4 and one model created for station B6SO2 in B6. For each model I estimated carbon flows between the prokaryote compartment (including Bacteria and Archaea), metazoan meiofauna (i.e., Nematoda on genera level, other meiofauna on higher taxonomic level), macrofauna (i.e., isopoda and polychaetes on family level, other macrofauna on higher taxonomic level), invertebrate megafauna, and fish. I also compared the sum of all carbon flows in the food web (i.e., total system throughput) and Finn's cycling index for both sites. Furthermore, I calculated specific carbon pathways (i.e., microbial loop and scavenging pathway) and contrasted the results with a comparable model developed for polymetallic nodule areas in the Peru Basin (South-East Pacific).

15:35 - 15:50

Nélia C. Mestre, Andrea Armatore, Miguel Caetano, Douglas P. Connelly, Tainá G. Fonseca, Daniel O.B. Jones, Amaya Menendez, Joana Raimundo, Maria João Bebianno

Ecotoxicological evaluation of deep-sea sediments and nodules

Few data are currently available on the ecotoxicological risks to deep-sea fauna from the potential release of toxicants during deep-sea mining activities. One fundamental uncertainty is whether the commonly used ecotoxicological end points established for shallow-water environments are applicable to deep-sea mining. Here we present results on the acute toxicity of deep-sea sediments and nodules from the Clarion-Clipperton Fracture Zone (North Pacific). Samples were collected from three different geomorphologies (trough, ridge and flat) in the APEI (Area of Particular Environmental Interest) 6 area during the RRS James Cook Cruise JC120 in May 2015. The EC50s (50% effective concentrations) of the inhibition of the bioluminescence of the bacterium Vibrio fischeri were obtained for the different layers of sediment cores and for crushed nodules. In addition, the EC50s related to the development of larvae of the sea urchin Paracentrotus lividus exposed to elutriates of sediments and crushed nodules were determined. Grain size and chemical composition (metal contents) of sediments, nodules and elutriates were also evaluated. Results indicate that crushed nodules are more toxic than sediments. Both bioassays produced similar EC50s for samples from the trough and ridge sites. The developing sea-urchin larvae of P. lividus was much more sensitive than the bacterium V. fischeri to samples from the flat site and crushed nodules. These standard toxicity tests may be a useful tool to compare the acute toxicity of different sites but cannot directly inform on the toxicity to local fauna. The specific challenges to recommending exposure limits in light of deep-sea mining activities will be discussed. Funding: European Commission - MIDAS project (Grant Agreement 603418); Fundação para Ciência e Tecnologia (FCT) and Direção-Geral de Política do Mar (DGPM) - JPIO Mining Impact 2 (Mining2/2017/001, Mining2/0004/2017); FCT (CEECIND005262017, UI/350/2020).

15:50 - 16:05

Chris Smith, HCMR, Telmo Morato, Meri Bilan, Marina Carreira-Silva, Nadia Papadopoulou, Andrew Sweetman, Dan Jones, Marjolaine Matabos, Cristina Gambi, Ana Colaço, Andrea Gori, Cristina Linares, Jozee Sarrazin, David Billet, Eva Ramirez-Llodra, Daphne Cuvelier, Katerina Sevastou, Anthony Grehan, Inês Martins, Laura Carugati, Maria Montseny, Teresa Amaro, Thanos Dailianis, Vasilis Gerovasileiou, Roberto Danovaro

Principles and key concepts for ecological restoration in the deep-sea

In 2016 the Society of Ecological Restoration published its International Standards for the Practice of Ecological Restoration with a more recent update considering recent advances. The standards included a set of principles and key concepts providing support for the technical application of ecological restoration across geographic and ecological areas, to improve biodiversity conservation outcomes for all ecosystems, secure the delivery of ecosystem services, ensure projects are integrated with socio-cultural needs and realities, and contribute to the 2030 Agenda for Sustainable Development. Application to strictly marine and European restoration has been very limited and within the EU funded H2020 MERCES marine restoration project, lessons learned from terrestrial and shallow water restoration along with previous deep-sea experience, were used to evaluate the principles, concepts and guidelines for ecological restoration of deep-sea ecosystems. Four deep-sea case studies were investigated, each affected by different pressures and requiring different degrees of intervention to assist their natural recovery processes. The case studies include a hydrothermal vent field in the mid-Atlantic that may be impacted by deep-sea mining (replacement of structures to speed up the development of hydrothermal vent chimneys), abyssal plain communities in nodulerich areas of the Pacific also of interest to deep-sea mining (replacement with chemically-conditioned artificial nodules), soft bottom communities in the Mediterranean impacted by rock drilling activities (natural regeneration) and cold-water coral ecosystems in the Azores impacted by deep-water fishing (coral transplantation). The study addresses the challenges posed in describing local native reference ecosystems, identifying and measuring key ecosystem attributes, knowledge gaps, time scales, uncertainties and challenges to deep-sea restoration. Restoration of marine ecosystems is an integral part of the new EU Green Deal and Biodiversity Strategy 2030 and a good understanding of the restoration process is essential to decide how we need to manage conservation and impacting activities.

16:05 - 16:20

Maila Guilhon, Luise von Pogrell, Luciana Yokoyama Xavier, Pradeep Singh, Sabine Christiansen Alexander Turra Ecosystem-based Management through the lens of International Seabed Authority stakeholders

The ocean is becoming increasingly threatened by human activities and climate change, which can undermine ecosystems' health. Consequently, it is of major importance to manage human activities considering an ecosystem perspective, such as through Ecosystem-based Management (EBM). EBM is an approach that seeks to harmonize human uses, usually represented by sectoral activities, with a holistic, participative and integrative understanding of the state of the ocean, and how potential pressures can impact the the maintance of ecosystems' integrity, processes, functions and services. By acknowledging uncertainties and applying a precautionary approach, EBM implementation in scenarios of limited knowledge and potentially irreversible impacts, such as deep sea mining (DSM), is highly pertinent. The International Seabed Authority (ISA), the international organization with the mandate to award mineral exploration and exploitation contracts on the international seabed, has recognized the need to incorporate the ecosystem approach in its recent instruments but has not specified how it can be done in practice. The lack of consensus on a common definition and how to operationalize EBM represent shortcomings for effective implementation. Taking this into account, the study aims (1) to ascertain whether different stakeholders are aligned in their general understanding of EBM in the DSM context and (2) to discuss the implications of possible discrepancies identified in such understanding. To achieve such objectives, a two-step approach was followed: first, the conduct of an online survey containing 24 statements to be ranked by stakeholders together with four open questions; second, in-depth interviews were performed with selected experts representing different stakeholder groups. Through multivariate data analysis, a set of "factors" representing the broad perception was identified. Content analysis was applied to open questions and interviews. The presentation aims to discuss and rationalize the results obtained to propose recommendations to the DSM process at the ISA.

General 2: Biodiversity

14:50 - 15:05

Poppy Keogh, Rylan J. Command, Evan Edinger, Aggeliki Georgiopoulou, Katleen Robert The Charlie-Gibbs Fracture Zone – Biodiversity, Community Composition and What Drives Them.

The Charlie-Gibbs Fracture Zone (CGFZ) is a prominent geological feature offsetting the Mid-Atlantic Ridge (MAR), consisting of two parallel fractures, creating a highly variable seafloor bathymetry. It has been defined as the most important latitudinal biodiversity transitional zone on the MAR, but the faunal communities living on the fracture zone have not been extensively described. A remotely operated vehicle (ROV) was utilized during the TOSCA (Tectonic Ocean Spreading at the Charlie-Gibbs Fracture Zone) survey to examine geological processes occurring at the CGFZ. The survey included 5 ROV video transects at depths ranging between 560m and 2,900m. The objectives of the current study were to use this video footage to quantify the biodiversity of the CGFZ, identify FAO-recognized VME indicator species, and determine the benthic community composition and its drivers. Species accumulation curves and generalized additive modelling showed that depth and the presence of hard substrates (bedrock and boulders) played an important role in explaining species richness and abundance on the CGFZ. Cnidarian taxa were more abundant between depths of 1,500m and 2,000m, while Porifera taxa were most abundant between 1,750m and 2,250m. Sponge densities on a ridge at those depths were high enough that the area could be described as a sponge ostur. Hierarchical clustering indicated the presence of eight distinct biological communities, including three associated with VME indicator species: soft sediment seapen, stalked crinoid and Acanella fields; hard bottom sponge aggregations; and coral (Antipatahria and Octocorallia) gardens with an abundance of echinoderms, arthropods, and boney fish. The high diversity and presence of VME indicator species found in this study highlight the need for detailed surveys to help support decisions made by governing bodies such as OSPAR (Convention for the Protection of the Marine Environment of the North-East Atlantic) on the protection status of the CGFZ.

15:05 - 15:20

Amy McAllister, Paul Snelgrove, David Cote, Zacchaeus Compson, Owen Sherwood Resolving food webs in the Labrador sub-Arctic deep sea

In a region of the global ocean experiencing rapid effects of climate change, marine food webs in the Labrador Sea require effective monitoring to understand and prepare for ecological change. Food webs are especially vulnerable to change because they encompass the biodiversity, species interactions, and structural and functional relationships of an ecosystem. The remote location of deep-sea environments limits the use of traditional methods for studying food webs, requiring adaptation of novel approaches such as isotopic analyses and environmental DNA (eDNA). Using a midwater trawl, we collected fishes and invertebrates at multiple sites from the Labrador shelf to the continental slope between 500 and 3000 m depths to obtain tissues for stable isotope analysis to evaluate species trophic levels within contrasting environments. Using a CTD-Rosette, we also collected water samples to obtain and extract eDNA to determine species presence. We then gleaned trophic information from open-source biological databases to infer trophic positions through modeling. By comparing food web properties across sites using isotopic and eDNA analytical tools, we evaluate the sensitivity of the tools and determine which are most appropriate for detecting ecological shifts across sites. Preliminary analysis indicates similar trophic levels of a given species between analytical tools and consistent trophic levels across sites for frequently occurring species. However, additional food web properties obtained from the eDNA model show greater variation across sites compared to trophic level alone. This work enhances understanding of deep-sea trophic dynamics and provides an ecological baseline of the Labrador Sea necessary for tracking future responses to rapidly evolving oceanographic conditions in the face of global environmental change.

15:20 - 15:35

Ana K. Avila, Maurício Shimabukuro, Daniel M. Couto, Paulo Y. G. Sumida, Fabiane Gallucci Whale falls as chemosynthetic 'stepping-stones': perspectives from the meiofauna

Organic islands represented by whale carcasses are among deep-water reducing chemosynthesisbased environments that show high species richness. During the sulfophilic stage, bones exhibit lineages of organisms comparable to other chemosynthetic deep-sea environments, such as hydrothermal vents and cold seeps, possibly acting as 'stepping-stones' for the dispersal of organisms on the sea floor. Such evidence is based mainly on macrofaunal taxa which exhibit planktonic larval dispersal. For the smaller meiofauna, data on whalebone assemblages is still lacking. Their direct development with no planktonic larvae and relatively low mobility suggests limited dispersion. As such, one might expect assemblages colonizing whale carcasses to resemble those from adjacent sediments, rather than from other chemosynthetic environments. On the other hand, evidence for long-distance passive dispersion of meiofauna, as well as for selective settlement in sulfidic substrates, supports the possibility of whale falls as 'stepping-stones' for dispersal of chemosynthetic meiofauna. To test these alternative hypotheses, we have investigated the colonization of experimentally deployed whalebones by meiofauna at 1500 and 3300 meters depth in the Southwest Atlantic Ocean, and compared assemblage's composition to other deep-sea environments, as well as to sediment samples adjacent to the carcasses. Whalebone assemblages were composed mostly by nematodes, dominated by the genus Halomonhystera. These assemblages were highly different from those inhabiting adjacent sediments and other deep-sea sedimentary environments, while it showed high similarity to assemblages from cold seeps and hydrothermal vents. These results challenge the notion of limited dispersion in deep-sea nematodes and support the idea that whale carcasses may act as intermediate environments for the dispersal of the meiofauna dependent on chemosynthetic environments. Such findings highlight the importance of organic islands for understanding the connectivity and phylogeny of benthic organisms, including representatives of the meiofauna.

FINANCIAL SUPPORT: This study was supported by FAPESP (2011/50185-1 and 2019/18526-5) and PETROBRAS/CENPES (Santos Project).

15:35 - 15:50

Stace Beaulieu, Michael Meneses, Lauren Dykman, Susan Mills, Daniel Fornari, Lauren Mullineaux Distinct fauna on inactive sulfides contributes to biodiversity on the East Pacific Rise

Inactive sulfide structures located within deep-sea hydrothermal vent fields are no longer actively discharging vent fluids, but appear to continue to support microbial production. To investigate whether they also support distinct invertebrate fauna, we characterized the inhabitants of two inactive sulfide features using the HOV Alvin and ROV Jason: Lucky's Mound and Sentry Spire, located off-axis southwest of the 9°50'N vent field on the East Pacific Rise. At both sites, we conducted quantitative down-looking surveys with a deep-sea 24MP digital still camera, and close-up scans with a 4K video camera. For comparison, we also surveyed the relatively flat basaltic seafloor at a similar depth and distance off axis. Preliminary analyses of megafauna visible in the down-looking surveys indicate that abundance and diversity are substantially higher on the inactive sulfide structures than on nearby bare rock seafloor. With the exception of one species, the galatheid squat lobster, the megafauna do not appear to be characteristic of active vents, but instead are representatives of typical deep-sea fauna, including holothurians, crinoids, ophiuroids, brisingid asteroids, sponges, and alcyonarians. In contrast, the close-up video reveals smaller species not typical of non-vent ecosystems. For instance, the upper, inactive chimneys of Sentry Spire are covered with limpets of the genus Neolepetopsis. Species of this genus have been reported from other vent fields and we have collected their larvae in plankton in the 9-10°N region, but have never before found the adults in this region. We are continuing to analyze the collected imagery to evaluate the hypothesis that inactive vents support a fauna distinct from both active vents and "ambient" deep-sea habitat, and that inactive sites contribute substantively to the biodiversity of vent fields. These findings are relevant to evaluations of ecological impacts of deep seafloor mining that target inactive seafloor massive sulfides.

15:50 - 16:05

Melissa Betters Rethinking Informative Traits: Environmental Influence on Shell Morphology in Deep-Sea Gastropods

Marine gastropod mollusks within deep-sea, chemosynthetic environments present unique challenges to taxonomic study because they are chronically under-sampled, yet are anomalously biodiverse along the ocean floor. While classifying gastropod diversity often relies on shell morphology, the accuracy of shells in delineating species is no longer clear, as genetic evidence increasingly confirms intraspecific morphological variation. Chemosynthetic environments, for instance, may present a uniquely heterogenous landscape where abiotic factors can affect gastropod shell formation and maintenance. In examining a snail species from the genus Provanna (Dall, 1918) (Gastropoda) from three hydrocarbon seeps along the Costa Rica Margin, preliminary data have found variation in traits that would typically be considered taxonomically informative. Evidence of shell morphology varying within a single gastropod species is not underheard of, however, the extent of this variation within Provanna, and what drives this variation, is still poorly understood. My current research addresses the question: Does the environment in which marine gastropods live have a significant effect on their intraspecific morphological variation? This project will examine how shell morphometry within a species of Provanna varies along environmental parameters associated with active hydrocarbon seepage, such as biogenic substrate, oxidative reductive potential, dissolved oxygen, and alkalinity. This research may elucidate the impact of heterogeneous chemosynthetic landscapes on gastropod morphology, and critically assess the reliability of shells in diagnosing chemosynthetic gastropod species.

16:05 - 16:20

Juan Carlos Azofeifa-Solano, Juan José Alvarado, Leonardo Chacón-Monge, Jorge Cortés Diversity and biology of deep-sea echinoderms from Costa Rica

Echinoderms are a highly diverse group of marine invertebrates, and probably one of the most conspicuous organisms in the deep sea, playing key roles as detritivores, suspesion feeders, and predators. Here we present a brief review about the history of expeditions and studies on deep-sea echinoderms in Costa Rica, including an updated list of species. We used information gathered from the databases of the California Academy of Sciences (CAS), the Benthic Invertebrate Collection (SIO, Scripps Institution of Oceanography), the National Museum of Natural History (NMNH, Smithsonian Institution), the Museum of Comparative Zoology (MCZ, Harvard University), and the Museo de Zoología (MZUCR, Universidad de Costa Rica). A total of 95 species have been collected at the Costa Rican deep sea, 82 found in the Pacific Ocean, 14 in the Caribbean Sea, and one species shared between the two basins. Here we report 18 new records for the Eastern Tropical Pacific, 30 for Central American waters, and 35 for Costa Rica. The most specious group was Holothuroidea with 30 species, followed by Asteroidea (24 spp.), Ophiuroidea (19 spp.), Echinoidea (14 spp.), and Crinoidea (8 spp.). The bathymetric distribution of richness was 31 species at the 200-1000 m depth range, 60 species at the 1000-2000 m range, 22 at the 2000-3000 m range, and only two species were found >3000 m depth, the crinoid Bourgueticrinus sp. (3031 m) and the ophiuroid Ophiosphalma glabrum (3400 m). Further efforts on identification will be required for a better comprehension of the diversity of deep-sea echinoderms since several specimens reported are identified at the genus level or identified with affinities to a species. In addition, little research has been done regarding the biology and ecology of deep-sea echinoderms in Costa Rica, and additional efforts will be necessary to understand their ecological function in these ecosystems.

General 1: Conservation

16:40 - 16:55

Thomas Dahlgren, Jon Thomassen Hestetun, Muriel Rabone, Adrian Glover Genetic barcode repository gap analysis – contrasting the beauty

A new deep-sea ‘blue economy’ will require long-term environmental monitoring of deep benthic ecosystems. To achieve this, metabarcoding of environmental DNA samples has been suggested as a possible complement or alternative to current morphological methods to assess biodiversity. However, as 95% of the deep-sea fauna is yet to be described, let alone with molecular data, the use of existing taxonomic resources with this methodology may be questioned. For the method to successfully characterise species assemblages, a public sequence database is necessary to match barcodes to species identity, however, these public sequence libraries must be expanded, and subjected to at least some degree of quality control. The oil and gas industry conducts large-scale environmental monitoring in the North Sea, one of the most heavily sampled marine areas worldwide and could therefore be considered a ‘best-case scenario’ for macrofaunal metabarcoding. In a recent study, we investigated the database coverage of two common metabarcoding markers, mitochondrial COI and the ribosomal rRNA 18S gene, for a complete list of 1802 macrofauna taxa reported from the North Sea monitoring region IV. For COI, species level barcode coverage was 50.4% in GenBank and 42.4% for public sequences in BOLD. For 18S, species level coverage was 36.4% in GenBank and 27.1% in SILVA. Results from this study is contrasted with data from an emerging deep-sea industrial target – the Clarion-Clipperton Zone (CCZ) in the equatorial Pacific. The critical need for molecular taxonomy in the deep-sea is highlighted through a comparison of recent metabarcoding studies both in the (relatively) well barcoded North Sea and the less catalogued CCZ.

16:55 - 17:10

Lara Atkinson, Colin Attwood, Natasha Karenyi, Kerry Sink, Charles von der Meden, Grant van der Heever Measuring change in a southern Benguela slope after cessation of trawling.

To investigate the effects of trawling on the benthic ecosystem of the Benguela shelf, a 7.5 x 6.0 km block spanning depths between 350 and 520 m, was divided into five lanes. Trawlers were channelled through lanes one, three, and five, leaving two and four untrawled. Towed camera transects and grab sampling was undertaken one year before and four years after the implementation of the lanes, yielding video segments and photographs of the seabed and the fishes just above it. Annually from 2014 to 2018, fifteen sites were chosen using a random stratified design, covering all lanes equally. Fishes and epifauna were identified and counted from videos and photographs. Infauna and sediment properties were quantified from grab samples. The intensity of trawling pre- and post-lane closure was estimated using fishing industry tracks and AIS records. Seventeen species of bony fishes dominated by spiny eels, six species of chondricthyans dominated by skates and one Myxiniform species were recorded. 75 species of epifauna, dominated by a brittle star and polychaete, and more than 300 infaunal species, primarily polychaetes and amphipods, were recorded. Fish (p=0.01), epifauna (p=0.02) and infauna (p=0.05) species composition was significantly influenced by depth, but trawl intensity and the interaction between trawl intensity and depth, were not significant. Fish and epifauna communities did not change significantly over the 5 year experiment, however, infauna showed a significant difference among years (p=0.05). If the change in trawl intensity applied at this localised scale influenced fish, epifauna or infauna, community level changes were not evident after four years. This unique in situ deep sea experiment showcases an opportunity for co-operative research through collaborations between industry and scientists.

17:10 - 17:25

Nicole B. Morgan, Amy R. Baco Recent fishing footprint of the high-seas bottom trawl fisheries on the Northwestern Hawaiian Ridge and Emperor Seamount Chain: a finer-scale approach to a large-scale issue

A standing data gap for management of high-seas seamounts of the Northwestern Hawaiian Ridge and Emperor Seamounts (ES-NHR) by the North Pacific Fisheries Commission is the footprint of fisheries activities on these seamounts. Using satellite AIS data and the algorithms of the publicly available Global Fishing Watch database, a spatial map of trawling in a 0.01 by 0.01-degree square grid was created to review the data available to map this footprint. From 2012 – 2018 much of the trawling effort was focused on Koko, Yuryaku, Kammu, and Colahan Seamounts at depths between 400 m (summits) and 1500m, the depth limit currently set by the North Pacific Fisheries Commission. Other seamounts with fishing activity included Annei (North Koko), Kinmei, Jingu, and Suiko. The remaining ES-NHR seamount locations showed no trawling in those years. Bottom contact fishing was predominately carried out by ships with flag states of Japan and Korea. To date there appears to be compliance with the recent small-scale closures on C-H seamount and Koko. An additional source of data comes from scientific Autonomous Underwater Vehicle (AUV) surveys in 2014 and 2015 from three of these seamounts, in which scars from bottom contact gear are readily visible. These cover a smaller spatial scale than the satellite data, but indicate the full footprint is not encompassed by the Global Fishing Watch data, suggesting either the fishing footprint is not fully captured by the AIS approach or that the footprint has shifted through time. AUV surveys also provide data on areas of abundant benthic megafauna, which can provide candidate starting points for VME management efforts and further closures, similar to ones already in effect in the ES-NHR. The combination of satellite and AUV data provide a finer-scale fisheries footprint for this region that can aid in management of these sites.

17:25 - 17:40

Peter Etnoyer, Amanda Demopoulos, Stacey Harter, Kris Benson After the Disaster: Plans for Coral Propagation Activities to Support Restoration of Mesophotic and Deep Benthic Communities Impacted by Deepwater Horizon Oil Spill

Background: Deep benthic communities are vast and complex ecosystems, and the foundation of Gulf of Mexico food webs. Nearly 2000 sq km of deep-sea and mesophotic habitat were injured by the Deepwater Horizon (DWH) oil spill. There were direct observations of injury to several hundred colonies of gorgonian octocorals near the wellhead at 1500 m, and in the mesophotic zone between 50-150 m. Since 2019, US federal trustees have been developing detailed work plans, inventories, and analyses of best available data to inform implementation of an 8-year project to develop techniques for propagation of the mesophotic and deep coral species injured by the spill. One primary objective of this presentation is to solicit community input on preliminary results of ‘planning phase’ analyses. Aims: The intention of this work is to prioritize species for propagation, identify a pool of taxa for monitoring, and develop a strategy to mitigate losses to biodiversity. The project intends to establish a network of partners, including cold water aquaria facilities equipped to meet the challenges of deep-water coral propagation. Description: Analysis teams identified 42 deep-sea coral species that may be impacted. Each was considered using criteria for degree of injury, frequency of occurrence, and management relevance, in order to rank taxa for propagation. These taxa were assessed in terms of their abundance and distribution, taxonomic status of knowledge, and their suitability for the laboratory environment. Spatial analyses used ArcGIS to identify targets for sampling, and sites for propagation. Plans are in place to inventory artificial structures, design, and deploy these in the field, to enhance recruitment. Labs will be engaged in cooperative studies of coral growth, feeding, reproduction, and thermal tolerance to support lab husbandry, in-situ fragmentation, and outplanting in temperatures as low as 4-5 o C, and as deep as 1800 m.

Special 1b: Spatial planning

16:40 - 16:55

Amelia E Bridges, David K Barnes, James B Bell, Rebecca E Ross, Lizette Vogues, Kerry L Howell Filling the data gaps – transferring models from data rich to data poor deep-sea areas to support spatial management

Spatial management of the deep sea including Areas Beyond National Jurisdiction (ABNJ) is challenging due to limited available data on the distribution of species and habitats to support decision-making. In the well-studied North Atlantic, predictive models of species distribution and habitat suitability have been used to fill data gaps. In the South Atlantic and other poorly studied regions this is not possible due to a lack of data. In this study, we ask whether models constructed in data-rich areas can be used to inform data-poor regions. We use a model transfer approach to identify whether a habitat suitability model for Desmophyllum pertusum cold-water coral reef, built in a data-rich deep-sea basin (North Atlantic), can be transferred to a data-poor basin (South Atlantic). The transferred model was built using the Maximum Entropy (MaxEnt) algorithm and constructed with 227 presence and 3064 pseudo-absence points, and 200 m resolution environmental grids. Performance in the new area was validated using an independent dataset of D. pertusum presences and absences, with assessments made using both threshold-dependent and - independent metrics. We find a model for D. pertusum reef fitted to North Atlantic data transfers well to the South Atlantic basin, with an area under the curve of 0.72. Suitable habitat for D. pertusum reef is predicted on 21 of the assessed 27 features including seamounts. In ABNJ, we find four seamounts that provide suitable habitat for D. pertusum reef are at least partially protected from bottom trawling, whilst three do not fall within closures. Marine Protected Areas/Zones designated by Saint Helena, Ascension Island and Tristan da Cunha provide significant protection for D. pertusum reef habitat. We conclude that model transfer approaches stand to provide significant contributions to spatial planning processes, particularly in ABNJ and areas that have previously undergone little scientific exploration.

16:55 - 17:10

Elisabetta Menini, Helena Calado, Roberto Danovaro, Patrick Halpin, Elisabetta Manea, Cindy Lee Van Dover Good news: Protection of active vent ecosystems is growing globally

Deep-sea hydrothermal vents support special ecosystems, with endemic biodiversity able to tolerate high pressure, strong geochemical and geothermal gradients, instability in space and time and fluids loaded with toxic compounds. All active deep-sea hydrothermal vents merit special protection implemented through a precautionary approach and qualify against criteria for Vulnerable Marine Ecosystem and Ecologically and Biologically Significant Areas. In the last decade, management and protection of these extreme ecosystems at national and international levels has increased to include about 25% of all active vents currently known and georeferenced. Just in the last three years, four new marine protected areas and area networks have been added to the existing sectoral and crosssectoral area-based management measures established by numerous sovereign countries and by Regional Fisheries Management Organizations. This growth in protective measures include moratoria on deep-sea mining implemented by Island States in the Pacific Ocean and at European level. Managed hydrothermal vents are found across all ocean basins and include different types of endemic hydrothermal fauna and biogeographical provinces. The natural capital of hydrothermal vent ecosystems is underscored by global interventions to protect them.

17:10 - 17:25

Kirsty McQuaid, Amelia Bridges, Kerry Howell, Kerry Sink, Mandy Lombard, Tiago Borges Ribeiro Gandra Mapping the South Atlantic to support regional Marine Spatial Planning

Marine management has historically adopted sector- and place-specific approaches, both within and beyond areas of national jurisdiction. However, connectivity is a key characteristic of marine ecosystems, and there is thus a drive towards more integrated, ocean basin-scale management, whereby larger regions and multiple sectors are managed in a holistic way. One approach to support the realisation of this vision is marine spatial planning, a process dependent on the production of habitat maps. This study brings together habitat mappers, biodiversity experts and ocean managers from multiple South Atlantic bordering nations to produce two regional benthic habitat classifications of South Atlantic Areas Beyond National Jurisdiction (ABNJ). The first approach combines pre-clustered abiotic variables selected through a literature search on biologically relevant environmental drivers, while the second uses an objective method to select abiotic variables through principal component analysis (PCA) and clusters these with an unsupervised k-means algorithm. The output habitat maps produced identify broad benthic habitat classes across the South Atlantic. We compare the outputs of both classifications, identifying areas of agreement and inconsistency. We also compare outputs to national habitat maps in the region, and explore the potential for applications to marine spatial planning at an ocean basin-scale in South Atlantic ABNJ.

17:25 - 17:40

Tammy Norgard, **Cherisse Du Preez** Identifying Representative Seamount Ecosystems in Large Marine Protected Areas

Seamounts cover vast areas of the Canadian Offshore Pacific Bioregion (~20,000 km2), with 50 of the 62 seamounts in existing or anticipated Marine Protected Areas. The remote nature and range of these seamounts make gathering comprehensive or representative data a challenge. To provide science advice to guide deep-sea marine spatial planning for seamount conservation and protection, Fisheries and Oceans Canada Science developed an evaluation, building on published methods and widely recognized important ecological criteria, to identify representative seamount ecosystems (e.g., by seamount class). Representative ecosystems are considered a collection of areas that captures examples of different biogeographic subdivisions that reasonably reflect the full range of ecosystems present at the scale of assessment, including the biotic and abiotic diversity of those ecosystems. The analyses aimed to maximize available data (mainly benthic), examining in detail the nature of seamount ecosystems from surveyed areas and predicting with some confidence the nature of unsurveyed areas. That said, the large offshore MPAs are three-dimensional dynamic systems with multi-scale spatial and temporal variability, and it is recommended that the methods presented here be used to update/reassess the nature of representative areas as new data becomes available.

Tuesday 14th September

Special 1f: Climate change

09:05 - 09:20

Chih-Lin Wei, William W. L. Cheung, Lisa Levin

Climatic Impact on Deep-sea Ecosystem and its Future Projection

We used climate projections from three 3-D fully coupled earth system models, as part of the Coupled Models Intercomparison Project Phase 5 (CMIP 5), to evaluate climatic impacts on deep-sea ecosystem. Projections were made under the current emissions scenario (also known as 'business as usual) in representative concentration pathway (RCP) 8.5 for bottom temperature, oxygen, pH and POC flux to the seafloor. Climate change was assessed by subtracting the historical average (1951-2000) from the future average (2081-2100). Time of emergences of climate change were defined as the year when the climate changes of all stressors exceeds their historical standard deviation. Exposure to climate change hazards were measured as the amplitude of climate change in the unit of historical variability (climate change divided by historical standard deviation). Climate velocity magnitude was calculated by dividing long-term trends of climate stressors (yr-1) by their spatial gradients (km-1) in a 3x3 neighborhood of cell. Cumulative impacts of climate change were calculated by integrating either climate change hazards or climate velocity magnitudes due to warming, declines in POC flux, deoxygenation, and acidification. Our results show that over 75% of seafloor are projected to see future climate changes exceeding historical variability by 2065. For 75% of the seafloor, the cumulative impact represented by accumulated warming, oxygen loss, acidification, and food shortfall, will be more than 30 times their summed modeled historical variability by 2081- 2100. The cumulative climate velocity magnitude of warming, oxygen loss, acidification, and food shortfall will increase > 8 km yr-1 by 2081-2100 (compared to the cumulative velocity in 1951-2000) for 75% of the seafloor. In conclusion, the earth-system model projections of climate-change parameters at the seafloor reveal negative impacts in projected climate hazard, time of emergence (beyond natural variability) and climate velocity magnitude for majority of the deep-sea ecosystem.

09:20 - 09:35

Owen Anderson, Fabrice Stephenson, Ashley Rowden, Erik Behrens

Predicting shifts in areas of habitat suitability for deep-sea corals in New Zealand

In New Zealand, most species of deep-sea corals are protected by law, but while this legislation prevents deliberate collection or damage to corals it offers no protection from incidental damage due to contact with mobile fishing gear or to the effects of climate change on the environmental conditions in which they live. In this study, we utilised a large, historical deep-sea coral sample dataset along with outputs from a locally-tuned Earth System Model (the NZESM) to predict the current and future (2100) distribution of twelve taxa of protected corals. Predicted future environmental conditions were based on two potential emissions scenarios: one with middle-of-theroad mitigation and adaptation and the other with a considerably more pessimistic future. For modelling, we used an ensemble of two species distribution models (Boosted Regression Trees and Random Forests) and estimated model precision using resampling methods. Models were driven by a range of environmental predictors, but seafloor concentrations of aragonite/calcite and oxygen were important for most taxa. Results indicated that for most deep-sea coral taxa the primary areas of current distribution will experience a substantial decline in habitat suitability over time, and the location of future areas of the highest habitat suitability will differ considerably from the current distribution, particularly under a pessimistic future scenario. In contrast, the distributions of two genera of stylasterids, were driven more by fixed variables such as sediment type and roughness, and may be more resilient to the effects of climate change.

09:35 – 09:50

Daniëlle S.W. de Jonge, Daniela Yepes-Gaurisas, Angelo F. Bernardino, Andrew K. Sweetman

Soft-sediment ecosystem functioning under climate projections at the Cape Verde Basin (North-East Atlantic)

Environmental conditions at the deep seafloor are projected to change under future climate scenarios, which in some cases can already be observed. With climate change, soft-sediment ecosystems are predicted to experience multiple stressors including deoxygenation, acidification, warming, and reduced quantity and quality of POM flux. How this suite of changes will impact benthic ecosystem functioning and consequently ecosystem services, is virtually unknown. As part of the iAtlantic project, we are assessing the impact of multiple climate stressors on soft-sediment ecosystem functioning through a combination of in situ and ex situ experiments, and food-web modelling. Cape Verde slope sediments (<100m) were incubated ex situ with 'fresh' and 'degraded' food input under present-day and future seafloor temperatures to study both single stressor and potentially synergistic effects on sediment community oxygen consumption (SCOC). Furthermore, in situ SCOC was measured for the first time at the Cape Verde Abyssal Plain (~4500 m) with a benthic respirometer lander to assess current ecosystem functioning at this location. At a later stage, our field measurements will be combined with literature data to construct a linear inverse food-web model to study ecosystem-wide carbon cycling under current and future climate scenarios. The combination of field data with modelling will help our understanding of future ecosystem functioning and services of these data-sparse systems and can help inform climate policy.

09:50 – 10:05

Daniela Yepes-Gaurisas, Daniëlle S.W. de Jonge, Andrew K. Sweetman, Angelo F. Bernardino Climate change impacts on Brazilian deep-sea benthic ecosystems

The Atlantic Ocean is experiencing abiotic changes due to current global warming that are expected to intensify in the coming decades. These changes will likely be more severe and faster in deeper ocean layers, making deep-sea ecosystems vulnerable to warming and other related effects such as a lower food supply. However, due to the lack of ecological studies and monitoring in deep-sea environments, we do not know certainty how climate change will affect deep-sea species composition and patterns. The Brazilian continental margin encompasses the Tropical and Subtropical Atlantic Ocean. A large part of the Brazilian Exclusive Economic Zone (EEZ) is within deep waters with a wide variety of seafloor geomorphological features, which are distributed along wide latitudinal and productivity gradients, suggesting a great diversity of ecosystems and associated species. In this work, we propose to review and consolidate biodiversity records within the deep Brazilian EEZ to help predictions of their resilience to expected climate change projections. We synthesized deep-sea benthos species occurrences and compared their distribution with the climate change models (IPCC RCP8,5) for the South Atlantic basin for the first time. The models predict current and future impacts of warming ocean temperatures and declining POC quality on these ecosystems for next century. We observed higher temperature changes in the Northern and Southern Brazilian EEZ, with up to 3°C and 0.8°C increase in bathyal and abyssal depths, respectively. These changes are expected to occur over vulnerable deep-sea ecosystems such as canyons and seamounts, with yet unknown consequences to species and the resources they provide. To analyse these predictions on deep-sea benthic assemblages, incubation experiments will be carried as part of the iAtlantic project (European Union) in Santos Basin (SE Atlantic) and over Cabo Verde (Equatorial Atlantic) to understand future changes in deep oceans and ecological responses in the benthic fauna.

Special 2a: Honor to Craig Smith

09:05 - 09:20

Ashley Rowden, David Bowden, Daniel Leduc, Sarah Seabrook, Andrew Thurber, Olivia Pereira, Lisa Levin, Kathleen Campbell, Gareth Crutchley, Jess Hillman Benthic community patterns at cold seep sites that face potential impact from gas hydrate exploitation

Cold seep ecosystems face potential threats from a number of human activities, which may in the future include drilling for sub-seafloor gas hydrate deposits. Reserves of gas hydrates have been identified along the Hikurangi margin of New Zealand. As part of a wider 5-year project that includes determining the geological characteristics, and economic and practical feasibility of exploiting these reserves, an ecological study was conducted to determine the benthic community structure at seep sites in the vicinity of the gas hydrate deposits. A gradient sampling approach was used to examine patterns in benthic mega-, macro-, and meiofaunal communities, as well as microbial communities, across three cold seep sites. Changes in community structure along the sampling gradient were related to physical and geochemical sediment parameters, and methane seepage pathways determined by seismic survey. This presentation will provide an overview of the results from these analyses, as well as preliminary results from trophic analyses that aim to determine the influence of the seeps on the wider margin ecosystem. Together, these data will be used to inform an assessment of the environmental risk associated with any future exploitation of gas hydrates, as well as the socioeconomic implications for the region.

09:20 - 09:35

Katharine T. Bigham, Ashley A. Rowden, David A. Bowden, Daniel Leduc Megafaunal community resilience to a turbidity flow in Kaikōura Canyon (Aotearoa New Zealand) demonstrated by time-series imagery

Turbidity flows (underwater avalanches) transport massive amounts of sediment across large distances and can have dramatic, long-lasting impacts on deep-sea benthic communities. A turbidity flow in Kaikōura Canyon triggered by a 7.8 (Mw) earthquake in 2016 provides a unique opportunity to examine the response of deep-sea benthic communities to a large-scale habitat-altering disturbance. Photographic transects showing mega-epibenthic fauna and lebensspuren (feeding and other life traces on the seafloor) were collected using a towed camera at five sites at 900 – 1200 m depths in the head of the canyon 10 weeks, 10 months, and 4 years after the event, and compared to transects collected along the same lines 10 years before. Immediately after the event there was little evidence of a living mega-epibenthic community. However, ephemeral patches of bacterial mat, like those seen in chemosynthetic environments, were observed. Four years after the turbidity flow, the visual surveys indicated a benthic community similar in structure to that seen before the event. Community recovery was investigated in relation to changes in the physical characteristics of the habitat caused by the disturbance using habitat topographic variables (depth, roughness, aspect, slope etc.) derived from high-resolution pre- and post-multibeam bathymetry data. This presentation is made to the special session 'Biodiversity and ecology of the deep-sea and polar benthos - in honour of Prof Craig R. Smith'. Prior to the turbidity flow, Kaikōura Canyon was identified as one of the most productive deep-sea benthic environments ever described; a finding that Prof. Smith was instrumental in discovering. The research in this presentation will contribute to improved understanding of the influence of natural disturbances in the deep sea and will also help understand the impact of anthropogenic disturbances such as seabed mining; a topic that has also been a focus of Prof. Smith's research.

09:35 - 09:50

Daphne Cuvelier, Ana Patricia Bras Silva, Joachim Jakobsen, Kirsten Jakobsen, Ana Colaço The first whale fall of the Mid-Atlantic Ridge and a year of its succession

While the Mid-Atlantic Region is a much frequented migration route for multiple cetacean species, to date, no whale falls were encountered or studied along the Mid-Atlantic Ridge. That changed in 2015 when a sperm whale was sunk south of Faial (Azores, Portugal) for the BBC's Blue Planet II series. Implanted at 750m depth, the development of the whale fall was followed for a year and 7 submersible dives were carried out during this time span. The decomposition and associated faunal succession was studied and, based on the imagery, 2 different successional stages, a mobile/scavenging and an enrichment/opportunistic stage were observed. However, when analysing the bones samples taken after 1 year at the deep-sea floor, a transition to the chemosynthetic-based stage appeared to have been initiated. Here we present the first results of the whale fall communities observed along the mid-Atlantic ridge. Its biogeographical relationship with other whale and organic falls will be discussed across oceans as well as its function and its linkages between various ecosystems in the Azorean waters.

09:50 - 10:05

Rob P. Harbour, Astrid B. Leitner, Carsten Ruehlemann, Annemiek Vink, Daniëlle S.W. de Jonge, Alycia Smith, Andrew K. Sweetman Benthic and demersal scavenger biodiversity in the Clarion- Clipperton Zone

In the Clarion-Clipperton Zone (CCZ) in the north-eastern Pacific Ocean ca. 30 billion tonnes of polymetallic nodules, rich in metals critical for frontier technologies, lay on the sediment surface over an area of 4 to 5 million square kilometres. For this reason, there is accelerating interest in deep-sea mineral mining in the CCZ. Few data exist concerning marine biodiversity in this enormous region and a solid understanding of baseline biodiversity and ecosystem function are necessary in order to inform effective management strategies, conservation and monitoring in the event that mining goes ahead in the CCZ. We have carried out 20 in situ baited-camera experiments in the eastern end of the CCZ as well as 4 baited traps. Numerous bait-attending taxa were observed, the most common of which were macrourid, ophidiid and zoarcid fishes, and dendrobranchiate shrimp. Successional patterns regarding their time of arrival were also observed. The bait consumption rate was measured, and a mean scavenging rate of 878 g d-1 ± 113 (SE, n = 9) was calculated in the BGR licence area, with the rattail Coryphaenoides spp. responsible for the majority of the bait consumption. Significant differences in community structure were found between different regions of the eastern CCZ (the OMS, BGR, NORI-D and UK1 licence areas). This ongoing study increases our knowledge of deep-sea scavenging communities in an area targeted for deep-sea mining and will monitor impacts and changes after a collector test has taken place in 2022.

Special 1c: Managing deep sea

10:05 - 10:20

David Bowden, Ashley Rowden, Owen Anderson, Fabrice Stevenson, Malcolm Clark Predicting distributions of seafloor fauna and communities: are we getting better at it?

Habitat suitability models, in which relationships between point observations of a taxon's occurrence and environmental gradients are used to predict occurrence in unsampled areas, are in common use in deep-sea research and environmental management. These methods are particularly appealing for use where observations of seafloor fauna are sparse. Performance metrics generated by crossvalidation of the original sample data generally suggest that such models are effective but their limitations are rarely examined in practice. Accumulating sufficient data to inform models generally involves merging available data across multiple sources and years, which limits analyses to presenceonly data, requires aggregation of taxa to coarser hierarchical groupings, and carries the implicit assumption that distributions will not have changed during the period in which sample data were collected. Furthermore, the environmental variables used as predictors in the models are fundamental to the credibility of the resulting predictions but are also a potentially major source of unquantified uncertainty. In New Zealand, we have been building and using habitat suitability models for more than a decade but have only recently developed a data set of independent seafloor observations sufficient for objective evaluation of their predictions. Here, we discuss our experience with use of SDM in the deep sea, how our predictions stand up against the independent data, and what we now need to do to improve.

10:20 - 10:35

Charlotte L. O'Brien, Peter T. Spooner, Jack Hudak Wharton, Eirini Papachristopoulou, Nicolas Dutton, David Fairman, Rebecca Garratt, Tianying Li, Francesco Pallottino, Fiona Stringer, David J. R. Thornalley Exceptional 20th century shifts in deep-sea ecosystems are spatially heterogeneous and associated with local surface ocean variability

Traditionally, deep-sea ecosystems have been considered to be insulated from the effects of modern climate change, but with the recognition of the importance of food supply from the surface ocean and deep-sea currents to sustaining these systems, the potential for rapid response of benthic systems to climate change is gaining increasing attention. However, very few ecological time-series exist for the deep ocean covering the twentieth century. Benthic responses to past climate change have been well-documented using marine sediment cores on glacial-interglacial timescales, and ocean sediments have also begun to reveal that planktic species assemblages are already being influenced by global warming. Here, we use benthic and planktic foraminifera found in Northeast Atlantic south of Iceland, Northwest Atlantic and Labrador Sea sediments to investigate whether anomalous oceanographic changes in the 20th century North Atlantic have altered benthic ecosystems, and if so, where. Our results reveal that at many sites, 20th century benthic foraminiferal abundance levels are exceptional compared to the prior several thousand years. These shifts are spatially heterogeneous and are associated with local surface ocean variability. The maximum benthic response occurs in locations beneath areas which have seen large changes in surface circulation, temperature and/or productivity. We infer that the observed surface-deep ocean coupling is due to changes in the supply of organic matter exported from the surface ocean and delivered to the seafloor. The local-to-regional scale nature of these changes highlights that accurate projections of changes in deep-sea ecosystems will require models capable of adequately resolving these relatively small-scale oceanographic features.

10:20 - 10:35

Telmo Morato, J. Murray Roberts Improved deep-sea biodiversity assessments inform sustainable development of the deep North Atlantic in a changing planet

The Horizon 2020 project ATLAS (WP3) applied a combination of techniques to improved deep-sea biodiversity assessments and inform sustainable development of the deep North Atlantic in a changing planet. During the ATLAS project new habitats and species were discovered, new Vulnerable Marine Ecosystems were identified and new biodiversity distribution patterns were revealed. The Global Open Oceans and Deep Seabed (GOODS) classification scheme in the North Atlantic was evaluated and adaptations were suggested. Protocols for assessing Good Environmental Status in the deep-sea were proposed. Habitat suitability forecasted a decrease in suitable habitat for cold-water corals and a shift in the suitable habitat of deep-sea fishes towards higher latitudes. Climate change were also suggested to affect the GES in the North Atlantic but predicting GES future trends will be challenging. The HSM emphasize the need to consider climate change in management decisions since it can be used to produce climate-relevant metrics to inform area-based management. ATLAS WP3 also developed a basin-scale analysis of important areas for deep-sea biodiversity that can be used to inform decision-making. Newly produced information have been used to support the nomination of EBSA candidates under the UN CBD, the implementation of the Nature 2000 Habitats directive, and the implementation of National Marine Protected Areas, including the Coral Habitat Area of Particular Concern off the southeast United States.

10:50 - 11:05

Mia Schumacher, Dr. ir. Veerle Huvenne, Prof. Dr. Colin Devey, Prof. Dr. Pedro Martínez Arbizu, Prof. Dr. Arne Biastoch, Stefan Meinecke The Atlantic Seascape A basin-wide automated Cluster Analysis of Atlantic Seabed Areas

Classifications of the marine environment give a comprehensive and unpretentious overview into regions of similar characteristics and can hence be a stepping stone for sustainable ocean resource handling and protection plans. There have been many efforts to categorise the marine realm into seascapes or hydro-morphologic provinces, using different approaches, applied at a wide range of scales. Some of those categorisations available are based on hierarchical classification schemes with often arbitrary thresholds or use simple algorithms which do not fully account for the high complexity of the data. This study presents a basin-wide classification of the Atlantic seafloor environment, based on nine global datasets: bathymetry, slope, terrain ruggedness index, topographic position index, sediment thickness, POC flux, salinity, dissolved oxygen, temperature, current velocity and phytoplankton. To reduce subjectivity within the analysis, an unsupervised classification was performed on the normalised data using Gaussian finite mixture models. Those models describe a latent distribution structure of the input data set from which the final clusters, here seabed areas (SBAs), are derived. This model-based clustering approach seeks to overcome the shortcomings of other classification techniques by trying to embrace the challenging complexity of the ocean floor environment. The result is a map of the Atlantic realm subdivided into nine SBAs. Some are clearly defined by geological and geomorphological properties, while others are dominated by hydrographic properties, or by a mixture of both sea floor terrain and water column characteristics. Larger SBAs cover the deep abyssal plain with low hydrographic and seasonal variation – in contrast to smaller SBAs including coastal waters that are subject to high seasonal variability. There are also differences in geographical distributions. The SBAs we found were further compared to other existing classifications (e.g. Global Ocean Seascapes, GOODS, EMU) and supplementary data (e.g. seamount locations) to assess in how far the objectively identified SBAs are represented in former classifications and studies.

Special 2a: Honor to Craig Smith

10:05 – 10:20

Andrew J Gooday, Brygida Wawrzyniak-Wydrowska, Teresa Radziejewska, Zofia Stachowska, Pedro Martinez Arbizu Macrofauna-sized foraminifera in core and epibenthic sledge samples frm the eastern Clarion-Clipperton Zone (equatorial Pacific)

We studied the diversity of macrofaunal monothalamids (>300 µm) in qualitative samples obtained using an epibenthic sledge within five contract areas (IOM, German, Belgium, French and APEI-3; ca. 4000-5000 m water depth) in the eastern Clarion-Clipperton Zone during RV SONNE cruise 239 (March-April 2015), and in quantitative multicorer samples collected during the same cruise at the IOM site disturbed during a simulated mining experiment in 1995 and the nearby resedimentation and control sites (3 replicates per site). The nine IOM core samples yielded 220 morphospecies (43- 85 per sample), with monothalamids representing 78%

of the total assemblage ('live' and dead, complete specimens and fragments). Tubular morphotypes accounted for 25% of species, followed by komokiaceans (18.2%), spherical morphotypes (10%) and unclassified monothalamids (8.2%). There were no significant differences in species composition between the three IOM coring sites, either because the foraminifera had recovered from the 1995 disturbance or the differences were too subtle to be detected based on three samples. The 12 epibenthic sledge samples (2-3 per area) yielded 224 morphospecies (24-50 per sample; total assemblage), of which the vast majority (95%) were monothalamids, reflecting the strong tendency of the epibenthic sledge to concentrate light forms that can be easily suspended from the sediment. Komokiaceans (34.4% of species) were the most abundant group, followed by tubular (17.4%) and chain-like (10.7%) morphotypes, while spherical morphotypes were a minor component. MDS plots revealed similar faunal compositions in the IOM, BGR and Belgium areas, while the geographically more distant French area and APEI-3 were somewhat distinct, suggesting the occurrence of faunal shifts at scales >1000 km. Our results show that core and epibenthic sledge samples both yield highly diverse macrofauna-sized foraminiferal assemblages, affirming the importance of monothalamids in this size fraction, while providing contrasting but complementary views of the faunal composition.

10:20 - 10:35

Guadalupe Bribiesca-Contreras, Thomas G. Dahlgren, Diva Amon, Stephen Cairns, Regan Drennan, Jennifer Durden, Marc P. Eléaume, Andrew Hosie, Antonina Kremenetskaia, Kirsty McQuaid, Timothy D. O'Hara, Muriel Rabone, Erik Simon-Lledó, Craig R. Smith, Helena Wiklund, Adrian G. Glover Benthic megafauna of the western Clarion-Clipperton Zone

There is a growing interest in the exploration of deep-sea mineral deposits, particularly on the abyssal plains of the central Pacific Clarion-Clipperton Zone (CCZ), which are rich in polymetallic nodules. In order to effectively manage potential exploitation activities, a thorough understanding of the biodiversity, community structure, species ranges, and connectivity across a range of scales is needed. The benthic megafauna plays an important role in the functioning of deep-sea ecosystems and represents an important component of the biodiversity. Megafaunal surveys in the area, from video and still images, have provided insight into the biodiversity and community structure, but the physical collection of samples of this fauna is still required to improve estimates of species richness and species ranges, and is very rarely carried out. Using a Remotely Operated Vehicle (ROV), we collected 55 specimens of benthic megafauna from seamounts and abyssal plains in three Areas of Particular Environmental Interest (APEI 1, APEI 4, and APEI 7) at around 3100-5100 m depth in the western CCZ. We found, using both morphological and molecular evidence, 48 different species belonging to five phyla, of which only eight represented known species, with the rest possibly representing species new to science.

10:35 -10:50

Ivan Cautain, Kim Last, David McKee, Bodil Bluhm, Paul Renaud, Bhavani Narayanaswamy Investigating the uptake of sympagic and pelagic carbon by Arctic benthos

The benthos plays a key role in carbon flow though Arctic ecosystems, being both an endpoint for much of the overlying production and an important food source for higher trophic levels. On Arctic shelves and over the basins, primary production occurs in both the pelagic and sea ice (or sympagic) habitats, by phytoplankton and ice algae respectively. These primary producers differ in their quantity of food delivered to the benthos, with sympagic carbon generally being a less abundant but potentially valuable food source. We investigated the relative abundance of sympagic vs pelagic carbon in Barents Sea shelf (200 - 400 metres deep) mega- and macrobenthos across seasons and different concentrations of sea ice. Samples were collected in the winter, spring and summer of 2018, along the 30° E longitude in the Barents Sea seasonal ice zone. We use highly branched isoprenoids – lipid biomarkers produced with distinct structures in sea ice and the water column – to determine the ratio of sympagic-to-pelagic carbon in various benthic feeding guilds. Preliminary results for summer samples indicate little difference between a station at the polar front and a more ice-influenced northern station. In both stations, megafaunal biomarkers indicated that around 5-11% of assimilated carbon came from sympagic sources, with the remainder from pelagic sources. While there is evidence of seasonal differences, they were only observed in subsurface deposit feeders. At the southern station, subsurface deposit feeders assimilated less sympagic carbon in the summer than winter, whereas in the northern station the opposite was observed. Other feeding guilds did not show similarly strong seasonal differences. Furthering our knowledge of the relative importance of sympagic- and pelagic-derived carbon to the Arctic benthos will allow a better understanding of how these seafloor communities will respond to an increasingly ice-free Arctic

10:50 - 11:05

Regan Drennan, Thomas Dahlgren, Katrin Linse, Adrian Glover Genetic diversity of annelid communities in a region recently covered by an ice shelf

The Prince Gustav Channel is a deep, narrow seaway located in the western Weddell Sea on the northeastern-most tip of the Antarctic Peninsula. The channel is notable for both its deep (>1200m) basins, and a dynamic glacial history, most recently including the break-up of the Prince Gustav Ice shelf, which covered the southern portion of the channel until its collapse in 1995. Understanding the biology of previously ice covered habitats is important in the context of the unprecedented ice shelf retreat and collapse along the Antarctic Peninsula in past decades, however until 2018 the channel remained virtually unsampled. A recent faunistic study by Drennan et al. (2021) provided some the first insights into the biology of the Prince Gustav Channel, describing the benthic annelid fauna of the channel and revealing diverse, spatially heterogeneous benthic communities in a dynamic habitat with continuing glacial influence. In this talk, we present the first results of molecular investigations describing the genetic diversity of the channel and assessing levels of cryptic diversity, in addition to comparisons with previous morphological assignments. These results will help us to understand the longer-term impacts of climatic change in Antarctica.

Special 1e: Pollutants

11:25 - 11:40

Serena M. Abel, Angelika Brandt, Gunnar Gerdts Plastic pollution in the abyssal and Hadal sediments of the Kuril Kamchatka trench.

Recently, deep-sea trenches were described as trash bins and ultimate sink of anthropogenic litter, mostly represented by plastic. The negative effects of plastic pollution on the deep environment are point of discussion in several topics, as it might be the cause imbalances of delicate ecological and biological interactions and affects the food web at all its levels. A comprehensive characterisation and realistic quantification of plastic pollution affecting these remote areas is therefore an important step required to estimate the level of environmental disturbance caused by these and the resulting negative effects. Moreover, it is not less important to establish the pathways wit with plastic is reaching the deep-sea floor, for a better understanding of the nature of pollution. Within the deep MiPoll project, in collaboration with Senckenberg World of Biodiversity and the Alfred Wegener Institute for Polar and Marine Research, we contribute to the evaluation of plastic pollution in the abyssal and hadal sediment of the Kuril Kamchatka trench, located in the North West Pacific Ocean. By analysing sediment samples collected during the KuramBio II expedition in summer 2016, we assessed the presence of microplastic in the trench by a systematic microplastic identification, in sediments at a depth range between 5143-8250 m. We also provide a first evaluation of microplastic sedimentation dynamics in the trench over the past 65 years and, on a larger scale, an identification of plastic items and their origin collected at the trench floor, down to 9.500 m depth.

11:40 - 11:55

Inês Martins, António Godinho, Beatriz Mano, Joana Goulart, Marina Carreiro-Silva Impacts of acute copper concentrations on cold-water corals under an ocean acidification scenario

The impacts of anthropogenic activities on deep-sea ecosystems have been raising a huge concern on scientific community. The synergistic effects of emergent pollutants, such as metal toxicity associated with deep-sea mining, and ocean acidification is particularly relevant under predicted global change conditions. To address this issue, a land-based experiment was designed to expose two habitatforming cold-water octocoral species, in the Azores Dentomuricea meteor and Viminella flagellum, to low seawater pH and high copper (Cu) concentrations scenarios. To answer the question: How corals responds to a predictive effect of Cu exposure under ocean acidification? corals were exposed to four different treatment conditions during 9 days: (1) ambient pCO2/pH (385 µatm/8.09) as measured in the in situ conditions with Cu exposure (2) increased pCO2/reduced pH (1000 µatm/pH 7,73) scenario with Cu exposure; (3) ambient pCO2/pH and (4) increased pCO2/reduced pH with no Cu addition. Respiration rates and metabolic (LDH, MDH, Hsp70, CA and RNA/DNA ratio), oxidative damage (SOD, GPx, CAT, LPO) and detoxification (GST) biomarkers were measured to evaluate cold-water corals “health” after the exposure period. Our results show that under a scenario of ocean acidification/Cuexposure, both D. meteor and V. flagellum triggered distinct cellular responses, although with similar mortality rates. Here we discuss octocoral sensitivity and physiological specificities to environmental risks of metal toxicity associated with deep-sea mining under climate change scenarios and expected ecological consequences to cold-water coral ecosystems.

11:55 - 12:10

Nina Vieira, José Manuel González-Irusta, Carlos Dominguez-Carrió, Telmo Morato, Joachim Jakobsen, Kirsten Jakobsen, Nina Schlapfer, Laura Perrez Herrera, Christopher K. Pham Modelling the distribution of Abandoned, Lost and Discarded Fishing Gear (ALDFG) on the deep seafloor of the Azores region

The deep seafloor is considered to be an important sink of marine litter, with fishing activities representing its main source when moving away from the continental shelf. Over the past decade, there has been an increasing international recognition of the need to address the ecological and socioeconomic impacts of losing fishing equipment at sea, also known as Abandoned, Lost or otherwise Discarded Fishing Gears (ALDFG). Since fishing gears are mostly made of synthetic and very durable materials, the amount and distribution of ALDFG has risen in the past decades, yet little is known about its distribution and abundance over the seabed at large spatial scales. The aim of the present study is to model the distribution of ALDFG over the seabed of the Azores down to 1500 m depth using a suite of environmental and anthropogenic factors. Data on the type and location of ALDFG used to run the model was obtained from a large video archive of seafloor footage (390 dives) collected in the region for over 15 years (2006-2019) by means of different imaging platforms. The overarching objective was to identify likely hotspots of ALDFG and evaluate the potential use of predictive distribution maps as proxies of pressures from bottom fishing activities. Linking such information with the distribution of sensitive benthic habitats will be essential to identify priority areas for conservation and/or define effective restoration programs. In addition, our assessment can serve as a valuable indicator of seafloor integrity in the framework of national and European strategies to assess the health of marine ecosystems.

12:10 - 12:25

Tracey Sutton, Kevin Boswell, April Cook, Maëlle Cornic, Kendra Daly, Tamara Frank, Kaitlyn Frasier, John Hildebrand, Rosanna Milligan, Jon Moore, Steven Murawski, Nina Pruzinsky, Andrew Remsen, Kelly Robinson, Isabel Romero, Jay Rooker, Michael Vecchione, R. David Wells, Marsh Youngbluth The Open-Ocean Gulf of Mexico and Deepwater Horizon: A Decadal Synthesis of Research

The open ocean (water column seaward of the 200-m isobath) in the Gulf of Mexico (Gulf hereafter) is the largest ecosystem component, occupying over 97% of its volume. Many assumed that this size would impart resilience to the Deepwater Horizon oil spill disaster (DWH), an assumption that factored into mitigation decisions such as the large-scale injection of subsurface dispersants at great depth. After a decade of research, spearheaded by the $500 million investment of the Gulf of Mexico Research Initiative, we have learned a great deal about the open-ocean Gulf and the impacts of DWH, though much remains unknown. Here we synthesize what we have learned about the openocean Gulf relative to DWH, including the epi-, meso-, and bathypelagic domains. We examine the spectrum of impacts across a wide range of biota, including phytoplankton, zooplankton, larval tunas/billfishes, deep-pelagic nekton (fishes, shrimps, and squids), and marine mammals. In some cases, particularly in lower trophic levels, there were no apparent long-term impacts. In other cases, particularly the meso- and bathypelagic assemblages, the impacts were catastrophic and remain so as of this writing. We will discuss attributes of vulnerability and resilience that likely contributed to the observed patterns, and highlight existing data gaps that require sustained observation to assess the full, long-term measure of DWH as well as the potential impacts of future deep-water oil spills.

Special 2a: Honor to Craig Smith

11:25 - 11:40

Marta Maria Cecchetto, Andrew K Sweetman, Annabell Moser, Craig R Smith, Dick van Oevelen Abyssal seafloor response to fresh phytodetrital input across regional spatial scales in 3 Areas of Particular Environmental Interest (APEIs) in the western abyssal Clarion-Clipperton Zone (CCZ)

The abyssal seafloor (3500-6000m), the largest solid ecosystem on Earth, remains largely unexplored and with anthropogenic impacts now reaching the deepest depths of the oceans, there is a growing necessity to preserve and safeguard deep-sea biodiversity and functioning. Consequences of polymetallic nodule mining remain poorly understood, especially in the Clarion-Clipperton Zone (CCZ), due to its large scale and the largely unknown ecosystem functions. Thus, baseline studies focusing on biodiversity, ecosystem functioning and connectivity across the CCZ are fundamental to assess mining impacts and manage the region as a whole. In situ pulse-chase experiments were conducted in three Areas of Particular Environmental Interest (APEIs) in the western CCZ using a benthic chamber lander and confirmed a positive relationship between the flux of ocean surface productivity to the seafloor, benthic respiration as well as macrofaunal abundance and biomass. In terms of C-cycling dynamics, most of the labile phytodetritus C was shunted into the DIC pool which confirmed that the benthic ecosystem in the western CCZ as respiration-dominated ecosystems. We detected lower rates of macrofaunal and bacterial C-uptake at our study sites compared to the eastern CCZ. However, our experiments confirmed bacteria as key players in the short-term (~1.5 d) cycling of C at the seafloor as already seen in the eastern CCZ. In our experiments, macrofauna processed more C per unit area per unit time when rates were normalised to biomass than in the eastern CCZ. Our study provides evidence of high variability exists in benthic C-cycling dynamics across the CCZ and between mine claim areas and APEIs highlighting the need of further baseline.

11:40 - 11:55

Alycia J Smith, Daniëlle SW de Jonge, Rory Davis Esq., Rob P Harbour, Tobias Hahn, Andrew K Sweetman Sediment Community Oxygen Consumption, CO2 production and bacterial activity determined in situ in the NORI-D license area of the Clarion-Clipperton Zone

Little is known about abyssal benthic communities and ecosystem functioning in the ClarionClipperton Zone (CCZ) situated across the eastern Pacific Ocean. Proposed polymetallic nodule mining activities in this region have the potential to drastically affect physical, chemical and environmental parameters, and impact deep-sea communities, ecosystem functioning and the services that the deep sea provides. Baseline characterisation of benthic habitats targetted for mining, as well as surrounding areas, is necessary to predict and mediate the likely destructive effects of mining activities. Baseline studies have been conducted in some licensed areas of the CCZ, but no information is currently available for the NORI-D license area. A benthic respirometer lander was deployed at seven sites within a test mining and preservation reference zone in the NORI-D license area of the CCZ in May 2021. The lander carried out benthic flux measurements and in situ pulse-chase experiments were undertaken in each lander deployment. In this talk, we will present data on seafloor respiration and CO2 production rates, as well as bacterial uptake rates of phytodetritus C, and we will compare our results to similar datasets from other license areas and APEIs. This data will be used to inform stakeholders about baseline ecosystem dynamics in the NORID area and help in assessing the effects from test mining in the NORI-D area, that is tentatively planned for 2022.

11:55 - 12:10

Adrian Glover, Guadalupe Bribiesca-Contreras, Thomas Dahlgren, Helena Wiklund, Erik Simon-Lledo, Andrea Waeschenbach, Amanda Ziegler, Regan Drennan, Muriel Rabone, Craig R Smith The biodiversity of animals living on polymetallic nodules

Although there have been a vast number of survey expeditions to the abyssal plains of the ClarionClipperton Zone (CCZ), almost nothing has been published on the small (macrofaunal-sized) animals that live on the polymetallic nodules that characterise this region. This is surprising given that the nodules are the main focus of attention with regards plans for deep-sea mining. To date, there are only two quantitative studies of the nodule fauna based on actual samples. The reasons for this are probably 1) most of the early survey work in the 1970-2000 period was based on protocols for dealing with the sedimented, muddy part of the habitat, when in fact the CCZ seafloor is an intriguing mix of hard and soft substrate, 2) in more recent times, most of the work on the nodule fauna has been based on megafaunal image surveys rather than samples, which provides excellent spatial coverage but excludes study of the small animals and 3) the specimens are small and rather easily overlooked, requiring skilled zoologists at sea examining every single nodule. Here we present the first data from a large quantitative biodiversity study of nodule macrofauna based on 98 box cores taken across a broad region of the eastern CCZ. Comparing our results with other studies of hardsubstrate deep-sea habitats we discuss the implications for understanding the drivers of high abyssal biodiversity, as well as the obvious conservation implications. We present in honour of Prof Craig Smith, someone who has spent more time than most in the CCZ and has contributed so widely to the study of deep-sea biodiversity and conservation.

12:10 - 12:25

Franck Lejzerowicz, Andrew John Gooday, Inés Barrenechea Angeles, Tristan Cordier, Raphaël Morard, Lidia Lins, Lénaick Menot, Angelika Brandt, Lisa Ann Levin, Pedro Martinez Arbizu, Craig Randall Smith, Jan Pawlowski Benthic nucleic acid from the Clarion-Clipperton Zone and other abyssal regions: what it says about eukaryotic biodiversity patterns

The abyssal seafloor is a mosaic of highly diverse habitats, including regions enriched in mineral resources, such as polymetallic nodules in the Clarion-Clipperton Zone (CCZ). Nodule mining attracts commercial interest but because it will be destructive, baseline data are necessary to measure impact on benthic communities. We interrogate environmental DNA and RNA by sequencing two eukaryotic rRNA gene markers targeting Foraminifera (37F region) and metazoans (V1V2 region), from 310 surface-sediment samples from the CCZ and other abyssal regions. Our results confirm huge gaps in our knowledge deep-sea biodiversity. Benthic Foraminifera are more common in CCZ samples than metazoans and dominated by clades that are only known from environmental surveys. The most striking results are the uniqueness of CCZ areas, both datasets being characterized by a high number of OTUs exclusive to the CCZ, as well as greater beta diversity compared to other abyssal regions. The alpha diversity in the CCZ is high and correlated with water depth and terrain complexity. Topography was important at a local scale, with communities at CCZ stations located in depressions more diverse and heterogeneous than those located on slopes. This could result from eDNA accumulation, justifying the interim use of eRNA for more accurate biomonitoring surveys. Our descriptions not only support previous findings and consolidate our general understanding of deep-sea ecosystems, but also provide a data resource inviting further taxon-specific and large-scale modelling studies. Nucleic acid analyses will be useful for deep-sea biomonitoring, but results must be validated experimentally for sound ecological interpretation, and notably because it may apply to more than eukaryotes.

Special session: Communication

12:25 - 12:40

Thomas Linley, Alan Jamieson Deep-sea tropes – to resist or play along?

It can be difficult to offer people a personal connection to the deep sea. As terrestrial air-breathing mammals, there are few habitats that differ from the world we know so completely and that represent so many of our innate fears. Our own language gives us away ‘deepest darkest fears’, the abyss – a bottomless pit in hell and Hadal from Hades – the underworld and its god. To many the deep sea may represent our repressed subconscious, or death*. The surface waters embody life, there is growth and productivity. The deep ocean is its antithesis, death, decay, and filth. The life found there is starving and inherently unclean.

Becoming frustrated with how our own work was often relayed through the media (and stranded in our homes) Alan and I started The Deep-Sea Podcast as a chance to speak with people directly about deep-sea science. We decided to actively push against the topes and the clichés in our own discipline: ‘we know more about the moon than the deep sea’, monsters and aliens of the deep etc. We tried not to oversimplify the science but rather help the listener understand the concepts. The response has been overwhelmingly positive, and I have had some wonderful interactions with listeners.

But there are many who like the ‘alien monsters’ and how remote and different the deep ocean feels. They like that anything could be out there, and we know so little. There is no single right way to communicate the deep ocean. We need diversity in tone, medium, style and the people who are communicating to engage the maximum audience and help them feel a personal connection with the deep sea.

*Jamieson AJ, Singleman G, Linley TD, Casey S, Browman H (2020) Fear and loathing of the deep ocean: why don't people care about the deep sea? ICES Journal of Marine Science doi 10.1093/icesjms/fsaa234

12:40 - 12:55

Torben Riehl, Gerd Hoffmann-Wieck, Gerd Hoffmann-Wieck "Deep-Sea and Marine Research" — The new exhibition at the Senckenberg Natural History Museum

The deep-sea environment covers the largest part of our planet and therefore deep-sea knowledge is essential for our understanding of the entire Earth system. At the Senckenberg Natural History Museum Frankfurt an immersive platform of mediation and learning, inspiring wonder and fascination about the deep oceans and marine research has been opened recently. By addressing a wide range of visitor groups and with first-hand scientific facts, original collection specimens and state-of-the-art scenography side by side, three show rooms raise awareness of the deep-sea ecosystems, its importance in the Earth system and Anthropocene threats. The making of these new show rooms integrated first-hand knowledge and research experience of Senckenberg and partners, foremost GEOMAR. By combining objects of our research collections and models, we place our research in context. Our museum is a window connecting the public with the scientific community, thus, making scientific objects and findings visible: With an intense scenographic contrast, visitors are caught by the design of the rooms: bright, laboratory-like atmosphere in the marine research, dark, mystical, and filled with creatures that dwell in the darkness of the deep sea. Once the eyes got used to the minimal light, the scenery allows visitors to literally dive into the largest ecosystem of our planet. Footsteps are muffled, strange sounds are heard, and sparse lighting reveals the fascinating, bizarre, and at times eerie organisms that withstand the extreme conditions of the deep sea. Deep-sea giants are presented side by side with microscopic organisms. Three important habitat types — black smokers, soft sediments and whale falls, each with its own specific biocoenosis — are presented in large and almost invisible display cases. A rusty beer can, half buried in the sediments and a degraded reef hint to the fact that even the most remote ecosystems are not out of reach for human activities.

12:55 - 13:10

Brandon Gertz, Mary Edmondson Podcasts as Tools for Deep Sea Science and Policy Communication

Podcasts can explain complex ideas in a unique and effective way to the global public. It has an accessibility not afforded by traditional scientific journals or documentaries, to be listened to at any moment, anywhere, at any time. Podcasts also have the advantage of not requiring multimillion dollar exploration missions to collect pictures to create vivid imagery. Podcasts on scientific topics allow research and storytelling to come together, creating an effective science communication tool. We applied these ideas to create a podcast episode bridging connections between the public and deepsea mining issues. Our episode explores the risks, rewards, and resistance deep-sea mining has sparked in three pacific island nations: Papua New Guinea, the Cook Islands, and Fiji. Along the way, we interview deep sea experts Dr. Cindy van Dover and Ph.D. student Elisabetta Menini from Duke University to help explain the environmental and human impacts of deep-sea mining and the actions that can be taken to avoid them. We found that the podcast format, especially when experts are invited to talk about their passions, was well-received by experts and students and is a promising method for deep-sea science communication.

Link to listen to "Deep-sea Mining: Risks, Rewards, and Resistance in Pacific Island Nations" (to be published on the Duke University Marine Lab's "Seas the Day" Podcast in October 2021):

https://soundcloud.com/brandon-gertz-415659967/edmondson-gertz-dsm-podcast/s-0x3qGOLTB73

Special 2a: Honor to Craig Smith

12:25 - 12:40

Emily Young, Craig Smith, Kenneth Halanych, Diva Amon, Janet Voight, Iris Altamira Biodiversity, community structure and ecosystem function of organic-rich habitats on the Washington-Oregon margin

Whale bones and wood at the deep-sea floor support ecologically dynamic faunal assemblages in an otherwise food-poor environment. Existing studies of organic falls involve parcels of differing sizes, qualities and seafloor durations, which confound our ability to isolate bathymetric and geographical drivers of diversity and community structure. We conducted a comparative experimental approach to examine the roles of depth, regional location and substrate type in structuring organic-fall faunal assemblages. Four replicate free-vehicle landers containing replicate wood, bone and inorganic hard substrates were deployed for 15 months to depths of ~1600 m and ~2800 m, spaced at ~400 km along the Washington-Oregon margin. The landers collected a total of 84,892 macro- and megafaunal individuals of 144 species. Wood, bone and inorganic substrates supported assemblages with different community structures, even within landers. Community composition was significantly different between depths and between landers within a depth, indicating variability on regional and bathymetric scales. Wood blocks at ~1600 m were heavily degraded by wood-boring xylophagaid bivalves, which were responsible for up to 92% of wood-mass loss. As key ecosystem engineers, xylophagaids increased and diversified habitat and nutritional niches, which allowed for highly abundant faunas to inhabit the wood interior. Xylophagaid abundance was positively correlated with infaunal abundance and species richness, and negatively correlated with assemblage evenness, which was driven by high abundances of dorvilleid polychaetes. Xylophagaid colonization was absent to mild in deeper wood blocks, which we suspect results partly from lower propagule supply at increased distances from terrestrial wood sources. Whale-bone degradation was low compared to some other NE Pacific whale-fall studies of similar duration, yet still exhibited reducing conditions and supported some sulphophilic species. Our study demonstrates quantitatively that co-located whale bones and wood falls support highly distinct, species-rich assemblages and thus promote biodiversity at the deep-sea floor.

12:40 - 12:55

Andrew Thurber, Lila Ardor Bellucci, Susie Cummings, Kerry McPhail, George Neuhaus, Sarah Seabrook, Nicole Raineault, Tamara Baumberger, Amanda Demopoulos Framing deep-sea research around ecosystem ecology and services to co-advance science and holistic management: A Case Study from Cascadia Margin's Cold Seeps

Methane seeps are a ubiquitous feature of vast regions of the deep sea, providing significant ecosystem services and incredible heterogeneity. Through an ecosystem approach, including analysis of biogeochemistry, metabolites, genomics, and community composition of microbes and animals, we quantified the diversity and impact of seeps on the Cascadia margin. We found that each seep often appeared unique: some had incredible dominance of particular microbial taxa (e.g. methanotrophs making up more than 60% of all microbes), others were covered by a blanket of seemingly voracious gastropods, and still others were little more than ephemeral pockets of weak seepage. Our results, further informed by our research in Antarctica, has expanded our view of the drivers of methane seepage to be more inclusive of successional dynamics, seepage duration, underlying geochemical variability, and fauna. In communicating these results, we have found that each aspect of this work resonates with stakeholders and managers in different ways. The role of seeps as a greenhouse gas sink, fish habitat, or potential epicenters of marine genetic resource discovery all were differentially important for different people. As a result of this project, we have further advanced our appreciation for the diversity of the deep and the variety of research results that can lead to management actions, including the recent designation of methane seeps as essential fish habitat in our region of research. We propose this abstract for the special session honoring Professor Craig Smith, a scientist who has embraced and taught the importance of robust, holistic ecological research from the deep to the poles and used it to inform effective management of vast ocean habitats.

12:55 - 13:10

Kenneth M. Halanych, Candace Grimes, Kyle Donnelly, Che Ka, Nusrat Noor, Andrew Mahon Benthic megafaunal invertebrate diversity of the West Antarctic Peninsula

Characterizing present and past marine fauna of the Southern Ocean's continental shelf sheds light on the previously underestimated Antarctic biodiversity and aids in predicting how they will respond to climate change by providing a baseline. This study provides benthic invertebrate faunal diversity and abundance across the Western Antarctic Peninsula (WAP) region before the collapse of several large ice sheets (e.g. Thwaites and Western Antarctic Ice Sheets) which may serve as an ecological baseline in coming years as temperatures rise. We employed photographic transects of the Antarctic bottom taken on two cruises around the WAP between 2012-2013 aboard the RVIB Nathanial B. Palmer and the ASRV Laurence M. Gould. Transects were conducted with the YoYo Camera, a submersible camera lowered to the benthos at 8 sites beginning on the eastern side of the Antarctic Peninsula moving westward to the Ross Sea. To the degree possible, we identified and counted sponges, tunicates, sea spiders, and echinoderms using 40-50 selected photos for 1km long transects located between 301-731m depth from the Weddell Sea to the Ross Sea continental shelf. The sites spanned 15 degrees of latitude, but we did not find significant evidence for a latitudinal trend in diversity, abundance, or richness. Montravel Rock, the northernmost site, had the highest abundance, richness, and Shannon Diversity values, but the remaining sites seemed to be influenced more by habitat characteristics, such as bottom type, and then latitude. Communities in the Bransfield Strait were dominated by sponges and sea spiders. However, brittle stars and sea cucumbers were relatively more abundant in the exposed sites like the Bellingshausen and Eastern Amundsen Seas. At present, benthic community members of the WAP experience relatively stable bottom ocean conditions, but as temperatures rise and ice melts, this environment will change drastically impacting the marine invertebrate abundance and diversity.

Special 2c: North-West Pacific

14:50 - 15:05

Hanieh Saeedi, Angelika Brandt Marine biodiversity in the NW Pacific and the adjacent Arctic Ocean

From our four expeditions to the NW Pacific deep sea (SojaBio, SokhoBio, and KuramBio I and II), we have mobilised 7,042 unique deep-sea taxa distribution records to open-access databases, of which 1,723 records were at the species level. Using this dataset and data collected from open-access databases, we analyzed species richness, endemism rates, and faunal community composition in the shallow and deep NW Pacific and adjacent Arctic Ocean. Our results supported the hypothesis that, although biodiversity is increasing in the tropics and coastal depths (especially in the Philippines) is highest, but decreases at the equator and at depths below ca. 2000 m. Despite the high species richness around the eastern Philippines, the Yellow Sea and Gulf of Tonkin had the highest benthic species endemism rates (ca. 70%), while the Aleutian Islands had the highest pelagic endemism rates (ca. 45%) among all the different ecoregions. Our generalized linear models (GAMs) showed that the combined effects of all environmental predictors provided the best model for species richness in both the shallow and deep seas of the NW Pacific . However, of all the predictors, dissolved oxygen, bottom temperature, and salinity were the most important environmental factors explaining deep-sea species richness in the NW Pacific and adjacent Arctic Ocean. These results provides baselines for marine conservation plans and inform the policy, as species richness and knowledge of endemic hotspots are necessary prerequisites for preventing biodiversity loss. Our book consists of 21 chapters with an introduction followed by 20 chapters on taxonomy and biogeography of various deep-sea taxa, including Porifera, Cnidaria, Brachiopoda, Entoprocta, Nemertea, Solenogastres, Bivalvia, Sipuncula, Polychaeta, Echiura, Nematoda, Kinorhyncha, Pygnogonida, Ascothoracida, Ostracoda, Decapoda, Amphipoda, Isopoda, Ascothoracida, Tanaidacea, Echinoidea, and Asteroidea. Our results also provide sustainable data for the upcoming United Nations Decade of Ocean Exploration and Sustainable Development (2021-2030).

15:05 - 15:20

Mizuki Ohta, Shigeaki Kojima How does the swimming ability of deep-sea isopods affect the vertical distribution and speciation?

Among the Asellote isopods (Isopoda: Arthropoda) living in the deep-sea, the species belonging to the family Munnopsidae have a unique ecological feature, namely, swimming ability. They are thought to have a large vertical distribution range due to their swimming ability, but in reality, the exact range of their species is unknown due to the presence of hidden species. Based on the hypothesis that deepsea benthic organisms speciate by adapting to changing environments as water depth increases, we hypothesized that such cryptic species appear in a depth-dependent manner, resulting in a limited vertical distribution range of "true" species. We sampled over 300 individuals of asellotes between the depths of 130 and 3,500 m around the landward slope of the Japan Trench, the northwestern Pacific, of which unique feature of our sampling along transects within a narrow area of ocean. They were classified based on morphological and molecular phylogenetic analyses. For the dominant genera, Ilyarachna and Munnopsurus, of the family Munnopsidae (having high swimming ability), Janirella of the family Janirellidae and Janiralata of the family Janiridae (having no swimming ability), we compared vertical distribution patterns of species and inter- and intraspecific genetic distances based on the nucleotide sequences of mitochondrial DNA. The results showedunexpectedly high species diversity. In addition, we analyzed the relationship between molecular evolution and morphological differentiation, eliminated environmental factors other than depth differences, and examined the vertical species distribution range. We will discuss how the swimming ability has influenced speciation and vertical distribution patterns of asellotes.

15:20 - 15:35

Joan M. Alfaro-Lucas, Chhaya Chaudhary, Angelika Brandt, Hanieh Saeedi Diversity patterns, endemism and bioregions of the Arctic Ocean

Climate change is altering marine biodiversity worldwide leading to the potential modification of the ecosystem functioning, which are especially critical since they directly affect the ecosystem services that mankind rely on. In the Arctic Ocean, climate change is occurring at faster pace than elsewhere. More than ever determining and understanding Arctic biodiversity distribution and patterns is of paramount importance. Here, in the extension phase of the BENEFICIAL Project (Biogeography of the NW Pacific deep-sea fauna and their possible future invasions into the Arctic Ocean), we aim to determine the species richness and endemism patterns as well as biogeographic region classification of the Arctic Ocean. We extracted, quality controlled, and cleaned distribution records of extant fish, polychaetas, bivalves, gastropods and amphipods from Ocean Biodiversity Information System (OBIS) and Global Biodiversity Information Facility (GBIF), from 70° to 90° N, and from the shallow to the deep sea, yielding over 175,000 distribution records of over 2,000 accepted marine species. Analyses were performed separately for shallow (=200 m) species distribution records. We divided the study area into 50,000 and 700,000 km² equal-area hexagonal cells where species turnover (β-diversity) was assessed with Simpson's dissimilarity index (βsim). Biogeographic regions were identified with different complementary approaches. Results of this study will help to understand the nuances of diversity patterns of the Arctic marine fauna and will thus provide a valuable baseline for future biodiversity status assessments being of practical interest for scientists, conservation and management initiatives.

15:35 - 15:50

Chhaya Chaudhary, Joan M. Alfaro-Lucas, Angelika Brandt, Hanieh Saeedi Global distribution of corals and their associated taxa under climate change

The biodiversity patterns and species distribution ranges of marine fauna are changing in response to climate change. The alarming northward shift in marine species richness in the northern hemisphere in the recent past has suggested that the tropics are facing regional loss in diversity, where majority of corals and their associated taxa are distributed. The Arctic species could be at a high risk of extinction because of geographical restrictions to move further north. To understand the effects of climate change, we need to identify new spots where species will arrive in the near future, under the expected rise in temperature. Coral reefs have proven to be of both ecological and economic importance worldwide and one of the strongest indicators of climate change. Since they provide food, habitat and shelter for many species, we may expect a similar type of geographic range variation in both corals and their associated species in the future. To understand how the coral reef ecosystem will cope with the warming effects, we are predicting the global distribution of 22 species of corals (tropical and Arctic) and 144 species of geographically associated taxa, in present and future. Here, we use species habitat modelling Maxent to predict the species range distribution under present and future scenarios (RCP 45 and RCP 85) for the years 2050 and 2100, using benthic environmental layers including sea bottom temperature, salinity, and current velocity from Bio-ORACLE, and depth as the explanatory variables. We aim to compare the predicted geographical range maps of the species under present and future scenarios. To understand how climate warming will affect species in the tropics and the Arctic, we will compare the tropical and Arctic species distribution in present and future. The results might suggest how the biodiversity associated with the coral reef ecosystem would move poleward under future climate scenarios, or whether the species expand or contract their ranges or will go extinct.

15:50 - 16:05

Dmitrii Pantiukhin, Henk-Jan T. Hoving, Gerlien Verhaegen, Charlotte Havermans

Modelling of Arctic gelatinous zooplankton distribution and abundance based on data from pelagic video transects in Fram Strait.

The profound environmental shifts in the Arctic region caused by global warming lead to far-reaching alterations of the composition and structure of marine communities. Such effects of global warming are particularly pronounced in the transitional zones such as Fram Strait where the increased inflow of warm Atlantic waters accelerates this process. In other ecoregions of the world's oceans warming has caused an increase in the biomass of gelatinous zooplankton (or jellies). Jellies are versatile predators in diverse marine ecosystems. Despite the potential impact of jelly communities on the Arctic food webs, their ecological roles have been poorly studied. We hypothesise that the Arctic pelagic community consists of a significant component of gelatinous fauna, some of which are expanding from the North Atlantic. To test this hypothesis, we obtained baseline data on vertical distribution and diversity of Arctic jellies using towed camera video transects during expeditions to the HAUSGARTEN LTER in Fram Strait in 2019, 2020 and 2021. The data include the abundance of 17 groups of gelatinous zooplankton, among which the most abundant were the family of Rhopalonematidae mainly consisted of Aglantha and Rhopalonema, and suborders of Physonectae and Calycophorae. Based on the obtained abundance data, we fitted bayesian joint species distribution models (JSDMs) in order to understand current patterns of species distributions at different depth layers and to provide predictive insights into community assembly processes. Variance partitioning over the explanatory variables showed that depth and temperature explained a substantial amount of variation for most of the taxa. The trained models will be later coupled with climate change scenarios (from CMIP6), which will allow us to forecast spatial niche range shifts in ecosystems and identify climate change winners and losers among the jelly taxa in the Fram Strait.

16:05 - 16:20

Henry Knauber, Angelika Brandt, Torben Riehl

Evolution and Biogeography of the Haploniscus belyaevi species complex

Species complexes are not only reportedly common within a large spectrum of deep-sea taxa but furthermore bear the potential to unravel deep-sea evolutionary mechanisms, thus improving our currently poor understanding of the origins of deep-sea biodiversity. Here we investigate the putative Haploniscus belyaevi Birstein, 1963 species complex from the abysso-hadal Northwest Pacific (NWP). The primary goal of this work is to test the hypothesis that H1) Haploniscus belyaevi comprises a complex of multiple, closely related species. Relating biogeographic with phylogenetic patterns will help to study historic differentiation across biogeographic borders, depth strata and large geomorphological structures to infer their effects on benthic species. We expect that H2) across these potential barriers both intraspecific differentiation and interspecific divergence will become apparent, thus providing fundamentals for future population-genetic and phylogeographic investigations on the NWP deep-sea benthos. By combining morphological, molecular, and biogeographic data in an integrative taxonomic approach ten haploniscid species could be identified of which several represent cryptic species, leaving only three morphologically distinguishable species. Based on the conducted analyses (i) a reconstruction of the ontogenetic development highlighting sexual dimorphism and allometric growth, (ii) a phylogenetic overview of the haploniscid isopods of the NWP and (iii) an analysis of their genetic distances by using haplotype networks is provided. The biogeography of these haploniscid species indicated that the Kuril-Kamchatka Trench and the Kuril Island Ridge of the NWP act as barriers to dispersal and thus promote diversification and eventually speciation.

Special 2a: Honor to Craig Smith

14:50 -
15:05

Amanda W.J. Demopoulos, Jennifer P. McClain-Counts, Jill Bourque, Carolyn Ruppel, Nancy Prouty, Sandra Brooke, Tracey Sutton, Erik Cordes, Samantha Joye

Stable isotopes reveal heterogenous carbon sources at several seeps along the U.S. Atlantic margin

Chemosynthetic environments support distinct benthic communities capable of utilizing reduced chemical compounds for nutrition. Along the U.S. Atlantic margin, hundreds of seeps have been documented, with detailed investigations at a few of these seeps revealing extensive mussel beds, microbial mats, authigenic carbonates, and most recently, vestimentiferan tubeworms. Stable isotope analysis (δ 13C, δ 15N) was used to characterize food webs at nine seep locations along the U.S. mid-Atlantic margin. Where present, mussel species and isotopic composition differed between the northern seeps (Bathymodiolus childressi, δ 13C: -84.4‰ to -54.4‰) and the southern-most seep (B. heckerae, δ 13C: -62.3‰ to -32.4‰), consistent with species-level differences in their methanotrophic and chemoautotrophic endosymbionts and/or spatial variation in source carbon isotopic composition, including methane. Chemosymbiotic tubeworms (cf. Escarpia sp., δ 13C: -35.2 to - 26.3‰) and clams (Acharax sp., δ 13C: -34.5 to -33.2‰) were 13C-enriched relative to mussels present along the margin, with δ 13C values potentially indicative of carbon fixed by their thiotrophic endosymbionts. Isotope values differed by tissue type for both mussels and tubeworms, possibly due to variations in isotopic routing among the tissues, tissue-specific turnover time, and the contribution of endosymbionts. Sites containing mussels had a greater spread of δ 13C data compared to sites without mussels, suggesting diverse carbon sources available. Heterotrophic consumers, including deposit (e.g., Echinus spp., ophiuroids, sipunculids) and suspension feeders (anemones and sponges) exhibited δ 13C values consistent with reliance on chemosynthetic production. In contrast, other taxa, including benthic (polynoid worms) and pelagic feeders (euphausiids and fishes) were 13C-enriched relative to chemosynthetic communities, indicating reliance on photosynthetically-derived organic matter. Additional analysis using sulfur isotopes will help resolve the relative contribution of chemosynthetic vs. photosynthetic-derived carbon to these seep inhabitants. The presence of seeps, and the diversity of food resources available within seeps along the margin, increase the overall trophic and community diversity of the U.S. mid-Atlantic continental slope.

15:05 - 15:20

Guilherme Siqueira Toledo de Carvalho, Flávio Dias Passos, Paulo Yukio Gomes Sumida

Wood-eating bivalves of the deep Southwestern Atlantic

The deep sea dimensionally represents the largest ecosystem on Earth and contains a high biodiversity, despite its overall scarcity of available food. However, large amounts of organic matter, such as wood, sporadically sinks to great depths and are quickly colonized by a group of wood-eating bivalves of the Xylophagaidae family. Acting as ecosystem engineers, they transform it into a more labile source of nutrients and help create a distinct, diverse, and rarely studied habitat. The aim of this preliminary study was to analyse the composition of these bivalves at a depth of 550 meters and 240 km off the coast of Santa Catarina, Brazil. To that end, we sought to identify the different morphotypes encountered, formally describe them, and understand their phylogenetic relationship to other xylophagaids. To obtain the specimens, an autonomous lander structure was used, containing wood blocks of different sizes and species, and was implanted at the ocean floor for ten months. After their recovery, the wood blocks were then sorted, their specimens were removed and preserved in 96% ethanol. According to their relevant morphological characteristics, observed under light and scanning electron microscopies(SEM), they were grouped into different morphotypes. From the eight identified morphotypes, two were predominant, one belonging to a probable new genus, currently under description, and the other to Xylopholas, each represented by hundreds of individuals. Both were never reported to the Southwestern Atlantic, with the possibility of additionalspecies as more samples are analyzed. This high xylophagaid diversity is possibly related to the existence of extensive forests along the Brazilian coast, environments that are possibly threatened by the extensive deforestation occurring over the last few centuries.

15:20 - 15:35

Jeroen Ingels, Sandra Brooke, Amy Baco, Steve Morey, Michael Martinez-Colon, Giovanni Santos, Patrícia Neres, Letícia Pontes, Flávia França, Raianne Cavalcante, Débora França, Matthew Poti, Arliss Winship, Adam Alfasso, Anthony Sogliuzzo, Gabriella Panto, Queriah Simpson, William Brantley

Assessing model-predicted hydrodynamic disturbance using meiofauna and nematode community metrics – a case study from the deep Florida Escarpment in the Gulf of Mexico

The eastern Gulf of Mexico (GOM) is dominated by a massive carbonate platform that slopes gently for over 200km offshore before dipping sharply down to abyssal depths. The deep slope and escarpment of this platform is one of the least accessible places in the GOM, it’s far from shore, very deep and subject to high current conditions. In the NOAA OER-funded HydroSMAC project, hydrodynamic current models were developed to enhance deep-water coral habitat suitability models. However, validation of these models is difficult in this environment, and traditional physical oceanographic tools do not capture the integrated effects of currents on infauna. Here, we analyzed meiofauna (32-500 um) communities to ground truth the hydrodynamic current model, an approach premised by experimental evidence that disturbances gradually shape meiobenthos communities. Sediment samples were obtained using ROV push cores (steep escarpment) and multicores (deep slope) at depths between 1473 and 2267 m. Over 25,000 individuals were identified to higher taxa level, and more than 5,000 nematodes to genus/species level. Deep community analysis, including disturbance metrics (based infaunal life history, trophic identity, and disturbance sensitivity), was compared against the model current data to investigate their usefulness in validating the model. Preliminary analyses show distinct differences between the deep slope and steep escarpment, which are likely subject to different localscale current and disturbance conditions. Importantly, however, for the deep slope, significant meiofauna community differences were found between all modelled current speed categories, suggesting our approach can offer accurate validation of hydrodynamic models in the deep sea. This paves the way for a re-assessment of how we ground truth models in areas where continuous oceanographic monitoring is difficult to achieve. Single point sampling of infaunal communities, which are shaped by the integrated effects of currents can be considered an effective hydrodynamic model validation tool.

15:35 - 15:50

Jill R. Bourque, Amanda W. J. Demopoulos, Jonathan Quigley, Jason D. Chaytor, Erik Cordes

Infaunal communities associated with deep-sea coral habitats in the western Atlantic

Deep-sea coral habitats support abundant and diverse sediment infaunal communities through the provision of highly complex three-dimensional structures that facilitate sediment accumulation and alter hydrodynamic regimes. While studies elsewhere (e.g. Gulf of Mexico, NE Atlantic) indicate that cold-water coral (CWC)-associated infauna are important contributors to deep-sea biodiversity and differ from the vast mud-dominated deep sea, little is known about infauna from CWCs in the MidAtlantic and Southeastern U.S. regions. Infauna provide several critical ecosystem functions and services and understanding this component of coral communities is vital in light of potential offshore development and global change. Recent exploration in these regions has documented extensive coral provinces along the western Atlantic margin. With little known regarding the ecosystem function of these habitats, examination of historical and new samples provides the first insight into CWC sediment communities in this region. We investigated macrofaunal abundance, diversity, and community structure from sediments collected near Lophelia pertusa, Enallopsammia sp., and Solenosmilia sp. colonies offshore of North Carolina to Florida, U.S (407-1334 m) and associated geochemical parameters (e.g. grain size, organic carbon content, stable isotope composition). Infaunal density and diversity was highest at shallow (< 500 m) sites with similar densities among deeper sites. Density of infauna was lower in Atlantic CWC habitats than those reported from similar habitats and depths in the Gulf of Mexico, suggesting different geophysical environments. Community structure varied among sites, primarily influenced by depth and grain size, with shallow sites containing higher proportions of coarse sediments indicating stronger currents and stony coral breakage. This study provides important baseline information on the connectivity of CWC sediment environments in the western Atlantic and the role of CWC in supporting biological diversity on shelf and slope environments in the region.

15:50 - 16:05

Marta Miatta, Paul Snelgrove Sea pen fields as biogenic habitats for macroinfaunal communities in deep-sea sediments: Evidence from the Laurentian Channel MPA

Pennatulacean octocorals (sea pens), one of the primary conservation targets of the Laurentian Channel MPA in eastern Canada, can occur at high densities in deep-sea sedimentary habitats. Considered important habitat-forming species for many megafaunal organisms, the effect of sea pens on nearby sedimentary macroinfaunal communities remains unexplored. We therefore sampled 9 stations within the MPA during two cruises (September 2017 and July 2018), including sea pen fields and bare sedimentary habitats (336-445 m depth). A subset of the cores directly sampled individual sea pens to assess small-scale influence. For each core, we evaluated macroinfaunal densities, taxonomic diversity, vertical distribution, community composition and biological trait expression, and investigated their variation between sea pen fields and bare sedimentary habitats. We examined a wide range of abiotic and biotic variables and used multivariate techniques to identify the drivers of macroinfaunal community composition and biological trait expression. Enhancement of macroinfaunal density and taxonomic diversity and higher percentages of organisms in the upper sediment layers characterized sea pen fields in the fall cruise, with more variable results in the summer cruise. Community composition and biological trait expression consistently differed in sea pen fields compared to bare sedimentary habitats, with average density of Pennatula sea pens as a primary driver, along with other environmental variables (depth, sediment granulometry, and food availability). We detected localized enhancement of macroinfaunal diversity in cores containing sea pens at stations characterized by predominantly bare sediments. Characteristics of communities within sea pen fields suggested higher environmental stability, confirmed by lower betweensampling period variability, coupled with higher sensitivity to disturbance. Our results indicate that sea pens play an important ecological role by shaping and sustaining macroinfaunal communities, perhaps by increasing food availability in adjacent sediments. Their role as biogenic habitat for macrofauna amplifies the need for protection of sea pens in deep-sea environments.

16:05 - 16:20

Lisa Levin, Kira Mizell, Olivia Pereira, Olivia Pereira, Guillermo Mendoza, Devon Vlach, Kaila Pearson Macrobenthos of phosphorite and Fe-Mn crust hardgrounds in the Southern California Borderland

Deep sea mineral hardgrounds are being considered for their mineral resource potential, and characterizations of concomitant ecosystems are needed to wholly inform environmental management of these resources. Specifically, quantitative information for small invertebrates is scarce on hard substrates in the deep sea. To address this, we sampled phosphorite cobbles (n=14) and iron-manganese crusts (n=7) in the rugged, bathyal Southern California Borderland (SCB) on a series of seamounts, banks, ridges and escarpments to provide baseline characterization of macrofauna (> 300 microns) in these mineral-rich settings to facilitate economic and conservation planning. Preliminary analysis of 20 rocks suggests macrofaunal densities were 3 times higher on phosphorites (5675 ind/m2) than on Fe-Mn crusts (1830 ind/m2). Annelids were dominant (55%), with syllids, polynoids and hessionids most abundant. Arthropods (18%), ophiuroids (17%), molluscs (4%) and sponges (3%) comprised much of the remainder. Among arthropods, isopods and gammarid amphipods dominated on phosphorites in contrast to tanaids on Fe-Mn crusts. The shallower depths and corresponding better oxygenation of most of the phosphorite locations (438-790 m) relative to the Fe-Mn crusts (690 – 1129 m) may be responsible for these trends, although most of the study area falls within a well-developed oxygen minimum zone. Macrofaunal densities observed on these mineral-rich hardgrounds were notably higher than on carbonates at the nearby Del Mar methane seep (1020 m), but comparable to densities on carbonates at Costa Rica seeps (1000 m). Ongoing work will assess macrofaunal biodiversity and functional attributes, as well as potential macrofaunamicrobe interactions linked to minerals in these hardground settings.

Wednesday 15th September

Special 2d: Bioluminescence

09:05 - 09:20

Manabu Bessho-Uehara, Warren R. Francis, Steven H.D. Haddock Biochemical characterization of diverse deep-sea anthozoan bioluminescence systems

Anthozoans are some of the most abundant luminous animals. Among luminous sessile organisms, the shallow-water sea pansy Renilla has been well studied for its chemistry and molecular biology. Aside from Renilla, however, little is known about the bioluminescent mechanisms of other anthozoans, especially deep-sea corals. In this study, we investigated the characteristics of bioluminescence in deep-sea anthozoans. The bioluminescent capabilities of Heteropolypus, Kophobelemnon, Paragorgia, and a hormathiid anemone are newly described. Coelenterazine, a substrate for bioluminescent reactions, was detected in extracts from octocorals. Coelenterazinedependent luciferase activity was found in all the anthozoans. Moreover, immunoreactivity against Renilla luciferase was detected in protein extracts of the specimens from the families Isididae, Alcyoniidae, Umbellulidae, Funiculinidae, Kophobelemnidae, and Protoptilidae, suggesting that all luminous octocorals may share a common biochemical mechanism, which utilizes coelenterazine and Renilla-type luciferase. Combining these results with improved phylogenetic study, we prose a hypothesis that bioluminescence in octocorals evolved in the Silurian period. Our finding provides fundamental observations of deep-sea corals and experimental evidence of their coelenterazinedependent luciferase systems.

09:20 - 09:35

Heather Bracken-Grissom, Charles Golightly, Danielle DeLeo, Lori Schweikert, Tamara Frank Deep-Sea Lights: The Diversification and Function of Photophores in Sergestid Shrimps

Deep-sea shrimp belonging to the family Sergestidae provide a unique system for studying the evolution of bioluminescence. Most species within the family have one of three distinct forms of photophores including lensed photophores, non-lensed photophores or internal organs of Pesta, while other species lack light organs completely. In this group, autogenic photophores are known to function in counterillumination, in which they can alter light emission to match downwelling sunlight and camouflage themselves from predators below. Over the past few years, our research group has used integrative methods to study the diversification of photophores and their role in counterillumination and congeneric recognition. Phylogenetic investigations suggest light organ type may be correlated with species' depth distributions. Non-lensed photophores evolved once across the family but were lost in the deepest living genus. Lensed photophores also evolved once within benthopelagic genera, suggesting a potential link between the evolution of lenses and the seafloor. The internal organs of Pesta represent the ancestral state for the family and can be found in species with the shallowest depth profiles. Photophore diversity extends beyond light organ type, as each species displays unique light organ patterns. We investigated if species-specific arrangements play a role in conspecific recognition, as darkness and low biomass make it challenging for animals to find and identify one another in the deep sea. By combining morphological and visual modelling we found sergestids to be capable of detecting bioluminescence over short distances, however limited spatial resolution suggests they cannot resolve organ pattern. Although species-specific patterns do not play a role in conspecific recognition, recent evidence suggests internal photophores not only emit light, but can also detect light. Combining transcriptomic, histological and physiological methods, our team found evidence for photosensitivity in organs of Pesta, which we predict may allow for regulation of light emission during counterillumination.

09:35 - 09:50

José Paitio, Daichi Yano, Shiro Takei, Masakazu Iwasaka, Yuichi Oba Light shading mechanism in neoscopelid fish Neoscopelus microchir

Myctophiformes include lanternfishes (Myctophidae) and neoscopelids (Neoscopelidae), both families have ventral-lateral photophores for counterillumination1 and diverged from a bioluminescent ancestral2 . Photophores' inner structure is similar within Myctophiformes, but some differences can be found. Lanternfishes have a modified scale cup and lens, and inner colored reflector3 . None of these structures is reported in neoscopelids which have pigment surrounding the photocytes4 . Coloured reflector allows lanternfishes to achieve adequate counterillumination but the mechanism of neoscopelids' photophores is not studied yet. Lanternfishes Diaphus watasei and neoscopelids Neoscopelus microchir were collected at Kochi Prefecture and Suruga Bay fishing ports, Japan. Fresh photophores were fixed for histology and deepfrozen fishes used for luciferase purification, fluorescence microscopy, and spectrometry. Similar scale lens to lanternfishes was found in N. microchir. Silver inner reflector is non-parabolic and composed by disarranged guanine crystals, projecting all visible light. Large photocytes area is surrounded by a branched pigmented tissue. Spectra of photocytes light transmitted by this pigment matches to mesopelagic downwelling light. Pigment color naturally occurs from yellowish to red and can be regulated by pH. In neoscopelids photophores, pigment may aggregate and disperse through the branches, shading photocytes light to control counterillumination intensity during vertical migrations. Lanternfishes have a parabolic colored reflector for the same purpose. Compared to lanternfishes, neoscopelids photophores have a simpler light projection mechanism and a less precise counterillumination. Each Myctophiformes family developed a different counterillumination mechanism based in photophores accessory tissues. Less complex light projection system and lower efficiency for counterillumination of neoscopelids photophores may be linked to its lower biological success than lanternfishes.

09:50 - 10:05

Jérôme Mallefet, Laurent Duchatelet The kitefin shark, Dalatias licha: first study and comparative aspects with lantern sharks.

Bioluminescence has been often seen as a spectacular uncommon event at sea but considering the vastness of the deep sea and the occurrence of luminous organisms in this zone, it is now more and more obvious that producing light at depth must play an important role structuring the biggest ecosystem of our planet. The Chatham Rise fish survey done in January 2020 by Niwa, gave us the unique opportunity to get access to shark species such as Dalatias licha, Etmopterus lucifer, and Etmopterus granulosus. Although these species are mentioned as bioluminescent it is the first time their luminescence is documented. Results through a diversity of technics [i.e. digital pictures (ventral, lateral, and dorsal views), histological description of light organs (photophore, iris-like structure pharmacological data) and hormonal control of long lasting-glow], highlight the evolutive conservation of the bioluminescence process within Dalatiidae and Etmopteridae. A special emphase is made on D. licha luminescence as representative of the largest luminous vertebrate with assumptions on the light emission function. Chatham Rise is a unique place since representatives of the three luminous sharks' families were observed in the same area. This survey revealed a glimpse of the diversity of shark bioluminescence making essential more research to understand the physiology of these unusual deep-sea inhabitants: the glowing sharks.

General 2: Biodiversity

09:05 - 09:20

Helen Armstrong, Brittany Finucci, Ashley Rowden Habitat use of deep-sea chondrichthyans

Of the 112+ species of chondrichthyans found in New Zealand waters, approximately 80% of species are found in the deep sea, and many have a high level of data deficiency. Habitat use has been identified as a knowledge gap for deep-sea chondrichthyans, and it is important to understand how different life stages utilise their environment when assessing risk to fishing activities and other anthropogenic impacts. In New Zealand, much of what is currently speculated about habitat use is based on bycatch data and has not been confirmed with in-situ observation. In recent years, there has been an increasing interest in deep-sea mining, resulting in an increase of projects dedicated to seabed mapping. Here, a series of readily available deep-sea video collections, including video surveys conducted by the National Museum of New Zealand (Te Papa) and the National Institute of Water and Atmospheric Research (NIWA)'s Deep Towed Imaging System (DTIS) have been analysed to characterise areas of importance for encountered deep-sea chondrichthyans. Confirmed sightings have indicated a potential nursery site for ghost sharks (Hydrolagus spp) and lanternsharks (Etmopterus spp) on sandy substrate on the Campbell Plateau and a previously unstudied seamount has been shown to be an egg laying ground for a large bodied deep-sea skate. This is the first confirmed nursery area for a deep-sea ghost shark and the first known skate egg nursery in NZ. This information is important in informing management of species' risk to fishing and other habitat disturbances, including future seabed mining in the deep sea.

09:20 - 09:35

Savannah Goode, Ashley Rowden, David Bowden, Malcolm Clark, Fabrice Stephenson

Using substrate and seafloor terrain variables to explain benthic community structure and predict community distributions on two New Zealand seamounts

The ability to predict community distributions relies on an understanding of the factors related to community assembly processes. Most deep-sea distribution modelling efforts to date have focused on one or few similar species. However, community-level modelling (for whole or partial assemblages) may be more useful for habitats characterised by high species richness and many rare records, such as seamounts. Seamounts are a common feature of the deep seafloor, and vulnerable to disturbances from several human activities, including fishing. These features can also be highly heterogeneous at a range of spatial scales. It is thus important to understand fine-scale community and patch dynamics, and the environmental drivers contributing to assembly patterns on seamounts to improve habitat mapping efforts on these features. We conducted a study to: 1) describe the structure and distribution of mega-epibenthic communities on two unfished seamounts off New Zealand; 2) determine which environmental variables best correlate with variation in community structure; 3) predict the distribution of the identified communities beyond the sampled areas; and 4) describe the patterns of the predicted spatial distributions of each community, in particular the community patch characteristics. We found that the environmental variables which best explained variations in community structure differed between the seamounts and at different spatial scales. These differences were reflected in the distribution models: communities on one seamount were predicted to form bands with depth, while on the other seamount communities varied mostly with broadscale aspect and the presence of pinnacles. The number and size of community patches, interpatch distances, and patch connectedness were found to vary both within and between seamounts. These results can be used to better assess the potentoal for benthic communities to recover from fishing impacts and to inform the spatial management of seamounts.

09:35 - 09:50

Akira Iguchi, Miyuki Nishijima, Eri Ikeuchi, Taiga Kunishima, Hiroyuki Yokooka, Hideki Sugishima, Kazumasa Ikeda, Ryuichi Miwa, Yoshiro Sekido, Nozomu Iwasaki, Masahiro Suzumura, Ayumi Tsukasaki, Yuichiro Tanaka, Shogo Kato, Junpei Minatoya, Nobuyuki Okamoto, Travis Washburn, Atsushi Suzuki

Comparative analysis of multiple size classes reveals complex dynamics of biodiversity among seamounts

The aim of this study was to evaluate the differences of biodiversity around seamounts with cobaltrich ferromanganese crusts from the aspect of multiple size classes of biological communities (i.e., microbes, infaunal benthos, and motile megafauna) in relation to both depth and distance between seamounts. A total of five seamounts were studies in the Northwestern Pacific at both the seamount summit and base. In the cases of microbes and infaunal benthos, we applied metabarcoding analyses using sediment samples. In the case of motile megafauna, we used a free-fall deep-sea camera lander known as "Edokko Mark I.", which can obtain high resolution images of deep-sea animals attracted by bait trap. We observed differences of biological communities between the summit and base of seamounts in all size classes. In contrast, community structure among seamounts showed different patterns for each size class of organisms, which may be attributed to the difference of main process related to different functional traits of each biological community. Our results will assist with forming ecological baselines of seamount communities and environmental impact assessments in consideration of future deep-sea mining projects.

09:50 - 10:05

Leah Bergman, Mehul Sangekar, Dhugal Lindsay The Kuruse Hole: A unique, warm deep-sea environment in the IzuBonin Arc, Japan dominated by viperfishes (genus Chauliodus)

The deep sea is categorized as a cold-water environment, typically 4℃ around 800 m depth near Japan. There are warm environments in the deep sea, including hydrothermal vents and the deep Mediterranean, Red and Sulu Seas; noted as having unique faunal communities that reflect the extraordinary environmental conditions. The Kuruse Hole, located in the Izu-Bonin Arc of Japan, is another example of a warm deep-sea environment. The warm temperature is attributed to geological activity, although no vent systems have been reported within it. The area has been surveyed/sampled on three occasions, twice by RV 'Natsushima' cruises in the year 2000 and once during a RV 'Kaimei' cruise in the year 2020. These expeditions utilized cameras on submersible platforms to film both the benthic and midwater communities. During the 'Natsushima' expedition, the bottom temperature was recorded to be around 11℃ at 820 m depth; in the 'Kaimei' expedition, the bottom temperature was recorded at around 18℃. In the year 2000, the dominant fish taxon was the family Trichiuridae, with around 30 individual observations from a total of 52. The ichthyofauna changed drastically between the 'Natsushima' (2000) and 'Kaimei' (2020) expeditions, with fishes in the family Stomiidae accounting for the majority of observations (2,056 individuals from a total of 2,475) during the 'Kaimei' expedition. Within the family Stomiidae the genus Chauliodus was dominant, with over 1,500 individual observations making up 62.23% of the total ichthyofauna observed within the Kuruse Hole. Many genera observed during the 'Kaimei' expedition, including Chauliodus, have never been recorded at such high temperatures. The fish community within Kurose Hole is unique when compared to other warm deep-sea environments, warranting further study on the trophic ecology of its inhabitants and the metabolic adaptations allowing them to survive at such warm temperatures.

Special 2e: Microbiology

10:05 - 10:20

Lines Salonen, Panagiota-Myrsini Chronopoulou, Hidetaka Nomaki, Dewi Langlet, Masashi Tsuchiya, Karoliina Koho Metabarcoding observations on species-specific microbiomes of deep-sea benthic foraminifera

Benthic foraminifera are abundant unicellular eukaryotes that play key roles in marine biogeochemical cycles; however, their ecology and interactions with prokaryotic communities remain poorly known, especially in the deep-sea. Recently, metabarcoding has emerged as a powerful tool in gaining in situ insights into the microbiome composition of deep-sea unicellular eukaryotes that are difficult to maintain in laboratory and therefore study using traditional experimental methods. Living foraminifera belonging to five species (Bulimina subornata, Globobulimina sp., Chilostomella ovoidea, Nonionella labradorica and Bulimina striata) were collected from Sagami Bay, Japan, from 750 m water depth. Specimens were isolated from the top 5 cm, representing various foraminiferal microhabitats, and including both shallow- and deep-infaunal taxa. Using 16S rRNA gene metabarcoding, the intracellular diversity of bacteria and chloroplasts was studied, and compared to bacterial communities living in the surrounding sediment. Results show that foraminifera harbor species-specific intracellular bacterial assemblages, indicating that differences in their preferred microhabitat and ecological strategy are likely reflected in the foraminiferal microbiome. Compared to the sediment community, the intracellular bacterial assemblage of foraminifera was less substantially diverse. Certain bacterial groups, such as such as the bacterial family Marinilabilaceae for C. ovoidea and Hyphomicrobiaceae for B. subornata and B. striata, were tightly associated to a specific foraminiferal species. Their consistent occurrence and high relative abundance in specific foraminiferal species implies that there may exist unique, potentially symbiotic relationships between foraminifera and bacteria that have been previously overlooked, therefore calling for further research focusing on these bacterial groups. In addition, we investigated the origins of intracellular chloroplasts found in foraminifera, discovering that they also originate from species-specific sources likely reflecting the different ecological and trophic strategies of each species.

10:20 - 10:35

Lara Macheriotou, Ann Vanreusel, Sofie Derycke Global patterns of deep-sea nematode genetic diversity

Nematodes (Phylum: Nematoda) are amongst the most widespread and numerically dominant invertebrate metazoans in the deep sea, constituting up to 90% of the soft-sediment fauna in oligotrophic ecosystems such as abyssal plains. Being so abundant, nematodes represent a vital biotic component of the global deep-sea habitat by providing various services such as denitrification, organic matter mineralization and heavy metal removal. Comprehensive inventories of diversity through morphological assessments are impeded by the high and undescribed species richness of this phylum, phenotypic plasticity of diagnostic characteristics, cryptic species and the fragility and small size of the specimens. DNA-based approaches such as metabarcoding offer a means by which nematode diversity can be examined rapidly and consistently, precluding taxonomic expertise. In this work, we compiled publicly available metabarcoding datasets targeting 18S rRNA (v1-v2) in marine sediments worldwide to assess global patterns in deep-sea nematode Amplicon Sequence Variants (ASVs). We highlight differences found between various ecosystem habitat types, depth zones and marine biogeographic realms with respect to alpha and beta ASV diversity as well as phylogenetic community structure and evolutionary distinctiveness thereof.

10:35 -10:50

Diana L. Salcedo, Patricia Velez, Jesica A. Hernández, Luis A. Soto Functional role of fungi in the trophic structure and carbon flux in deep-sea hydrothermal vents of the southern Gulf of California, Mexico

The biological diversity and trophic interactions of the macrofauna and bacteria of deep-sea hydrothermal vents have been widely analyzed, demonstrating their importance in energy transfer. However, the occurrence of fungi and their functional role in these ecosystems remain poorly studied. Herein, we assessed the role of benthic fungi in the trophic structure and carbon flux in hydrothermal vents, through the analysis of the isotopic signatures of carbon (δ13C), nitrogen (δ15N), and sulfur (δ34S) in fungal isolates obtained from surficial sediment samples collected in three hydrothermal fields of the southern Gulf of California (Pescadero Basin, Pescadero Transform Fault, and Alarcón Rise). The fungal diversity of the sediments was previously analyzed by culturedependent and independent methods, and 27 isolates were selected for isotopic analyses. The analyzed material included members in the Pleosporales, Eurotiales, and Sordariales, being acknowledged as conspicuous terrestrial decomposers. Our results revealed that fungi are involved in important deep-sea ecosystem processes. These osmotrophs represent an important link in the recycling of the organic carbon stored in the sediments and its incorporation into the trophic web. According to the δ 13C values of the fungi, they might be feeding on chemosynthetic and/or heterotrophic bacteria since they have similar isotopic signatures. Their δ 15N values suggest the assimilation of local depleted nitrogen sources. Their δ 34S values suggest the assimilation of local sulfur of volcanic origin instead of sulfates from the water. We suggest that fungi might represent secondary consumers in the trophic web of hydrothermal vents, transferring the organic carbon to higher levels through the detritivores/bacterivores, likely feeding on a mixture of bacteria and fungi inhabiting the sediments.

10:50 - 11:05

Pierre-Antoine Dessandier, Ewan Pelleter, Dimitri Kalenitchenko, Jean-Hervé Ogor, Giuliana Panieri, Jozée Sarrazin Benthic foraminiferal adaptability to hydrothermal conditions: a case of study from the Lucky Strike vent field (Mid-Atlantic ridge).

Hydrothermal vent fields represent dynamic environments hosting extremely rich ecosystems based on interactions between chemosynthetic microbial communities and invertebrate species thriving on active sulfide edifices. At the Mid-Atlantic ridge, the Lucky Strike (LS) vent field has been the focus of multiple biological studies, thanks notably to the establishment of the EMSO Azores observatory. While ecological studies have been focusing on microbial and macrofaunal communities, more recently efforts have been paid to better understand the ecology of meiofauna in these environments. However, some groups still remained out of the scope. In this study, we present for the first time, an ecological study of benthic foraminifera inhabiting soft sediments in the direct vicinity of hydrothermal edifices and their peripheries at LS. A total of twelve blade cores were collected. We combine microhabitat environmental descriptors (major elements, organic carbon) with faunal density and diversity of benthic foraminifera (living & fossil) and microbial DNA to investigate the impact of hydrothermal activity on their ecology. The far periphery, ~150 m away from hydrothermal activity, harbors a community of diverse foraminifera feeding on pre-degraded organic matter characterized by a phytoplankton detrital signal. Communities located at intermediate distance from venting showed the presence of opportunistic species likely feeding on chemosynthetic microorganisms. Finally, environments closer to active sites (few meters) showed very low abundance of living individuals, as the presence of harsh environmental conditions (high sulfur content) may limit faunal growth. Unexpectedly, the presence of widespread iron-oxidizer bacterial biofilms was associated to the dissolution of all biogenic carbonate content raising questions on their impact on regional carbon budge.

General 2: Biodiversity

10:05 - 10:20

Javier Montenegro, Erik Thuesen, Tiffany Bachtel, Hiromi Kayama Watanabe, Ehsan Kayal, Allen Collins, Dhugal Lindsay Towards a standardized threshold on the molecular identity of gelatinous zooplankton: study case of family Halicreatidae at the Clarion-Clipperton Zone

Deep midwater marine environments are considered to be the largest ecosystems on earth. However, given its extension, it is difficult to estimate the diversity and richness of species inhabiting midwater ecosystems through traditional sampling and taxonomic approaches. eDNA has emerged as a cost-effective alternative to study the diversity of this ecosystem. While sequencing and bioinformatic technologies have come a long way, a major flaw of eDNA analyses remains the quality of the databases used as references for taxonomic determination. Furthermore, the absence of clear thresholds in genetic distances and alignment identities compromises the accuracy of the taxonomic inferences derived from eDNA analyses. We propose the creation of a taxonomically-curated database including molecular data, and standard molecular identity thresholds at genus and species level. As a proof of concept, in this study we aim to set a standardized molecular identity threshold for jellyfish species in the family Halicreatidae. First, vouchers and newly-collected specimens from multiple locations were identified using in-situ imaging and traditional taxonomic analyses. Second, total DNA was extracted, and mitochondria 16S sequences were determined. Amplified sequences were used to estimate the genetic distances across localities per species and across congeneric species. Based on these results, the existence of a barcoding gap across genera and species was established. Thereafter, basic BALST statistics were estimated and standard thresholds for genus and species levels were computed. Establishing a taxonomically-curated database with clear thresholds on genetic distances and relevant BLAST statistics promises to facilitate the detection of cryptic species and increase the accuracy of eDNA barcoding analyses. Such a tool will be invaluable in enabling Environmental Impact Assessments of proposed deep-sea mining sites to be carried out without the real time input of an on-board taxonomist to identify these fragile organisms based on morphology, and will also facilitate studies on connectivity.

10:20 - 10:35

Camille Poitrimol, Eric Thiébaut, Claire Daguin-Thiébaut, Anne-Sophie Le Port, Marion Ballenghein, Adrien Tran Lu Y, Didier Jollivet, Stéphane Hourdez, Marjolaine Matabos

Contrasted phylogeographic patterns of hydrothermal vent gastropods along Southwest Pacific back-arc basins

Understanding drivers of biodiversity patterns are essential to evaluate the impact of potential deepsea mining and ecosystems resilience. Although the Southwest Pacific forms an independent biogeographic province for deep-sea hydrothermal vent fauna, different degrees of connectivity among basins have been reported for a small number of species. This study compares phylogenetic patterns of several hydrothermal vent gastropods across Southwest Pacific back-arc basins by analysing partial cytochrome oxidase subunit I (COI) gene variations. We focused on six genera from four families of vent gastropods widely distributed in the region: Shinkailepas (Phenacolepadidae), Lepetodrilus (Lepetodrilidae), Desbruyeresia and Provanna (Provannidae), and Lamellomphalus and Symmetromphalus (Neomphaloidae). A large-scale sampling was conducted during the CHUBACARC cruise held in 2019. Samples were collected at different vent fields in the Futuna volcanic-arc, and the Manus, Woodlark, North Fiji and Lau basins. A total of 320 individuals from the six gastropod genera were morphologically identified and their mitochondrial COI gene were sequenced. To determine the occurrence of cryptic species and explore the genetic structures of each taxon, different genetic analyses were conducted: phylogenetic trees using the Neighbor-joining method with Kimura 2 parameters model of substitutions, haplotype networks and the Automatic Barcode Gap Discovery (ABGD) method with the same model. Results showed contrasted phylogeographic patterns among species, even between closely related species within the same genus. While some species are widely distributed across basins (i.e. Shinkailepas tollmanni and Desbruyeresia melanioides), others are present in only one (i.e. Shinkailepas tufari complex of cryptic species, Desbruyeresia cancellata and D. costata). Other species showed intermediate patterns with different lineages separating the Manus from the Lau/North Fiji basins, individuals from the Woodlark basin being related to either of the lineages (i.e. Lepetodrilus schrolli, Provanna spp.). Results are discussed according to the dispersal potential of the species and the geological history of the Southwest Pacific.

10:35 -10:50

Florence Pradillon, Pierre Methou, Iván Hernández-Ávila, Cécile Cathalot, Jozée Sarrazin, Marie-Anne Cambon-Bonavita

Apartment-sharing at deep-sea hydrothermal vents: how Rimicaris spp. vent shrimps co-exist on the Mid-Atlantic Ridge

Among the endemic and specialized fauna from hydrothermal vents, Rimicaris shrimps surely constitute one of the most important and emblematic taxa. On the Mid Atlantic Ridge (MAR), two species affiliated to this genus co-occur: Rimicaris exoculata and Rimicaris chacei differ by their morphology, their trophic regimes and their abundance. The first forms large and dense aggregations on active chimney walls in close proximity to vent fluid emissions, whereas the second is much less conspicuous, living mostly in scattered groups or solitary further away from the fluid influence. During the BICOSE 2014 & BICOSE2 2018 cruises at the TAG and Snake Pit vent fields on the MAR, we observed marked variations in the local distribution of sexes and life stages of the two species, resulting in different local assemblages, and pointing different habitat uses along their life cycles. “Nurseries” of R. chacei appeared to be strikingly abundant, contrasting with the low densities of their adult counterparts, suggesting a possible post-settlement collapse of the population and contrasting with the demography of its congener R. exoculata. Additionally, our results highlight distinct niches for the earliest juvenile stages of both species compared to all the other life stages. In the light of the observed variability in population structures, we propose a hypothetical scenario depicting the benthic part of the life-cycle of each species, and discuss the potential drivers of the cooccurrence of these two closely related species at a small spatial scale.

10:50 - 11:05

Genki Ishiyama, Tsuyoshi Takano, Hiroaki Fukumori, Hajime Itoh, Kazunori Hasegawa,

Shigeaki Kojima, Yasunori Kano Geographic distance matters: diversification process in the deep-sea snail genus Bathyancistrolepis (Gastropoda: Buccinidae)

Little is known about the speciation of benthic animals in the deep sea, where few obvious barriers exist to prevent admixture of individuals. Intense environmental gradients with depth, rather than geographic separation, would thus play a central role in genetic differentiation and speciation (the depth-differentiation hypothesis). Several empirical studies have corroborated this idea for lineages of bivalves, amphipods and octocorals. However, difficulties in sampling have hampered detailed documentation of existing diversity and hence past speciation process in the deep sea. Here we show—with among the most extensive datasets for a clade of deep-sea benthos—that geographic distance may play as significant a role in speciation as depth-related factors do, presumably depending on the dispersal ability of individuals. Direct-developing snails of the buccinid genus Bathyancistrolepis are endemic to the northwest Pacific (Sea of Okhotsk to Pacific coasts of Japan to southwest of Taiwan) with a depth range from 550 to 5,500 m. Specimens from 120 localities encompassing their geographic and vertical distributions were classified into seven biological species, five of which were new to science. Sister species had either sympatric or allopatric distributions, with or without an overlap of depth ranges. Genetic distances between conspecific individuals increase with their geographic distances, but not with differences in depth, suggesting that both sympatric and allopatric speciation occurred in the evolution of this bathyal–abyssal clade. We aim in the future to time-calibrate the divergence events with their Miocene to Pleistocene fossils; the extensively uplifted areas of Japan provide an unrivaled opportunity to examine bathyal taxa of as recent as 0.6 million years ago.

Special 2e: Microbiology

11:25 - 11:40

Sarah K. Hu, Erica L. Herrera, Rika Anderson, Amy R. Smith, Maria G. Pachiadaki, Virginia P. Edgcomb, Jeffrey S. Seewald, Jeffrey S. Seewald Microbial eukaryotic diversity & grazing activity at deep-sea hydrothermal vents

Our current understanding of microbial food web dynamics and ecology at deep-sea hydrothermal vent ecosystems is incomplete without including the role of microbial eukaryotes. Vent fluids mixing with seawater at hydrothermal vent systems support hotspots of biological activity by microbial chemosynthetic primary producers. Single-celled microbial eukaryotic (protistan) trophic interactions, especially in the form of grazing, undoubtedly impact the distribution and richness of the resident bacteria and archaea, as well as the flow of carbon in these ecosystems. Here, we used a qualitative and quantitative approach to explore the diversity and distribution of protists at deep-sea hydrothermal vent sites and measure the predation pressure that protistan grazers exert on vent bacteria and archaea. Sequence surveys of microbial biodiversity from several hydrothermal vent ecosystems, including Axial Seamount, Gorda Ridge, and Mid-Cayman Rise (Piccard and Von Damm), revealed a diverse assemblage of putative grazers, parasites, and symbiotic hosts. To further investigate the ecological impact of protists, grazing experiments conducted with discharging hydrothermal vent fluids from the Gorda Ridge and Mid-Cayman Rise demonstrated increased grazing pressure on vent bacteria and archaeal communities compared to the background seawater. Together, this work provides novel insight into underexplored protist communities at hydrothermal sites and relevant trophic interactions which form the foundation of deep-sea marine food webs and mediate carbon transfer to higher trophic levels.

11:40 - 11:55

Jesica Abril Hernandez-Monroy, Diana L. Salcedo, Laura Espinosa-Asuar, Tzvetanka Dimitrova Dinkova, Eduardo Lujan-Soto, Silvia Pajares, Luis A. Soto, Marcos Paolinelli, Jaime Gasca-Pineda, Patricia Velez Pairwise fungal-bacterial interactions as a model to understand dynamics in deep-sea hydrothermal systems at the southern Gulf of California

The heterotrophic microbial communities in deep-sea hydrothermal vents include a wide variety of taxa such as fungi and bacteria. Heterotrophic bacteria inhabiting vents have been characterized as important players in carbon cycling processes; whereas fungi have been hypothesized to accomplish a fundamental role making carbon available to the overall community. Additionally, the crosskingdom interactions between fungi and heterotrophic bacteria in terrestrial ecosystems have been proved to be important for the overall community due to the physical and metabolic relationships that facilitates the nutrient uptake, production of by-products, and for the synergistic interaction degrading organic matter. Nevertheless, the ecological interactions between these groups in deepsea hydrothermal systems remains unexplored, leaving a knowledge gap in the understanding of the ecological dynamics and functioning of these ecosystems. Therefore, the aim of this work was to characterize fungal-bacterial ecological interactions using a comparative transcriptomic approach in order to understand the molecular interactions between them. To accomplish this objective, microorganisms isolated from the deep-sea hydrothermal system The Pescadero Transform Fault located at the southern Gulf of California were used. Two filamentous fungi Aspergillaceae and Eurotiales, were growth in pairwise in vitro bioassays with Bacillus. The comparative transcriptomic analysis revealed a specific response of each organism, exposing a complex molecular interaction and crosstalk between them. This research opens a new paradigm of how fungi and bacteria are important interacting groups with a functional and ecological role in deep-sea hydrothermal systems.

General 2: Biodiversity

11:25 - 11:40

Ana Colaço, Marie Creemers, Neus Campanyà-Llovet, Christopher Pham Should I lodge or should I devour? The functional role of Pheronema carpenteri to its associated fauna

Sponges are benthic species of high ecological importance for many deep-sea ecosystems. They are known to provide habitats and food to other fauna. Sponge grounds host rich and heterogeneous faunal assemblages. However, the ecological role of sponges as single entities to support small benthic macrofauna remains understudied. We investigated the role of the glass sponge Pheronema aff. carpenteri as habitat and food provisioning for associated organisms at two stations of the Azores archipelago (North Atlantic). In order to study the relations between sponge morphology and their associated fauna abundance and richness, sponge weight, external and internal biometric parameters such as size, volume and porosity were measured. Epifauna and infauna were collected by hand from outside and inside individual sponges, as well as from around the sponges using a ROV suction sampler. All the associated fauna was classified into operational taxonomic units (OTUs) representing distinct morphospecies. Sponge associated fauna was dominated by infauna, mainly foraminifers and annelids. Interestingly, a high abundance of juvenile crustaceans was found at one of the two study sites. Results on the food transfer from sponges to the associated fauna (epifauna and infauna) using carbon and nitrogen stable isotopes show that the associated macrofauna uses mainly carbon sources from the environment but in some cases also produced by the sponges. This suggest that for the majority of the associated macrofaunal species the sponge ground primarily serves as a habitat, with some species however showing a high trophic dependence of the sponge.

11:40 - 11:55

Roberto Danovaro, Cristina Gambi Resilience of the Palinuro Seamount ecosystem after mechanical disturbance

The increasing global demand for metals and rare-earth elements has urged the requests to the International Seabed Authority for contracts to explore minerals on the deep-sea bed in the Pacific, Atlantic and Indian Oceans. Recent technological advances may make deep-sea mining economically viable in soon but raise global concerns about potential ecological impacts of these activities in remote ecosystems. In the last decade rock-drilling and dredging activities have been conducted on the top of the Palinuro seamount (Mediterranean Sea), due to the presence of mineral deposits, provoking substrate removal and re-deposition along with habitat modification. The Palinuro seamount can represent a case study to investigate the effect of unassisted restoration (i.e., natural regeneration according to the Society for Ecological Restoration guidelines) on benthic ecosystem after the end of the disturbance comparing impacted vs. not impacted (control) sites. We investigated the progress of the resilience of ecosystem functions and benthic fauna diversity (meiofaunal taxa and nematode species) on the top of Palinuro seamount after 7 and 10 years from the mechanical disturbance. Our results suggest that Palinuro seamount shows high resilience of the ecosystem functions and meiofaunal abundance after 7 years from the end of the rock-drilling and dredging activities but the recovery rate does not increase after 10 years. The resilience rate is different when different attributes of the ecosystem are considered and major differences still remain between impact and control sites for benthic assemblages' composition, independently of the taxonomic level and sampling period investigated. The results obtained in this study provide the first insights on the potential and progress of the unassisted ecological restoration on benthic ecosystem affected by deep-sea mining.

Special 2f: Microbiology

11:55 - 12:10

Blandine Trouche, Miriam Brandt, Caroline Belser, Covadonga Orejas, Stéphane Pesant, Julie Poulain, Patrick Wincker, Jean-Christophe Auguet, Sophie Arnaud-Haond, Loïs Maignien Diversity and Biogeography of bathyal and abyssal seafloor Bacteria and Archaea along a Mediterranean – Atlantic gradient

Seafloor sediments cover the majority of planet Earth and microorganisms inhabiting these environments play a central role in marine biogeochemical cycles. Yet, description of the biogeography and distribution of sedimentary microbial life is still too sparse to evaluate the relative contribution of processes driving this distribution, such as the levels of drift, connectivity, and specialization. To address this question, we analyzed 210 archaeal and bacterial metabarcoding libraries from a standardized and horizon-resolved collection of sediment samples from 18 stations along a longitudinal gradient from the eastern Mediterranean to the western Atlantic. Overall, we found that biogeographic patterns depended on the scale considered: while at local scale the selective influence of contemporary environmental conditions appeared strongest, the heritage of historic processes through dispersal limitation and drift became more apparent at regional scale, and ended up superseding contemporary influences at inter-regional scale. When looking at environmental factors, the structure of microbial communities was correlated primarily with water depth, with a clear transition between 800 and 1200 meters below sea level. Oceanic basin, water temperature, and sediment depth were other important explanatory parameters of community structure. Finally, we propose increasing dispersal limitation and ecological drift with sediment depth as a probable factor for the enhanced divergence of deeper horizons communities.

12:10 - 12:25

Kathrin Busch, Ute Hentschel Biodiversity of deep-sea sponge microbiomes across environmental gradients

Sponge-dominated communities are found in diverse deep-sea environmental settings such as seamounts, mid-ocean ridges, canyons, slopes, shelves and fjords. This project investigates the biodiversity of microbial consortia associated with deep-sea sponges in the North Atlantic. 20 deepsea expeditions were conducted within the EU H2020 consortium “SponGES” to collect data for a next-generation biodiversity assessment of deep-sea sponge-microbiomes that were integrated with extensive oceanographic and ecological metadata. Our study aims to determine the main drivers of microbiome variability within deep-sea sponges. Amplicon data reveal that sponges represent diverse reservoirs of microbes in the dark ocean. We find that different host individuals harbor their own, characteristic microbiomes which are different from seawater and sediment microbiomes originating from the same sampling location. Based on a set of 24 environmental/ biogeochemical parameters, we examined how microbial diversity within deep-sea sponges is related to factors such as depth, nutrients, temperature and oxygen. Our results suggest a strong nestedness of deep-sea sponge microbiomes within their ecological context and reveal stably- and loosely-associated microbial community members across environmental gradients. With more than 1000 sponge individuals analysed in the present study, we are spanning spatial scales from the individual sponge holobiont to the North Atlantic Ocean ecosystem.

12:25 - 12:40

Andrew K, Sweetman, Alycia Smith, Danielle de Jonge, Rory Davis, Rob P. Harbour, Jennifer Pratscher In situ rates of dark inorganic C fixation in the abyssal Pacific and possible key microbial players: in situ results from 3 mine-lease areas

Abyssal seafloor ecosystems cover 55% of the Earth’s surface and are viewed as almost exclusively dependent on the input of organic carbon (Corg) from the surface for biomass production. Microbial communities comprise most of the biomass at the abyssal seafloor and play key ecosystem roles, but their importance in dark inorganic C fixation (DICF; the synthesis of biomass [eg. lipids] from inorganic C) has been estimated to be minor here compared to in the euphotic and deep pelagic zone. Recent in situ studies have revealed extremely high rates of DICF in the eastern abyssal Pacific, which suggest that DICF could be an important C-cycle process in abyssal ecosystems that provides an additional Corg input pathway to abyssal benthic communities. To better understand the importance of DICF in abyssal sediments, we carried out a series of in-situ lander experiments in May 2021 in the abyssal equatorial Pacific to estimate rates of DICF and C transfer from microbes to protozoans and metazoans. We additionally undertook studies to quantify rates of phytodetritus Cturnover by the benthic community. In this talk, we will provide preliminary data on rates of inorganic C uptake into microbial biomass and compare these results to phytodetrital C-uptake results. We will also provide data from DNA/ RNA stable isotope probing analysis identifying the microbial organisms fixing inorganic C and the genes being used in this process. It is hoped that these results will deepen our understanding of the role of DICF in deep-sea sediments, and deep-sea benthic ecosystem functioning in general.

12:40 - 12:55

Paraskevi Mara, David Geller-McGrath, Virginia Edgcomb, Maria G. Pachiadaki Microbes along the permanently stratified redoxcline and the deep euxinic zone in Cariaco Basin contain diverse secondary metabolite gene clusters

Oxygen-depleted water columns (ODWCs) are regions of globally important biogeochemical cycling. The Cariaco Basin on the Venezuelan continental shelf is a permanently stratified ODWC with a redoxcline that extends from ~200 m to 350 m depth, below which the water becomes euxinic (anoxic and sulfidic) with sulfide concentrations approaching 80 µM near the basin floor. Microbiallymediated biogeochemical cycling in Cariaco Basin has been studied, yet identification of potential secondary metabolites and their role in shaping Cariaco’s microbial communities remains poorly understood. Genome mining was applied to identifiy secondary metabolite biosynthetic gene clusters (smBGCs). Metatranscriptomes constructed from water samples filtered and fixed in situ were used to assess the differential expression of gene from microbial communities identified in the particle-associated (PA) and free-living fractions of water samples along the redoxlcline, and within the euxinic zone (900m) of the Cariaco Basin. Numerous prokaryotic phyla expressed smBGCs within both water fractions. The majority of biosynthetic gene clusters were solely expressed in the FL or PA fractions without overlap. The increased expression of genes from smBGCs including ribosomal, and non-ribosomal peptides, polyketides, terpenes, and non-ribosomal and polyketide hybrids in the PA communities relative to their FL counterparts provides evidence of a competitive lifestyle on particles which may depend on the secretion of secondary metabolites for successful survival.

12:55 - 13:10

Anne E. Dekas, Nestor Arandi-Gorostidi, Alma E. Parada A single-cell view of microbial activity in the deep-sea with nanoscale secondary ion mass spectrometry (nanoSIMS)

Our knowledge of the diversity of marine microbes has expanded significantly in recent years. However, our understanding of microbial activity, including its rates, distribution, and physicochemical controls, has lagged behind. Nanoscale secondary ion mass spectrometry (nanoSIMS) offers a quantitative single-cell approach to characterizing the anabolic activity of uncultured microbes, and is particularly well suited to studying low activity, low biomass samples. Here, we use nanoSIMS to analyze microbial cells from the epi-, meso-, and bathypelagic northeastern Pacific Ocean incubated with 15N-ammonium, 13C15N-amino acids, and 13C15N-urea to assess microbial activity, nitrogen preferences, and C/N relative use efficiencies with depth. We find the percentage of active cells decreases from 90% in the epipelagic to ~20% in the bathypelagic in the open ocean (300 km from shore), but stays high, >50%, down to 3000 m at the base of the continental slope (150 km from shore). We quantify the intracommunity distribution of activity using the Gini Coefficient – a metric for (in)equality -- and find that the distribution is increasingly uneven with water depth (fewer cells responsible for a greater percentage of total activity) at the continental slope site, while the trend was more variable at the open ocean site. We observed that microbial cells assimilate more nitrogen from amino acids than ammonium or urea throughout the water column, but urea becomes a relatively more preferable nitrogen source with increasing water depth. Additionally, we observe that microorganisms preferentially assimilate carbon over nitrogen from amino acids at greater water depth, consistent with increasing carbon limitation. Although not performed under in situ pressures, our results suggest that the majority of deep-sea cells are active at the edge of continental margins, and highlight the potential importance of nitrogenous organic matter as a source of both nitrogen and carbon in the bathypelagic.

General 2: Biodiversity

11:55 - 12:10

Davide Di Franco, Katrin Linse, Huw J. Griffiths, Angelika Brandt

Environmental drivers of peracarid assemblages from the Southern Ocean

Benthic fauna is affected by several physical parameters in the deep sea and on continental shelves; in the Southern Ocean, climate change is rapidly changing environmental variables and this will have consequences for the benthos. Among Southern Ocean benthic communities, peracarid crustaceans are one of the most dominant and species-rich groups. Our study investigated the distribution pattern and assemblage structure of peracarid crustaceans from the Southern Ocean at different spatial scale and bathymetrical range. The analyses included peracarid samples collected using an epibenthic sledge during expeditions of RRS James Clark Ross and RV Polarstern. A total of 183606 peracarids were analysed from 109 sampling stations, at a depth range of 160 – 6348 m. We assessed the correlation between isopod species richness (648 species) and environmental variables in the Atlantic sector of the Southern Ocean. Depth and ice coverage were the main phyisical driver shaping peracarid assemblage structure. These two environmental variables were positively correlated with peracarid abundance and species richness. Results confirmed the exceptional occurrence of shelf fauna at depth assigned to the deep sea in non-Southern Ocean settings and also showed the vulnerability of benthic assemblages to shifts in sea-ice concentration. Climate change is rapidly changing the environment and drastically reducing sea-ice concentration, our results showed that such changes are a threat not only to benthic assemblages living on the continental shelf but also to those living in the deep sea.

12:10 - 12:25

Denise Swanborn, Veerle Huvenne, Simon Pittman, Tony Watts, Lucy Woodall

Quantifying and assessing the importance of seamount habitat heterogeneity

Seamounts are often conceptualised as single habitat type, yet deep ocean surveys have revealed that seamounts support highly heterogeneous habitat structure. Complex spatial gradients and patchiness exist in environmental conditions such as substrate type, topographic relief, and hydrodynamic exposure, shaping biological assemblages, habitats and ecological processes. However, methods to quantify the spatial patterns of benthic seascapes in the deep sea and evaluate its potential ecological consequences on biological distributions remain scarce. Land- and seascape ecologists have developed metrics and multi-scale analyses to quantify seascape composition (relative abundance of habitat types) and configuration (the spatial arrangement and orientation of habitats) from categorical habitat maps. Seascape ecology has provided new insights in shallow water ecosystem and the approach is now gaining attention from deep-sea ecologists. We combine unsupervised habitat mapping methods with categorical spatial pattern metrics to apply a novel ecological framework to study seamount habitat heterogeneity and its ecological consequences. We focus on five seamounts along the South-West Indian Ridge with highly varying sizes, shapes and summit depths (Rogers and Taylor, 2012). This region is amongst the least scientifically studied globally but is affected by anthropogenic impacts such as industrial fishing. We use swath bathymetry, backscatter and oceanographic data to produce broad-scale potential habitat maps of each seamount and quantify environmental structure using spatial pattern metrics. These are used to study the relation of seamount-associated demersal fish identified from ROV observations with habitat composition and configuration. Results provide insights into: 1) the environmental parameters that determine potential habitats on seamounts; 2) the ability of spatial pattern metrics to quantify habitat heterogeneity; and 3) the importance of habitat composition and configuration for demersal seamount fishes with relevance for ecosystem-based management.

Rogers, A. D., and Taylor, M. L. 2012. Benthic biodiversity of seamounts in the Southwest Indian Ocean Cruise report – https://www.bodc.ac.uk/resources/inventories/cruise_inventory/reports/jc066.pdf

12:25 - 12:40

Jade Castel, Thomas Broquet, Florence Pradillon, Claire Daguin-Thiébaut, Stéphanie Ruault, Jean Mary, Erwan Corre, Stephane

Hourdez, Didier Jollivet A story of divergence and inter-specific exchanges in deep-sea hydrothermal vent gastropods Alviniconcha

Deep-sea hydrothermal vents are highly fragmented, ephemeral and unstable at multiple temporal scales. Such a spatial and temporal dynamics of the environment is likely to play a non-negligible role in speciation. Little is however known about the evolutionary processes that drive population-level differentiation and the subsequent speciation of the vent species and more specifically how geography and habitat specialization interplay in the history of divergence. In this study, we assessed the distribution and genetic divergence of three species of the hydrothermal symbiotic snails Alviniconcha that occupy active vent fields in the West Pacific Ocean, by using sequence variation in the mitochondrial Cox1 gene, species transcriptomes and ddRAD-seq data, and tested whether these species have already fixed morphological differences by looking at the shell biometry and its bristle ornamentation. Combining morphological description, sequence variation for mitochondrial Cox1, transcriptomes, and RAD-sequencing across 5 back-arc basins, we confirm that A. kojimai, A. boucheti and A. strummeri have partially overlapping distributions across the West Pacific and found the high level of divergence previously described for mtDNA Cox1 to be representative of the nuclear genome as well. A. kojimai and A. strummeri have recently split with divergences of 9% (mtDNA) and 2% (gDNA) when compared to A. boucheti which is the most divergent of the three species (12.5% and 3.2% respectively). Information from population models with both gene flow and population size heterogeneities along genomes indicated that these three species are still able to exchange due to secondary contact between populations after a long period of isolation, and this may explain why the evolutionary rate may slightly differ from expectations between nuclear and mitochondrial genomes for the strummeri/kojimai pair. Finally, extending previous morphological descriptions, we found that the three species can be distinguished based on external morphology by observing the distribution of bristles and the shape of the columella.

12:40 - 12:55

Barbara Górska, Thomas Soltwedel, Maria Włodarska-Kowalczuk Macrobenthic biodiversity response to climate warming driven environmental change in the Arctic deep-sea (HAUSGARTEN, Greenland Sea 79°N)

Large-scale simulations of global climate predicts continuous increase in air and water temperature, leading to further reduction in ice-cover in Arctic. Monitoring of natural, temporal variability of characteristics of deep sea ecosystems in that climate change sensitive area, are crucial for capture of the moment and the nature of the biological response to changes in environmental regimes.

Research was localized in HAUSGARTEN area, where the long-term interdisciplinary monitoring program of structures and functions of deep sea ecosystem in Arctic was established by Alfred Wegener Institute in Bremenhaven (AWI, Germany). HAUSGARTEN is located on the border between the Arctic Ocean and the northern North Atlantic in the region of marginal ice zone - an area very sensitive to possible effects of the global climate change. Between years 2004 and 2008, the anomalously warm surface waters (with temperatures >3°C), called Warm Water Anomaly (WWA), occurred in the central HAUSGARTEN area. It had a significant influence on the whole marine ecosystem – from pelagic zone to the deep sea bottom.

We aimed to explore the response of macrobenthic communities to environmental change in HAUSGARTEN region. The study is based on samples collected before (2000) and after the WWA (2010, 2017). Macrofauna samples were collected from board of r/v "Polarstern", at stations located along the bathymetric gradient from shelf to abyssal plain (230-5561m). Macrofauna species composition and diversity has been compared among the three sampling years to explore if and how it responded to the climate warming driven environmental change.

12:55 - 13:10

Saskia Brix, Stefanie Kaiser, Anne-Nina Lörz, Morgane Le Saout, Mia Schumacher, Frederic Bonk, Hrönn Egilsdottir, Steinunn H. Olafsdottir, Anne Helene S. Tandberg, James Taylor, Simon Tewes, Joana R. Xavier, Katrin Linse Habitat variability and faunal zonation at the Aegir Ridge, a canyon-like structure in the deep Norwegian Sea

The Aegir Ridge System (ARS) appears as a canyon-like structure in the Norwegian Sea, but is an extinct spreading axis extending from the upper slope northeast of Iceland as part of its EEZ to a depth of ~ 3800 m in the Norwegian Basin. The main objective of this study was to characterize benthic habitats along the ARS based on macro- and megabenthic communities, substrate, depth and water mass variables. During the IceAGE3 expedition (Icelandic marine Animals: Genetics and Ecology) onboard the RV Sonne, in June 2020, the benthic communities of the ARS were surveyed and physically sampled by means of a remotely-operated vehicle (ROV KIEL 6000, GEOMAR) and an epibenthic sledge (EBS). For this purpose, two working areas were selected, including abyssal stations in the northeast and bathyal stations in the southwest of the ARS. Qualitative video and still images of the seabed were used to describe benthic habitats based on the presence of habitat-forming taxa and the physical environment. These biological data were complemented by high-resolution bathymetry data acquired with the vessel's multibeam echo sounder system. First results do identify differences in macro- and mega-faunal communities associated with a depth gradient. A biological canyon effect became evident in dense aggregates of megafaunal filter feeders and elevated macrofaunal densities. Finally, the presence of several Vulnerable Marine Ecosystem (VME) indicator taxa (e.g. sponges and corals) highlights the importance of our study in support of sustainable management of parts of the ARS towards the long-term conservation of its biodiversity and associated ecosystem services.

Thursday 16th September

08:30 - 09:00

Keynote Johanna Weston Thriving under pressure: What amphipods can teach us about the ecological and evolutionary dynamics across the hadal zone

The ocean's deepest zone, the hadal zone, is an enigmatic ecosystem comprised of subduction trenches, troughs, fracture zones, and trench faults that plunge to depths of 6 to ~11 km. These geomorphologically complex features are considered to function as ecological and evolutionary independent units due to long-term geographic isolation and selection pressures. The order Amphipoda, particularly scavenging amphipods, has emerged as a model taxon for understanding drivers of diversity and ecology across the hadal zone as they can be readily and consistently recovered with baited landers. Further, the number of expeditions to both Pacific and non-Pacific Ocean features has increased over the past five years. This talk will focus on advances in hadal amphipod research, including: 1) an expansion of the described diversity through integrative taxonomy, 2) the sampling beyond subduction trenches to examine how the community dynamics are shaped by the topography of a non-subduction feature, and 3) that population genomics is showing that populations of the globally distributed *Bathycallisoma schellenbergi* are highly restricted to their individual feature. Together, these findings are beginning to illuminate how changing plate tectonics and paleo-oceanic conditions have contributed to shaping speciation across the hadal zone. Building on these findings, we are looking to pair extensive specimen collections with advances in genomics, geochemical, and palaeogeological analyses to find the origin of hadal fauna and untangle the complex interaction of biological, chemical, and geological factors shaping the ecology of the deepest marine ecosystem.

Special 4a: Vision

09:05 - 09:20

Tom Cronin, Karen Osborn Tribute to Michael Land

At the end of last year, the deep-sea scientific community lost one of its scientific stars. Michael F. Land, known to all as just "Mike", passed away on December 14, 2020. Mike was a truly special person: scientific pioneer, talented and humorous personality, and a deeply original and observant researcher. Mike is best known for his research on comparative vision. He began his career during his doctoral research, studying the eyes of scallops. But it didn't talk long for him to immerse himself in the visual specializations of all sorts of unusual creatures, including those that inhabit the open ocean. On the British research vessels RRS Discovery and RRS Challenger, he was eager to claim the odd creatures of the mesopelagic, most eagerly the midwater crustaceans such as ostracods, hyperiid amphipods, or mirroreyed deep-sea shrimp. But he was not limited to arthropods and also studied the odd double-eyed squids and fishes found in the mesopelagic. Mike was said to be capable of joining the ship, suitcase and notebook in hand, and disembarking with a fully documented scientific paper ready for publication! While Mike's interests ranged far beyond deep-sea animals, or even marine invertebrates, his fundamental impact on our understanding of deep-sea sensory biology is unmistakable. We will talk about Mike's impact on our knowledge of vision in the deep-sea, his lasting impact on the field and finally the unanswered questions that remain and some of the ways we will pursue those questions in the coming years. In this session on deep sea vision, this talk will set the stage for the session and future directions of the field.

09:20 - 09:35

Anna-Lee Jessop, Zahra Bagheri, Karen J. Osborn, Julian C. Partridge, Jan Hemmi Eye diversity in mesopelagic hyperiid amphipods

The visual adaptations of hyperiid amphipods are highly diverse, ranging from species without eyes to species with eyes as large as one third of their body length. This diversity is extraordinary considering the amphipod suborder (Hyperiidea) contains a relatively small number of species (~350 of the ~10,000 Amphipoda). A pertinent question is how such a small suborder has evolved so many different eye 'designs'. Animal eyes have evolved many remarkable adaptations that can generally be interpreted from a sensory ecology perspective, but, for most hyperiid species, detailed information about their ecology and their eye 'designs' is lacking, making interpretations challenging. In this study we have examined the vision of three distinct hyperiid genera: Phronima, Streetsia, and Hyperia, using a new micro-CT based technique. The technique allows us to map the entire visual field of their eyes in great detail and extract important visual parameters. We show that the visual fields of these genera are very different and exhibit some extremely specialised features. We also incorporate extracted visual parameters into a computational model that predicts the sighting distance of potential predator and prey items. We discuss these results in the context of what is known about the visual ecology of hyperiid amphipods. For example, the depth at which they live is thought to drive aspects of their eye morphology, with light levels decreasing with depth, and the sensing of bioluminescence being a relevant visual task. Furthermore, a fact that has received little consideration in the context of hyperiid eye evolution is that many species are symbionts of gelatinous zooplankton, and that these symbioses can be specific and formed by different modes of association. Overall, our study provides new insights into the visual capabilities of the three study genera and provides a more holistic view of the diverse evolution of hyperiid eyes.

09:35 - 09:50

Tamara Frank Unusual Visual Pigment Systems in Deep-sea Crustaceans Correlated with Bioluminescence

Blue wavelength light travels the furthest in clear oceanic water, and therefore deep-sea species with functional photoreceptors would be expected to possess a single blue visual pigment to maximize sensitivity to the remaining downwelling light. Most of the deep-sea pelagic crustaceans that have been studied to date have a single blue visual pigment system and, if they are bioluminescent, possess either photophores or a bioluminescent spew, but not both. However, several species of deep-sea oplophorid crustaceans have a near-UV visual pigment in addition to the expected blue visual pigment, and these species all possess both photophores and a bioluminescent spew. This dual visual pigment system may optimize their ability to distinguish between photophore emission, which might be used to attract mates or to counterilluminate, and spew emission, which always indicates a predator threat. In addition, several species of deep-sea benthic crabs and shrimp also possess a similar dual visual pigment system, but these species are not bioluminescent. However, these species are most commonly found sitting amongst the branches of deep-sea octocorals, using their long claws to pick off edible plankton that sticks to these tree-like structures. Here, the possession of a dual visual pigment system may enhance their ability to distinguish between the greenish bioluminescence emitted by their non-edible benthic cnidarian hosts and the bluish bioluminescence emitted by the edible plankton whacking into the cnidarians. Lastly, new data will be presented from a species of pandalid crustacean that has been found to possess both near-UV and blue sensitivity maxima, that also appears to be correlated with their possession of both a bioluminescent spew and photophores.

09:50 - 10:05

Eric Warrant, Kerstin Fritsches, Eva Landgren, Richard Brill A tale of two fishes: The visual ecology of two deep-sea predatory fishes

Despite their great economic importance, almost nothing at all is known about the ecologies of deepliving swordfishes (Xiphias gladius) and escolars (Lepidocybium flavobrunneum). In my talk I will describe how the eyes of these two fishes can provide a window into their virtually unknown lives. The eyes of the swordfish are large and very sensitive, with acute frontally directed foveae. They are also heated by a specialised ocular muscle that produces fast vision (flicker fusion: 32 Hz) even in the very cold water of the deep. These results reveal that swordfishes are most likely to be fast visual predators at depths of up to 500 m during the day. The eyes of the escolar are also large and even more sensitive than those of the swordfish, but are more poorly resolved. Nevertheless, they possess foveae directed both dorsally and frontally. Since they lack ocular heating, escolar vision is slow, although it is fastest in warm surface waters (flicker fusion: 8 Hz). These results reveal that escolars are most likely to be slow nocturnal visual predators; cruising ”smash and grab” hunters in warm surface waters at night when vision is fastest, spotting their prey from below.

10:05 - 10:20

Ron Douglas, Martin Genner, Julian Partridge, Wen-Sung Chung, Justin Marshall, Bruce Robison, Jochen Wagner The evolution of complex ocular diverticula in deep-sea barreleye spookfish (Opisthoproctidae)

Sunlight underwater diminishes with depth but is always more intense from above. Consequently, members of several families of mesopelagic fish, have developed, upward-pointing, tubular eyes that maximise sensitivity to the dim downwelling light in this ‘twilight zone’. However, arguably a more important source of light in the deep sea is bioluminescence. As this can occur all around an animal, much bioluminescence remains undetected by the limited, dorsal, visual fields of conventional tubular eyes.

All species within the mesopelagic Opisthoproctidae whose detailed ocular anatomy has so far been examined possess some form of ventrolaterally-directed, light-sensitive, diverticulum that extends the otherwise limited visual field of their tubular eyes. Some genera (Opisthoproctus, Monacoa, Winteria) have only very small rudimentary diverticula that are simple outpouchings of the lateral wall of their tube eye that have no means for focussing the light. Some genera (Bathylychnops, Dolichopteryx, Rhynchohyalus, Macropinna), however, have more extensive diverticula resulting in bipartite eyes that simultaneously focus dorsal illumination onto the retina of a tubular eye using a lens, and ventrolateral light using diverticula that produce focussed images using either refraction or, uniquely among vertebrates, reflection. Such eyes, represent some of the most optically complex eyes of all vertebrates.

This range of ocular morphologies among the Opisthoproctidae presents a unique opportunity for examining how the complex eyes of this family may have evolved. To this end a phylogeny of the Opisthoproctidae was reconstructed using available mitochondrial and nuclear DNA sequences, including all the species whose eye types are known. Mapping the different types of diverticulum onto this phylogeny indicates a process of repeated evolution of complex ocular morphology from rudimentary diverticula in response to similar selective pressures within the deep sea.

10:20 - 10:35

Fanny de Busserolles, Lily Fogg, Daniel Papinczak, Fabio Cortesi, Wen-Sung Chung, Karen Cheney, Justin Marshall Nocturnal coral reef fishes shed light on the function of the multibank retina, a common visual adaptation in deep-sea fishes

Many deep-sea teleost fishes rely heavily on vision to detect prey, predators and mates, communicate, camouflage and/or navigate. To be able to see in their dim environment, they have evolved a multitude of visual adaptations. One of these adaptations is a multibank retina, a retina composed of several banks of rod photoreceptors stacked into layers. Even though multibank retinas have been found in over 28 families across the deep-sea teleost phylogeny, their function is still unknown. Two non-mutually exclusive hypotheses were proposed: (1) they enhance visual sensitivity, and (2) they enable colour vision in dim light. Support for either hypothesis is lacking, mostly due to the difficulty in accessing live deep-sea specimens to conduct physiological and/or behavioural experiments. However, the recent discovery of multibank retinas in the nocturnal coral reef fish family Holocentridae (squirrelfish and soldierfish) offers the chance to test these hypotheses. Holocentrids make an ideal model since they are easily accessible, have a particularly well-developed multibank retina ranging from 6 to 17 banks, and have an ecological and evolutionary connection to the deep-sea. Live individuals of three holocentrid species, as well as two control species without multibank retinas (cardinalfish and triggerfish), were captured on the Great Barrier Reef (Australia) and held in aquariums to test the two hypotheses. The sensitivity hypothesis was investigated using electroretinography, a technique that measures the response of the retina to light stimuli over a range of frequencies and intensities. ERG results indicate that multibank retinas do enhance luminous sensitivity by allowing vision to function over a broader range of light intensities, including dimmer signals. To test the colour discrimination capabilities of the different species, behavioural experiments using Ishihara-style stimuli are currently being conducted under several light intensities. Results from these experiments will also be presented here.

10:35 -10:50

Zuzana Musilova, Fabio Cortesi To see and not to be seen with 38 rhodopsins: silver spinyfin (Diretmidae, Teleostei) extraordinary vision

In the dim light environment, such as deep sea, fish generally obtain visual information through light-sensitive photopigments based on a single rod opsin (rhodopsin 1 = RH1). Vast majority of teleost fishes possess one or two copies of the rhodopsin gene in their genome. In the deep sea fishes, however, an extreme adaptations of rhodopsins have been found. We have recently discovered a species, silver spinyfin (Diretmus argenteus), with the highest number of visual opsins among vertebrates (two cone opsins and 38 rod opsins). Such an extraordinary set up has evolved in the extreme conditions and suggests unique mode of vision, albeit its exact mechanism remains elusive. The peak sensitivity of the rhodopsin photoreceptors spans the blue-green light spectrum of 444 to 519 nm, having actually one of the shortest-sensitive rhodopsins known in vertebrates. In evolution, the extreme diversity of the rhodopsin genes has raised through multiple gene duplications followed by the series of amino acid mutations, which cause changes of the protein function (=sensitivity). Following the original discovery, we will present new findings on the whole genome properties of this species, as well as differential selection on function of vision during ontogeny when larvae need to see in the shallow while adults in the deep.

10:50 - 11:05

Fabio Cortesi Current challenges facing deep-sea vision research and possible ways forward

The deep-sea is a place of infinite wonders, a proverbial candy shop where one can pick and choose from the most scurrile and incredible creatures on earth. In particular, the eyes of deep-sea critters have intrigued and inspired myths and legends since ancient times. However, when it comes to studying deep-sea animals, we face a dilemma. As beautiful and intriguing as they may be, learning about these critters' (visual) behaviours in their natural environment is exceedingly difficult, if not outright impossible. Consequently, we are often left staring at the (semi-)dead bodies of our study objects, wondering how they might pursue their lives in the relative darkness of the deepest oceans? Fortunately, though, not all things are lost, and one can make an informed guess about deep-sea visual ecology from what their eye anatomy, physiology, and molecular building blocks can teach us. Recent technological advances in imaging, molecular sequencing, filming and ROV space have made it possible to study deep-sea vision in greater detail and across many more species than ever before. Likewise, advances in computational algorithms to study deep-sea vision evolution and investigating visual behaviours in shallow-living relatives provide exciting new functional insights. However, none of this work would be possible without much of the anatomical and physiological groundwork that has been laid by the pioneers in the field, some of which I hope will be able to attend this special session.

Special 2b: Hadal

09:05 - 09:20

Anna Sobek, Hamed Sanei, Zhe Li, Stefano Bonaglia, Gisela Horlitz, Sebastian Abel, Ronnie N Glud Organic matter degradation leads to higher concentrations of persistent organic pollutants in hadal sediments

The biological pump plays a major role for the transport of hazardous persistent organic pollutants (POPs) to deep sea regions. In the photic zone, POPs partition to phytoplankton and other particulate organic matter and reach deep-water layers and sediments through vertical export with sinking particles. 1 Hadal trenches represent the deepest part of the global ocean and trenches act as hot spots for both deposition and decomposition of organic material.2,3 In this study, we analysed POPs in sediment from the Atacama trench (3 hadal sites at ~8000 m, 1 site on the slope ~6000 m, 1 site on the abyss ~2500 m), to reveal the biogenic-mediated transport and fate of POPs to the deepest places on Earth. Concentrations of polychlorinated biphenyls (PCBs) were at the pg/g dwt level, with the highest concentrations observed at the deepest, hadal sites, in sediment with the lowest total organic carbon content (TOC). Hence, these results contrast the current paradigm of TOC being a significant driver for sediment POP concentrations. The observed PCB concentrations in the Atacama trench support earlier findings that other sources are significant for sediment-living hadal organisms containing high POP concentrations4,5. In the investigated samples, PCB concentrations increased with the relative contribution of inert TOC, suggesting that degradation of TOC within the trench creates sediment with a higher capacity to bind and store POPs.

09:20 - 09:35

Peter Stief, Clemens Schauberger, John Paul Balmonte, Ronnie N. Glud Marine snow in the deep sea: Effect of hydrostatic pressure on microbial degradation and colonization of model diatom aggregates

Phytoplankton aggregates forming in the sunlit layers of the ocean are densely colonized by diverse microbes that degrade the microalgal organic matter while the aggregates sink to the deep ocean. Microbes attached to fast-sinking diatom aggregates (i.e., >100 m/d) are quickly exposed to high levels of hydrostatic pressure, which may significantly reduce their respiration activity and thus organic matter degradation. We hypothesized that suppression of pressure-sensitive microbes attached to the aggregates impedes microbial aggregate degradation. During 2-day incubations in a rotating pressure tank, microbial respiration activity was incrementally reduced by increasing pressure levels. Using 16S rRNA gene amplicon sequencing, we show that the complete inhibition of respiration activity at pressure levels of 80-100 MPa was accompanied by substantial phylum-level changes in bacterial community composition. Bacterial groups apparently not adapted to the fast increase in pressure level were observed to decrease in relative abundance, while other groups had a similar relative abundance as in non-pressurized controls. In contrast, pressure levels of 10-70 MPa induced only partial inhibition of respiration activity and subtle bacterial community changes. We speculate that longer-term experiments, which mimic the more gradual increase in pressure experienced by sinking microbes, induce more pronounced changes in community composition by the time hadal pressure levels have been reached. In conclusion, (1) the partial or complete inhibition of aggregate degradation by pressure will enhance the amount of labile organic matter that is deposited on the seabed, while (2) the suppression of different bacterial groups by pressure has the potential to re-shape the microbial communities transported from surface waters to the deep sea.

09:35 - 09:50

John Paul Balmonte, Rie Pors, Peter Stief, Carol Arnosti, Ronnie N. Glud Microbial enzymatic activities from surface to hadal hydrostatic pressures

Throughout the marine water column, microbial communities initiate the degradation of high molecular weight organic matter by producing diverse extracellular enzymes. However, the extent to which microbial enzymatic activities are affected by elevated hydrostatic pressures (HP) up to levels experienced in hadal waters remain little understood. Understanding the effect of elevated HP on microbial enzymatic activities is as relevant for shallow marine-derived microorganisms—including those associated with sinking particles or those in shallow sediments that seed deep-sea environments by down-slope dispersal—as it is for deep water microbial communities adapted to high pressures. Using pressure chambers, we quantified the effect of increasing (surface water to hadal) pressure levels on the enzymatic activities of several microbial communities, including those from 1) coastal surface waters and sediments, 2) mesopelagic and bathypelagic waters, and 3) copepod and phytoplankton cultures. Enzymatic activities assayed include leucine aminopeptidase, β-glucosidase, chitinase, and a range of polysaccharide hydrolases. Rates were simultaneously measured at distinct levels of elevated HP and at surface water (atmospheric) pressure (AP), to calculate a pressure effect (PE = RateHP/RateAP). Our results showed that PE varied for different enzymes, but most values were < 1, with few that were ≥ 1, suggesting different degrees of pressure tolerance among diverse microbial communities. Preliminary experiments on cell-free, dissolved leucine aminopeptidases from surface microbial communities demonstrate up to 60% loss of enzyme activities when subjected to hadal HP; however, elevated pressure reduced the activities of dissolved β-glucosidases and chitinases to a lesser extent. Overall, these results suggest that increasing pressure dampens to varying degrees the rates at which microbial enzymes can degrade specific components of sinking organic matter. Through its effect on microbial enzymatic activities, pressure may influence the quantity and quality of surfacederived organic matter that reach great oceanic depths.

09:50 - 10:05

Ronnie N. Glud, B.Thamdrup, Matthias Zabel, Kazumasa Oguri, F. Wenzhöfer Microbial carbon and nitrogen mineralization in hadal sediments

Hadal trenches act as depo-centers for organic material, but the extent this material is retained or mineralized remain largely unknown. Based on in situ benthic O2 consumption rates and process rate studies in recovered sediment cores, we explore respiration rates of hadal communities. Data from different trench systems are used to explore environmental factors that govern differences in activity levels within and between different trench systems and to assess the carbon mineralization efficiency of hadal communities. Furthermore, data are used to assess the potential quantitative importance of anaerobic respiration in hadal sediments and the extent.

10:05 - 10:20

Clemens Schauberger, David Seki, Bela Hausmann, Blandine Trouche, Sophie Arnaud-Haond, Lois Maignien, Frank Wenzhöfer, Ronnie N. Glud, Bo Thamdrup Effects of biogeochemistry and biogeography on benthic microbial community composition of hadal sediments

Marine sediments store huge amounts of organic carbon and microbially mediated processes in these systems impact global nutrient cycles. The hadal zone represents the endpoint in the oceanic depth continuum and is hence relevant for studying selective processes that shape benthic microbial communities in the deep-sea. Recent advances in hadal microbiology indicate that hadal communities are distinct from those of adjacent abyssal environments. Potential factors contributing to this dissimilarity include biogeochemical differences, depositional regimes, and adaptation to extreme pressure. Here we assessed how such factors affect microbial community composition in the Kermadec and Atacama trenches. We collected sediment cores at multiple sites within both trenches, sliced each core at high vertical resolution, and determined the microbial community composition of more than 400 samples by sequencing 16S rRNA genes. At all hadal sites, microbial community composition changed gradually over sediment depth. These down-core succession patterns resulted in larger differences in community composition with sediment depth at centimeter scale than among sites along the 430 kilometer long transect of the Atacama Trench axis. The down-core successions appeared unaffected by fluctuations in organic carbon content and associated subsurface peaks in microbial abundance, which suggests that communities may be shaped mainly by conditions in their respective sediment layers rather than by the original composition of communities imported to the trench interior via marine landslides. Comparisons with biogeochemical data revealed that redox zonation imposed a strong selective force on these microbial communities, leading to the contrast between high horizontal similarity and stark centimeter-scale downcore turnover in community composition. Selection associated with oceanic depth and organic carbon concentrations was less prominent, yet hadal communities still appeared clearly distinct from adjacent abyssal environments. Determining the factors that cause these distinctions will require a more holistic approach that incorporates changes in meiofauna populations and a higher spatial resolution.

10:20 - 10:35

Mathias Middelboe, Clemens Schauberger, Daniel Castillo, Sachia Jo Traving, Bo Thamdrup, Ronnie N. Glud Bacteria and viruses in hadal sediments: Spatial variations and evidence of prophage-encoded genes supporting bacterial growth.

Hadal trenches represent the deepest part of the global ocean, and are depocenters with intensified prokaryotic activity. Here we compared the distribution and drivers of prokaryotic and bacteriophage abundance in hadal (>8000 m depth) and abyssal (~6000 m depth) sediments, in Kermadec and Atacama trenches, representing regions with contrasting surface productivity. In abyssal sediments prokaryotic and phage abundances were lower than at hadal sites and declined exponentially with sediment depth, closely correlated with the attenuation of total organic carbon availability. In contrast, the hadal sediments exhibited variable depth profiles of prokaryotes and phages with many subsurface peaks. The prokaryotic abundance correlated well to fluctuations in organic carbon content on the centimeter scale, which were likely caused by recurring mass wasting events. While prokaryotic and phage abundances cross-correlated well in abyssal sediments, there was no clear correlation in the hadal sites. These results suggest that dynamic depositional conditions and higher substrate availability result in a high spatial heterogeneity in phage and prokaryotic abundances in hadal sediments in comparison to more stable abyssal settings. Further, analysis of a phagePseudomonas sp. system isolated from Kermadec trench sediments demonstrated a prophageencoded chitinase gene, which supports host growth in the presence of chitin. We argue that the conditions in deep trench sediments enhance the relative importance of phages for shaping prokaryotic communities and their functional properties.

10:35 - 10:50

Daniel Leduc, Ashley A. Rowden, Malcolm Clark, Daniela Zeppilli, Mauricio Shimabukuro, Timothy Shank, Frank Wenzhöfer, Ronnie N. Glud Distribution of hadal infauna and their contribution to Kermadec Trench biodiversity

The Kermadec Trench is the fifth deepest in the world with a maximum depth at ca. 10 000 m and extends from approximately 26° to 36°S northeast of New Zealand. Since the early work undertaken during the Galathea and Vityaz expeditions in the 1950s, much of the sampling within the trench has focused on bait-attending fauna, leading to valuable insights into the biology and ecology of amphipods, fish and other epifauna. More recently, core sampling within the trench has revealed the presence of relatively abundant and diverse infaunal communities (comprised almost exclusively of meiofauna-sized organisms) extending from the edge of the trench to its deep axis. In 2017, several sites were sampled within the deep basins of the Kermadec Trench axis (>9000 m), providing the deepest core samples ever obtained from the trench. Here, we present new results on the distribution of infauna within and across the trench, and combined with previously published data, we describe distribution patterns in relation to bathymetric, longitudinal and surface productivity gradients. We also explore relationships with sediment parameters and oxygen uptake rates in order to better understand the role of food availability on infauna distribution. Lastly, we provide an overview of all biodiversity data available for the trench and show that infaunal nematodes account for about half of the 200+ metazoan species recorded. Although our knowledge of Kermadec Trench diversity remains incomplete, it is clear that nematodes are not only numerically dominant but also represent a substantial proportion of total diversity in this and presumably other hadal ecosystems.

10:50 - 11:05

Maurício Shimabukuro, Daniela Zeppilli, Daniel Leduc, Frank Wenzhöfer, Ashley A. Rowden, Ronnie N. Glud High hadal meiofauna standing stock and linkage to food availability

The Atacama Trench is underlying one of the globally most productive open-ocean regions and the few available data suggest that the trench seafloor is a hotspot for meiofauna density and biomass. We tested this hypothesis by quantifying meiofauna standing stocks (density and biomass) at six trench axis sites, two adjacent abyssal sites and one bathyal site. The vertical distribution of meiofauna standing stock and infaunal respiration was highest in the top centimetre of sediment and rapidly decreased in subsurface layers. The general meiofauna vertical distribution was clearly correlated to the volume specific oxygen consumption rates of the sediment indicating strong linkage between intensified diagenetic activity and meiofauna standing stock. Indeed, the depth integrated meiofauna standing stock (down to 5 cm sediment depth) was correlated with concentrations of organic carbon and diffusive oxygen uptake rates, implying that meiofauna distribution is governed by food availability and microbial activity. Meiofauna standing stock along the trench axis was markedly higher than the abyssal plain site. The regional variations between trench systems in standing stocks are correlated to the variations in surface productivity. This study supports the hypothesis that the relatively steep bathymetry of hadal trenches focuses organic material along trench axes and thereby sustains elevated infauna abundance and biomass relative to adjacent abyssal plains.

General 4: Adaptation

11:25 - 11:40

Mark Royer, Kim Holland, Carl Meyer, Kelsey Maloney, Edward Cardona, Kate Whittingham, Chloé Blandino, Guilherme Silva

Scalloped hammerhead shark swimming performance and thermoregulation strategies during deep dives into cold water – evidence of marine mammal-like breath holds?

Adult scalloped hammerhead sharks (Sphryna lewini) utilize oceanic habitats around the Hawaiian Islands where at night they dive repeatedly to depths exceeding 800m and water temperatures as low as 4°C, presumably to forage on deep-dwelling prey. We hypothesized that S. lewini dive duration is limited by ambient water temperature at depth because body cooling associated with excursions into cold water can reduce muscle power output, cardiac function and visual acuity. To determine how S. lewini respond to cold ambient water temperatures experienced during deep dives, we equipped adult individuals with instrument packages capable of directly measuring depth, ambient water temperature, activity rates, orientation and intramuscular temperature. Our specific objectives were to determine (1) whether S. lewini maintain core body temperature during deep dives via simple thermal inertia or instead employ active, physiological thermoregulation and (2) whether swimming performance changes during deep, repetitive dives into cold water. We obtained 180 total days of data from 9 free-swimming adult S. lewini. Our data show 'warm' core muscle temperatures are maintained throughout the deepest portion of each dive and core muscle cooling only occurs during ascent to the surface. However, once initiated, this cooling is rapid. After sharks return to the warm surface layer, it takes 45 to 75 minutes for swimming muscles to fully equilibrate to ambient mixed layer water temperatures, but the shark will begin the next dive while the core temperature is still rising. The delayed onset and subsequent rapid rate of cooling followed by the slower rate of rewarming indicate evidence of physiological thermoregulation akin to a marine mammal-like dive reflex (i.e. breath holding and/or modulation of blood flow). Understanding how S. lewini, a warm-water species, are physiologically able to exploit resources in deep, cold habitats provides important insights into the broader ecology of this regionally endangered shark.

11:40 - 11:55

Batour Maria, Chamieh Hala, Taha Samir, Jebbar Mohamed

Characterization of polysaccharide degradation enzymes in hyperthermophilic archaea and their role in adaptation to high hydrostatic pressure

Since the reclassification of life into three domains (Bacteria, Eukarya and Archaea) in 1990 by Carl Woese,most archaea are considered extremophiles occupying extreme ecological niches in terms of temperature and high hydrostatic pressure (HHP) such as deep-sea hydrothermal vents (DSHVs). DSHVs are located in the oceans at depths ranging from a few meters to almost 4,960 m in the Cayman Trough. Living in vicinity of DSHVs, these archaea are facing high temperature and HHP. Thermococcus barophilusis the first hyperthermophilic, true piezophilic archaeon isolated from a chimney collected at the Snake Pit site at 3,550 m depth on the Mid-Atlantic Ridge. In T. barophiluscells subjected to HHP, it was demonstrated that carbohydrate metabolism genes were overexpressed. The degradation of polysaccharides (e.g. maltodextrins, pectin, etc.) by T. barophilus requires the secretion of enzymes degrading these polymers. T. barophilus, possesses many genes and gene clusters encoding enzymes that could be involved in carbohydrates degradation. The objective of PhD project is i) to study a new family of polysaccharide lyases from Thermococcale, ii) to provide their biochemical characteristics and iii) to decipher their roles in adaptation to HHP. Indeed, the growth characteristics of T. barophilus WT and derivatives were monitored, when cells were grown in TRM rich medium supplemented with or without sulfur in the presence of carbohydrates at low (0.1 MPa) or HHP (40 MPa). The secretome of various growth conditions, wasstudied and then proteinsseparated on SDS-PAGE were identified by mass spectrometry and therefore their encoding genes localized on the genome. An overexpression, purification and characterization of a new Pectate lyase from another hyperthermophilic archaea Pyrococcus horikoshiiOT3, using the pBAD System was performed. The properties of the recombinant enzyme were analyzed and showed an enzymatic activity on pectin at high temperature.

11:55 - 12:10

Lorenzo Carré, Eric Girard, Etienne Henry, Ghislaine Henneke, Didier Flament, Bruno Franzetti

High pressure effect on DNA polymerases activities from deep-sea and surface thermophilic microorganisms

Hydrothermal abyssal environments display unique ecosystems based on chemosynthesis and without the need for solar light. Microorganisms thriving in these environments, particularly those colonizing chimneys, face various extreme conditions such as high temperature and high pressure. Extremophilic bacteria and archaea from these environments have been extensively studied as a source of exceptionally thermoresistant biomolecules. Notably, many archaeal DNA polymerases have been commercialized for high-fidelity PCR. It is often assumed that abyssal microorganisms, like those adapted to other extreme conditions, possess various molecular traits associated with pressure-tolerance. However, investigating pressureadaptation at the biochemical and structural levels is challenging. In particular, it is unclear how high temperature and high pressure compensate each other and the effects of high hydrostatic pressure on complex cellular machineries remain poorly understood. To explore response of biological systems from abyssal hydrothermal vents to high pressure, we conducted an enzymological analysis of DNA polymerases under pressure ranging from 0.1 to 100MPa. We used an in vitro real-time fluorescence assay to monitor different activities of DNA polymerases under various pressure/temperature/salinity combinations. Our main model is the DNA Polymerase B from the hyperthermophilic and pressure-tolerant archaea Pyrococcus abyssi, which has been isolated from a 2km deep-sea hydrothermal vent (PabPolB). Our results showed that, unlike strand displacement activity, elongation activity of PabPolB was stimulated by 10-50MPa at 70°C. We then compared PabPolB pressure-tolerance to similar enzymes from other thermophilic archaea and bacteria, isolated in either abyssal or surface environments. All the other enzymes, including those from other abyssal archaea, displayed reduced activities at 10MPa. Pressure inhibition of the PabPolB, at values above 50 MPa, was shown to be reversible and not compensated by high-salt conditions (KCl). Hence, P. abyssi evolution may have compensated inhibitory pressure of abyssal pressure on DNA replication, which would otherwise limit microbe dissemination in deep-sea environments.

12:10 - 12:25

Sébastien Duperron, Bérénice Piquet, Bruce Shillito, François H. Lallier, Ann C. Andersen The dynamics of gill tissue in symbiont-bearing Bathymodiolus mussels: first visual insights into apoptosis, cell proliferation and differentiation patterns

Deep-sea mussels Bathymodiolus spp. harbor high densities of bacterial symbionts in their gills that contribute to hosts nutrition. Despite that the gill organ also exists in similarly-sized non-symbiotic mussels, several features of Bathymodiolus gills are assumed to be adaptations to symbiosis, the most spectacular being their large size. Symbiosis flexibility including symbiont abundances variation is key to mussel’s ability to colonize a broad diversity of habitats, some of which are highly variable over time and space. Investigating the mechanisms underlying organ development and dynamics is thus key to understanding what makes this symbiosis one of the most efficient and successful in deep sea reducing habitats. Various studies have pointed to patterns of over and under-expression of genes involved in pathways associated with host cell proliferation and apoptosis. Yet, these do not reach clear-cut conclusions, as to whether cell death actually occurs in the gills or not. In an attempt to address the role of candidate mechanisms, we conducted microscopy-based investigation of patterns of host cell apoptosis and proliferation in gill tissue of vent and seep Bathymodiolus species using protocols that were not previously used on mussels. Results identify gill developmental patterns that differ from those in nonsymbiotic Mytilus, including higher apoptosis and proliferation rates, and regionalized distribution of these processes in the gill filament, possibly related to the localization of symbionts. Bathymodiolus gills appear as dynamic organs with rapid cell turnover. Observations from lab-based starvation experiments indicate that symbiont loss is accompanied by major modifications of the gill epithelium ultrastructure. After 2 months, gill epithelial cells resemble those of non-symbiotic Mytilus. This could be the consequence of a possible dedifferentiation process, a hypothesis that warrants further investigation because it could provide insights into the evolution of mussel gills towards symbiosis. Allowing for cellular-level resolution of processes, microscopy-based evidence offers a necessary complementary approach to the high-throughput gene/protein expression studies. Therefore, microscopic evidence should be used in tandem with these methods to achieve detailed understanding of the cellular processes that underly the symbioses, which are essential to sustain the high levels of productivity characteristic of deep-sea chemosynthetic habitats.

12:25 - 12:40

Jie. Lyu, Anne. Godfroy, Tom. Mariotte, David. Francois, Nadège. Bienvenu, Valérie. Cueff-Gauchard, Claire Geslin Extremophilic marine viruses from deep sea hydrothermal vents

Viruses are estimated to be more abundant than prokaryotes in deep-sea hydrothermal ecosystems. Viruses are known to play a critical role in biogeochemical cycles and may drive the evolution and adaptation of their cellular hosts [1].
However, the viral diversity, the nature of virus-host interactions and their functional roles in these extreme marine environments are not well known. To date, only 11 viruses have been isolated and characterized from deep sea hydrothermal vents, including 3 archaeoviruses and 8 bacterioviruses [2, 3].
To better understand virus-host relationships and viral influence on microbial ecology in deep-sea hydrothermal ecosystems, we perform viral infections and follow viral cycles under variable environmental conditions.
In a bioreactor, we built a simple microbial community, with one bacteria and one archaea and their viruses. MPV1 that infects Marinitoga piezophila which is a thermophilic, anaerobic and piezophilic bacterium, and virus IRI that infects Thermococcus sp. which is a hyperthermophilic, anaerobic, sulfur-reducing archaeon. Under varying environmental parameters (temperature, sulfur, oxygen, carbon sources) in continuous culture, hosts and viruses’ abundance is monitored by flow cytometry, combined with qPCR targeting 16S rDNA gene, viral MCP (Major Capsid Protein) gene and plasmid gene. We want to explore the cascading effects caused by possible shifts in viral life cycle strategies (lysogenic versus lytic) in response to naturally encountered stressors in deep-sea hydrothermal vents. These effects may involve horizontal gene transfer and result in improved adaptability of hosts to their environment.

Keywords: Deep sea hydrothermal vents, virus-host interactions, bacteria, archaea, continuous culture.

[1] A. Dell’Anno, C. Corinaldesi, R. Danovaro (2015). Virus decomposition provides an important contribution to benthic deep-sea ecosystem functioning. Proc. Natl. Acad. Sci. U.S.A. 112: E2014-9

[2] J. Lossouarn, S. Dupont, A. Gorlas, C. Mercier, N. Bienvenu, E. Marguet, P. Forterre, C. Geslin (2015). An abyssal mobilome: viruses, plasmids and vesicles from deep-sea hydrothermal vents. Res Microbiol. 166: 742-752

[3] S. Thiroux, S. Dupont, C. L. Nesbø, N. Bienvenu, M. Krupovic, S. L'Haridon, D. Marie, P. Forterre, A. Godfroy, C. Geslin (2020). The first head-tailed virus, MFTV1, infecting hyperthermophilic methanogenic deep-sea archaea. Environ Microbiol. 00: 00–00

12:40 - 12:55

Jacob R. WInnikoff, Itay Budin, Steven H. D. Haddock Grease under pressure: Temperature-Independent Depth Adaptation of Ctenophore Lipidomes

In deep-sea organisms, the properties of lipid membranes are adaptively tuned to maintain cellular integrity at ambient temperature and pressure. Classic studies have reported direct correlations between cold habitats, deep habitats, and membrane-fluidizing lipid compounds in fish and microbes, but little has been done to isolate the effects of temperature and pressure on the lipid pool. To address the difference between depth- and cold-adaptation of membranes, we measured the composition of fatty acids in 105 ctenophores and intact lipids in a subsample of 15 animals. Our dataset encompasses 21 species, depths from sea level to 4000 meters, and temperatures from -2° to 28° C. Thanks to the incredible taxonomic and habitat diversity of phylum Ctenophora, we identified fatty acid profiles and phospholipid classes related specifically to depth and to temperature. This finding informs lipid metabolism requirements for invertebrate lineages colonizing the deep sea, and may also be relevant to midwater trophic ecology. We will also report on ongoing experiments to determine the biophysical basis for environmental composition trends.

12:55 - 13:10

Magali Zbinden, Julia Machon, Philippe Lucas, Steffen Harzsch, Jakob Krieger, Thomas Chertemps, Nicolas Montagné, Bruce Shillito, Juliette Ravaux How do hydrothermal shrimps perceive their environment?

Since the discovery of hydrothermal vents, the question of the detection of vent emissions by endemic species and their ability to navigate in this chaotic and locally deleterious environment was put forward (1). In these aphotic environments, hydrothermal shrimps face recognition of active hydrothermal sites at different times of its life. After dispersal in the water column, larvae need to find a vent site to settle. As adults, shrimp have to navigate in the environment, find food, mates, fluids fueling their symbiotic bacteria, or just remain in an appropriate range of physicochemical conditions. Vision (of the very dim light emitted by hydrothermal vents), chemoreception (of specific chemical compounds of the fluids like sulfide), thermoreception (of the thermal gradient between fluid and seawater) or even mecanoreception (detection of acoustic vibrations emitted by vent emission) have been proposed as possible navigational cues for the detection of hydrothermal vents (2-6). To try to understand the sensory modalities by which hydrothermal shrimp perceive their environment, we used several approaches and developed various experimental technics regarding morphology, molecular biology, electroantennography, behavioural studies and brain architecture. Our different approaches were carried out in parallel on several hydrothermal shrimp and related coastal species in order to investigate possible specific adaptations to the hydrothermal environment.

General 2: Biodiversity

11:25 – 11:40

Ella Treloar, Harriet Baldwin, Craig M. Robertson, Furu Meinis, Gerard C.A. Duineveld, Marc Lavaleye, Andrew J. Davies Benthic Community Trends Along a Habitat Complexity Gradient Within the Deep-sea Coral Reefs of The Rockall Bank, NE Atlantic

Cold-water corals are habitat-forming species that are classified as vulnerable marine ecosystems due to sensitivity to anthropogenic impacts and disturbance. Desmophyllum pertusum and Madrepora oculata are habitat-forming coral species in the NE Atlantic, creating structurally complex three-dimensional substrate which are known to promote diverse benthic assemblages, facilitate niche micro-habitats and act as species refugia. To date, very few quantitative studies exist investigating the biodiversity and habitat facilitation in D. persutum reefs and little is known regarding the macrofauna associated with these diverse and fragile ecosystems. This study aimed to assess macrofaunal habitat facilitation across a habitat complexity gradient transversely over one of the largest coral mound structures in the Logachev Mound complex on Rockall Bank, NE Atlantic. The study utilised 8 boxcore samples collected by the crew of the RV Pelagia (2013), from two-cross mound transects from four verified habitat types: coral rubble, low, dead and live coral framework. The following hypotheses were answered: (1) diversity positively corresponded to increased habitat complexity; (2) beta diversity and community structure have significantly great association with habitat heterogeneity. Preliminary results showed that 68% the macrofauna species richness was found in high coral complexity habitats compared to 32% in those habitats with low reef structural complexity. Total abundance was almost one order of magnitude higher in live coral framework, the majority of individuals observed at high coral framework belonged to the Families Syllidae and the Polynoidae. A significant reduction in macrofaunal abundance was observed between live framework and coral rubble. Habitat complexity is an important factor in determining biodiversity in these understudied habitats. This study furthers our understanding of coral-associated sediment communities in the Rockall Bank and provides insight into the role of ecosystem engineers in maintaining deep-sea macrofaunal biodiversity, guiding future conservation and management activities.

11:40 - 11:55

Neus Campanyà-Llovet, Daphne Cuvelier, Amanda E. Bates, Marina Carreiro-Silva, Eva Giacomello, Christopher Pham, Rui Prieto, Ana Colaço Application of a trait-based approach on Marine Protected Areas from the Mid Atlantic Ridge

Quantifying community structure and diversity based on species and biological/ecological traits can combine to provide tools for monitoring conservation outcomes and targets of Marine Protected Areas. We aim to compare not only species but also functional diversity in protected and unprotected areas of the Azores Marine Park in the Mid Atlantic Ridge. There, we find deep-sea seamounts, unique and resourceful ecosystems facing well characterized (i.e., fishing and climate change) and prospective threats (i.e., seabed mining) as human activities continue to expand into the deep ocean. We first compiled a list of species and selected a variety of traits (e.g., fragility, motility, habitat provisioning, size, and trophic level) to characterise the roles of species and functional diversity of communities in seamounts with different categories/levels of protection.

Species and trait data were extracted from public and University repositories such as EMODNET and COLETA, BIOTIC, FishBase, SealifeBase, TraitBank, and WoRMS. Finally, we build a trait database standardized across different groups of taxa (i.e., macro- and megafauna, demersal and pelagic fishes, cetaceans, etc.) representing > 1000 species (whereby the pelagic realm the most sampled, and the benthic realm the most taxonomically diverse). We also found variable functional diversity among seamounts with some of the Southern Chain Seamounts represented by small benthic species, and some of the Azores EEZ seamounts represented by larger pelagic species. This novel information can help identify areas of high sensitivity and vulnerability to a specific disturbance and areas with important functions in the Azores Marine Park (e.g., habitat provisioning), depending on the distribution of traits. Specifically, combining sensitivity and vulnerability will identify functional and species diversity hotspots for prioritizing areas of conservation (e.g., sensitive to disturbance and important role in ecosystem function, or highly resistant that can help re-populate disturbed areas).

11:55 - 12:10

Francisca Correia de Carvalho, Astrid Schuster, Shirley A. Pomponi, Hans Tore Rapp, Manuel A. Malaquias, Joana R. Xavier

Diversity patterns and biogeographic affinities of North Atlantic deep-sea rock sponges

Lithistids, also known as rock sponges, are globally distributed in temperate and sub-tropical areas, constituting an important component of deep-sea benthic communities where they can form structurally complex and vulnerable marine ecosystems (VMEs). This study provides the first basinscale assessment of the diversity and biogeographic patterns of lithistid sponges across the North Western and Eastern Atlantic (NWA and NEA), and Mediterranean Sea (MED). Through an extensive compilation of data from the literature and institutional databases, morphological analysis of new samples, coupled with molecular phylogenetics, we investigated the faunal composition, bathymetric and geographical distributions of lithistid species across these areas. Our results indicate: i) latitudinal and longitudinal gradients with an increase of diversity towards the tropics and from the NEA to the NWA, ii) a general decrease of the diversity with depth, and iii) a clear distinction of taxonomic composition between the three regions (NWA, NEA and MED), with few species shared between them. Of the 108 species reported in these realms, 78 are found in the NWA, indicating that tropical latitudes in the NWA represent a diversity hotspot for lithistid tetractinellids. We further discuss the phylogenetic and biogeographic affinities of this upper bathyal fauna in the context of the biogeographic classification systems currently used, and its implications for the conservation of these species.

12:10 - 12:25

Magalie Castelin, Paco Cardenas, Sarah Samadi

Diversity and structure of Porifera and symbiotic microbial communities living on the seamounts of the New Caledonian EEZ

In the deep sea, geological reliefs surrounded by strong currents, such as seamounts, banks, ridges, and continental slopes are dominated by reef-building filtering organisms whose three-dimensional structure hosts a rich and diversified macrobenthic fauna. These deep-sea gardens are characterized by a high spatial heterogeneity whose determinants are unknown. Many studies established on shallow-water reef-building sponges show that the structure and diversity of symbiotic microbial communities are intimately related to the health and specificity of habitats and can be used as a bioindicator for habitat distinctiveness.

Based on trawl samples from deep-sea cruises carried out by the Tropical Deep-Sea Benthos program, we investigate the diversity of sponges and associated microbial communities across the seamounts and continental slopes of the New Caledonian EEZ. The aim is to characterize the diversity and dissimilarity of microbiomes associated with different sponge species co-occurring in different seamount habitats, and determine whether symbiotic microbial communities can be used as a bioindicator for seamount habitat distinctiveness. More specifically we try to assess whether spongeassociated microbial communities are sponge-species specific, or reflect regional and bathymetric differences.

DNA barcoding approach was performed on 200 demosponges to assess species identity. Overall, our results show a higher species diversity of sponges than expected with the morphological identification of specimens. The microbiomes of 32 sponges distributed on different seamounts and at different depths were analyzed using fragments of the V1-V2, V3, and V4-V5 regions of the bacterial 16S rRNA gene using Illumina technology. These data seem to reflect the geographic and bathymetric structuration of the microbial communities associated with the deep-sea sponges.

12:25 - 12:40

Van Audenhaege Loïc, Matabos Marjolaine, Brind'Amour Anik, Drugmand Jonathan, Laës-Huon Agathe, Sarradin Pierre-Marie, Sarrazin Jozée

7-year monitoring of the spatio-temporal evolution of hydrothermal assemblages at the centimeter-scale of a diffuse-flow habitat

At deep-sea hydrothermal vents, a number of environmental and biotic factors interact to shape benthic communities at different temporal and spatial scales. Due to their remoteness, infra-annual dynamics remains poorly described, while understanding scales and drivers of ecological variability is essential to fully understand ecosystem functioning. This study aims to characterize factors driving the weekly dynamics of a diffuse-flow vent assemblage dominated by Bathymodiolus azoricus. We analyzed a 7-year time-series of images and environmental data collected at 1700 m depth at the base of the active Eiffel tower edifice at the Lucky Strike vent field (Mid-Atlantic Ridge). We surveyed an area of 1.5 m^2 using images acquired weekly by the TEMPO ecological module connected to the EMSO-Azores observatory (EMSO-ERIC, www.emso-fr.org/fr/EMSO-Azores). The dynamics of different species inhabiting the faunal assemblage was assessed in relation to changes in habitat environmental conditions monitored daily.

The habitat displayed a relative stability with small-scale variability related to tidal periodicity and local temperature anomalies. Consequently, the mussel and zoanthid assemblages exhibited a remarkable constancy. Decimeter-scale movements of the mussel assemblage were induced by changes in fluid exposure and substratum instability. Microbial mats were more dynamic, displaying redundant infra-annual changes characterized by aperiodic growth and decline. Their development patterns were not entirely resolved by environmental conditions, as other factors, including biotic interactions, may be at stake. Scales of variations and driving factors were compared to those governing intertidal zones. The outcomes of this study question the general assumption that vent fauna experience frequent and intense disturbances because of highly variable and extreme environmental conditions. On the slow-spreading mid-Atlantic Ridge, mussel assemblages appear to be under relatively stable and mild environmental conditions compared to their coastal counterparts.

12:40 - 12:55

Mari Heggernes Eilertsen, Jon A. Kongsrud, Anne Helene S. Tandberg, Tom Alvestad, Nataliya Budaeva, Tone Ulvatn, Rolf Birger Pedersen, Hans Tore Rapp The fauna of Loki's Castle vent field on the Arctic Mid-Ocean Ridge

The Loki's Castle vent field was discovered in 2008 at 73 °N on the Arctic Mid-Ocean Ridge. The vent field hosts both black smoker chimneys with fluids of up to 320 °C and sedimented areas with diffuse venting at around 20 °C. Several new species have been described from Loki's Castle, and selected taxa from this site have been included in phylogenetic and population genetic studies. However, a complete faunal inventory of the Loki's Castle remains to be completed. This study aims to compile data from seven cruises between 2008-2019 to generate a voucher-linked dataset of species records from Loki's Castle, including DNA-barcodes (COI, 16S) for the majority of the fauna. The dataset will be used to describe the different faunal assemblages within the vent field, and to discuss the habitatspecificity of the fauna and links to other chemosynthesis-based ecosystems in the Arctic, as well as from other oceanic regions.

12:55 - 13:10

Chris Yesson, Stephen Long, Martin Blicher, Nanette Hammeken Arboe, Mona Fuhrmann, Michael Darling, Kirsty Kemp, Rasmus Nygaard, Karl Zinglersen Deep-sea benthic habitats and trawling impacts in the offshore Greenland halibut fishery, Davis Strait, west Greenland

The offshore Greenland halibut (Reinhardtius hippoglossoides) fishery in the Davis Strait, west Greenland, employs demersal trawl gear at depths of 800-1,400 m. In contrast to many other examples of deep-sea fisheries, the target stock remains stable despite a long history of exploitation and the fishery is of significant economic importance. Recent Marine Stewardship Council certification of this fishery has highlighted the paucity of knowledge of benthic habitats and the impacts of trawling. This study employs a towed benthic sled to address these knowledge gaps. The spatially discrete northern and southern areas of the fishery are found to be markedly different in terms of the communities present, with the northern area exhibiting a lower abundance and diversity of epi-fauna. Non-metric multidimensional scaling suggests the temperature is the primary driver of the differentiation between the communities in the colder northern water and warmer southern ones. Extensive physical evidence of trawling was observed in imagery from within the fishery footprint. Trawling effort is significantly linked with community composition and we see a negative association of trawling effort and abundance of some taxa, including vulnerable marine ecosystem (VME) indicator species. Three potential VMEs are identified: i) Flabellum alabastrum cup coral meadows; ii) a Halipteris finmarchica sea pen field; and iii) areas exhibiting mixed assemblages of VME indicators at notable collective densities. Of immediate conservation concern is a H. finmarchica field, which seems to be at least regionally rare, is situated within the fringes of existing trawling effort and is currently afforded no protection by management measures.

14:15 – 14:50

Keynote Stéphane Hourdez Metazoan adaptation to deep-sea hydrothermal vents

The vast volume and expanse that the deep-sea in general represents a challenging environment to colonize. Pressure is the most basic of these challenges but the cold temperature, absence of light, food scarcity, and sometimes limited oxygen supply have been the focus of many studies over the years. Since the discovery of deep-sea hydrothermal vents in the late 1970's our perception of the deep-sea has changed. In these habitats, food scarcity is no longer an issue because of the local primary production by microbes that use reduced chemicals contained in the vent fluid (chemosynthesis). For metazoans, taking advantage of this food source, however, requires specific adaptation to deal with the harsh conditions that are encountered near hydrothermal vents. In particular, the chaotic mixing of the hydrothermal fluid with the cold deep-sea water creates highly variable -and unpredictable- conditions. For these animals, temperature and low oxygen concentrations are probably the first constraints to deal with. The hydrothermal fluid also contains compounds that are toxic (heavy metals, H_2S, …), and its pH is very low compared to seawater. All these challenges require specific adaptations that are found in vent species. This explains at least in part the fact that 95% of the species are endemic of this type of environment.

General 4: Adaptation

14:50 - 15:05

April Stabbins, Erik Cordes, Shana Goffredi, Victoria Orphan, John Maygar and Ryan Gasbarro Importance of chemosynthetic productivity to a recently discovered methane seep coral from the Pacific Costa Rican margin

Finding food in a nutritionally limited environment is a challenge faced by all deep-sea organisms. Consequently, they often evolve novel feeding strategies such as forming symbiotic relationships. In shallow waters cnidarians are known for their symbiotic associations with photosynthetic zooxanthellae, yet very few studies have shown evidence of similar relationships between deep-sea corals and chemosynthetic microbes. Along the Pacific coast of Costa Rica, a variety of deep-sea corals inhabit methane seep landscapes, opportunistically attaching to authigenic carbonates once seepage has subsided. One species in particular has been observed thriving in active methane seep habitats, where nutrition is supported primarily through chemosynthetic means and local conditions are toxic to many species not adapted to reducing environments. Therefore, the aim of this study is to understand the ecophysiology of this species, and if it has adapted a mixotrophic feeding strategy, obtaining part of its nutrition from chemosynthetic means. Here we report the distribution of a recently described seep coral, Swiftia sahlingi, across a well-known Costa Rican seep site, Mound 12. Initial results from underwater photo transect surveys carried out by AUV Sentry show evidence this species is capable of thriving in very close proximity to active seeps, often adjacent to endemic symbiont baring species, as well as in transition zones. Observations of physical samples collected from active areas also visibly demonstrate filamentous bacteria associated with healthy coral tissue. Additional results from stable isotope analysis further suggest part of this corals diet is being obtained from seep-derived carbon, with δ 13C values as low as -28.6‰, lower than surface POC. By using a variety of microanalytical techniques alongside incubation experiments, microbial profiling and video analysis, this study will increase our understanding of how corals can interact and overlap with deep-sea chemosynthetic communities and elucidate the role they play in local biogeochemical cycles.

15:05 - 15:20

Mackenzie Gerringer, Abbey Dias, Abby von Hagel, James Orr, Adam Summers, Stacy Farina Habitat influences skeletal morphology and density in the snailfishes (family Liparidae)

We tested the hypothesis that deep-sea fishes have poorly mineralized bone relative to shallowerdwelling species using data from a single family that spans a large depth range. The family Liparidae (snailfishes, Cottiformes) has representatives across the entire habitable depth range for bony fishes (0 m–> 8000 m), making them an ideal model for studying depth-related trends in a confined phylogeny. We used micro-computed tomography (micro-CT) scanning to test three aspects of skeletal reduction in snailfishes (50 species) across a full range of habitat depths: 1) reduction of structural dimensions, 2) loss of skeletal elements, and 3) reduction in bone density. Using depth data from the literature, we found that with increasing depth, the length of the dentary, neurocranium, and suborbital bones decreases. The ventral suction disk decreases width with increasing maximum habitat depth and is lost entirely in some deeper-living taxa, though not all. Although visual declines in bone density in deeper-living taxa were evident across full skeletons, individual densities of the lower jaw, vertebra, suction disk, hypural plate, and otoliths did not significantly decline with any depth metric. However, pelagic and polar taxa tended to show lower density bones compared to other species in the family. We propose that skeletal reductions allow snailfishes to maintain neutral buoyancy at great depths in the water column, while supporting efficient feeding and locomotion strategies. These findings suggest that changes in skeletal structure are non-linear and are driven not only by hydrostatic pressure, but by other environmental factors and by evolutionary ancestry, calling the existing paradigm into question.

15:20 - 15:35

Timothy M. Shank, Michelle L. Neitzey, Kate R. Castellano, Rachel J. O'Neill Deep-Ocean Genomes Project: accelerating discovery of deep-sea adaptations and biodiversity

The deep sea hosts a broad spectrum of habitats including hydrothermal vents, methane seeps, oxygen minimum zones, seamounts, canyons and trenches with evidence suggesting deep-ocean life is richly diverse and highly adapted. In partnership, Woods Hole Oceanographic Institution and the University of Connecticut have established the Deep-Ocean Genomes Project (DOG) as an Affiliate program for the global Earth Biogenome Project. DOG aims to implement genomics technologies and address diverse ecological and evolutionary hypotheses within and across a myriad of species found in deep-sea habitats. Founded on a cryo-repository of >500 species from >17 phyla, spanning >30 habitat types below 200 meters depth, DOG was established to use genome sequencing and comparative genomics approaches to study species adaptations to extreme environments, including immense pressures (>15,000 psi), near-freezing to near-boiling temperatures, absence of sunlight, toxic chemical conditions, and diverse energy sources. To date, 20 species of 100 projected for phase 1 are currently in our EBP standard genome sequencing pipeline including annelids from vents, fish from hadal regions and cnidarians from canyons and seamounts. As examples of phase 1 progress, we have developed a reference-level tunicate genome and the first deep-sea coral genome from the family Primnoidae using short and long-read sequencing technologies. Progress includes genome sequencing and comparative studies among pairs of similar species inhabiting two chemically and spatially distinct habitats, such as the siboglinid worms Riftia pachyptila and Tevnia jerichonana from low-temperature diffuse flow habitats (2°C to 25°C) and the annelids Alvinella pompejana and Alvinella caudata inhabiting elevated temperature habitats (2°C to 60°C) on the sides of active polymetallic sulfide chimneys. Challenges and progress in high molecular weight nucleic acid extraction methods of cryopreserved samples, sequencing workflows, and the assembly, annotation, transcriptomic, epigenomic and comparative genomic analysis (exploration of gene, regulatory, and noncoding content) pipelines will be presented.

General 2: Biodiversity

14:50 - 15:05

Paulo Vinicius Ferraz Corrêa, Paulo Yukio Gomes Sumida Megafaunal community structure on ferromanganese crusts and adjacent areas on Rio Grande Rise

The Rio Grande Rise (RGR) is a large and geomorphologically complex feature located in the Southwest Atlantic and it has become a region of great commercial and scientific interest due to its potential for mining rare earth elements. Mining activities are potentially harmful to deep-sea ecosystems and will likely cause some extent of biodiversity loss. Thus, understanding the biodiversity and ecological patterns of RGR will lead to better management of mining areas and help the conservation of deepsea fauna from its potential impacts. A scientific expedition conducted by the RSS Discovery in 2018 lead to 13 successful dives with the ROV HyBIS on a small area in RGR (30°35'S – 31°03'S, 35°36'W – 36°16'W, 600 – 1500 m depth). It was equipped with a Full HD camera and produced 36 hours of video transects of the seafloor, which were analyzed for the description of structuring factors and to record benthic megafauna occurrences. Videos exhibited highly heterogeneous habitats, composed of different types of substrates such as Fe-Mn crusts, volcanic rocks, steep slopes, flat calcarenite pavements, and sediments. They also revealed a patchy distribution of specimens, with areas dominated by different species, namely sponges, brisingids, fishes, sea urchins, and black corals. In contrast, many sites were practically composed of deserts, with nearly no megafauna. Over 17 thousand megabenthic organisms were recorded and classified in 83 OTUs and 6 different phyla, from which Porifera (42.7%) and Cnidaria (41.5%) were the most representative. The habitats with Fe-Mn deposits were characterized by distinct communities, dominated by the hexactinellids Sarostegia oculata and Aphrocallistes cf. beatrix, which were rarely observed in other habitats. Additionally, there were variations in community structure at regional scales (20 – 30 km), with distinct communities on each side of a large, deep rift, and at the southwest of the study area.

This work was funded by NERC/UK and FAPESP grants 2014/50820-7 and 2017/11884-8

15:05 - 15:20

Marcelo R. S. Melo, Rayane S. França, Flávia T. Masumoto, Amanda A. Gomes, Heloisa Caixeta, Claudio Oliveira DEEP-OCEAN project: revealing the diversity of deep-sea fishes in the Brazilian EEZ, western South Atlantic

For a long time, the diversity of deep-sea fishes in the western South Atlantic (WSA) had been neglected. The first discoveries were based on the specimens collected during the passage of the Challenger Expedition in the 1800's, nevertheless, after the 1980's a few oceanographic expeditions conducted onboard USA, French or Japanese vessels permitted a more comprehensive understanding about the diversity and composition of the WSA deep-sea ichthyofauna, resulting on discoveries of several new species and records of unexpected occurrences. In Brazil, this scenario rapidly changing in the past decade, with a greater number of cruises and more Brazilian ichthyologists becoming interested on the taxonomy of deep-sea species. Hitherto, a total of 712 species of deep-sea fishes have been recorded in Brazilian waters, including five species of Myxini, six species of Holocephali, 81 species of Elasmobranchii, and 620 species of Actinopteri. The objectives of the project "Diversidade E Evolução de Peixes de Oceano Profundo - DEEP-OCEAN" are to increase the taxonomic sampling in the Brazilian EEZ, and to foment taxonomic studies using modern technologies. The three predicted cruises are being conducted onboard the Brazilian R/V Alpha Crucis off Southeastern Brazil, using a semi-balloon otter trawl with 23 meters in the lower hope and mesh size of 100 mm in the wings and main body and 25 mm in the cod-end. The first expediction focused the continental slope in depths from 400 to 1,500 m, and resulted on the capture of 12 species of chondrichthyans and 78 species of actinopterygians. The taxonomic analysis includes the use of traditional morphology, osteological micro-CT 3D reconstruction, and COI-based DNA barcoding. Preliminary results revealed the discovery of eight new species, including two chimerids, four anguilliforms, a grenadier, and a blind clusk eel. Funding: FAPESP (2017/12909-4), CNPq (433050/2016-0).

15:20 - 15:35

Virginia Biede, Brendan Roark, Amy Baco Cold-water coral assemblages on Koko Guyot in the Emperor Seamount Chain

Koko Guyot lies at the bend of the Northwestern Hawaiian Ridge and Emperor Seamount Chain (ESC) in the North Pacific and is the largest seamount in the ESC. Koko is a heavily impacted seamount after several decades of fishing effort, but investigations into these disturbed communities can be important for understanding the effects of trawling disturbance and the potential for resilience. Despite the heavy fishing efforts, recent studies using AUV imagery on this seamount have documented vulnerable marine ecosystems and areas that appear to be recovering, as well as areas of significant adverse impacts. The angle of the AUV camera and height above the bottom prevents the resolution of taxa below the class or family level in most cases. Therefore, to obtain a more detailed understanding of the distribution of megafauna on this seamount at a higher taxonomic resolution, replicate 500m transects were conducted with the Pisces IV and V submersibles. At depths of 500m and 600m, diverse coral gardens, patches of cold-water coral reef, and sponges were observed. Dominant fauna at 500m included small yellow acanthogorgiid octocorals and at 600m included small white branching scleractinians. Total abundance and overall community structure were significantly different between the two depths, however diversity indices were similar at both depths. Debris from trawling was observed on most transects including fishing lines, nets, rockhopper gear pieces, and plastic. Continued investigations incorporating bathymetry, substrate, and other environmental factors will help to elucidate the influence of bottom contact gear versus environmental variability within the study areas.

Special 6a: Biomimicry

15:35 - 15:50

Julia Sigwart, Robert Blasiak, Marcel Jaspars, Jean-Baptiste Jouffray, Deniz Tasdemir

Unlocking the potential of marine biodiscovery

The tremendous diversity of life in the ocean has proven to be a rich source of inspiration for drug discovery, with success rates for marine natural products up to 4 times higher than other naturally derived compounds. Yet the marine biodiscovery pipeline is characterized by chronic underfunding, bottlenecks and, ultimately, untapped potential. For instance, a lack of taxonomic capacity means that, on average, 20 years pass between the discovery of new organisms and the formal publication of scientific names, a prerequisite to proceed with detecting and isolating promising bioactive metabolites. The need for "edge" research that can spur novel lines of discovery and lengthy highrisk drug discovery processes, are poorly matched with research grant cycles. Here we propose five concrete pathways to broaden the biodiscovery pipeline and open the social and economic potential of the ocean genome for global benefit: (1) investing in fundamental research, even when the links to industry are not immediately apparent; (2) cultivating equitable collaborations between academia and industry that share both risks and benefits for these foundational research stages; (3) providing new opportunities for early-career researchers and under-represented groups to engage in high-risk research without risking their careers; (4) sharing data with global networks; and (5) protecting genetic diversity at its source through strong conservation efforts. The treasures of the ocean have provided fundamental breakthroughs in human health and still remain under-utilised for human benefit, yet that potential may be lost if we allow the biodiscovery pipeline to become blocked in a search for quick-fix solutions.

15:50 - 16:05

Sylvia Colliec-Jouault, Agata Zykwinska, Corinne Sinquin, Laetitia Marchand, Sandrine Bonnetot, Véronique Verrez-Bagnis, Christine Delbarre-Ladrat

Deep-sea hydrothermal vent bacteria: a unique source of glycosaminoglycan-mimetic exopolysaccharides for biomedical applications

Bacteria have developed a unique strategy to survive in extreme adverse conditions through a synthesis of an extracellular polymeric matrix conferring to the cells a protecting microenvironment. The important structural component of this complex network constitutes high-molecular weight hydrophilic macromolecules, namely exopolysaccharides (EPS). EPS composition with the presence of particular chemical features may closely be related to the specific conditions in which bacteria evolve. Deep-sea hydrothermal vent bacteria from Ifremer collection are able to produce EPS rich in hexosamines and uronic acids, sometimes slightly substituted by sulfate groups [1,2]. Such a particular composition ensures interesting functional properties, including biological activities mimicking those known for glycosaminoglycans (GAG), such as hyaluronic acid and heparin. In particular, two deep-sea hydrothermal vent bacteria have been shown to exhibit GAG-mimetic properties that can be explored for several biomedical applications, e.g. tissue engineering and cancer therapy. Native EPS produced by Alteromonas infernus and its derivatives have shown their beneficial properties in cartilage regeneration [3,4]. Their antimetastatic activities have been also reported [5]. Native EPS secreted by Vibrio diabolicus, presenting structural similarities to hyaluronic acid, displayed suitable biological activities on bone [6] and skin [7] repair. Both EPS are currently being explored for their gelling properties to elaborate functional matrices, such as hydrogels structured at micro and macro scales, for tissue engineering applications [8]. It comes out from these different studies that deep-sea hydrothermal vent bacteria from Ifremer collection constitute a unique source of high-added value compounds with a huge potential in health issues.

References: [1] Delbarre-Ladrat, C.; Sinquin, C.; Lebellenger, L.; Zykwinska, A.; Colliec-Jouault, S. Exopolysaccharides produced by marine bacteria and their applications as glycosaminoglycan-like molecules. Front. Chem. 2014, 2, 85. [2] Zykwinska, A.; Marchand, L.; Bonnetot, S.; Sinquin, C.; Colliec-Jouault, S.; Delbarre-Ladrat, C. Deep-sea hydrothermal vent bacteria as a source of glycosaminoglycan-mimetic exopolysaccharides. Molecules. 2019, 24, 1703. [3] Merceron, C.; Portron, S.; Vignes-Colombeix, C.; Rederstorff, E.; Masson, M.; Lesoeur, J.; Sourice, S.; Sinquin, C.; ColliecJouault, S.; Weiss, P.; et al. Pharmacological modulation of human mesenchymal stem cellchondrogenesisbyachemicallyover-sulphatedpolysaccharideofmarineorigin: Potential application to cartilage regenerative medicine. Stem Cells 2012, 30, 471–480. [4] Rederstorff, E.; Rethore, G.; Weiss, P.; Sourice, S.; Beck-Cormier, S.; Mathieu, E.; Maillasson, M.; Jacques, Y.; ColliecJouault, S.; Fellah, B.H.; et al. Enriching a cellulose hydrogel with a biologically active marine exopolysaccharide for cellbased cartilage engineering. J. Tissue Eng. Regen. Med. 2017, 11, 1152–1164. [5] Heymann, D.; Ruiz-Velasco, C.; Chesneau, J.; Ratiskol, J.; Sinquin, C.; Colliec-Jouault, S. Anti-metastatic properties of a marine bacterial exopolysaccharide-based derivative designed to mimic glycosaminoglycans. Molecules 2016, 21, 309. [6] Zanchetta, P.; Lagarde, N.; Guezennec, J. A new bone-healing material: A hyaluronic acid-like bacterial exopolysaccharide. Calcif. Tissue Int. 2003, 72, 74–79. [7] Senni, K.; Gueniche, F.; Changotade, S.; Septier, D.; Sinquin, C.; Ratiskol, J.; Lutomski, D.; Godeau, G.; Guezennec, J.; Colliec-Jouault, S. Unusual glycosaminoglycans from a deep-sea hydrothermal bacterium improve fibrillar collagen structuring and fibroblast activities in engineered connective tissues. Mar. Drugs 2013, 11, 1351–1369. [8] Zykwinska, A.; Marquis, M.; Godin, M.; Marchand, L.; Sinquin, C.; Garnier, C.; Jonchère, C.; Chédeville, C.; Le Visage, C.; Guicheux, J.; et al. Microcarriers based on glycosaminoglycan-like marine exopolysaccharide for TGF-β1 long-term protection. Mar. Drugs 2019, 17, 65.

16:05 - 16:20

Ryan M. Young, Sam Afoulouss, Nicole E. Avalon, Joshua Welsch, Howard O. Fearnhead, Mark P. Johnson, Bill J. Baker, A. Louise Allcock

Diving Deep for Drug Discovery

Only 2% of the described marine metabolites are from the deep sea, despite most marine habitat being deep. Improvements in technology are starting to make the deep-sea habitats more accessible. Currently, there are six drugs of marine shallow water origin on the market for treatments ranging from severe pain to metastatic breast cancer. The biodiscovery potential from deeper habitats remains relatively unexplored. We highlight our efforts to collect, screen and ultimately isolate and describe bioactive deep-sea metabolites from the Irish deep-sea canyons. We have screened the chemical extracts of collected corals and sponge species in a range of biological assays ranging from anticancer to anti-microbial. Biological diversity of the deep-sea collections is reflected in chemical diversity. Specific examples are antimicrobial bisindole alkaloids from a demosponge; a potential neuroinflammatory inhibitor from the nephtheid soft coral Drifa sp.; an apoptosome inhibitor from zoanthids growing on the hexactinellid sponge Aphrocallistes beatrix, antiplasmodial sesquiterpenes from the scleraxonian coral Paragorgia arborea and cytotoxic oxidated steroids from a bamboo coral Keratoisinae sp. By linking chemical novelty to the economic potential of these biodiverse hotspots, we can illustrate their conservation and ecosystems services value.

16:20 - 16:35

Deniz Tasdemir, Fengjie Li, Dorte Janussen

Discovery of Novel Anticancer Metabolites from the Deep-sea Latrunculia Sponges from Antarctica

Marine natural product (MNP) discovery has provided 14 MNP-derived drugs that entered into the clinics, particularly against cancer. Shallow water sponges represent the best studied marine organisms, contributing 30% of all MNPs. Antarctica, one of the most hostile environments on earth, is also one of the oldest, stable and well-structured marine systems with a rich benthic community. Sponges often represent a diverse and dominant invertebrate communities of Antarctic ecosystems.

Marine sponge genus Latrunculia is predominantly distributed in cold-water regions of the southern hemisphere. Latrunculia species are a major reservoir of pyrroloiminoquinone-type alkaloids that show prominent anticancer activity and serve as chemotaxonomic markers for the family Latrunculiidae.

In the continuation of our search for anticancer metabolites, we studied the metabolome and anticancer activity of several Antarctic deep-sea Latrunculia biformis specimens. UPLC-MS/MS-based molecular networking (MN) type metabolomics strategy applied on the crude organic extract of the first L. biformis specimen (from -303 m depth) showed, for the first time, the presence of tsitsikammamine type bispyrroloiminoquinone alkaloids in this sponge genus. The combination of MN and anticancer activity-guided isolation scheme led to the targeted isolation of tsitsikammamine A (1) and its new 16,17-dehydro analogue (2). The same strategy allowed isolation of a number of oligomeric discorhabdins from another L. biformis specimen (collected from -291 m), including the first trimeric (3) and dimeric (4) discorhabdin alkaloids bearing a novel C–N bridge (C-1/N-13’) between discorhabdin monomers. The purified compounds exhibited significant anticancer activity against human colon cancer cells and/or showed affinity to established cancer targets, e.g., topoisomerase I-II and indoleamine 2,3-dioxygenase enzymes by molecular modeling and docking studies. This presentation will deal with our efforts to find medically relevant secondary metabolites from Antarctic deep-sea demosponges.

16:35 - 16:50

Janna Nawroth, Joost Daniels, Kakani Katija, Alex Hoover

Developing workflows for bioinspired design studies on rare, deep-sea animals

The field of bioinspired design often involves studying animal features in constrained laboratory environments. These observed behaviors are often suspect, and study systems are limited to those that can be maintained in a laboratory. However, if we were able to conduct observations in situ and apply quantitative techniques to inform relevant topics like ecomechanics, novel biological systems could be interrogated for bioinspired design. One particular question that has vexed the biomechanics community is why the structure of flexible propulsors are conserved throughout Animalia. In marine mammals, birds, bats, fish, etc., their propulsors (e.g., wings and fins) have the same ratio of rigid to flexible surfaces. This observation is consistent even in animals that use their propulsors to swim and feed, as is the case of midwater giant larvaceans (or appendicularians; genus: Bathochordaeus) pumping their tails in mucus filtration houses. Given their simplified morphology and their status as basal chordates, can studying larvacean ecomechanics shed light on this long-standing question? Here we demonstrate how remotely operated vehicles equipped with high-resolution cameras and laser illumination (DeepPIV) were used to quantify the pumping kinematics of giant larvaceans in their mucus houses. Animals were subsequently collected and histologically analyzed to characterize their musculature and material properties. These measurements then inform a computational model of a larvacean tail, whose motion emerges from the interaction between hydrodynamic forces and ratio of rigid to flexible components. We find that the greatest fluid pumping performance corresponds to the observed kinematics in giant larvaceans, thereby suggesting that the highly conserved flexible propulsor structure across animals is tuned to produce efficient fluid transport for swimming and feeding. We conclude that our novel workflow can provide new insight into the role of flexibility in biological propulsors and other ecomechanics topics, with broad implications for the design of human-engineered systems.

General 2: Biodiversity

15:35 - 15:50

Emily Cowell, Erik Cordes

Assessing biogenic habitat successional thresholds across the methane seep landscape of the Costa Rican Pacific Margin

Methane seepage enables the formation of diverse chemosynthetic communities on the deep-sea floor. They support microbial assemblages, which act as food sources or symbiotic partners for dense aggregations of biogenic habitats, and are a source of deep-sea primary productivity. This high organismal biomass, coupled with authigenic carbonate precipitation, sequesters the majority of methane released from seep sites, preventing what would otherwise be a dramatic increase in greenhouse gas emissions. It is vital to identify the successional patterns present at the seep sites, and determine the biotic and abiotic thresholds that drive these changes to ensure that disturbance regimes do not disrupt seep succession and megafaunal community formation. We aim to identify the thresholds that influence biological succession and associated megafaunal community composition across the Mound 12 and Jaco Scar survey sites off the Costa Rican Pacific Margin using a regression tree approach coupled with underwater phototransect surveys. Initial results indicate clear successional stages occurring within the seep, with age and intensity of seepage along with carbonate rock formations determining the presence and coverage of biogenic habitats. These biogenic organisms in turn appear to support distinct associated megafaunal communities, altering the community composition of these important diversity hotspots. Using a regression tree approach to calculate the abiotic thresholds which drive these successional shifts will increase our understanding of the clear spatial and temporal zonation patterns present at seep sites, as well as the "tipping points" of different seep-associated organisms. This will enable future identification of those organisms that are highly threatened by environmental change, as well as potential bioindicator species. Without understanding these thresholds, we risk disrupting established successional patterns at seep sites through climatic or human disturbance, reducing community formation and biomass accumulation, and therefore the diverse and essential ecosystem services provided by methane seep communities.

15:50 - 16:05

Danielle M. DeLeo, Cheryl Morrison, Makiri Sei, Veronica Salamone, Amanda Demopoulos, Andrea M. Quattrini Genetic diversity and connectivity of chemosynthetic seep mussels (Bathymodiolus spp.) from the U.S. Mid-Atlantic margin

Deep-sea mussels in the genus Bathymodiolus have unique adaptations to colonize hydrothermal vent and cold seep environments throughout the world's oceans. These invertebrates function as important ecosystem engineers, creating heterogenous habitat and promoting biodiversity in the deep sea. Despite their ecological significance, efforts to assess the diversity and connectivity of this group are extremely limited. Here, we present the first genomic-scale diversity assessments of the recently discovered bathymodiolin cold seep communities along the U.S. Mid-Atlantic margin, dominated by Bathymodiolus childressi as well as known communities of B. heckerae. Bathymodiolus childressi mussels were collected at various depths from three seep sites- Norfolk Canyon Seep, Baltimore Canyon Seep and Chincoteague Seep. The vast majority of B. heckerae samples were collected from a deeper site at Blake Ridge. DNA was extracted and sequenced using a Restrictionsite Associated DNA (RAD) sequencing approach from a total of 177 bathymodiolins with confirmed species identities as either B. childressi (n=81) or B. heckerae (n=96). RADseq data was assembled discretely for each species with iPYRAD using a reference genome and analyzed to examine genetic diversity and population structure within and between seep sites. Assessments of genetic differentiation using SNP data revealed high gene flow and minimal diversification among individuals, as well as high inbreeding for both species. No evidence was found for diversification with depth in B. childressi likely due to their life histories, including high dispersal capabilities. Kinship analyses indicated a high degree of relatedness among individuals indicative of local recruitment, though our data suggest shallower communities serve as source populations for deeper seep sites. We also discovered loci under selection in B. childressi (400 - 2200m) and B. heckerae (2200 - 3300m) that elucidate depth-related adaptations, potentially lending to the diversification of Bathymodiolus mussels despite the high gene flow and widespread dispersal capabilities of this group.

16:05 - 16:20

Rachel Eckley, Tracey Sutton Population dynamics, vertical distribution, and trophic ecology of whalefishes (Cetomimidae) in the bathypelagic Gulf of Mexico

The whalefishes (Stephanoberycoidei: Cetomimidae) are a systematically challenging group of primarily bathypelagic fishes. Physical limitations accompanied with sampling the deep-sea have resulted in lower incidence of collection of cetomimids compared to other midwater fishes, and thus poorly understood taxonomy and biology. Per the Ocean Biogeographic Information System, 764 global records exist of which 52 have occurred from the Gulf of Mexico.

In the present study, cetomimids were collected from the Gulf of Mexico using high-speed rope trawls from surface to 1600 m and a multiple-opening-and-closing net system that sampled five depth strata from surface to 1500 m. The population dynamics were assessed through morphometric analysis. Vertical distribution patterns, including diel variation, specific to species and life-history stages were described by analyzing the standardized abundance per collection depth strata. The trophic ecology of larval cetomimids was described via gut-content analysis.

In total, 493 cetomimids were collected representing five genera and 16 species. Six new records occurred for the Gulf of Mexico (Cetomimus compunctus, C. picklei, Danacetichthys galathenus, Gyrinomimus bruuni, G. grahami, and "Ataxolepis") and one new record occurred for the Atlantic Ocean (C. compunctus). Two globally distributed species (Cetostoma regani and Ditropichthys storeri) comprised over 54% of the assemblage. The life-history stage data suggest highly skewed sex ratios favoring larger females. The vertical distribution data suggest that cetomimids have wide vertical ranges but are most commonly collected from the bathypelagic zone (depth greater than 1000 m). Vertical migration likely occurs in C. regani and D. storeri. Larval cetomimids ("Eutaeniophorus") gorge on copepods over short periods of time and may target large swarms. Feeding likely occurred in the epipelagic zone as many shallow-water copepod species were identified as prey. Larval vertical distribution patterns and trophic analyses indicate that ontogenetic descent may be rapid.

16:20 - 16:35

Thomas F. Hourigan, Christopher D. Kelley, Robert McGuinn, Meagan Putts, Sarah Bingo, Derek Sowers, Arvind Shantharam Varied and Valuable: Characterizing High-Density Deep-

Sea Coral and Sponge Communities of the Hawaiian Region

The deepwater habitats around the Hawaiian Archipelago and nearby waters are among the best studied, and within U.S. waters, the best protected, in the insular North Pacific. Until recently, however, most of our knowledge of benthic communities in the region was limited to depths shallower than 1500 m. Expeditions conducted from 2015 to 2018 aboard the National Oceanic and Atmospheric Administration (NOAA) Ship Okeanos Explorer and Ocean Exploration Trust Vessel E/V Nautilus have extended the geographic and depth range of surveys and revealed rich new high-density coral and sponge communities. Based on their functional role as habitat and their fragility, these communities represent hot spots of biodiversity in the deep sea. Discovering and characterizing these communities on seamounts and island slopes has been a major focus of these deep-sea expeditions by NOAA and its partners.

We analyzed coral and sponge observations from 85 remotely-operated vehicle (ROV) dives ranging from 300-4800 m depths on island slopes, ridges, and seamounts surrounding the Hawaiian Archipelago, Johnson Atoll, and Musicians Seamount Range. These surveys revealed 30 high-density (>3,000 corals and sponges/km) and seven very high-density (>10,000/km) communities at depths from 300 m to 2700 m. While there is clear differentiation among assemblages at different depths or temperatures, there was a significant amount of additional variation. This paper explores the coral and sponge taxon composition of these communities in relation to underlying geomorphology and oceanography. We will further discuss the implications of our findings for their conservation, particularly as it may relate to planning for potential deep-sea mining of cobalt-rich ferromanganese crusts on seamounts of the north central Pacific.

16:35 - 16:50

Olívia S. Pereira, Sean W. Mullin, Connor Coscino, Victoria K. Orphan, Erik E. Cordes, Lisa A. Levin Connections between microbial and macrofaunal response to methane seepage

Macrofauna depend on microbes at methane seeps for food, substrate, settlement cues or inhibition, detoxification, and more. Because seepage at methane seeps is dynamic, microbial response to changes in seepage activity and other disturbances could drive the macrofaunal response. Here, we examined synchronously microbial community composition based on 16S rRNA gene and invertebrate macrofauna community composition at methane seeps on in situ and transplanted carbonate rocks across a seepage gradient for 17 months. By analyzing whether there is a correlation between microbial and macrofaunal communities response to changes in seepage activity, we observed that (1) active sites are dominated by ANME-2a/b and microbial grazers such as neolepetopsid limpets and provannid snails; (2) at sites with lesser seepage activity, ANME-1b, ANME-2c, and Lokiarchaeia are more abundant, and the macrofaunal community is composed of background species including chrysopetalid polychaetes, peracarid crustaceans, and hydroids; (3) the microbial community exhibits characteristics of both the start and the end communities in the transplant experiment, while the macrofaunal community seems to change/adapt more quickly to the new seepage activity at the end site; (4) When microbes associated with anaerobic oxidation of methane (i.e., ANMEs and SRBs) persist under a decline in seepage activity, the seep macrofauna also persists and retains low δ13C signatures indicative of methane-derived carbon. This study suggests that there is facilitation by microbes enabling macrofaunal resilience to disturbances.

Special 1d: Stewardship

17:10 - 17:25

Kerry Howell, Ana Hilario Challenger 150 - an inclusive, global deep Ocean Decade program

Macrofauna depend on microbes at methane seeps for food, substrate, settlement cues or inhibition, detoxification, and more. Because seepage at methane seeps is dynamic, microbial response to changes in seepage activity and other disturbances could drive the macrofaunal response. Here, we examined synchronously microbial community composition based on 16S rRNA gene and invertebrate macrofauna community composition at methane seeps on in situ and transplanted carbonate rocks across a seepage gradient for 17 months. By analyzing whether there is a correlation between microbial and macrofaunal communities response to changes in seepage activity, we observed that (1) active sites are dominated by ANME-2a/b and microbial grazers such as neolepetopsid limpets and provannid snails; (2) at sites with lesser seepage activity, ANME-1b, ANME-2c, and Lokiarchaeia are more abundant, and the macrofaunal community is composed of background species including chrysopetalid polychaetes, peracarid crustaceans, and hydroids; (3) the microbial community exhibits characteristics of both the start and the end communities in the transplant experiment, while the macrofaunal community seems to change/adapt more quickly to the new seepage activity at the end site; (4) When microbes associated with anaerobic oxidation of methane (i.e., ANMEs and SRBs) persist under a decline in seepage activity, the seep macrofauna also persists and retains low δ13C signatures indicative of methane-derived carbon. This study suggests that there is facilitation by microbes enabling macrofaunal resilience to disturbances.

17:25 - 17:40

Carlos Dominguez-Carrió, Jorge Fontes, Telmo Morato The Azor drift-cam: an affordable and easy-to-use underwater video system for a rapid appraisal of deep-sea benthic habitats

Deep-sea exploration using visual methods has significantly increased during last decades due to advances in marine technology. Underwater imaging tools, especially ROVs, are currently the most common approach to study deep-sea benthic communities. Nonetheless, the use of cutting-edge technology implies complex equipment, large oceanographic vessels and specialized crews, only accessible to few research institutions due to its elevated costs. Current commitments to protect marine biodiversity would therefore benefit from tools that can generate scientific data at a reasonable cost, making deep-sea exploration easier, simpler, cheaper and accessible to many.

The Azores region is mostly deep-sea, with most of its seafloor below 200 m depth. The Mid-Atlantic Ridge provides a complex geomorphological setting, and more than 100 underwater features (seamounts/ridges) inside the Azores EEZ have their summits below 1000 m depth. The need to characterize and map the distribution of benthic species and communities across such an extensive area led us to the development of the Azor drift-cam, a cost-effective tool to visually document deep-sea benthic communities and habitats to 1000 m depth. This simple yet robust imaging system is made of off-the-shelf products, taking advantage of small action cameras, pressureresistant lights and a simple live-view system to obtain high-quality images of the seabed. It can be deployed from small vessels and moves over the seafloor following the vessel's drift, with its position controlled using a hydraulic winch based on the images provided by the live-view feed. In the past two years, we have performed 250+ video transects with the Azor drift-cam in 15 seamount/ridges of the Mid-Atlantic Ridge and many seamounts/slopes around islands of the central group . We believe that by sharing this technological development we can contribute to facilitate deep-sea research to countries/institutions currently excluded due to monetary and technological constraints.

17:40 - 17:55

Joana R. Xavier, Ana Sofia Soares, Inês Gregório, Celso Domingos, Daniel Despujols, Sandra Ramos, Isabel Sousa-Pinto, José Teixeira, Eunice Sousa, Corina Chaves, Teresa Moura, Jorge Lobo, Cristina Pita, Ana Hilário, Telmo Morato, Marina Carreiro-Silva

DEEPbaseline – co-developing a knowledge baseline on the diversity and distribution of deep-sea vulnerable marine ecosystems of the Portuguese mainland shelf and slope

Sponges and corals form a variety of highly structured habitats known as sponge/coral gardens, aggregations and reefs. They are particularly prevalent in the deeper areas of the continental shelves and slopes, and play key roles in ecosystem function, from recycling of major nutrients to provision of habitat, nursery and feeding grounds for many other invertebrate and fish species. Their vulnerability to the impacts of anthropogenic activities is increasingly recognized and led to their classification as Vulnerable Marine Ecosystems (VMEs). Yet, large knowledge gaps still exist on their taxonomic composition and distribution, limiting the implementation of measures for their conservation and sustainable management at regional and even European scales. DEEPbaseline, an awardee of the Ocean Conservation Fund, is an interdisciplinary project aimed at developing a framework for the co-development and co-delivery of a knowledge baseline of the diversity and distribution of deep-sea vulnerable marine ecosystems of the continental shelf and slope of mainland Portugal. It brings together scientists, local fishing communities and associations, fisheries managers, and the wider society to foster awareness and advance conservation actions towards their sustainability. The project is gathering Local Ecological Knowledge from local fishers on the spatial and historical occurrence of sponge and coral species and habitats, and combining it with Conventional Scientific Knowledge, e.g. bycatch data from multi-annual bottom-trawl scientific surveys, and integrative taxonomy of bycatch samples. Training activities are being developed to capacitate and engage local fishers and fisheries observers on the identification and reporting of VME-indicator species. Knowledge and data obtained and generated will be translated into management-support tools (identification guides, distribution maps) and transferred to key endusers to inform the selection of high biodiversity areas to be protected, and support the implementation of regional and (inter)national regimes for conservation and sustainable management of VMEs.

DEEPbaseline (www.deepbaseline.org) is funded by Oceano Azul Foundation and Oceanário de Lisboa.

17:55 - 18:10

Maria Baker, James Bell, Emma Cavan, Mark Costello, Harriet Harden-Davies, Nomaki Hidetaka, Nick Higgs, Sandra Maier, Emma McIntosh, Ross Mounce, Nguyễn Văn Nguyên, Angelique Pouponneau, Hannah Sharman, Eulogio Soto, **Paris Stefanoudis**, Elin Thomas, Clive Trueman, Paul Tyler

Assessing the open access landscape in deep-sea biodiversity research: status, progress and options

Openly accessible ocean research and data is pivotal to advance science, and scholarship and robust management. Since the 2000s there has been a shift towards open access publishing with most journals nowadays offering an option to publish open access in exchange for a fee. However, in most cases open-access fees are prohibitively high for institutions with limited financial resources, leaving only a handful of scientists from wealthy institutions – typically concentrated in the Global North – dominating the open-access landscape. Here, we focus on the publication landscape relating to the largest environment on Earth – the deep ocean – and conduct a global analysis of scholarly articles published over the last 10 years that focus on deep-sea ecological research. We present the most widely-chosen journals, and how that relates with accessibility (open access vs. subscription) as well as authors' institutional affiliations. Furthermore, we comprehensively review all available openaccess options for the deep-sea research community, including financially-accessible choices. Our results will hopefully help the deep-sea stakeholder community to make informed choices when it comes to publishing, with the ultimate aim of advancing research, improving decision-making, and helping move towards greater equality in scientific dissemination and data accessibility.

Friday 16th September

08:30 - 09:00

Keynote Kim Juniper So, what's the deal with cabled observatories in the deep sea?

Cabled observatory technologies offer unique opportunities for ecological research in the deep sea. They enable continuous, long-term, high-frequency time series observations, real-time monitoring, and can support in situ experimentation in well-characterized locations. We will briefly review cabled observatories currently supporting ecological studies and then use examples from the deep-sea cabled installations of Ocean Networks Canada in the northeast Pacific Ocean, to illustrate how networked observing systems operate and how they are being used for observation of Essential Biodiversity Variables (EBV) in the deep sea. Examples will include benthic ecology studies using EBV data from fixed and mobile observing platforms in submarine canyon and hydrothermal vent habitats, and a growing inter-disciplinary collaboration around deep-scattering layer dynamics that combines observations from a neutrino observatory, vertical ROV transects, and seabed cameras and sonars.

Special 5b: Artificial Intelligence

09:05 - 09:20

Mehul Naresh Sangekar, Simon-Martin Schröder, Rainer Kiko, Mitsuko Hidaka, Hiromi Kayama Watanabe, Jean-Olivier Irisson, Dhugal Lindsay Dealing with Diversity: Data-driven unsupervised clustering on diverse deep-sea image collections

Midwater marine environments are one of the largest ecosystems on earth. Collecting visual data of a quality from which identifications can be made is difficult due to limited survey opportunities. Often during dives, long video recordings are made, which need to be analyzed in real-time or in post processing for annotating observations. Although manual annotations are reasonably accurate, the process is time consuming with few taxonomists available to annotate. Various machine learning approaches are getting popular for automatic classification of marine species from visual data. Most methods require predefined classes for training, making them difficult to use in marine datasets due to the many undescribed species. A different approach to automatic annotation has been demonstrated in a new tool called MorphoCluster.

The tool provides a data-driven approach for fast annotation of large data sets of single object images without predefining classes. It combines unsupervised clustering with an interactive tool allowing the annotator to revise the initial clusters, arrange them hierarchically, manually correct the hierarchy and annotate the clusters. This enables exploring the groupings inherent in the data, and to spot novelties and unexpected patterns. Identified groups of similar images can then be annotated as a whole, to enable consistent manual review of large amounts of data in a rather short time.

Visual observation devices have enabled us to record different types of images, such as flatbed scanner-acquired plankton images, shadowgraphs, dark-field illuminated colour images, framegrabs from videos, developed holograms, etc. In this work, we aim to report the results of evaluating the MorphoCluster software with a variety of different data types. We shall assess the influence of the quality and type of raw images on groupings made using the software. The effects of pre-processing the raw images on the outputs are also reported by running various experiments.

09:20 - 09:35

Erin Browne, Emily Hutchinson, David Hutchinson, Nils Piechaud, Kerry Howell Development of a method for real-time AI analysis of live ROV video

Technological developments enable the collection of larger seafloor imagery datasets at a rate too great to process. Annotation of seafloor images and video by skilled human para-taxonomists is a significant bottleneck in turning this imagery into quantitative data. Artificial Intelligence, specifically deep learning, offer a possible method to rapidly turn imagery into data. However, these methods have yet to be tested in the field of deep-sea biology. The aim of this study was to develop and test a method for real-time AI analysis of live ROV video. To develop our AI model we used archived manually annotated ROV frame grabs as training data. All annotated taxa were grouped into visually similar classes for model training purposes. The VIAME (Video imagery analysis for the marine environment) software was used to train various YOLOv3 models in order to investigate model performance and optimise our approach. All model performances were assessed using mean Average Precision (mAP) calculated using previously unseen manual annotations. A final model was then trained for application to real-time data in the field. During the investigation phase, mAP generally increased with training set size. The visually distinctive squat lobster class achieved second best average precision with 6.4% of the maximum training images, in one case detecting an instance missed by the annotator. A 'cup coral' class however performed poorly – perhaps due to visual differences between class members. Further optimisation of classes is required. New results from the field trial of the final trained model this summer will be presented and the pipeline to process a realtime ROV feed is described.

09:35 -09:50

Nils Piechaud, Rhodri Irranca-Davies, Kerry Howell Investigating the advantages of semi-automated counting of a benthic species for studying fine scale distribution patterns

New sampling technologies (HD cameras, AUVs…) have considerably increased the size and complexity of benthic image collections. The development of more efficient analysis methods is critical to take full advantage of these technologies. New AI-assisted methods are efficient if carefully implemented but at present require a significant investment of time and resources by ecologists. This limits the time effectively gained in the short-term by shifting from manual to automated annotation, which may thus not be suited to small-scale projects or teams.

In this study we investigated how a semi-automated benthic species counting method can provide a dataset capable of answering a simple ecological question. Our objective was to precisely determine the abundance of the xenophyophore Syringammina Fragilissima and better understand its finescale distribution pattern in the North Atlantic, with a large dataset of AUV images. This is performed with the MAIA extension of BIIGLE that allowed us to quickly train a Mask-r-CNN model on a small (1000) number of manual annotations. Predictions were then made on another batch of manually annotated images to measure the performances of the model. We calculated the recall and precision of the model, as well as the correlation between the number of xenophyophores provided by manual and semi-automated methods in each image. MAIA achieved a recall of 0.76 and a precision of 0.85. The correlation between manual and semi-automated counting was 78%.

As these performances were satisfactory, we used the same trained model on the entire dataset of 50,000 images. We discuss the ecological findings and the benefit of the automation of the semiannotation process, as well as potential caveats and possible routes to improve performances and move towards full automation. We hope to provide useful insights to other researchers considering similar approaches for studying benthic megafauna and help inform the conservation of xenophyophores.

09:50 -10:05

Marjolaine Matabos, Sébastien Rochette, Roland Duffau, Anne-Charlotte Philippe, Catherine Borremans Deep Sea Spy: from citizen annotation to articial intelligence

The assessment of the status and trends of marine systems in a changing ocean requires long-term monitoring of ecosystems. The recent development of multidisciplinary seafloor observatory increased our capacity to study the deep sea and its associated biodiversity. Since 2010, the TEMPO(-mini) ecological module recorded about 7 500 hours of video sequences, which processing is time-consuming and challenging. The Deep Sea Spy (DSS) project, is a free open online image annotation tool that enables the contribution of citizens to the analyses of the large imagery archive. Since 2017, over 1 200 citizens contributed to the annotations of 47 000 images. However, the analysis of citizen data requires the implementation of validation protocol to insure a proper assessment of benthic communities diversity and trends. In addition, observatories are designed to operate over decades and data keep flowing, requiring a long-term solution for standardized, quick and reliable image annotation protocol.

The first mission of DSS included 3 800 images that were all annotated 10 times by different citizen annotators and an expert scientist. We developed a statistical tool to combine spatial multi-user data into one annotation set at different levels of agreement among users. This sets and the expert data were then used to train machine learning (ML) algorithms. The quality of citizen annotations greatly varied depending on the species considered, which corresponded to different task difficulties. As expected, machine learning algorithms performed better with expert data, but results suggest that a proper validation of citizen data can produce a usable training dataset. Finally, validation by the citizens of pre-processed images (i.e. ML algorithms outputs) will help improve the performance of the machine in the future. While observations systems are developing around the world, our approach provides a general workflow from acquisition to artificial intelligence application.

10:05 - 10:20

Chloe A. Game, Michael B. Thompson, Graham D. Finlayson Broad benthic habitat classification: a ‘user-friendly’ and simple approach to streamline analysis of image surveys

Identification and mapping of benthic habitats is fundamental to marine spatial planning and conservation of deep-sea communities. With increasing acquisition of marine imagery, particularly from autonomous platforms, extracting data is severely restricted due to the time and resource constraints of manual annotation. Machine learning approaches to image classification are widely believed to be essential to alleviating this problem and have become increasingly popular over the last few decades. In particular, domain-driven training and tuning of pre-trained convolutional neural networks (CNNs), also known as transfer learning, has shown promising results. However, for a nonspecialist, these methods are often inaccessible, as they require large investments in time and computational resources.

We demonstrate that these methods are more feasibly exploited by using an ‘off-the-shelf’ CNN, VGG16, to extract benthic image features (with no further training) and used alongside a simpler classification algorithm, Support Vector Machine (SVM), to classify broad benthic habitats. SVM’s are a classical method and offer a good trade-off in terms of complexity, performance, computational demand and time.

We classify a dataset of 10,000 images (80% training, 20% test) from deep Norwegian waters, into 3 broad classes; soft substrates (sands and muds), hard substrates (gravels, cobbles and boulders) and reef (Desmophyllum pertusum). SVM hyperparameters were tuned using 5-fold cross validation of the training set. The final classifier performed well on the test data (accuracy = 0.94). Precision and Recall results were also high with 0.95|0.98 for soft substrates, 0.93|0.90 for hard substrates and 0.92|0.92 for reef habitat, respectively.

This approach is simple, fast and consistent. It allows segregation of images based on features of interest and can support annotation by grouping images into similar categories, with similar fauna. It’s usage at sea could also provide quick, albeit crude, insights into habitat presence. Future work will involve classification at a finer resolution.

10:20 - 10:35

Abdul Qayyum, Abdesslam Benzinou, Kamal Nasreddine, Catherine Borremans, Daniela Zeppilli A comprehensive review of artificial intelligence-based approaches for biodiversity studies in the deep sea

Faced by the rapid increase of anthropogenic pressures on deep-sea ecosystems, the scientific community has to cope with the growing need for monitoring the biodiversity and to carry out rapid and accurate impact assessments. The majority of deep-sea infauna is undoubtedly one of the best models for monitoring all kind of human impacts, but also one of the most difficult groups to study, requiring time and highly-skilled specialists.

Therefore, the scientific community has underlined the urgent need to explore imaging-based tools that can provide fast and automatic analysis of huge amounts of data for biodiversity studies in the deep sea.

In this study, state-of-the-art methods in artificial intelligence (AI) and machine learning (ML) for biodiversity studies in deep sea are explored to investigate existing architectures, their key concepts, the concept drift due to variant datasets, or the optimization of hyperparameters for training models.

AI and ML techniques would achieve high efficiency for deep-sea biodiversity studies on communities such as microbial eukaryotes, marine plankton, benthic fauna and foraminifera. It is a need to investigate what are the limitations, and what will be the solution based on the limitation in the current AI and ML techniques. Even though deep learning is widely used for the automatic image identification, classification and segmentation, the deep learning architectures are black boxes in nature that transform the input data into the output decision probabilities without providing any interpretation inside the architecture. That is why, we will also inspect the explain ability or interpretation of hidden parameters for improved decision making in the deep learning models.

General 3: Life-history traits and connectivity

09:05 - 09:20

Craig M. Young, Caitlin Q. Plowman, Shawn M. Arellano, David B. Eggleston, Amy K. Burgess, Ruoying He Isotopic evidence for demersal development in the larval shells of cold-seep mussels, and a possible bet-hedging dispersal strategy

Biophysical models predicting larval dispersal and genetic connectivity require parameter estimates not only for current speed and planktonic larval duration, but also for swimming behaviors that influence the depths of dispersal. Hypothetical LTRANS models predict large differences in dispersal distance and direction for long-lived larvae of the seep mussel Gigantidas childressi, a slope species in the Gulf of Mexico and on the Northwestern Atlantic Margin. Previously, we have found planktotrophic larvae of this species both in the upper water column and in tube traps on the sea floor. The latter occur at a wide range of sizes, suggesting that they may drift for extended periods in the benthic boundary layer. To estimate the relative proportions of demersal drifters and ontogenetic vertical migrators, we compared oxygen isotopes of larval shells (prodissoconchs) and juvenile shells (dissoconchs) of recently settled individuals. In fifty-four percent of the fifty paired samples analyzed, there was no significant difference in the temperature signal of calcium deposition between larval and juvenile shells, indicating demersal development. Forty percent showed evidence for significantly warmer deposition in larval than juvenile shells, suggesting some level of ontogenetic migration. Six percent of larvae had developed in water colder than their settlement depth, suggesting colonization from downslope metapopulations. Thus, these seep mussels produce some larvae with swimming behaviors that facilitate long-distance dispersal in the water column and some that stay near the bottom where they are more likely to encounter seep habitats suitable for settlement. This is analogous to the well-studied dispersal dimorphisms found in nudibranchs, vascular plants, and insects. Whether the behavioral dimorphism in larval mussels occurs at the individual or population level remains unknown, but the observation is consistent with the hypothesis that seep mussels have evolved a bet-hedging dispersal strategy.

09:20 - 09:35

María Belén Arias, Sergi Taboada, Paco Cárdenas, Vasiliki Koutsouveli, Francisca Correia de Carvalho, Ellen Kenchington, Hans Tore Rapp, Ana Riesgo Population structure and connectivity patterns of the artic deep-sea sponge Geodia hentscheli

Deep-sea sponge grounds are common ecosystems in the North Atlantic Ocean where dominant sponges play fundamental roles in ecosystem functioning and community composition. Sponge grounds provide crucial complex habitat for many marine species enhancing local biodiversity, act as food resources and drive biogeochemical cycles. North Atlantic sponge grounds are currently under threat by anthropogenic activities, especially bottom-contact fisheries, which highlights the necessity of conservation strategies for these unique ecosystems. Despite their ecological role, little is known about the dispersal, genetic diversity, gene flow and population connectivity in deep-sea sponges, information that is crucial to develop effective management and conservation plans.

Here, we used double digest restriction site-associated DNA sequencing (ddRAD) to screen for single nucleotide polymorphisms (SNPs) and investigate the genetic diversity, structure and molecular connectivity of a keystone species in artic sponge grounds, the tetractinellid demosponge Geodia hentscheli. Over 120 specimens were collected from eight areas covering different bathymetrical ranges, spanning ca. 6,000 km over its entire distribution range in the North Atlantic and Arctic Oceans. We obtained ca. 3,500 SNPs which allowed the identification of a strong genetic structure separating the populations into two distinct genetic clusters segregated by depth. Populations inhabiting areas between 139 to 1300 m formed a single cluster (Shallow-Cluster), while those dwelling in depths from 1300 to 2,959 m formed another (Deep-Cluster). While the 1,300 m isobath was the strongest potential dispersal barrier for G. hentscheli, geographic distance, circulation patterns, and bottom topographical structure could be behind the substructure detected in the ‘Shallow-Cluster’, which separated populations from the West North Atlantic (Davis Strait) and the East North Atlantic and Arctic Oceans (including Karasik seamount). Our results highlight the strong gene flow occurring across isobaths in the deep-sea but also identifies populations showing more restricted connectivity, indicating areas where conservation actions should be directed to ensure the protection of the local genetic diversity.

09:35 -09:50

Anna Patova, Pedro A. Ribeiro, Lindsay Beazley, Javier Murillo, Ellen Kenchington, Ana Riesgo, Sergio Taboada, Shirley Pomponi, Hans Tore Rapp†, Joana R Xavier Population genomics of Vazella pourtalesii sponge grounds of the Northwest Atlantic: implications for conservation of deep-sea Vulnerable Marine Ecosystems

Sponges are key ecosystem engineers that globally shape structure and enhance the biodiversity of shallow and deep-sea benthic communities. The habitats they form – known as sponge grounds, aggregations, and reefs - are highly vulnerable to anthropogenic activities, particularly to deep-sea bottom-contacting fisheries. Ensuring these habitats' long-term sustainability and preservation of their ecosystem functions requires the design and implementation of conservation and management areas based on a sound knowledge of the ecological processes underpinning persistence and recovery of the structuring species and their populations. We implemented a population genomics approach to investigate the genetic diversity, structure, and connectivity of a deep-sea habitatforming glass sponge, Vazella pourtalesii (Schmidt, 1870). This species is widely distributed across the Northwest Atlantic and forms a unique habitat on the Scotian shelf off East Canada. The analyses of 1102 neutral single-nucleotide polymorphism (SNPs) derived from restriction site-associated DNA sequencing (RADseq) provided evidence of a moderate but significant genetic structure of Vazella pourtalesii with the presence of two distinct geographical groups: one on Florida-Carolina Shelves and one on the Scotian Shelf. Moderate levels of genetic diversity were observed with low migration across considerable distances (over 1000s km) and high connectivity at smaller scales (<300km). Levels of genetic diversity found within the two Sponge Conservation Areas (Emerald Basin and Sambro Bank), currently established to protect this habitat from the impacts of bottom-fisheries, were slightly lower to those found outside these closure areas. We discuss our findings in light of existing area-based management tools aimed at protecting deep-sea vulnerable marine ecosystems.

09:50 -10:05

Karin Steffen, María Belén Arias, Sergi Taboada, Ana Riesgo, Paco Cárdenas Sponge ground connectivity across Atlantic waters: case study of Geodia barretti using ddRADseq

Sponge grounds, particular deep-sea habitats characterised by dense aggregations of sponges, were discovered in the North Atlantic in the 1990s and listed as threatened habitats (OSPAR) and Vulnerable Marine Ecosystems (VMEs) only twenty years later. Understanding connectivity, that is the extent of gene flow between different populations, in deep-sea habitats is challenging yet paramount to conservation management of these habitats. With the keystone demosponge species Geodia barretti, we investigated the connectivity of boreal North Atlantic sponge grounds. We collected 161 samples across the North Atlantic covering different oceanographic settings in European and Canadian waters, from fjords to continental shelves and slopes, to the upper bathyal; all in all covering a depth range from 28 to 1560 meters. Sponge specimens were genotyped using double digest restriction site-associated DNA (ddRAD) sequencing. We also produced a draft reference genome of G. barretti in order to discriminate between polymorphisms (SNPs) of the sponges and those of their numerous microsymbionts. We tested the hypotheses that i) isolation-bydistance (i.e. distant populations share less genetic material than close populations) and ii) isolationby-water-mass (i.e. populations within the same water mass share more genetic material) processes control population structure. Our results confirm these hypotheses but also raise new questions with respect to deep-sea sponge connectivity.

10:05 - 10:20

Coral Diaz-Recio Lorenzo, Pedro Martinez Arbizu, Stefan Laurent, Sabine Gollner Genome-wide Single Nucleotide Polymorphisms (SNPS) uncover fine-scale population structure and demographic histories of vent-endemic copepods: Implications for resilience to deep-sea mining

Deep-sea hydrothermal vinet meiofauna contributes >50% to metazoan biodiversity at vents, with Copepoda being the most abundant taxon in these systems where hard substrate is available. To date, no population genomic studies have been conducted on vent meiofauna. Understanding the genetic connectivity of populations is of upmost importance to understand whether these populations are resilient to potential future impact by polymetallic massive sulphide mining. We report how Single Nucleotide Polymorphisms (SNPS) discovered with restriction site associated DNA sequencing (2b-RAD) can reveal fine-scale diversity in deep-sea vent-endemic copepod populations of Stygiopontius lauensis within the Lau Basin (Southwest Pacifie). Our results are consistent with the wide and local-scale current circulation and biophysical models of dispersal of the area. Using demographic-modelling software FastSimCoal2, we aim to estimate demographic parameters and investigate for example past bottleneck events. This coalescent modelling may then be harnessed to predict the gene flow strength and direction of future populations under different disturbance scenarios, allowing us to infer their resilience to human activity in the deep-sea.

10:20 - 10:35

Sylvie Marylène Gaudron, Sébastien Lefebvre, Gonçalo Montairo Marques Inferring functional traits in a deep-sea wood-boring bivalve using dynamic energy budget theory

In the deep sea, there is a gap of knowledge on functional traits of species at any stages of their life cycle. Dynamic Energetic Budget (DEB) theory was proven to be an efficient framework to estimate functional traits along life cycle using simulation modeling. An abj-DEB model was successfully developed in the deep-sea Atlantic woodeater Xylonora atlantica. Most of core and primary parameter values of the abj-DEB model of X. atlantica were in the range of those found in shallow marine bivalve's species. However, the energy conductance and the energy required to reach puberty were much lower for the same range of body size, and the maximum reserve capacity was higher. Consequently, size at first reproduction is lower and a better survival in starvation conditions is expected. A series of functional traits were simulated according to different scenarios of food density and temperature. Results evidenced weak cumulative number of oocytes, low Von Bertalanffy growth rate and small maximum body size, but an extending pelagic larval duration at deep-sea environmental conditions. Moreover, DEB-modeling has helped to explain how some male X. atlantica individuals remain dwarfs while still reproducing by possibly changing the Kappa value to 0.06 (instead of 0.72). The modeling of these traits is critical to decipher fundamental ecological knowledge and we suggest the use of DEB-modeling in further deep-sea studies.

General 5: Access

10:35 -10:50

Melissa Hanafi-Portier, Laure Corbari, Tin-Yam Chan, Wei-Jen Chen, Jhen-Nien Chen, Mao-Ying Lee, Christopher Mah, Thomas Saucede, Catherine Borremans, Karine Olu, Sarah Samadi When imagery and physical sampling work together: towards an integrative methodology of image-based megafauna identification

Imagery has become a major tool for deep-sea megafaunal biodiversity assessment, historically based on fishing gears. Image datasets provide quantitative and repeatable estimates, small-scale spatial pattern knowledge and habitat description. However, taxon identification from images is challenging and often relies on morphotypes without considering a taxonomic framework. This is particularly critical in regions where the fauna is poorly known and/or highly diverse. Furthermore, efficiencies of each method may vary among habitat types.

We have compared biodiversity metrics (alpha and gamma diversity, composition) between dredge and trawl catches and towed camera images from Papua New Guinea continental slopes (sedimented slope with wood-falls, canyon and cold seeps) and Mayotte volcanic island outer slopes dominated by hard bottoms. The comparison was done for selected taxa (Pisces, Crustacea, Echinoidea, Asteroidea) which are good candidates for identification on images. Identification ranks obtained on images vary among these taxa (e.g. Family/Order for fishes, Genus for echinoderms). At these ranks, imagery provides a higher taxonomic richness in hard bottoms and complex habitats; partly explained by difficult trawling in these environments. For the same reason, the gamma diversity of Pisces and Crustacea is also higher from images while no contrasted difference was observed for echinoderms. In soft bottoms, collecting provides higher alpha and gamma diversity for fishes and crustaceans, but these differences tend to decrease for crustaceans as identified at Species/morphospecies level on images. Collecting and imagery are selective against some taxa (e.g. according to their size or behaviour), therefore providing differential views of the biodiversity. Finally, specimens collected at larger scale helped megafauna identification from images.

From this complementarity, we propose a more robust methodology for image-based faunal identification relying on a taxonomic framework, from a collaborative work with taxonomists. This has led to the development of the first identification keys on deep-sea images.

Thesis co-funded by TOTAL & Ifremer as part of the Passive Margin Exploration Laboratories scientific project.

10:50 - 11:05

Véronique Merten, Till Bayer, Oscar Puebla, Thorsten Reusch, Fleur Visser, Julia Stefanschitz, Julian Stauffer, Henk-Jan T. Hoving, Katja Metfies Environmental DNA metabarcoding to uncover patterns of diversity and distribution in deep-sea cephalopods

Cephalopods are key players in marine food-webs, connecting higher and lower trophic levels as predators and prey. They contribute to carbon cycling during their life and also after their single reproductive cycle when they die, sink and are scavenged. Identifying and quantifying their role in the carbon cycle requires knowledge on the distribution and diversity of living cephalopods in the water column and of dead cephalopods on the seafloor (so-called foodfalls). However, this knowledge is limited due to technological and logistical challenges to study the deep sea. Additionally, the size, swimming capacity and sensing capabilities of cephalopods result in avoidance behaviours and biases in net and video surveys. Environmental DNA (eDNA) can circumvent some of those biases and be used to survey living and dead cephalopods. Foodfalls are often missed by other censuses due to their scarcity and rapid scavenging rates. We present the development, application and challenges of cephalopod eDNA metabarcoding from deep-sea water and sediment from the Atlantic and Arctic Ocean. We designed a primer targeting the nuclear 18S rRNA gene of cephalopods. We detected 39 cephalopod taxa off the Azores (50-1600 m depth), including the giant squid Architeuthis, new regional records, and reconstructed the cephalopod prey communities in the foraging habitats of cetaceans. Combining eDNA with trawls and video surveys, we established a cephalopod biodiversity baseline off Cabo Verde in the Atlantic detecting 68 species, including the elusive squids Taningia danae and Magnapinna, rendering Cabo Verde a cephalopod biodiversity hotspot. Abyssal sediment and water column samples (50-2500 m) from the Arctic Ocean are currently under investigation for cephalopod and fish foodfalls and biodiversity. Our efforts show that the detection of cephalopod eDNA in sediment is a challenge, but that eDNA is an excellent tool to study regional biodiversity, potential range expansions and prey spectra in foraging habitats.

General 3: Life-history traits and connectivity

10:35 -10:50

Autun Purser, Lilian Boehringer, Laura Hehemann, Teresa Morganti, Jonas Blendl, Beate Slaby, Antje Boetius *In situ* observations from the central Arctic and Weddell Sea indicate sponge locomotion in under-ice environments plays a role in juvenile dispersal

Three RV Polarstern recent expeditions to the central Arctic (PS101, 2016), the western Weddell Sea (PS118, 2019) and the eastern Weddell Sea (PS124, 2021) have all deployed the Ocean Floor Observation and Bathymetry System (OFOBS) to visually and acoustically habitat map the seafloor and investigate the abundances and distributions of megafauna in near permanently ice covered environments.

During all three research cruises sponges of 10s of centimeter diameter have been observed adjacent to extended trail features, indicative of movement. In the central Arctic, an abundant sponge ground was observed to cover the Langseth Ridge seamount chain, comprising Geodia parva, G. hentscheli and Stelletta rhaphidiophora sponge species, all of which appear to be capable of locomotion. In Antarctica, in the Weddell Sea, individuals of an unidentified Geodia sp. Species were also observed associated with trail features.

At present, the driving force behind this observed locomotion has not been firmly identified. One potential driving factor however is as an aid to juvenile distribution. In this study we quantify and present the abundances of juvenile sponges observed during the numerous seafloor survey transects conducted during these three expeditions, and relate these abundances to the occurrence of associated sponge trail features.

10:50 - 11:05

Pierre Methou, Chong Chen, Hiromi K. Watanabe, Marie-Anne Cambon-Bonavita, Florence Pradillon Reproductive strategies in vent shrimps shaped by feeding ecology with intriguing seasonality

Variations in reproductive patterns according to feeding strategies or food supply have been widely recognized in many animals from various ecosystems. Despite an unusual trophic structure, these relationships remain largely under-studied in chemosynthetic ecosystems and are mostly limited to species from the northern hemisphere. Here, we use Rimicarisshrimps, one of the most emblematic species endemic to deep-sea hydrothermal vents, as a case of study to explore the relations between reproduction, diets and food supply in these environments. For that, we have compiled data on the presence of reproductive individuals from the past 35 years and compared reproductive outputs for three vent shrimps with different diets and inhabiting vent field with opposed latitudes. We report widely distinct reproductive patterns between Rimicaris species according to their trophic regime regardless of the variations related to their body size. In addition, we observed for most the period of reproduction was between January and early April. Intriguingly, this reproductive periodicity does not correspond to seasonal variations with a presence of ovigerous females either during boreal winter or during austral summer for species from the northern and southern hemisphere respectively. These observations contrast with the long-standing paradigm in deep-sea species for which periodic reproductive patterns have always been attributed to seasonal variations of the photosynthetic production sinking from the surface. Our results indicate the presence of intrinsic basis for biological rhythms in the deep-sea, a much-neglected frontier for future research into the secret life of these animals.

General 5: Access

11:25 - 11:40

Arnaud-Haond, S., Pradillon, F., Günther, B., Trouche, B., Zeppilli, D., Maignien L., Cambon-Bonavita M., Matabos, M., Sarrazin J., M., Brandt, Henry, N., Pesant, S., Poulain, J., Wincker, P., de Vargas, C. eDNAbyss: Toward a concerted DNA-based exploration of the largest biome on earth

The deep sea floor is by far the largest biome on Earth, yet remains a biodiversity black box. Pioneer studies in the 60s and 70s at local scale revealed a tremendous amount of patchily distributed benthic biodiversity at local scale. Yet the vastness of the task, the attention attracted by the discovery of chemosynthetic ecosystems and the difficulty to integrate localstudies made by different operators / teams to obtain a broad picture deterred further progresses in our understanding of the extent and distribution of benthic biodiversity at global scale. Progresses allowed by the metabarcoding and metagenomics reconstruction of environmental DNA now rendered possible the gathering of large, interoperable and easy to integrate datasets at local and regional scales to gain a new appraisal of the extent and distribution of deep sea biodiversity, and of the contribution of deep sea benthic ecosystemsto large biochemical cycles. In the framework of the project Pourquoi Pas les Abysses (2016-2019), launched by Ifremer in 2016 and of the following France Génomique project eDNAbyss (2018-ongoing), we tested various protocols to find the best trade-off between the logistic complexity ofsampling at depth, and the efficient and reliable assessment of benthic diversity across the Tree of Life. We developed a standard set of sampling, molecular and bioinformatic steps adopted in the framework of eDNAbyss project to assess biodiversity inventories across the tree of life, and propose to use this first effort as a seed to open exchanges and trigger the large international and concerted effort needed to gain a global holistic view of the vastest biome of our planet.

11:40 - 11:55

Thomas Y. Chen Classifying and Semantically Segmenting Deep Sea Fish in Imagery with a Novel Automated Machine Learning Methodology

The study of wildlife that inhabit areas below the photic zone is notably limited in scope due largely to the environmental conditions that have in the past prevented in-depth understanding. However, with the development of technology and especially the rise of artificial intelligence, there are many opportunities to study deep sea fish, particularly. Common deep sea fish species include the lanternfish (Myctophum punctatum), flashlight fish (Anomalopidae), cookie cutter shark (Isistius brasiliensis), bristlemouths (Gonostomatidae), anglerfish (Lophiiformes), and viperfish (Chauliodus). Deep learning-based computer vision has been a key tool in recent literature for identifying, classifying, and semantically segmenting wildlife in imagery. However, this has largely been confined to terrestrial animals, and this technique has certainly not been extended to deep sea biology. Therefore, in this ongoing work, we propose the curation of an appropriate computer vision dataset, including images of the categories of the aforementioned fish taxa. We collect this data by utilizing web scraping and Google Images using queries of both the colloquial and scientific names of each taxon but recognize that this may not result in a dataset of a sufficient quantity for machine learning purposes. In the next stage of this work, we launch a large-scale worldwide operation to capture additional imagery of deep-sea fish species. Subsequently, we collect labels (categories and bounding boxes for individual fish) using a crowdsourcing platform such as Amazon Mechanical Turk. Finally, we train a convolutional neural network of the SqueezeNet architecture to classify and segment the fish in the imagery dataset. The goal of this preliminary work is to introduce a novel automated method for recognizing deep sea fish, which allows for the assessment of individuals and populations, leading to a greater understanding of species trends and conservation mechanisms that can be implemented by local governments and nonprofit organizations.

General 3: Life-history traits and connectivity

11:25 - 11:40

Jim Barry, Andrew DeVogelaere, Erica Burton, Chad King, Steve Litvin, Chris Lovera, Amanda Kahn, Geoff Wheat Hydrothermal warm springs: hot spots for deep-sea octopus reproduction

Thousands of abyssal octopuses (Muusoctopus robustus) are known to nest in warm hydrothermal springs at the “Octopus Garden” located in foothills along the base of Davidson Seamount near 3200 m depth. We hypothesize that the metabolic boost from warm temperatures at these springs benefits M. robustus through accelerated embryonic development. Reproduction in octopuses is linked tightly to environmental temperature with rapid embryonic development in warm seas and exponentially slower rates in cooler waters. Deep-sea octopuses typically have long brood periods, requiring as much as ~1590 days in bathyal Granadelone boreopacifica living in ~3.5 o C waters, the longest known brood period for any organism. M. robustus inhabits waters near 1.6 o C, where predicted brood period exceeds 10 years, a seemingly incredible feat. Using repeated visits with submersibles from 2019 to 2021, we estimated egg development rates and nest residence times for female M. robustus, and logged temperature and oxygen measurements in nests. Brood periods for 26 females averaged 576 days and nest residence times were from 559 – 644 days. Temperatures near nests varied from 1.6 to 10.5 o C and mean temperature adjacent to egg clusters was 5.1 o C. Based on the development: temperature relationship observed among other octopus species, the expected incubation period at 5.1 o C is 623 days. Although the risk of thermal stress may be high, the accelerated development possible in hydrothermal springs appears to have led to selection for this breeding behaviour in M. robustus. Hydrothermal vents have received great attention due to their role as oases of deep-sea life, mainly due to the reduced compounds available to support chemosynthetic life. However, the potential benefits of increased metabolism from thermal energy at deep-sea heat sources, including mediating growth, reproduction, feeding, predator-prey interactions, or other processes, have received little attention.

11:40 - 11:55

Vincent Mouchi, Christophe Pecheyran, Fanny Claverie, Didier Jollivet, Thomas Broquet, Thierry Comtet Connectivity of the deep-sea hydrothermal gastropod species *Shinkailepas tollmanni*: a geochemical approach by elemental fingerprinting

Recent connectivity of populations of hydrothermal vent species is still poorly described due to challenging access and sampling. Moreover, little is known on larval dispersal of vent species in terms of duration and trajectory, although physical models provide information on water mass circulation. Therefore, the spatial scale at which populations are connected between distant hydrothermal vent systems remains also poorly defined. Genetic approaches based on the analysis of genetic variability among adult individuals or populations are promising, but particularly challenging in species with large population sizes because they may be genetically homogeneous regardless of their connectivity.

As an alternative, we investigated the potential of elemental fingerprinting to infer connectivity in a vent gastropod. As the larval shell forms, it incorporates chemical elements from the seawater. Thus, the shell composition should reflect that of its surrounding environment. Provided that sites differ in their composition, measuring the elemental composition of the larval part of juvenile shells could allow to determine their natal site. Validating this approach first requires to estimate differences in elemental fingerprints between sites. The gastropod Shinkailepas tollmanni is a model of choice for such an approach as females lay capsules containing larvae that form a shell prior to dispersal, thus incorporating an elemental signature specific of their natal site.

Encapsulated veliger larvae sampled from active sites in five hydrothermal vent provinces of the Southwestern Pacific Ocean were digested to obtain cleaned shells of approximately 100 µm in diameter. Such minute size and weight (a few tens of ng) require the use of a cutting-edge analytical technique to measure the elemental composition of individual shells. A triple-quadrupole inductively-coupled plasma mass spectrometer was used with a femtosecond laser ablation system. We here assessed the site-specific elemental fingerprint of a series of individual S. tollmanni larval shells across western Pacific vent fields.

Special 5a: Ecosystem dynamics

11:55 - 12:10

Andrew Gates, Jennifer Durden, Susan Hartman, Stephanie Henson, Tammy Horton, Richard Lampitt, Corinne Pebody, Brian Bett

Understanding multidecadal change in the deep ocean: atmosphere to seafloor at the Porcupine Abyssal Plain Sustained Observatory, NE Atlantic

Despite pressing social needs, the world's oceans remain critically under-sampled in space and time. With concerted international actions and advances in sensor and platform technologies, multidisciplinary ocean observatories are increasingly capable of providing meaningful time-series monitoring of our ocean.

The Porcupine Abyssal Plain Sustained Observatory (PAP-SO; NE Atlantic) is one of a small number of oceanic sites that has achieved multidecadal monitoring of seafloor ecology (1985-), water column particle flux (1992-), and surface ocean and atmosphere parameters (2003-). The observatory is currently serviced by an annual cruise that enables conventional ship-based observation and sampling, and increasingly employs both fixed and mobile autonomous systems to expand and enhance the multidisciplinary time series.

From its inception, the PAP-SO has been an international collaborative effort that has sought to understand long-term change in the ocean – from surface to seafloor. Initially focussed on intra- annual seasonality in the deep ocean, now increasingly concerned with the causes and consequences of multidecadal change. Here we examine uptake, transfer, and storage of carbon in the deep ocean, whether there are decadal changes in the oceanic ecosystem, and what may be driving such change.

12:10 - 12:25

Pierre- Marie Sarradin , Julien Legrand , Mathilde Cannat, Marjolaine Matabos, Wayne Crawford , Valérie Ballu , Valérie Chavagnac , Jozée Sarrazin , Anne Godfroy, Céline Rommevaux , Jérôme Blandin , Nadine Lantéri , Laurent Gautier , Guillaume Roullet , Ana Colaço and the EMSO Azores Regional team

Temporal dynamics of the Lucky Strike hydrothermal vent field – the EMSO Azores observatory

Introduction

The EMSO-Azores observatory was first deployed in 2010. It aims at understanding the links between geological, physical and chemical processes and their effects on the dynamics of the hydrothermal fauna at different spatial and temporal scales at the Lucky Strike vent field (1700m depth, Mid Atlantic Ridge).

Methods

The autonomous observing system comprises two Sea Monitoring Nodes providing the energy, controlling the sensors, archiving and transmitting the data. The first node is deployed on the Lucky Strike fossil lava lake and measures the seismic activity and the vertical deformation of the sea floor. The second one is deployed at the base of the Tour Eiffel active edifice and monitors the variability of the edifice and its associated ecosystem. The nodes are acoustically linked to a surface buoy, ensuring satellite communication to the land base station. Data are available on the EMSO-Azores web page. The observatory setup comprises sets of autonomous instruments. A complementary site studies program is implemented during the cruises to increase the set of accessible parameters and to extend the spatial coverage of the project.

Results

Over the last 10 years, decisive results were obtained on the establishment of the fluid circulation in the hydrothermal system, on the key role of hydrothermal emissions in in the iron content of the oceans or on the spatial dispersion of particles and larvae of organisms by local currents. The stability of these hydrothermal communities on a decadal scale was highlighted and we showed for the first time the existence of biological rhythms on a deep-sea hydrothermal species! Conclusion The technologies developed and the knowledge acquired is a step forward to respond more effectively to the evaluation of the impacts of human activities in the deep sea (pollution, mineral resource exploitation, etc.).

This work has received funding from the European Union Seventh Framework Programme (FP7/2007-2013) under grant agreement n° [312463], the French ANR project Luckyscales ANR-14-CE02-0008.

12:25 - 12:40

Helena Hauss, Björn Fiedler, Johannes Karstensen, Rainer Kiko, Elizandro Rodrigues, Nele Weigt, Arne Körtzinger

Epi- and mesopelagic zooplankton time series at the Cape Verde Ocean Observatory

The Cape Verde Ocean Observatory as an open ocean site located windward of the Cabo Verde archipelago in the Eastern Tropical North Atlantic. Here, continuous moored observations as well as shipboard point observations were carried out since 2006. While the first years only hydrographic and chemical data were collected, we have expanded this time series to include zooplankton observations since 2012. Here we present results of repeated shipboard net samplings (five depth strata to a maximum of 1000m depth, day and night haul pairs) that were processed using the ZooScan system and analysed in terms of abundance, biomass and vertical migration for 41 taxonomic groups. This also allows to estimate active carbon flux by zooplankton, which we compare to NPP and passive particle flux derived from Underwater Vision Profiler (UVP5) profiles. Further, we used the acoustic backscatter continuous time series from the moored ADCP (upper 300m) to gain insights on temporal variability of zooplankton biomass in relation to environmental drivers.

12:40 - 12:55

Rylan J. Command, Fabio C. De Leo, Fabio C. De Leo Temporal dynamics of the deep-sea pink urchin Strongylocentrotus fragilis at the upper slope of Barkley Canyon

The Northeast Pacific continental margin is characterized by strong seasonal upwelling, which drives high primary productivity, and supports high diversity and biomass of benthic megafauna. The recent occurrence of a marine heat wave ("The Blob", sensu Kintisch, 2015) in 2013-2016 resulted in changes to phytoplankton community composition and loss of coastal kelp abundance and diversity, reducing gross primary productivity in the region. However, cumulative effects of marine heat waves and ongoing basin-scale deoxygenation in deep-sea ecosystems remain poorly understood. Here, we use a 7-year time series of physicochemical and video imagery data from Ocean Networks Canada's NEPTUNE observatory to investigate temporal dynamics of the deep-sea pink urchin Strongylocentrotus fragilis in relation to multi-year environmental variability. Using generalized additive models, we show that local S. fragilis abundance at Barkley Upper Slope (420 m) fluctuated over time in response to changes in dissolved oxygen concentration and suspended particulate matter in the benthic boundary layer (ADCP backscatter), with high abundance corresponding to high oxygen and low backscatter.

Seafloor dissolved oxygen ranged from 0.80-1.89 mL/L and varied seasonally, exhibiting a clear negative correlation with sea surface primary productivity (MODIS satellite Chl-a data), corresponding with the onset of yearly upwelling conditions. However, during the anomalously warm years affected by ‘The Blob’, vertical stratification dampened upwelling and maintained higher dissolved oxygen conditions near the seafloor. S. fragilis abundance declined during ‘Blob’ conditions, likely in response to reduced kelp and phytodetritus subsidies from coastal waters. We propose a foraging-respiration trade-off hypothesis, whereby S. fragilis forages in deeper water during weak upwelling and migrates to shallow habitats during low oxygen conditions. S. fragilis is an important bioturbator and detritivore; changes in the abundance and distribution of this species will directly affect sediment turnover rates and nutrient cycling on the continental margin, with consequences for surface and coastal productivity.

12:55 - 13:10

Mallory Ringham, Zhaohui ‘Aleck’ Wang, Mingshun Jiang, Sandra Brooke Exploration of fine-scale physical-biogeochemical environment over deep coral reefs on the West Florida slope using integrated ROV-lander-sensor systems

Deep-sea corals create complex structures that support diverse assemblages of invertebrates and fishes, some of which are economically important. Numerous abiotic factors influence the development of these ecosystems. Understanding spatio-temporal variation of the physicalbiogeochemical-environmental conditions, particularly carbonate chemistry, can provide insight into the distribution of deep coral ecosystems, and how they may be affected by future changes in ocean conditions. Information on the spatial and temporal dynamics of carbonate chemistry has been limited by the availability of precise in-situ sensors that can collect data for extended periods from mobile and stationary platforms.

The study objective was to document fine-scale and long-term physical-biogeochemical conditions over four deep coral habitats on the West Florida slope, Gulf of Mexico. In 2019, the ROV Global Explorer conducted visual surveys over scleractinian (Lophelia pertusa/ Desmophyllum pertusum) reefs and rocky slope habitats. The ROV was equipped with state-of-the-art carbon sensors including the dissolved inorganic carbon sensor Channelized Optical System II (CHANOS II) (Wang et al., 2015), and additional pCO2, pH, and other sensors. These collected high resolution data within and outside dense coral habitats. In addition, two benthic lander systems were equipped with pH/pCO2/CTD/DO/ADCP sensors, and deployed for 11 months in two locations within the study area; one was adjacent to a coral reef, and the other off a deep ridge. In-situ experiments of coral growth and skeletal dissolution were attached to the landers. Using these two approaches, we explore and characterize environmental variations at these coral communities with high resolutions (meters) and high-frequency (hours to days), and examine : 1) the sub-mesoscale spatial variability and drivers of the carbonate system over the deep coral sites, 2) temporal variability of carbonate chemistry over hourly to seasonal scales, and 3) the potential spatial correlation between the distribution of environmental conditions and coral coverage/ species distribution.

General 3: Life-history traits and connectivity

11:55 – 12:10

Vasiliki Koutsouveli, David Balgoma, Nadiezhda Santodomingo, Maria

Conejero, Hans Tore Rapp, Paco Cárdenas, Ana Riesgo

Reproductive biology of the deep-sea sponge genera Geodia and Phakellia: histological, lipididomic and transcriptomic approaches

Boreo-arctic sponge grounds are essential structural habitats that provide important services for the deep-sea ecosystem. Demosponges of the genera *Geodia* and *Phakellia* often dominate these habitats but many aspects of their basic biology are poorly known. Here, we studied ecological and molecular aspects of the sexual reproduction of five *Geodia* species and *Phakella ventilabrum* from the North Atlantic to understand their resilience by evaluating: 1) the seasonality and fecundity, 2) the molecular toolkits regulating the gametogenesis, and 3) the lipid metabolism for yolk nutrient formation during oogenesis (in *P. ventilabrum*).

All the studied species were oviparous and gonochoristic and their reproductive season spanned from late spring to early autumn. While Geodia spp. had synchronous gamete development at individual and population levels, and their oocytes had mostly lipid yolk, P. ventilabrum had asynchronous oocyte development and its oocytes had lipid and protein yolk. Both genera had much higher density of oocytes than most temperate and tropical oviparous species studied elsewhere. Our lipidome analysis revealed that, as oogenesis progressed, the signal of most triacylglycerides (TGs) increased, while that of other lipids decreased. In addition, genes involved in the biosynthesis of TGs were upregulated in female tissues, strongly suggesting that TGs might be the main component of lipid yolk in these sponges. Finally, we found that the molecular toolkit regulating oogenesis and spermatogenesis has been conserved from sponges to vertebrates.

The fecundity rates for both genera explain their high population densities. However the continuous disturbance of these ecosystems, essentially due to bottom trawling, might not allow the future populations to recover. Their reproductive seasonality might be used to design conservation strategies for the North Atlantic deep sea. Finally, this study provides essential clues for understanding the origin of the lipid yolk content and the evolution of gametogenesis in Metazoa.

12:10 - 12:25

Adrien Tran Lu Y, Claire Daguin-Thiébaut, Stéphanie Ruault, Pierre-Alexandre Gagnaire, Nicolas Bierne, Sophie Arnaud-Haond, Didier Jollivet, Stéphane Hourdez, François Bonhomme

Global to fine-scale patterns of genomic connectivity of hydrothermal vent gasteropod Ifremeria nautilei in the Western Pacific.

Understanding population connectivity is a central issue for evolutionary ecology and its applications in conservation and management. The use of indirect genetic approaches has been particularly useful in cases where direct observation of migration is not possible, as in most marine environments, including the deep sea. Since their discovery in the late 1970s, hydrothermal ecosystems have drawn considerable attention for their unique fauna, habitat and distribution. However, they have also recently attracted interest from deep-sea mining.

Previous studies have met with limited success in inferring fine-grained structure because many approaches have used few loci and generally provide a global but noisy picture of the demo-genetic events affecting them. By providing access to thousands of markers across the genome, it is now possible to identify loci with more information about the fine-grained population structure and individual ancestry. In this study, we explored the range-wide population connectivity of Ifremeria nautilei, a deep-sea hydrothermal vent snail, using restriction site associated DNA (RAD) sequencing. The global picture unraveled with ~10,000 markers is two panmictic genetic clusters isolated into two distinct set of oceanic back-arcbasins separated by 2000 km.

While the global analysis appears to depict two isolated populations, multi-marker inference of the demographic history and connectivity of these two populations allowed us to demonstrate that they began to diverge about 70,000 generations ago while still exhibiting weak and asymmetric gene flow. Furthermore, a careful analysis of outlier markers showed that these two groups are in fact two highly connected metapopulations with subtle limitation of connectivity. These results illustrate the use and application of large genomic datasets to understand pattern of population connectivity from the global to the fine scale in high gene-flow marine species.

12:25 - 12:40

Lauren Dykman, Carolyn Tepolt, Armand Kuris, Charles Blend, Lauren Mullineaux

Discovering the complex life cycles of hydrothermal vent parasites

Parasites are integral members of most ecosystems, and many must pass through more than one host species to complete their life cycle. Previous investigation into parasites at the 9°50’N vent field on the East Pacific Rise has revealed parasites are absent in many vent invertebrates but are diverse and abundant in the vent fishes Thermarces cerberus (Zoarcidae) and Thermichthys hollisi (Bythitidae). The most abundant group of parasites, found as adults in vent fishes, were digenetic trematodes. These typically require two other host species to complete their life cycle, yet the specific hosts used in vent ecosystems are unknown. During two HOV/ROV cruises in 2019 and 2021, we dissected a wide range of potential host fauna from the 9°50’N vent field and documented all stages of the trematode life cycle. While most gastropod species were parasite-free, 10% of the glass limpet Eulepetopsis vitrea (1st intermediate host) were infected by trematode parthenitae, which castrate the host. Cercariae, the free-living larval stage, were recovered with benthic samples. Although a number of snail and worm species hosted metacercariae, the shrimp Alvinocaris lusca (2nd intermediate host) was the most heavily infected. Out of 12 shrimp examined, all had metacercariae encysted in the abdominal muscle, with the heaviest burden being 344 cysts. Since fish, the definitive host, are infected by feeding on prey, the heavy infection we documented in shrimp can explain how vent fish achieve burdens of up to 600 worms. We also present genetic results linking the different life stages in an attempt to complete the life cycle of a deep-sea trematode species for the first time. The diversity and abundance of trematodes in a select few vent species indicates intimate feeding relationships that have persisted over evolutionary timescales, and which likely play a role in shaping vent communities.

12:40 - 12:55

Graeme Guy, Anna Metaxas Recruitment of deep-water corals and sponges on the continental slope off Nova Scotia, Canada: Implications for population connectivity and conservation

Deep-water, structure-forming invertebrates, such as corals and sponges, provide habitat complexity and shelter for many fauna, contributing to the health of deep-sea ecosystems. These animals are vulnerable to anthropogenic disturbances such as fishing and climate change because they grow slowly and have long life spans. This vulnerability has led to the protection of several deep-water coral and sponge aggregations on the continental shelf and slope in Atlantic Canada, specifically focused on the corals Paragorgia arborea and Primnoa resedaeformis, and the sponge Vazella pourtalesi. Because populations of these species are discontinuous and spatially fragmented, selfrecruitment and population connectivity are important in regulating their distribution, and potential for recovery from perturbations. However, population connectivity is poorly understood, and measures of recruitment are rare. Here, we present evidence of high coral and sponge recruitment occurring only at a few locations on the continental slope off Nova Scotia, Canada. Based on size frequency distributions recruitment of corals varied with depth, whereas a single, newly recorded sponge aggregation was dominated by juveniles. We suggest that both pre- and post-settlement processes are responsible for the observed size distributions. These data on recruitment can be incorporated into high resolution hydrodynamic models, and in combination with particle tracking, used to assess population connectivity between patches of P. arborea, P. resedaeformis and V. pourtalesi on the Scotian continental margin. This knowledge can allow for more effective conservation measures to protect these vulnerable species.

12:55 - 13:10

Michelle Hauer, Corinna Breusing, Elizabeth Trembath-Reichart, Julie Huber, Roxanne Beinart Population genomics of the symbionts of hydrothermal vent snail Alviniconcha hessleri reveals greater differentiation by vent site than by host-associated vs free-living states

Deep-sea hydrothermal vents support complex ecosystems and immense animal biomass due to chemoautotrophic bacteria that live as mutualistic symbionts with their animal hosts. The bacterial symbionts oxidize chemical reductants (e.g., H2S, H2, CH4) in venting fluids to obtain energy for the production of organic matter, which often provides the only food source for the animal host. Alviniconcha hessleri, the dominant animal species at vents in the Mariana back-arc, hosts a specific phylotype of intracellular gamma-proteobacterial symbiont in its gills that is acquired from the environment, yet nothing is known about the symbionts in their free-living state. Using a population genomics approach that assessed genetic polymorphisms in shared genes, our results show that there is greater population differentiation between the symbionts from different hydrothermal vent localities than when comparing host-associated and free-living populations. Similarly, we found that functional differences based on gene content vary by vent site and not by lifestyle (host-associated vs. free-living). Altogether, this work provides evidence that Alviniconcha hessleri associates with geographically differentiated strains of symbiont that it acquires from a local, environmental population.

Special session: Arts & Science

14:30 - 14:45

Christine Paillard, Jozée Sarrazin Marine immersion in arts & sciences

The complexity of the marine ecosystems in relation to climate change and other anthropogenic impacts confronts us with the need to interact with many scientific disciplines, but also with artists, whose multifaceted visions allow us to explore the unknown and the imaginary by "doing" and "living" in complete sensitive immersions. Several “art and science” experiments, mixing scientists from different disciplines with artists working on different media -including visual and sound artists, performers, choreographers, theatre artists, filmmakers-, are organized within the framework of the Interdisciplinary Graduate School for the Blue Planet (IS Blue). These experiments question the evolution of the co-construction process needed to favor transdisciplinary approaches. This “hybridization process” is of particular interest to the “science, art and creation” research, and not only the result or the production itself. “Art” is not there only to share or disseminate the science but also to question our scientific approaches and trigger new ideas in the development of research strategies. Restitutions and public experiments allow the artists and scientists that were involved well as the general public to be confronted with the dynamics and evolution of the research process and to promote ecological awareness. Arts and sciences festivals such as RESSAC (REsearch ScienceS Arts and Creation) initiated by the University of Western Britany in 2019, in conjunction with CNRS, Ifremer, IRD and local and national cultural partners, attempt to explore and immerse the public in this transdisciplinary “arts and sciences” approach. As the ocean, and the deep-sea in particular, is encountering great challenges in the near future, it is crucial to involve and engage with the next generation.

14:45 - 15:00

Jozee Sarrazin, Marjolaine Matabos, Lucie Delauney, Julie Tourolle, Catherine Borremans, Sandra Fuchs, Olivier Dugornay, Pierre-Marie Sarradin and many others EMSO-

Azores: a tool to raise awareness on deep-sea wonders

In the context of increased anthropogenic activities in the deep sea, we should take responsibility for raising awareness on the presence of various ecosystems, their uniqueness and fragility and also on the immense knowledge gaps we are facing. Issues about future mining scenarios have to be raised and explained and alternatives debated. In addition, we feel that it is of upmost importance to inform the society about our research, especially since they occur in inaccessible areas. Since 2010, the EMSO-Azores observatory monitors hydrothermal processes, from the sub-seafloor to the water column, at the Lucky Strike vent field, at the heart of a marine protected area managed by the Azorean government. The annual maintenance cruises of this observatory (Momarsat) offer unprecedented opportunities to plan outreach activities and bring artists on board. For the last 10 years, we have proposed various original actions to make the science, the people and life onboard accessible to the public and classrooms. In addition to the traditional online logbook, remote live events and interactions with school children were regularly organized. The development of the citizen science project Deep-Sea Spy pushed further the involvement of the public with a direct contribution to our research. Our activities also inspired a number of art production from books to theater.

Our 10 year experience taught us that successful outreach activities should involve a wide range of collaborations with dedicated structures including aquaria, associations and school academia. Over time, we have touched a variety of stakeholders from the general public to scholars, managers and policy makers. Some tools, such as the virtual visit to Eiffel Tower, were even used to promote our research and enhance Ifremer's image with the French ministries and inter-governmental agencies. Finally, through all these actions, we can share our passion while harvesting energy from the outside!

15:00 - 15:15

Dorte Janussen, Dorte Sukavi

Polar and deep-sea light as communication medium and source of inspiration

Light in all its appearances is the energy source of all life and evolution. Even in the deep-sea, light -- e. g. as bioluminescence-- plays a major role in the communication between organisms. In nature, the games of light and color have fascinate mankind since the onset of human culture. Working as a marine scientist, deep-sea and polar researcher and also as an artist, it is my priviledge being to find inspiration in lights and colors, of the marine organisms and landscapes. Especially at polar latitudes, the incident sunlight into water and ice generates scenaries and plays of light which enchant and inspire our imagination and fantasy. In my artwork, I experiment with reflexions and mirror images to create living light spaces. My light objects are partly or completely made of glass, such as different glass crystals and filter-interference glasses, which divide the incoming light (from spots) and reflect it in all directions as pure light colors. As light objects move naturall with the air, many visitors report that they feel spaced out in dancing lights, enraptured into stary space, or the deep-sea. With focus on marine and deep-sea environments, exemples are shown how nature-inspired light art can be utilised as a communication medium to transport crusial messenges, such as the beauty and protection worthiness of species and biotopes diversity. In videos, I show some of my moving light objects inspired by deep-sea animals such as medusae, and their effects of danceng lights in different ourdoors and indoors surroundings. And if possible, I would like bring one of my smaller light objects into a darker corner of the conference venue, to show this in real.

15:15 - 15:30

Teresa Radziejewska, Grażyna Czernik

Children's art as a pathway to ocean literacy

Achieving ocean literacy can be addressed in different ways. A particularly promising approach seems to couple an early start (working with children) with expression in art. We are showing how the artwork of schoolchildren – pupils of a private art school – following a series of talks and presentations elucidating the ocean life and challenges it faces, reflects the children's appreciation of the ocean in general and of the deep-sea.

15:30 - 15:45

Jonatha Giddens, Denley Delaney, Alan Turchik

Drawing the ocean closer: Deep-ocean cameras and an art-integrated exploration approach provide windows and mirrors into the deep sea

While new developments in ocean observing technology are expanding scientist's ability to study the deep ocean, communicating the value of the deep sea to society remains a top challenge for ocean scientists working in these remote areas. Transdisciplinary approaches to knowledge generation and communication can advance ocean literacy by coupling technological innovation with artistic inspiration. To this end, the Deep Sea Research Project of the National Geographic Society Exploration Technology Lab (ExTech) developed tools to advance cost-effective biological observation in the deep ocean, and an approach to advance ocean literacy through the integration of technology, science, and art. The ExTech Lab developed an autonomous benthic lander platform with a baited camera system to conduct stationary video surveys of deep-sea megafauna. With these camera systems, we are empowering explorers to expand our knowledge of deep-sea species distributions, life history, and patterns in biodiversity across regions. Moreover, we are creating new opportunities to communicate ocean science by reimagining the knowledge-generation process. We developed an art-integrated deep-sea observation methodology to more comprehensively investigate and communicate experiences of our ocean research. In the tradition of the early naturalist's journals and the illustrations of pioneering deep-sea explorers, a field-journaling course was developed in 2019. During a month-long expedition to the Galapagos, this course guided 10 researchers to enhance our ocean observations through field journaling, and we shared our insights broadly with society through pictures, presentations, and stories. This innovative approach can be used to connect people and communities to the ocean, and inspire them to engage in pro-environmental behaviours. The camera system technology provides a window to the deep-ocean, and the art-integrated field journaling course provides a mirror for researchers to see ourselves in relation to these remote areas, and to share our ocean inspirations with society.

15:45 - 16:00

Vincent Rousselot, DOUCHA Music Association, Joëlle Nassiet, Lucile Pichereau, Xavier Normand, Julien Ouvrard, Galatée Dietrich-Sainsaulieu COELACANTH PROJECT – MUSIC FROM THE DEPTHS

[ART & SCIENCE] Short performance with deep sea sounds and artistic science mediation

The five musicians of French band DOUCHA are working with the OHA-SIS-BIO program of the Geoscience Ocean research laboratory deploying hydrophones in the Indian Ocean for the CNRS. They also collaborate with the ASTI (Underwater Acoustics and Information Processing) attached to the F.O.F. (French Oceanographic Fleet) and managed by IFREMER, as well as the CHORUS Bioacoustics Research Institute.

The crackling of glaciers, the rubbing of tectonic plates, the songs of narwhals or the squeaking of shrimps... The musicians propose a poetic and musical diversion of scientific materials. They mix their instruments (accordion, cello, musical saw, clarinet, saxophone, double bass, drums) with recordings of the ocean floor collected from scientists. They reuse these sounds as notes and chords blending with instruments and singing and speaking voices telling of the ocean floor.

The reproduction of these sounds is done via devices that control the sound through movement (Leap Motion© and ultrasound sensors). Processing and sampling with Ableton Live© also allows the sounds to be assigned to musical instruments: the Antarctic pygmy whale can thus sing on all the notes of the piano. This artistic project immerses us under the surface to listen to what is being sung in the abyss: to meet the Coelacanth!

General 2: Biodiversity

14:30 - 14:45

Alessia C. Ciraolo, Paul Snelgrove, Andrew K. Sweetman, Marta M. Cecchetto Seafloor ecosystem functioning within the oxygen minimum zone along the continental slope of Vancouver Island

Global warming has reduced the overall dissolved O2 inventory of the global ocean, contributing to ongoing physical, chemical, and biological changes. The oxygen minimum zone along the continental slope of the Northeast Pacific Ocean (600-1200 m depth) offers a unique opportunity to study ecosystem response along an oxygen gradient on the continental slope off Vancouver Island. Using a multicorer we collected sediment cores from 3 sites (200, 475, 800 m depths) with contrasting oxygen concentrations in near-bottom waters (77, 40, and 10μm/L, respectively). We performed shipboard pulse-chase tracer incubations in which we added labelled algae (Phaeodactylum sp.) to some replicate cores but not others. Our goal was to examine the effects of depth and dissolved oxygen on macrofaunal communities and their response to phytodetritus and associated benthic nutrient fluxes. Our preliminary results show oxygen collinearity with depth, and significant impacts on macrofaunal communities. Infaunal diversity and abundance decreased with increasing depth and decreasing oxygen, but with higher evenness in hypoxic sites than in well-oxygenated sites. PERMANOVA indicated that O2 conc/depth explained 75.9% of macrofauna community composition variation. Spionid and paraonid polychates contributed most to faunal differences among the three sampling sites. Not surprisingly, total abundances were lower in the 5-10 cm layer than in shallower sediment horizons. In addition, benthic nutrient fluxes were different among sites and treatments. We found the highest net nutrient uptake in the shallowest site (200 m) and the less de-oxygenated site (475m), with highest nutrient regeneration at 850 m depth. The addition of algae in some cores of the two de-oxygeneted sites led to nitrate and silica uptake, ammonium regeneration, release of nitrite at 475 m and uptake at 850 m and, phosphate consumption at 475 m and regeneration at 850 m. The oxygen minimum zone thus exerts contrasting effects on macrobenthos and on associated ecosystem processes.

14:45 -15:00

Beatriz E. Mejia-Mercado, Amy R. Baco Characterization and spatial variation of the deep-sea fish assemblages on Pioneer Bank, Northwestern Hawaiian Islands

Knowledge of the spatial variation of deep-sea fish assemblages is a critical gap in our understanding of seamount ecology. Pioneer Bank in the Papahānaumokuākea Marine National Monument has no known history of human impacts; thus, it is a good location to further describe deep-sea fish assemblages. From replicated Autonomous Underwater Vehicle (AUV) transects at 300, 450, and 600 m on three sides of Pioneer Bank, 4,190 fishes were observed representing 81 species. Fish assemblages were dominated by Gadiformes, Perciformes, and Stomiiformes. The relative abundance of fishes was significantly different among sides of the seamount and the interaction of side and depth, with the NW side having the highest relative abundance at 450 m. Species richness, rarefaction estimates of expected species richness, Shannon diversity, and Simpson dominance showed significant differences by side, but not by depth. These differences were between the S and NW sides; with the S side having the lowest diversity and high dominance. The structure of the fish assemblage had significant differences among both sides and depths, with depth as the most important factor. Fish assemblage structure was most strongly correlated with % rugosity, Chl-a, and mean direction of the substrate. These scales of spatial variability both with depth and across short horizontal distances on a single seamount are similar to those found on other seamounts, which reaffirms the spatial heterogeneity in deep-sea fish assemblages on these underwater features. This study can be considered as an ecological baseline for the management and conservation of seamounts.

15:00 - 15:15

Craig R. McClain, Granger Hanks, S. River Bryant, Avery Hatch, Phil Manlick, Seth Newsome, Clifton Nunnally, Greg Rouse, Chiara Romano, John Whiteman Functional Diversity and Non-Random Assembly Connect Diversity and Ecosystem Function on the Bottom of the Ocean

Enhanced biological diversity bestows enhanced ecosystem function. The biodiversityecosystem function (BEF) relationship is detectable across scales of diversity, ecosystem processes, organisms, habitats, and empirical and theoretical treatments. However, despite BEF research stemming back to Elton and the reawakening and exponential growth of the field in 1990's, many questions remain. The answers to these questions are urgent in understanding the impacts of accelerated worldwide loss of biodiversity. We examine BEF relationships, community assembly, composition, and niche diversity in deep-sea xylophagid bivalve wood-fall communities. In May 2017, 32 wood falls were deployed at two sites at 2171 and 1970m in the northern Gulf of Mexico. A total of 18,767 individuals from 14 xylophagid bivalve species were identified. The amount of consumed wood in wood falls increased significantly with both abundance and species richness of xylophagid bivalves. Wood fall communities also changed nonrandomly as xylophagid diversity increases. Individual xylophagid species also inhabited unique trophic and spatial niches, but species individual effects on total wood consumption greatly varied. Overall, we find that functional redundancy is minimal in xylophagid bivalves, with increased richness conferring greater ecosystem function. Yet, the connections were complex with differential species effects and non-random assembly of xylphagid bivalve communities.

15:15 - 15:30

Jennifer Le, Peter Girguis, Lisa Levin Using deep-sea imagery to examine ecosystem services associated with methane seeps

This study was a first-step towards ecosystem services characterization and quantification using deep-sea imagery, which can often be underutilized. In 2015, Ocean Exploration Trust conducted an expedition on the E/V Nautilus to visit several methane seeps off the coast of southern California (USA). As has become routine on many deep-sea expeditions, remotely-operated vehicle (ROV) Hercules captured continuous video during each dive, yielding a tremendous amount of imagery (pictures and videos). We leveraged these dive videos and biological trait analysis to develop an approach to use deep-sea imagery for examining ecosystem services, in addition to biological community descriptions essential to our knowledge and ability to protect deep-sea habitats. This proof-of-concept qualitatively describes and compares megafaunal communities and their ecosystem services potential, specifically those related to fisheries and carbon cycling. Three methane seeps were used in this demonstration: Point Dume (~725 m), Palos Verdes (~506 m), and Del Mar (~1023 m). A total of 100 megafaunal morphotypes were observed and were assigned ecosystem services scores. This enabled comparison of potential ecosystem services among the methane seeps and their adjacent areas, identifying areas of possible high conservation value. Our results suggest that the Del Mar methane seep provides the greatest contribution to fisheries and carbon services relative to other sites. In one case, non-seep areas are associated with higher ecosystem services scores (Point Dume) whereas in another, the seep transition areas scored the highest (Palos Verdes), which emphasizes the unique habitats that methane seeps comprise.

15:30 - 15:45

Elizabeth Miller, Christopher Martinez, Sarah Friedman, Peter Wainwright, Samantha Price, Luke Tornabene Alternating Regimes of Shallow and Deep Diversification in Marine Fishes

The deep sea contains a surprising diversity of life including iconic groups such as anglerfishes, lanternfishes and viperfishes. Still, about 70% of teleost fish species are restricted to the photic zone (>200 meters). Our goal was to uncover the historical events and evolutionary processes that generated this disparity in marine species richness. Possible explanations for higher shallow richness include: more time spent in shallow versus deep habitats, faster shallow speciation rates, and the rarity of shallow-to-deep transitions. We used biogeographic models and a time-calibrated phylogeny of teleosts to identify the timing of individual colonisations of the deep sea and rates of speciation within each habitat following colonisation. We found that no single process adequately explained the disparity. Instead, we discovered alternating periods that favored either shallow or deep diversification over the 200-million-year history of teleosts. We also found that deep colonisation rates varied through time, with evidence of time-variable ecological filtering on morphologies associated with deep adaptations. Teleosts originated in the shallow zone; however, shallow and deep diversity became similar around 125 mya due to a burst of deep originations. Later, shallow diversification outpaced that of deep fishes, creating an inflection point in relative diversity ~100 mya. Deep diversification and colonisation rates increased again over the most recent 15 million years, suggesting we are currently living in a time favorable for deep sea fishes. These phases are consistent with an early hypothesis by Andriashev (1953) that deep sea fishes are composed of "ancient" and "secondary" forms. We conclude that most fishes today are shallow because of elevated origination from 100-15 mya (but not recent diversification) and the resulting accumulation of diversity over a 75-million-year period.

References:

Andriashev, A.P. 1953. Ancient deep-water and secondary deep-water fishes and their importance in a zoogeographical analysis. Notes on Special Problems in Ichthyology, Moscow.

15:45 - 16:00

Bryant River, Craig McClain Functional diversity analysis reveals deep-sea energetic niche expansion driven by trait tradeoffs

Anthropogenic stressors are already having known effects on deep-sea communities, and global climate change is shifting the landscape of energy availability in the world's oceans. This is predicted to have impacts on community composition, largely determined by functional diversity. Shifts in the community functional space have strong impacts on important aspects of ecosystem functioning, so it is paramount that we understand the impacts of energy on functional diversity in the deep sea. We investigate patterns of functional space, functional type, and functional traits of bivalve communities across the energetic gradient of the deep Atlantic Ocean. We use three traits related to energetic demands to define the axes of functional space, the unique combination of these traits as functional types, and the proportion of species employing these traits to investigate functional tradeoffs across the energetic gradient. As species richness increases with energy, new species are added into functional space through niche expansion rather than niche packing. Underlying this pattern are complex dynamics of gains and losses of individual functional types, with few adapted to the low- and high-energy extremes, and most occurring within intermediate energy regimes. Adaptive qualities of specific traits are evidenced by those functional types occuring at energetic extremes. Tradeoffs between these traits within the intermediate energy zone underlie an increased coexistence of functional types, which in turn drives the unimodal pattern of functional types, expansion of utilized functional space, and alpha-diversity as a whole. This work suggests that deepsea benthic communities may be especially vulnerable to continued shifts in food availability through the Anthropocene, as this may have long-term effects on community composition and ultimately lead to declines in ecosystem functioning of the deep benthos as a whole.

Special: open session

16:20 – 16:35

Horowitz Jeremy, Andrea M. Quattrini, Mercer R. Brugler, Tom C.L. Bridge, David J. Miller, Peter, F. Cowman Morphological innovations drove the persistence of black corals through deep time

Deep-sea lineages are thought to have evolved from shallow-water ancestors, but this hypothesis has yet to be tested for many taxonomic groups. Invading deeper habitats can decrease ecological competition; however, survival in nutrient-poor environments requires morphological adaptations to address different abiotic conditions. Corals are significant contributors to the faunal diversity of the deep sea, but how and when lineages invaded this biome remains unclear. Here, we reconstruct a time-calibrated phylogeny from genomic capture data to estimate ancestral depth ranges of the Order Antipatharia (black corals), which occur in all oceans and depths from 3 to >8,000 m. We found that black corals first diversified during the early Ordovician (443 Ma) in slope habitats (250–1,999 m) and then expanded into shelf depths (0–249 m) from the late Carboniferous to early Permian (295 Ma). Invasion of the abyss (>2,000 m) occurred relatively recently, in the Oligocene (30 Ma). Ancestral state reconstruction suggested that pinnules, specialized branch features that maximize surface area, first appeared ~188 Ma following the Triassic-Jurassic extinction event. This adaptive feature enhanced the ability to filter feed and likely enabled black corals to diversify and persist into the abyss. Together, these results demonstrate that bathymetric transitions of anthozoan fauna across deep time are more complicated than originally hypothesized, and that novel morphological adaptations may be necessary to invade and persist in novel habitats.

16:35 – 16:50

Alexandra A.-T. Weber, Adnan Moussalli, Andrew F. Hugall, Sophie Arnaud-Haond, Jozée Sarrazin, Matthew D. McGee, Timothy D. O'Hara Giant genomes uncover ecological speciation in the deep ocean

The deep ocean is the largest biome on Earth and yet it is among the least studied environments of our planet. Hence, the genomic mechanisms underlying the formation of species in the deep sea remain virtually unknown. Here we present the assembly of one of the largest sequenced invertebrate genomes. We used 10x chromium linked-reads, ONT long reads and transcriptomic reads to generate a draft genome assembly. The abyssal brittle star *Ophiosphalma armigerum* (Echinodermata: Ophiuroidea) genome is 8 Gb large and contains about 52% repeats. We further sequenced 123 *O. armigerum* individuals spanning the whole species geographic (from the North Atlantic Ocean to South Australia) and bathymetric range (from 2200m to 4800m depth). We found significant bathymetric structuring among bathyal (~2500m) and abyssal (~4000m) populations, suggesting ecological speciation along a depth gradient in *O. armigerum*. We then describe genomic islands of speciation and candidate genes for deep-sea adaptation. When focusing on the individuals from abyssal depths, we uncovered high levels of gene flow among localities around Australia. Remarkably, trans-oceanic connectivity was detected as individuals from the North Atlantic Ocean and individuals from South Australia were connected by significant levels of gene flow at abyssal depths. This study provides unprecedented marine invertebrate genomic resources and sheds light on speciation and connectivity mechanisms in the largest biome of the planet.

16:50 – 17:05

Henk Jan Hoving, Björn Fiedler Helena Hauss, Arne Körtzinger Pelagic cephalopods as nutrient vectors in the deep sea

The Republic of Cabo Verde is an African islands state that is located in the eastern tropical North Atlantic and is a hotspot of biodiversity, large-scale fisheries and climate change. The large exclusive economic zone of Cabo Verde features diverse benthic habitats (abyssal plain, seamounts and steep island slopes) that are furthermore impacted by strong spatiotemporal variability of the pelagic habitat. Seasonal and mesoscale productivity differences lead to changes in particle export flux as well as mesopelagic oxygen minimum zone intensity. Altogether, this makes Cabo Verde a very interesting region for deep-sea biological research. Cabo Verde is an "ocean science hub" in the eastern tropical Atlantic and includes the

Cape Verde Ocean Observatory oceanic time series and the Ocean Science Centre Mindelo, which hosts research laboratories and facilitates local and regional research campaigns with logistical and technical support for national and international researchers. Here we present research results obtained in Cabo Verde waters during four expeditions (MSM49, MSM61, POS520, POS532) between 2015-2019 which general aim was to document the diversity, ecosystem functioning and role of pelagic fauna in the biological carbon pump in oceanic and coastal deep seas of Cabo Verde. We collected pelagic and benthic in situ observations with towed camera systems and the manned submersible JAGO, and performed net and eDNA sampling in the water column. Results include the documentation of the vertical community structure of pelagic fauna in relation to oxygen minimum zones and mesoscale eddies, the identification of pelagic tunicates as foodfalls and other vectors in the biological carbon pump, and novel regional records of gelatinous taxa, crustaceans, fishes and molluscs. We present new and ongoing scientific initiatives to study Cabo Verde deep-sea ecosystems with the overall goal to collect baseline information that will aid in knowledge-based conservation and sustainable exploitation management plans for the region.

17:05 – 17:20

Vanessa I. Stenvers, Helena Hauss, Andrew K. Sweetman, Henk-Jan T. Hoving Impacts of global warming and deep-sea mining induced sediment plumes on the mesopelagic medusa Periphylla periphylla

While the deep pelagic ocean remains largely unexplored, it is becoming increasingly apparent that the inhabitants of this vast realm are under growing threats from human activities. Stressors such as resource extraction, pollution and global warming can lead to loss of biodiversity and associated ecosystem services. This is particularly worrisome as deep pelagic fauna play a vital role in atmospheric carbon sequestration, nutrient recycling and provisioning of commercially important fish stocks. In spite of this, species-specific responses of pelagic fauna to anthropogenic stressors remain poorly documented. Here, we investigate the effects of global warming and sediment plumes that will be produced during deep-sea mining on the mesopelagic jellyfish Periphylla periphylla. This species was chosen for its cosmopolitan distribution, occurrence from the surface down to 4000 m depth and high abundance in several mesopelagic Norwegian fjords. Given that sediment suspension in the pelagic ocean is generally low and temperatures at depth are buffered, we hypothesized that pelagic animals would have a high sensitivity threshold. Through a series of ex situ experiments, using P. periphylla collected from the Lurefjord, Norway, we measured the metabolic response (ammonium excretion and respiration) and expression of stress related RNA transcripts. Three temperatures (in situ, +2°C, +4°C for 7–9 hours) and five abyssal sediment concentrations (0, 16.7, 33.3, 166.7, 333.3 mg·L-1 for 24 hours) were tested. Our first results show that a four degree increase in temperature doubled respiration rates and that ammonium excretion increased over five-fold. Suspended particle load showed a visible negative effect on P. periphylla at concentrations >33.3 mg·L-1. More detailed insights into the responses of P. periphylla will be gained from ongoing experiments and analyses. We present and discuss one of the first datasets on speciesspecific tolerances towards warming oceans and mining induced sediment suspension in a deep pelagic gelatinous organism.

16th DSBS Deep-Sea Biology Symposium

Brest, 12-17 September 2021

Version 29th of August 2021

Posters

General & Special Sessions 1 Conservation topics and stewardship (natural/anthropogenic impacts, conservation, governance)

- ### Deep Sea Biology and the Ocean Decade in Europe

  François H. LALLIER

The United Nation Decade of Ocean Science for Sustainable Development has just begun this year. Deep sea is mentioned in the road map for the Ocean Decade as a frontier of science and discovery, calling for research to advance understanding of deep-sea ecosystems, their functions, vulnerabilities, and services to society. Scientists gathered in the Deep-Ocean Stewardship Initiative (DOSI) promote a healthy deep ocean able to contribute to the wider Earth system, through its sustainable management informed by independent science. They have published some papers giving recommendations and prompting for actions, and the Ocean Decade is certainly offering the perfect framework to turn these into concrete realizations. At the European level, the Horizon 2030 Mission Ocean identified deep sea as an important target focusing on filling the gap in knowledge and increasing ocean literacy on these largely unknown regions of the ocean that should be better explored before considering any exploitation. The European Marine Board, the renowned scientific think-tank, is considering the launch of a deepsea related working group to identify more precise targets and programs to be sustained by European countries. For example, in France, a newly funded program on Ocean & Climate, clearly designate the deep sea as a priority. This presentation at the Deep Sea Biology conference will serve as a focal point to promote discussion and envision future coherent and complementary operations within our international, and specifically European, community.

Special session 1b# Spatial planning in the deep - lesson learned and new opportunities.pdf – Menini

- ### Coordinating Area-based Management Tools for an Integrated Governance of the Ocean Resources

  Giovanni Ardito, Marzia Rovere

Due to the different and conflicting uses of marine areas beyond national jurisdiction (ABNJ) and their resources, the deep ocean is increasingly under pressure.

Despite political pledges, only 2.7 % of the Ocean is currently preserved through area-based management tools (ABMT) or marine protected areas (MPA), most of which are sectoral in nature and only aimed at protecting the marine environment from specific human activities or sources of pollution. The main reason for this is the absence of a global legal framework for the establishment of ABMT and MPA in ABNJ, aimed at the comprehensive protection of their biodiversity.

In the last years, States are in the process of concluding a legally binding instrument on the conservation and sustainable use of biological diversity in ABNJ (BBNJ treaty). While one of its pillars precisely concerns the establishment of ABMT in the high seas and the Area, it is still unclear how to operationalize the required coordination among the existing global and regional frameworks and bodies having a competence in this regard.

As the International Seabed Authority is approaching the last stages of the negotiation for the regulations on exploitation of mineral resources, its contribution to the protection and conservation of biodiversity beyond national jurisdiction has come to the fore. Interestingly, in the draft regulations, there is no provision explicitly requiring the Authority to consult other competent bodies before approving a plan of work for exploitation, should its geographical scope intersect an existing ABMT.

This presentation will highlight areas of possible geographical overlaps and underline the need for a better coordination among existing international bodies. In particular, it will discuss the inclusion of appropriate clauses in the draft to ensure that ABMT for certain anthropogenic activities are taken into account when recommending the approval of a plan of work for deep-sea mining.

- ### From theory to practice development of a deep-sea ecosystem services framework

  Giulia La Bianca, Kerry Howeel, Sian Rees, Martin Attrill, Kerry Sink, Mandy Lombard

Scientists agree that despite its remoteness, the deep sea has been affected by human activity and changes are already noticeable. To understand the implications of these changes to human society, it is urgent to determine and assess the services provided by unique and diverse ecosystems in the deep sea. However, progress in this area is limited by the lack of an appropriate framework. This study qualitatively assesses popular ecosystem services frameworks and their suitability in deep-sea ecosystem services (ES) assessment, and proposes the first ES framework for the deep sea. We review and summarise existing scientific literature related to marine ES frameworks and extract and compare services that are relevant to deep-sea habitats. Following this review we adopt aspects of the UK National Ecosystem Assessment (UK NEA), Options for Delivering Ecosystem Based Marine Management (ODEMM) and the Common International Classification for Ecosystem Services (CICES) frameworksfor use in a new deep-sea ES framework.Our proposed framework consists of 7 supporting services; 4 regulating services; 2 provisioning services and 3 cultural services. More peer-reviewed evidence relating to deep-sea habitats was available on supporting services than final ecosystem services. This is not surprising, as supporting services relate to ecological functions, which have been studied more extensively than natural capital and ecosystem services. We discuss knowledge gaps in the linkages between supporting and final services, which stem from the lack of detailed information on life histories and habitat dependencies of deep-sea benthic organisms.

Special Session 1c# Managing Deep-sea Ecosystems at Ocean Basin Scale.pdf – Morato & Roberts

- ## Random Forest Classification of Deep-Sea Habitats in the North Atlantic Basin using Predicted Species Assemblages as Proxie
  Oisin Callery, Anthony Grehan

Assessing the impact of human activities on the environment and on marine species and habitats is fundamental to the development of effective ecosystem based management. Assessment of the impact(s) of a given anthropogenic stressor on a given marine habitat requires that the sensitivity of that particular habitat-stressor combination be individually considered. The UK Marine Evidence-based Sensitivity Assessment (MarESA) database compiled by the Marine Life Information Network (MarLIN) represents the most comprehensive sensitivity dataset currently available. The MarESA database (supplemented where necessary with sensitivity assessments carried out in projects such as the MB0102 project) provides sensitivity scores for a diverse range of marine habitats classified under the European Nature Information System (EUNIS). The EUSeaMap which provides a broad-scale EUNIS seabed habitat map for Europe can be used as a basis to conduct impact assessments for a large portion of the North-East Atlantic. A major limitation at the basin scale, however, is that the EUSeaMap doesn't extend much beyond European waters, thus precluding the use of the MarESA database to conduct impact assessments across the wider geographical area. Here, we present a novel approach using the predicted distribution of species generated by habitat suitability models as proxies to enable application of the EUNIS classification to areas beyond EUSeaMap. A multiclass habitat classification model was built in R using the RandomForest package and the predicted distributions of 6 deep-sea fish and 6 cold-water corals as predictor variables. This model was found to correctly classify the area covered by the EUSeaMap with over 90% accuracy. The model was subsequently used to extend the EUNIS classification system to the entire North Atlantic Basin, facilitating the use of the MarESA database to conduct impact assessments for human activities across the entire region.

- ## Vertical walls as refuge areas for ancient black coral communities in the Azores
  Marina Carreiro-Silva, Carlos Dominguez-Carrió, Timm Schoening, Eva Giacomello, Jorge Fontes, Kirsten Jakobsen, Joachim Jakobsen, Telmo Morato

Vertical walls (seabed structures >70º) are common geological structures associated with the steep submarine morphology of island slopes and seamounts in the Azores. However, they have seldom been studied due to the technical challenges posed by complex reliefs when surveying with traditional video platforms (e.g. ROVs and towed camera systems). To overcome this limitation, the DeepWalls project made use of the submersible LULA1000 (Rebikoff-Niggeler Foundation) to characterize and map the benthic communities associated with deep-sea vertical walls down to 1000 m depth in the southern slopes of São Jorge and Pico Islands.

Diverse benthic communities were identified, including those formed by deep-sea oysters, cold-water corals and sponges, with a clear bathymetric zonation along the island slopes. We found high diversity of black corals, with the presence of Leiopathes sp. at 800-1000 m depth. These large black corals harboured numerous associated species, including crustaceans, anemones, molluscs, hydrozoans and fishes. In some areas, black corals also harboured the eggs of deep-sea sharks, indicating the importance of such communities, not only as refuge and feeding areas for associated fauna, but also as potential nurseries for deep-sea fauna.
Large black corals (which could reach ages of several millennia) have rarely been found on seamounts, suggesting that high relief areas, such as vertical walls, could provide natural refuges from fishing impacts. Such areas may constitute some of the last pristine habitats hosting century-to-millennia old deep-sea communities, which are documented in historical records but are hardly encountered in present times. Thus, in the frame of the Marine Strategy Framework Directive (MFSD) of the European Union, large black corals on vertical walls may constitute good proxies for reference sites (i.e. baseline data) for deep-sea communities in the Azores, and can help better defining what constitutes a Good Environmental Status (GES).

- ## Long-lived New Zealand black corals as tools for paleoceanographic reconstructions to guide climate modelling in the Southwest Pacific
  Ashley N. Davis, Daniel J. Sinclair, Dianne M. Tracey, Nicholas T. Hitt, Stewart J. Fallon, Erik Behrens

Deep-sea black corals (Order Antipatharia) can live for centuries to millenia and are distributed globally. Their skeletons can be radiometrically dated to high precision providing age and growth rate data useful in understanding their potential for recovery after disturbance. These corals also incorporate environmental geochemical signatures into their skeletons which can be sampled at subdecadal resolution making them valuable for reconstructing oceanography over modern timescales. The National Institute of Water and Atmospheric Research (NIWA) houses an extensive collection of corals from the Southwest Pacific making it a valuble resource for biological and paleoceanographic studies.

Ten black corals from three genera (Antipathes, Antipathella, and Leiopathes) were identified from NIWA's collection and radiocarbon-dated for our project which aims to reconstruct the last 300 years of water circulation and nutrient dynamics around New Zealand. Here, we present the age and growth rate data of the black corals. Life spans ranged from ~35 years (Antipathella fiordensis) up to 2,185 years (Antipatharia). Growth rates ranged from ~8-314 µm/yr. The age data advances our knowledge of the longevity of these organisms, the variability in ages and growth rates between species, and their vulnerability to physical disturbances (i.e. trawling) due to slow recovery rates.

Here, we also discuss how these corals are used to reconstruct historical ocean conditions to inform climate model forecasting. New Zealand sits in the southwest of the South Pacific Gyre which has intensified due to anthropogenic climate change, thus leading to physical and biogeochemical oceanographic changes that could impact New Zealand's marine resources. Our coral paleorecords will provide a fuller picture of regional ocean variability. These paleorecords will then be used in conjunction with model data derived from the New Zealand Earth System Model to help provide more accurate climate forecasts necessary for scientists and policy makers to manage critical marine ecosystem resources.

- ### Habitat suitability mapping of VME indicator taxa to inform deep-sea fisheries management in the Southern Indian Ocean

  Berta Ramiro-Sánchez, Boris Leroy, Alexis Martin

The United Nations General Assembly (UNGA) resolutions require states and regional fisheries management organisations to protect vulnerable marine ecosystems (VMEs), ecologically important habitats in the deep sea considered to be especially at risk from anthropogenic activities such as fishing. The Southern Indian Ocean Fisheries Agreement (SIOFA) adopted in 2019 a list of VME indicatortaxa that will allow agreeing specific provisions to meet obligations in the Agreement Area. In order to develop appropriate bottom fisheries and spatial conservation measures, the SIOFA Scientific Committee subsequently directed the development of maps of VME indicator taxa to guide advice on the identification of areas where VMEs are known or likely to occur. The aim of this study was to model the predicted distribution of VME indicator taxa in the SIOFA Area and produce several bioregionalisation schemes. The distribution of individual VME taxa was predicted based on an ensemble modelling approach. Ensemble models were constructed for individual taxa using models available in the biomod2 R package: generalised linear models, generalised additive models, multivariate adaptive regression splines, artificial neural networks, random forests, boosted regression trees and flexible discriminant analysis. On a first approach, the ensemble models were stacked and clustered based on biogeographical networks. On a second approach, we predicted patterns in beta diversity applying generalised dissimilarity modelling. Given the paucity of data, predicted bioregions were based on environmental data and the chosen models, rendering important uncertainties. The two predictive approaches, however, provide complementary pictures of the distribution of bioregionsfor VME indicatorsin the SIOFA Area that allow hypothesising between different processes driving biogeographic patterns. Determining the spatial distribution of VME indicator taxa is critical for supporting improved spatial management of fisheries in the SIOFA Area. Habitat suitability plays an increasing role in designing protection measures for cumulative impacts on VMEs.

- ### Prediction of Multi-Taxon Vulnerable Marine Ecosystems in the U.S. West Coast EEZ

  Arvind Shantharam, Matthew Poti, Arliss Winship, Robert McGuinn, Thomas Hourigan

Vulnerable marine ecosystems (VMEs) are defined by the functional significance of the habitat they form, structural complexity, fragility, and life history traits, and particularly their sensitivity to anthropogenic activities. While the occurrence of VMEs is assessed in relation to specific threats, their characteristics can be used more generally to identify ecosystems vulnerable to various anthropogenic impacts. The U.S. has not designated VMEs sensu stricto, thus the distribution of such VMEs in U.S. deepwater is poorly known. However, intensive mapping of deep-sea coral and sponge assemblages and recent MaxEnt species distribution modelling (SDM) has provided an opportunity to make predictions about the occurrence and of VMEs. Here we leverage these latest developments to generate novel predictions of the extent of deep-sea benthic VMEs in the US west coast economic exclusive zone (EEZ). Out of 45 deep-sea benthic taxa with SDMs in the U.S. west coast EEZ, 39 were identified as potential VME indicator taxa based on indicator species databases amassed for the Atlantic and Pacific Oceans. The VME indicator taxa included sea pens, black corals, soft corals, stony corals, stylasterids and sponges. Cluster analysis of SDM outputs identified eight different groups of potentially co-occurring taxa that represent unique multitaxon VMEs. We discuss the location and distribution of these VMEs within the biogeographic and bathymetric boundaries of the modeling domain, as well as the implications of our findings for the conservation and management of these unique ecosystems.

- ### Modelling tools to study deep-sea sponges connectivity in the Azores, using a particle tracking model, and a 3-dimensional biogeochemical model to better understanding deep-sea dynamics and ecosystem connectivity

  Cláudia Viegas, Manuela Juliano, Ramiro Neves, Ana Colaço

A hydrodynamic and a biogeochemical 3-dimensional models were implemented for the Azores region, enabling to study physical, biological and ecological processes in the entire water column, from the surface until the deep-sea bed. MOHID biogeochemical model simulates the cycles of oxygen, and the main nutrients controlling phytoplankton growth (phosphate, nitrogen, silica), and the plankton dynamics (considering phytoplankton, diatoms and zooplankton). These models were implemented and calibrated for the Azores region, and validated at surface using in-situ and remote sense data (for sea surface temperature, chlorophyll-a and salinity), and along the water column (for salinity and temperature) using Argo-buoys data. Biogeochemical model results were compared with World Ocean Atlas climatology (WOA-2018) and CMEMS model results.

Taking advantage of the high resolution hydrodynamic model, a particle tracking model was applied to study the connectivity of deep-sea sponges aggregations, a vulnerable marine ecosystem (VME). Considering the scarce data about deep-sea sponges' biology, different scenarios were tested, including different pelagic larval durations, and seasonal spawning, in order to study the connectivity between known sponge aggregations location in the Azores. Furthermore, these results are complemented with biogeochemical model results, providing additional and relevant data to study this connectivity. These biogeochemical model results reduce the current gap on deep-sea understanding, providing valuable information to study not only the hydrodynamic and bathymetric barriers, but also the biotic patterns in the bottom layers. The applied methodology and the first results are presented. This model integration approach provides a better understanding of ecosystem connectivity and deep-sea dynamics in the Azores region, helping to improve the understanding about VME connectivity in the deep-sea, providing new information to support conservation and management plans.

Special session 1e# Pollutants and debris.pdf – Mestre

- First Report of Deep-Sea Litter from the Southwest Atlantic
  Flávia Masumoto, Amanda Gomes, Rayane França, Marcelo Melo

Marine litter is defined as any persistent, manufactured or processed man-made solid material that has been discarded or abandoned directly in marine environments (sea based) or into rivers or near to the coastline and transported from land to the sea by rivers, sewage or wind (land based). The debris can be long-distance transported by marine currents both before and after sinking, making its precise source identification exceedingly difficult. The first reports of marine litter date back to the 1960's in shallow waters but, nowadays, it is becoming a general problem to all marine environments. In the deep-sea, the reports are still relatively scarce and more focused to the Mediterranean Sea, North Pacific and North Atlantic, which may be an artefact caused by the amount of scientific investment to those areas. In this contribution, we make the first report of deepsea litter from the Southwest Atlantic. Collections were made onboard the R/V Alpha Crucis using a semi-balloon otter trawl with 23 meters in the lower hope and mesh size of 100 mm in the wings and main body and 25 mm in the cod-end. Sixteen hauls were conducted on continental slope off Southeastern Brazil, in depths from 400 to 1,500 m. The items were sorted, dried, counted and weighted. The litters were collected in 81% of the stations, totalling 392 items and about 10 kg, and categorized into five classes: plastic (56%), metal (21%), textile (16%), fishing gear (5%), glass (3%) and miscellaneous (19%). Plastic was the most common, and the only item present in all samples, and glass was the heaviest composing 26% of the total weight. The most frequent items include plastic bags (58%) and food or beverage cans (35%).

- Plastic Ingestion by Pelagic and Benthic Crustaceans at the Charlie Gibbs Fracture Zone of the Mid-Atlantic Ridge
  Daniella Milanese, Michael Vecchione, Tracy Sutton, Tamara Frank

Plastic debris is a widespread pollutant found in all marine environments and it is known to have detrimental effects both on the environment and on a variety of organisms. Research over the past decade has documented plastic ingestion in pelagic fish species, however there are few studies examining plastic ingestion in deep-sea crustaceans. We quantified plastic ingestion in deep-sea decapod crustacean species with respect to habitat (pelagic vs. benthic), geography, and hydrography of the Charlie-Gibbs Fracture Zone (CGFZ) of the Mid-Atlantic Ridge (MAR). Pelagic specimens were captured at four discrete depths from 0-2900 m depth, benthic samples were obtained along the seafloor at depths between 1900m-3500m, from stations north and south of the CGFZ. Plastics were extracted from the digestive tract and gills and categorized by size as mesoplastics, microplastics, or mini-microplastics, and by type as fiber, film, fragment, and pellet. Plastic ingestion in benthic species was similar in samples collected both north and south of the CGFZ. While all types of plastics were present, the highest percentage was in the fiber category. Plastics ingestion in pelagic species was higher in samples collected north of the CGFZ vs. the southern samples. The only plastic type present in the pelagic species from either region was fibers. This study is the first to compare plastic contamination in deep-sea benthic vs. pelagic species collected from the same area at the same time.

- Occurrence of marine litter along abyssal areas of the Gloria Fracture Zone (NE Atlantic)
  Sofia P. Ramalho, C. Ferreira, Christian Hensen, Pedro Terrinha, Mark Schmidt, Thomas Müller, Kasia Sroczynska, Helena Adão

Marine litter pollution is a recognized form of anthropogenic disturbance that affects widely the marine environment, particularly near the continental margins, although also present at abyssal and bathyal depths. This study reports the occurrence of marine litter distribution and abundance in four abyssal basins along the Gloria fracture zone in the NE Atlantic. Litter items occurrences were analysed using TV-CTD video surveys carried out during the multidisciplinary activities of the R/V Meteor M162 cruise. The surveys reached depths between 3500-4500m and covered 16 km of seafloor, between the Terceira ridge and the Madeira-Tore Rise. Litter items were annotated and categorized by type (i.e., plastic, fishing gear, metal, glass, other unknown items). Results revealed that litter was exclusively found on soft sediment habitats across all areas, i.e. depositional areas, with the overwhelming dominance of plastics items (71%), such as plastic containers, cups and bag fragments. Although less common (6-8%), metal, glass and lost fishing gear were also observed. Litter density was on average 9 times higher in the easternmost area near the Madeira-Tore ridge, when compared to the other areas. Higher litter densities are likely explained due to the proximity to the Madeira-Tore seamount complex targeted by the fishing industry and nearimportant corridors of marine traffic between various Atlantic and Mediterranean locations. The observations provide new quantitative records of long-lasting marine litter presence in abyssal areas inside and outside Portuguese EEZ.

- Utilising seafloor imagery to assess marine macro-litter in The Canyons Marine Protected Area
  Laura Robson, Liam Matear, Emma Novak, Charlie Howarth, Kirsten Dinwoodie, Tom Tangye

The Canyons Marine Protected Area (MPA) is located to the South West of the UK and extends from the continental shelf down to ~2000 m. The MPA is designated for a range of deep-sea habitats including deep-sea bed, cold-water corals, coral gardens and sea-pens and burrowing megafauna, and is the only known example of cold-water coral in England's offshore waters. JNCC is responsible for providing scientific advice to the UK Government and the devolved administrations on MPAs in UK offshore waters.

Understanding of the distribution of marine macro-litter across the UK's MPAs is limited, but litter is known to disseminate from land-based activities, impacting marine species from shallow waters to the deep sea through entanglement, smothering and ingestion. Canyon habitats have been found to be hotspots for marine litter, due to the transport of litter via oceanographic circulation and entrainment in bottom currents. Surveys conducted in 2007 and 2015 to The Canyons MPA found evidence of marine litter occurring in contact with protected coral features.

This project sought to identify marine litter from seafloor imagery, using still image data from MPA research surveys, to determine the prevalence of marine litter within UK offshore MPAs. Following initial review of a range of offshore MPA survey datasets, the project focused on The Canyons MPA as it was identified as one of the best surveyed sites, with highest counts of litter. Images were inspected using Biigle software, and were annotated with information on litter, categorized by ICES/MSFD seafloor litter categories, and interactions with biodiversity. This talk will present the analysis and results from this project and look at the policy relevance for understanding impacts of marine litter in UK MPAs.

- Long-term PAH bioaccumulation in deep-pelagic organisms after the Deepwater Horizon spill
  Isabel C. Romero, Tracey Sutton, Heather Judkins, Michael Vecchione, April Cook, Marsh Youngbluth

The Deepwater Horizon oil spill (DWHOS) in 2010 highlighted the lack of baseline data for marine ecosystems in the Gulf of Mexico (GoM), critical for assessing the environmental impact on this ecosystem. Continuous observations after the DWHOS were conducted to distinguish natural variability from ecosystem change. Specifically, we analyzed polycyclic aromatic hydrocarbons (PAHs), known for their mutagenic, genotoxic, and carcinogenic effects. To understand exposure trends in PAH composition and concentration in the open-ocean ecosystem of the GoM, deep-pelagic fishes, cephalopods, and gelatinous zooplankton species were analyzed within a period of eight years after the DWHOS. Specifically, samples collected in 2010-2011 indicated an increase up to 10-fold in PAH concentration relative to pre-spill values, which then decreased over the following years for all taxonomic groups except cephalopods. Analysis of %lipids shows lower content in cephalopod species in 2011, potentially due to a lower dietary intake or dietary quality, suggesting potential effects of the spill to the trophic web. The composition of PAHs also varied among taxonomic groups, indicating gelatinous species may have less capacity to excrete PAHs; however, they are more sensitive to elevated concentrations of PAHs. In addition, analysis of gonads and ovaries indicates a significant maternal transfer of contaminants in gelatinous and fish species. Overall, the temporal trends suggest an episodic contamination event in 2010 that continued through the following years with long-term bioaccumulation driven by dietary intake or maternal transfer of PAHs. Our findings demonstrated the importance of monitoring the persistence of organic contaminants in the deeppelagic GoM (and other regions subjected to deepwater oil drilling), potentially explaining the decline in abundance observed recently in most species.

Special session 1f# Climatic changes and deep-sea biodiversity.pdf – Yasuhara & Levin

- The morphological response of benthic foraminifera Nuttallides umbonifer and Oridorsalis umbonatus to deoxygenation in the deep oceans
  Kyawt Aye, Daniela N Schmidt

The substantial rise in anthropogenic CO2 emissions since the industrial era induced a global decline in oxygen ventilation in the deep oceans through ocean warming. The global loss of 2% (77 billion tonnes) of oxygen in the oceans over the past 50 years have proliferated oxygen minimum zones and has severely impacted deep ocean biota (1). Among them are benthic foraminifera. Deoxygenation produces considerable threats to benthic foraminifera as oxygen is utilised for respiration and nutrient remineralisation, but to date, research in species-specific adaptations of benthic foraminifera to oxygen loss in the deep oceans have been limited. This research assesses the impacts of various oxygen concentrations on the growth and reproductive mode of two species of benthic foraminifera Nuttallides umbonifer and Oridorsalis umbonatus in the modern deep oceans of the South Atlantic, the South Atlantic Polar Front, and of Oridorsalis umbonatus during the glacial and interglacial cycles of the Arabian Sea over the last 170ka. The growth and reproduction were quantified using AVIZO generated 3D reconstructions of both species to measure the test diameter, chamber number, surface area to volume ratio (growth response) and proloculus diameter (reproduction response). Results indicate that oxygen exerts a higher influence on reproduction than growth as both Nuttallides umbonifer and Oridorsalis umbonatus in the modern oceans and Oridorsalis umbonatus during the glacial cycles of the Arabian Sea were still able to maintain large growths under oxygen-reduced conditions but lower oxygen concentrations induced a larger distribution of smaller proloculus, sexually reproducing species. Both Nuttallides umbonifer and Oridorsalis umbonatus were able to adapt to oxygen-reduced oceans provided other environmental resources such as organic flux to bottom waters remained constant.

Ongoing and upcoming Cold-Water Coral Multi Stressor Experiments

Kelsey Archer Barnhill, Cristina Gutiérrez-Zárate, Marina Carreiro-Silva, J. Murray Roberts, Covadonga Orejas, Alfredo Veiga, Inês Martins, Maria Rakka, Juancho Movilla, Uwe Wolfram, Elisa F. Guallart, Marta Álvarez, Andrea Gori, Sebastian Hennige

Cold-water corals (CWC) play a fundamental role in promoting deep-sea ecosystem diversity due to their ability to form complex 3-dimensional structures, such as coral reefs and coral gardens, that provide habitats for thousands of associated species. However, knowledge about their ecophysiological response to global change stressors is still very limited, as well as their synergies associated with this threat and how they interact with local stressors such as the impacts from mining and trawling activities.

Here we present experimental design and ongoing work of multi stressor experiments exploring the combined impact of several environmental stressors based on the IPCC projections (warming, acidification, deoxygenation and food limitation) on the ecophysiological response of three CWC species across different regions in the North Atlantic: the scleractinians Lophelia pertusa in Norway and Dendrophyllia cornigera in NW Spain, and the octocoral Dentomuricea aff. meteor in the Azores. Different analyses are performed on response variables including skeletal growth and microporosity, respiration and excretion rates, and tissue retraction, among others. The design of each experiment varies depending on the selected combination of stressors and response variables, as well as previous knowledge on the ecophysiology of the three species. The L. pertusa experiment includes repeated 3D imaging using computed tomography of live and dead skeletons to quantify ocean acidification impacts on the coral skeleton. The D. cornigera experiment includes tissue regeneration, simulating the simultaneous impacts from physical damage due to fishing activities and global change. Further experiments will include the addition of particles from mining or trawling activities to study their physical damage and ecotoxicological effects. The results from these multi stressor studies will increase the knowledge about the deep-sea coral species and ecosystems that will be most sensitive to global change and human impacts to support science-based marine spatial planning for the North Atlantic.

Suitable habitat and depth-driven climate refugia for Lophelia pertusa and faunal associates on the southeastern US margin

Ryan Gasbarro, Alex Margolin, Derek Sowers, Erik Cordes

Reef-forming corals on the deep seafloor support numerous ecosystem functions and harbor a diverse and abundant associate fauna, yet their ecological niche boundaries and spatial distribution remain poorly resolved. In 2018-19, mapping expeditions and submersible dives on the U.S. Atlantic margin confirmed the presence of numerous sites hosting rich coral reef ecosystems where previous, coarser predictive models placed a low probability for suitable coral habitat. Here, we use these newly acquired bathymetry and coral distribution data to create ensemble habitat suitability models for both the presence and abundance (% cover) of Lophelia pertusa, the primary reef-forming species in the region. In addition, we use the latest global climate data from the IPCC's Climate Model Intercomparison Project to project the distribution and abundance of the species from present-day to 2050 and 2100 in four emissions scenarios ranging from a 'sustainable future' to 'business-asusual.' Our results suggest that the deeper, more eastward sites in the region may act as spatial climate change refugia for L. pertusa, and that this deep refugia effect will be more pronounced in higher emissions scenarios. While the present-day model extends the known distribution of L. pertusa, the climate projections predict some degree of range contraction regardless of scenario. Using megafaunal data generated from video annotation of 14 submersible dives in the region, we also create joint species distribution models to predict functional diversity shifts with climate change and the concomitant decline in live coral cover. These novel first-order estimates presented of climate-driven declines in L. pertusa and the downstream effects on associate biodiversity will be key in prioritizing areas for management, exploration, and in creating energy budgets for this highly productive region.

- Crossing the Drake: Lessons from the brittle star Astrotoma agassizii
  Candace Grimes, Kyle David, Andrew Mahon, Damien Waits, Ken Halanych

The Antarctic is home to numerous endemic species with the Antarctic Polar Front (APF) considered to be the open-ocean barrier that has isolated organisms to the Southern Ocean. However, this barrier, which global climate change threatens to make more permeable, has been leaky in the past resulting in isolated but closely related populations of animals living in either temperate waters or cold polar waters. The filter-feeding brittle star Astrotoma agassizii is one such animal with distinct populations on either side of the APF. In order to explore how populations have adapted to these different environments including thermal regimes, we have sequenced the 2.2 Gb genome of A. agassizi using PacBio technology to explore and identify genetic differences between populations north and south of the APF. Previous work using a 2b-RAD genomic approach has identified unique single nucleotide polymorphisms (SNPs). Here, we placed these SNPs in the annotated genome to identify regions of the genome that differ between the two populations. We emphasized gene familes known to be sensitive to the thermal environment, for example genes related to thermal stress and ossification (such as heat shock proteins and alx family, respectively). We are also attempting to identify genomic regions of positive selection to help understand the genes that are directly influenced by environmental differences. Additionally, we sequenced the 2.9 Gb genome of the related basketstar, Gorgonaocephalus antarcticus, to facilitate comparative analyses. The goal of this work is to understand the genomic mechanisms that have allowed organismal adaptation to the Antarctic environment.

- In situ experimental evidence for responses of abyssal benthic biota to shifts in primary producers of the surface ocean linked to global climate change
  Hidetaka Nomaki, Eugenio Rastelli, Nanako O Ogawa, Yohei Matsui, Masashi Tsuchiya, Elisabetta Manea, Cinzia Corinaldesi, Miho Hirai, Naohiko Ohkouchi, Roberto Danovaro, Takuro Nunoura, Teresa Amaro

Abyssal plains cover more than half of Earth's surface. The main source of nutrition in these ecosystems is phytodetritus which is mainly originated from primary producers in the euphotic zone of the ocean. Global climate change is influencing the phytoplankton abundance, productivity, and species compositions, hence altering the quantity and quality of organic carbon supplied to the abyssal seafloor as phytodetritus, consequences of which remain largely unknown. Here, we investigated the response of the benthic abyssal assemblages to experimental supplies of different types of phytoplankton (i.e., diatoms or cyanobacteria) labeled with stable carbon and nitrogen isotopes. Responses of abyssal biota were compared at two sites in the western Pacific Ocean differing in trophic settings, at equatorial oligotrophic (1°N) and temperate eutrophic (39°N) sites. Meiofaunal and macrofaunal organisms at 39°N incorporated more phytoplankton than those at 1°N, and in general preferred diatoms. Prokaryotes and viruses, on the other hand, showed higher responses to supplies of cyanobacteria than diatom. At both sites, irrespective of the type of phytoplankton supplied, the response of prokaryotes and viruses was rapid, highlighting their major role in determining the early fate of phytodetritus. Overall, our results suggest that benthic deep-sea eukaryotes will be negatively affected by the shift in dominant phytodetritus from diatoms to cyanobacteria projected at higher latitudes by current scenarios of climate change. Conversely, such change can enhance prokaryotic metabolism and microbial organic matter cycling, in turn hampering carbon transfer to higher trophic levels. These effects have strong potential to alter the benthic food webs and their biodiversity and consequently carbon sequestration capacity at the global scale.

- The ChEReef project: what threats on cold-water coral reefs in the Bay of Biscay, how to monitor and how to predict them?
  Lénaick Menot, **Julie Tourolle**, Karine Olu, Bertrand Moreau, Ricardo Silva Jacinto, Bruce Shillito, Franck Lartaud

Similar to their tropical analogues, cold-water colonial scleractinians are autogenic engineers that create complex habitats while fixing carbon dioxide in the form of aragonite and thus provide important support, provision and regulation services. In the Bay of Biscay, these cold-water corals (CWC) thrive in the many submarine canyons incising the continental margin, where they are sheltered from deep-sea trawling. Submarine canyons however are conduits for sediments and pollutants from shallow waters to the deep sea that may funnel down sediments resuspended by trawling as well as marine litter. Beyond trawling and terrigenous pollution, CWC shall also cope with the cumulative threats of ocean warming, deoxygenation and acidification.
With support from the Life Integrated Marha (2018-2025) and ANR ARDECO (2021-2025) projects, ChEReef (Characterisation and Ecology of cold-water coral Reefs) will aim at defining the resilience and tipping points of the three reef-building scleractinians Desmophyllum pertusum (formerly Lophelia pertusa), Madrepora oculata and Solenosmilla variabilis to cumulative impacts. Marha project will implement a biogeophysical monitoring platform for five years in the Lampaul submarine canyon of Brittany. The instrumented platform will record daily videos of a CWCreef together with turbidity, currents, particles fluxes, temperature, salinity and pH. In-situ and ex-situ experiments on the growth and reproduction of reef coral species will also be conducted in the framework of the ARDECO project, which will support the development of innovative pressurized tanks allowing months-long experiments at in situ pressure on deep-sea corals. The key question addressed by these projects is how should one assess, monitor and predict the

conservation status of coral habitats in the Bay of Biscay in response to past, current and future anthropogenic pressures.

Special session Deep Sea Minning 1g#: Deep-seabed mining - impacts, conservation, governance.pdf – Gollner & Haeckel + 1h#: Polymetallic Nodule Mining - Integrating scales, processes, impacts and knowledge.pdf – Baldrighi et al.

- ## Heavily disturbed seafloor shows recolonization by Paleodictyon nodosum within 26 years

  Lilian Boehringer, Autun Purser, Yann Marcon, Antje Boetius

In 1989 the DISCOL (Dis-turbance and Re-Col-onization) experiment was an early attempt to simulate physical disturbances which may be associated with polymetallic nodule deep-sea mining. The experiment was conducted in the Peru Basin, with the seafloor being impacted by dragging an 8 m wide plough harrow repeatedly across the surface, pushing nodules into the underlying sediments or to the sides of the tracks. 26 years later, the SO242 cruise revisited the DISCOL area, imaging the seafloor with the Ocean Floor Observation System (OFOS). In ploughed areas, seven strikingly hexagonal hole patterns were observed, identified as Paleodictyon nodosum traces. These patterns were formerly interpreted as graphoglyptids, and are known from casts of ancient turbidites assumed to represent a subsurface hexagonal tube network. The modern P. nodosum are identified by the arrangement of the vertical outlets extending from each intersection of the subsurface tube network to the sediment surface. Despite the extensive study conducted by Rona et al. (2009), the origin of these patterns, and how they reflect on the mode of life of the forming organism, remains unknown.

The occurrence of P. nodosum on the ploughed substrate sheds some light on the lifecycle of these poorly known organisms, demonstrating that they can recolonize disturbed habitat and produce the identifiable and regular seafloor trace networks in less than 26 years. Nevertheless, the density on ploughed substrates was significantly lower than the densities observed on undisturbed substrates during the same survey campaign. We therefore hypothesise that, along with the majority of other sessile and semi-sessile benthic deep-sea fauna, the organisms are prone to disturbance, and even after 26 years populations have not recovered to pre-physical disturbance levels.

- ## Illuminating the “dark” abyssal biodiversity: Echinodermata

  Magdalini Christodoulou, Tim O'Hara, Andrew F. Hugall, Christopher Mah, Andrey Gebruk, Rich Mooi, Marc P. Eleaume, Pedro Martinez Arbizu

The most commercially appealing abyssal accumulations of polymetallic nodules rich in nickel, cobalt and manganese are found in the Clarion-Clipperton Zone (CCZ), in the NE Pacific Ocean. Additional important occurrences are known from the DIS-turbance and re-COLonisation (DISCOL) Experimental Area (DEA) in the Peru Basin, off South America. The lack of adequate baseline information at the onset of commercial-scale mining may result in serious species declines before this biodiversity is discovered and described. Our limited knowledge of these dark taxa ensures that they remain in the shadows of research and conservation policies. Therefore, Echinodermata (Asteroidea, Crinoidea, Echinoidea, Holothuroidea, Ophiuroidea) collected during ten scientific cruises across the CCZ and the DEA were examined. Over 850 specimens were genetically analysed using a gene fragment of the mitochondrial COI, while the specimens were morphologically identified to the lowest possible level through imagery to propose primary species hypotheses. Neighbour-joining trees were constructed, while tree-based and distance-based methods of species delineation (ASAP, BINs, GMYC, mPTP) were employed to propose secondary species hypotheses (SSHs) among the echinoderms collected. Concordant results from the species delimitation analyses indicate 84 deep-sea echinoderm SSHs, revealing an unexpectedly high diversity and showing that diversity of even the most conspicuous invertebrates in abyssal plains has so far been considerably underestimated. As a result, a curated DNA reference library for the CCZ-DEA echinoderms was created in BOLD, including DNA sequences, photographs, collection, and taxonomic data. Furthermore, barcodes (COI, 28S) were mapped onto an ophiuroid tree of life to show unprecedented levels of abyssal ophiuroid phylogenetic diversity, including at least three ancient (>70 mya), new clades. This study provides the foundation for biogeographic and functional analyses that will shed light on the community structure and densityrelated sensitivity to disturbance of nodule fields, and factors for policy-making as commercial ventures impinge on dark abyssal biodiversity.

- ## Biodiversity of Solenogastres (Mollusca Aplacophora) in the Clarion Clipperton Fracture Zone

  M. Carmen Cobo, Kevin M. Kocot

Deep-sea polymetallic nodule mining is an anthropogenic activity for which the nature and extent of potential impacts on deep-sea ecosystems are poorly known but of great concern. Before the impacts of this activity can be assessed, determining the biodiversity of these habitats is essential. Here we present preliminary results of an integrative taxonomic study on a collection of 38 Solenogastres (Mollusca, Aplacophora) from the Clarion-Clipperton Fracture Zone (CCZ) during the SO 205 MANGAN cruise. Solenogastres are one of the least known molluscs, although they are diverse and essential to understanding the evolution of the phylum. They are common in the global benthic malacofauna, but often go unnoticed, or are simply avoided as their identification usually requires complex and time-consuming methods. To determine solenogaster diversity in the CCZ, specimens were first classified into morphospecies based on their habitus and mantle sclerites. At least one specimen of each morphospecies was selected for detailed study. These were sectioned in three parts with the middle region imaged under a low-vacuum, low-accelerating voltage SEM, which makes it possible to obtain ultrastructure-level data on the mantle sclerites and high-quality DNA (for 16S and COI barcodes) from the same sample. The anterior and posterior regions were preserved for further analysis (histology for complete species identification). Morphological and molecular results indicate that this relatively small collection is surprisingly diverse: we identified roughly seventeen distinct species representing six different families. Moreover, and as usual in solenogasters from remote locations, most of them appear to be new to science. Thus, solenogaster studies are fundamental to understand the valuable biodiversity of polymetallic nodule areas, and in turn the study of these areas leads to a better understanding of the richness of these interesting molluscs.

Acknowledgments: The authors are grateful to Pedro Martínez-Abizu for providing this material. This work was funded by SO 205 Projekt MANGAN and NSF award 1846174.

Observed behavioural response and recovery of a sponge to sedimentation

Jennifer M. Durden, Johanne Vad, Michael Clare, Andrew R. Gates

Suspension and filter feeders, and sponges in particular, are important to benthic diversity and ecosystem function. They are vulnerable to smothering by suspended sediments and deposited particles, which are a common result of anthropogenic activities including deep-sea mining, hydrocarbon drilling, dredging, and trawling. The response to such disturbance has been measured in experiments using shallow water species, and in observations comparing conditions before and after disturbance, but no in-situ observations have been made during disturbance. We observed the behavioural response of a sponge to the accumulation of particulate organic matter and suspended sediments from the drilling of an oil well west of Shetland (156m water depth) using hourly timelapse photography over 48 days. Additional environmental data was collected using a current meter, and by assessing sedimentation in the images. Initial pulses of sediment disturbance occurred over ~5 days, followed by the deposition of coarse drill cuttings, and approximately 1000h of observed recovery time. We provide preliminary results of the observed impacts of the disturbance event on sponge behaviour and recovery. Sediment initially accumulated on the sponge, which later recovered by clearing this material. Sponge movement over the period may be related to both the deposition event and the tidal cycles. These observations provide important in situ context to complete laboratory studies useful for the risk assessment of disturbance activities important in project planning and the development of Environmental Impact Assessments.

Ophiotholia (Ophiuroidea): a little-known deep-sea genus present in polymetallic nodule fields

Angelina Eichsteller, Alexander Martynov, Magdalini Christodoulou, Tim O'Hara, Pedro Martìnez Arbizu

The Clarion Clapperton Zone (CCZ) in the Northeast Pacific Ocean holds the largest deposits of polymetallic nodules at abyssal depths of 4000-6000 m in the world. These nodules are rock formations containing valuable metals and minerals targeted for mining. Polymetallic nodules support a rich sessile and mobile fauna. Little is known so far on the taxonomy, natural history and biogeography of these deep-sea animals which is vital for accurate assessment of the risk of species extinctions from large-scale mining. One of the most abundant megafaunal groups in the CCZ is the Ophiuroidea (brittle stars), of which Ophiotholia is one of the most common genera found in the area. The genus Ophiotholia has a world-wide distribution and currently holds six species. In order to study the taxonomy of this genus Ophiotholia, material collected from seven scientific cruises to the CCZ was examined. Furthermore, comparative material from all the known species was studied. The specimens were morphologically examined although their small size and the damage caused during sampling often impeded their identification. For this reason, the specimens were further genetically analysed using a fragment of the mitochondrial COI gene. Finally, Scanning Electron Microscope images of the key microstructural characters were made using specimens from CCZ as well as from the comparative material. Within the specimens of the CCZ, four different lineages of Ophiotholia were recognised, while two morphotypes were recognised from examining the non-damaged material. Preliminary results indicate that one morphotype belongs to the known species Ophiotholia supplicans Lyman, 1880, while the second seems to be new to science. The most relevant morphological characters such as the umbrella spines and the arrangement of their articulations on the lateral arm plate, used for the taxonomy of the genus Ophiotholia are discussed and a revised identification key of all known Ophiotholia species is provided.

Restoration after polymetallic nodule mining-impact

Sabine Gollner, Matthias Haeckel, Felix Jannsen, Nene Lefaible, Massimiliano Molari, Stavroula Papadopoulou, Gert-Jan Reichart, João Trabucho Alexandre, Annemiek Vink, Ann Vanreusel

Deep-sea polymetallic nodule mining will cause multiple long-term impacts for the benthic microbial and faunal communities, including for example loss of habitat by removal of nodules and habitat modification of top sediment layer by the operating mining vehicle. A tool to manage biodiversity risks is the mitigation hierarchy, which includes the avoidance and minimization of impacts, followed by rehabilitation/restoration of the impacted ecosystem when there has been significant biodiversity loss, followed by offsets as a last resort. An important objective is the re-establishment of pre-existing ecosystem processes and biotic integrity. While these actions are commonly applied in Environmental Impact Assessments for terrestrial and coastal habitats with varying degrees of success, potential ecological restoration within the deep sea remains understudied. Moreover, further research is needed to define a clear ecosystem baseline in order to achieve effective restoration.

Here, we present scientific experimental set-ups to test the feasibility of restoration actions after a test-mining impact at polymetallic nodule fields in the Clarion Clipperton Fracture Zone at ~4000 meters depth. We developed and deployed artificial ceramic nodules to explore the role of substrate type for settlement success of biota and impact on sediment biogeochemistry. In addition, sediment on the deep seabed was loosened by means of a metal rake to test the feasibility of sediment decompaction as a restoration measure to facilitate soft-sediment recovery. Considering the slow natural recovery rates of deep-sea communities, these experiments represent the beginning of a long-term scientific pilot study for which we expect to gain insights throughout the following decades.

In situ oxygen flux baseline studies to quantify impacts of manganese nodule mining on benthic activity in the Clarion Clipperton Fracture Zone

Felix Janssen, Antje Boetius, Matthias Haeckel, Massimiliano Molari, Duygu Sevgi Sevilgen, Frank Wenzhöfer, Batuhan Cagri Yapan

Sediment community oxygen consumption is an established measure of benthic activity and recommended by the International Seabed Authority for baseline investigations as part of exploration activities (document ISBA/25/LTC/6). It addresses rates of organic matter remineralization as a key function of seafloor ecosystems. In 2019, oxygen flux measurements were carried out at locations approx. 1000 km apart in the Clarion Clipperton Fracture Zone (CCZ) within the German and Belgian exploration license areas. Rates of total (TOU) and diffusive oxygen uptake (DOU) were quantified in situ with benthic chambers and microprofilers manipulated by remotely operated vehicle (ROV). The study was carried out in the framework of the European collaborative project MiningImpact under the Joint Programming Initiative Healthy and Productive Seas and Oceans (JPI Oceans). The primariy aim was to settle a baseline in preparation of a subsequent assessment of the environmental impacts associated with the first test of a manganese nodule collector pre-prototype in international waters. In both license areas, replicate measurements were obtained at different sites across several kilometers distance. Based on this extensive data set, the presentation aims to assess the requirements (e.g., in terms of replication, relevant spatial scales, methodology) for oxygen uptake observations in the context of environmental baseline studies. Lateral variability in fluxes is addressed as well as differences between total and diffusive fluxes and relations to other biogeochemical data obtained in sediment and pore water samples (e.g., nutrients, organic matter, chloroplastic pigments). In addition, first data on immediate effects of the recently performed pre-prototype collector test on oxygen distribution in the upper sediment layer are presented.

Protecting deep sea hydrothermal vent biodiversity through ABMTs

Lise Klunder, Sabine Gollner, Henko de Stigter, Erik Molenaar, Catherine Blanchard

Deep-sea hydrothermal vents are unique and vulnerable ecosystems, that may be at risk by the imminent start of deep-sea mining. Conservation of the vent biodiversity can be regulated through area based management tools (ABMTs). These ABMTs are best described as a set of regulations on human activities for a specific area.

In order to be able to protectvent biodiversity, the dimensions of ABMTs need to be determined. Hydrothermal vent fields are clusters of active and inactive vents or chimneys which might or might not be biologically connected. Although biodiversity has been studied extensively for active vents, there is almost a lack of knowledge with regard to inactive vents, the surrounding areas and the biological connectivity between them.

In this project we investigate the connectivity between the active vent field and its pelagic and benthic surroundings. For this, we use the Rainbow hydrothermal vent field at the Mid Atlantic Ridge as a model study system. First results, based on eDNA metabarcoding, demonstrated significant differences in community composition in the soft sediment surroundings. Differences were related to distance from the vent as well as influence from the vent's plume. Further, we aim to use eDNA to determine the presence of active vent organisms in the surroundings to further gain insight in the connectivity and biodiversity around hydrothermal vents.

Insight for deep-sea mining ecotoxicology: Biomarker development based on comparative proteomics study on in situ copper exposed deep-sea amphipods

Yick Hang KWAN, Dongsheng ZHANG, Nelía C. MESTRE, Jin SUN, Peiyuan QIAN

In recent decades, attention in terms of environmental impacts generated from seabed mining raised alongside the increasing technological feasibility. Biomarker's identification, such as discovering the genes or proteins molecules that participate in the animals coping mechanisms with environmental stress, are often used to understand the resilience of the deep-sea animals towards mining impacts, which are critical information for determining the baseline information. In this study, deep-sea amphipods, Abyssorchomene distinctus, were selected to examine the effectiveness of biomarker discovery towards copper exposure by in situ exposure experiment approach. 48 h of copper exposure experiment on amphipods were performed in situ and Inductively Coupled Plasma-Mass Spectrometry (ICP-MS) was used to confirm successful exposure. Whole protein extraction was conducted, and the identification and quantification of expressed protein abundance were assessed through tandem mass tag-based coupled with two-dimensional liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS). A total of 1918 potential biomarker proteins were continued for biomarker screening based on their abundance and dependence with copper concentration, out of 2937 identified and functionally annotated proteins. Screening results proposed that proteins such as Na+/K+ ATPase, cuticle, chitinase, and other proteins with unknown function were potential biomarker candidates in deep-sea mining baseline monitoring. The result also highlights a novel approach to investigate ecotoxicology data in future impact assessment of seafloor mining.

Testing the Seamount Refuge Hypothesis for Predators and Scavengers in the Western Clarion-Clipperton Zone

Astrid B. Leitner, Jeffrey C. Drazen, Craig R. Smith

Abyssal seamounts are the most numerous but least understood seamount habitats. Here we report results from the first baited camera deployments on abyssal seamounts. Observations were made in the Clarion Clipperton Zone (CCZ) polymetallic nodule region, which will likely experience large-scale deep-sea nodule mining in the near future. The

Seamount Refuge Hypothesis (SRH) posits that the seamounts found throughout the CCZ provide refuge for fauna disturbed by seabed mining, providing potential source populations for recolonization of mined areas. Here we use baited cameras to test this hypothesis for mobile predators and scavengers. We deployed two systems on three abyssal seamounts and their surrounding plains in three Areas of Particular Environmental Interests (APEIs), areas protected from mining. We found that the two habitat types have distinct communities. Seamounts were found to have higher species richness and lower evenness than abyssal plains due to high dominance. Relative abundances were generally higher on seamounts than on the plains, but this effect varied significantly among the taxa. Seven morphotypes were exclusive to the seamounts, including the most abundant species, the cutthroat eel Ilyophis arx. Differences in community compositions were driven largely by habitat type and productivity changes. Abyssal-plain deployments hundreds of kilometers apart were more similar to each other than to seamount deployments ~15km away. No morphotype was exclusive to the abyssal plains; thus, we cannot reject the SRH for the mobile megafaunal predator/scavenging fauna from CCZ abyssal plains. However, it is not known whether abyssal plain fauna occur on seamounts at numbers sufficient to act as a source population for recolonizing the abyssal plains post mining disturbance. Because seamounts have unique community compositions, they contribute to the beta biodiversity of the CCZ, and indirect mining impacts on these unique seamount communities are of concern.

Differential impacts of sediment plumes generated by the extraction of seafloor massive sulfides and ferromanganese nodules on cold-water octocorals

Sandra Marques, Inês Martins, António Godinho, Mariana Cruz, Ana Colaço, Joana Raimundo, Miguel Caetano, Marina Carreiro-Silva

Sediment plumes generated during mining activities for deep-sea mineral resource extraction, such as seafloor massive sulfides and ferromanganese nodules, are expected to strongly affect benthic ecosystems. The deposits differ in mineralogy, metal composition and particle morphology, potentially resulting in different mechanical and ecotoxicological impacts on organisms.

Here we describe an aquaria-based experiment designed to test the differential impacts of sediment plumes generated during mining activities for the extraction of nodules in the Clarion-Clipperton Fracture Zone (CCFZ), northeastern equatorial Pacific Ocean and seafloor massive sulfides from a hydrothermal vent field in the Azores, northeast Atlantic, on the physiology of the cold-water octocoral Dentomuricea aff. meteor. Corals were exposed, for a period of four weeks, to two concentrations (10 and 50 mg/L) of suspended plumes of sediments from nodule fields and hydrothermal polymetallic sulfide particles and a control treatment with no sediment addition. Sediment concentrations were selected based on plume dispersal models, as close-field and far-field plume dispersal scenarios. Sediments from the CCZ were obtained from abyssal depths of 4000m in the Belgian license area for the exploration of polymetallic nodules. Polymetallic sulfide particles were obtained by grinding broken dead sulfide chimneys collected at the hydrothermal vent field Lucky Strike at 1750m depth.

The physiological effects of sediments were measured every week at different levels in the organism: at the whole-organism level (survival, polyp activity, respiratory metabolism, excretion), tissues composition (C:N-ratio, metal bioaccumulation), and at the molecular level (protein expression). Preliminary results showed high sensitivity to polymetallic sulfide particles, with survival for only 96 hours in both particle concentrations, but full survival for 4 weeks under nodule field sediments. Results are discussed in the context of effects on the physiology of the organism, the potential consequences of mining activities in areas close to cold-water coral gardens, and recommendations for mining industry operations.

Polymetallic nodule size and distribution of sessile megafauna in the eastern Clarion-Clipperton Zone

Alejandra Mejia, Simon-Lledó, Diva Amon, Katja Uhlenkott, Pedro Martinez Arbizu, Anemiek Vink, Daniel Jones

The availability of hard substratum is a key factor structuring seabed communities from shallow to deep ecosystems worldwide. Hard surfaces provide stable sites for anchoring and development of filter-feeding sessile species, which can be abundant or even dominate in particular deep-sea habitats. Abyssal polymetallic nodule fields, such as the Clarion-Clipperton Zone (CCZ) in the northeastern abyssal Pacific, are a mosaic habitat where the hard substratum provided by nodules combined with the background sediment increases habitat heterogeneity, promoting the development of highly diverse communities. Increases in substratum patch sizes are usually associated with increases in the diversity and size of inhabiting fauna. We assessed the relationship between the size and shape of the nodules on which the most abundant sessile megafauna taxa were encountered based on seabed imagery collected across the eastern CCZ. We show that noduledwelling taxa differ in nodule size and shape preference, as well as in the relative placement upon them. We also show that organism body-size is positively related to nodule patch size. This suggests that variations in nodule size and typology play a key role modulating habitat complexity within nodule field areas, with a direct effect on the distribution of megabenthic filter-feeder communities at the CCZ. Our results have direct implications for environmental management plans in the area and suggest that the heterogeneity derived from the presence and varying type of hard substratum structures in abyssal environments may have been historically overlooked.

Effects of copper in Cancer bellianus

Nélia C. Mestre, Manon Auguste, Andreia Carvalho, Antonio Godinho, Maria João Bebianno

In light of deep-sea mining, it is important to understand the effects of metals on deep-sea organisms. This type of information can help defining threshold limits for such activity, promoting a reduction of the potential negative environmental impact of deep-sea resources exploitation. This study investigated the effects of 4 µM of Cu exposure for 68h in the deep-sea crab Cancer bellianus, collected from 660 m near the Condor Seamount, Azores, North Atlantic, in 2016. The copper concentration was measured in different tissues, muscle and gills, and in their sub-cellular fractions: insoluble fraction (IF), high molecular weight (HMW) and low molecular weight (LMW) fractions. Biomarkers of oxidative stress (superoxide dismutase – SOD, catalase – CAT, glutathione peroxidase – GPx), metal exposure (metallothionein – MT), biotransformation (glutathione-S-transferase – GST), oxidative damage (lipid peroxidation – LPO) and neurotoxicity (acetylcholinesterase – AChE) were measured in the different tissues. A differential sub-cellular distribution of Cu in the different fractions between tissues was noted. Higher Cu concentration was found in the IF and LMW fractions of gills of Cu-exposed crabs when compared to controls. Results suggest that copper induced significant effects in enzymatic activities related to biotransformation and oxidative damage in C. bellianus. In Cu-exposed crabs, the higher concentration of copper in the IF fraction, that contains amongst others cell membranes, is associated to the observed higher lipid peroxidation of cell membranes. A prolonged exposure to metals, as predicted in the case of industrial mining activities, would most likely induce cumulative effects including metabolic impair that could compromise the ability of the species to adapt or survive in an environment affected by deep-sea mining. Funding: European Commission - MIDAS project (Grant Agreement 603418); Fundação para Ciência e Tecnologia (FCT) and Direção-Geral de Política do Mar (DGPM) - JPIO Mining Impact 2 (Mining2/2017/001); FCT (CEECIND005262017, UI/350/2020).

How could the exploitation of deep-sea polymetallic nodules potentially impact benthic microbial assemblages?

Massimiliano Molari, Batuhan Cagri Yapan, julia Marén Otte, Felix Janssen, Frank Wenzhöfer, Matthias Haeckel, Antje Boetius

Industrial-scale mining of deep-sea polymetallic nodules will remove nodules in large areas of the sea floor. The regrowth of the nodules by metal precipitation is estimated to take millions of years. Thus, for future mining impact studies, it is crucial to understand the role of nodules in shaping microbial diversity and microbially-mediated processes in deep-sea environments. In this study, we investigated the abundance, diversity and extracellular enzymatic activity (EEA) of microbial assemblages associated with polymetallic nodules collected from the Clarion Clipperton Zone (CCZ) in the equatorial North-Central Pacific Ocean, at 4050-4550 m water depth across a spatial scale of approx. 1000 km. During RV SONNE expedition SO268, 58 nodules were collected with box-corer and remotely operated vehicle (ROV). Aliquots of the nodules were taken from three different microenvironments: the upper part exposed to seawater, the nodule core and the bottom part buried in the sediments. The total microbial cells were counted via acridine orange direct counts (AODC), and active bacterial and archaeal cells were enumerated applying fluorescence in situ hybridization (FISH). EEA measurements were carried out to assess the potential hydrolysis rates of several different enzymes (i.e. aminopeptidase, chitobiase, glucosidase, esterase). Bacterial and archaeal diversity was investigated by sequencing of hypervariable region V3-V4 and V3-V5 of 16S RNA gene, respectively. Our results provide for the first time a quantitative estimate of the microbial biomass hosted by polymetallic nodules and their potential contribution to organic matter degradation. The potential impact on benthic processes and diversity caused by the removal of polymetallic nodules by deep-sea mining activities is depicted by comparison with sedimentary data including sedimentation rates and relations with characteristics of the nodules themselves, in terms of their organic matter content, the presence of sessile epifauna (i.e. corals or anemones) on them, as well as their density.

Are we ready for deep-sea mining? State of the knowledge on ecosystems of the deep-sea mineral deposits after 20 years of exploration contracts

Tina Molodtsova, Diva Amon, Ana Colaço, Jeffrey Drazen, Livia Ermakova, Sabine Gollner, Lénaick Menot, Craig Smith

Exploitation of deep-sea mineral deposits has been of interest since the 1960s. At that time, however, deep-sea mining was considered difficult to access and economically inefficient. Advances in technology, depletion of commercially valuable minerals on land, and the increased need for these resources for rapidly developing electronics, computer technology, batteries, machinery and industry have brought seabed minerals back to the attention of interested parties. In March 2001, three contracts for exploration for polymetallic nodules in the Clarion-Clipperton Fracture Zone were signed with the International Seabed Authority, followed by formal exploration for deep sea mining. By March 2021, 20 years later, 31 contracts had already been signed for exploration for cobalt-rich ferromanganese crusts (5), polymetallic nodules (19) and polymetallic sulphides (7) in the Pacific, Atlantic and Indian Oceans.

Based on published data, we would like to (1) analyze the impact of the past 20 years in terms of increasing scientific knowledge of the composition, structure, and functioning of the seafloor mineral ecosystems, (2) evaluate which data collected from exploration contracts were actually used in peerreviewed scientific publications, (3) estimate the extent to which ISA contractors collaborate with the scientific community, (4) list the potential risks of deep sea mineral mining discovered in last 20 years, and (5) identify the major knowledge gaps that need to be addressed to fully understand potential impacts of mining in the deep-sea.

Exploring the potential of metabarcoding as a reliable tool for monitoring meiobenthos in potential future deep-sea mining areas

Ellen Pape, Lara Macheriotou, Kenny Bogaert, Holly Bik, Taruna Schuelke, Annelien Rigaux, Ann Vanreusel

Polymetallic nodule mining is expected to occur in the near future in the Clarion Clipperton Fracture Zone (CCFZ), Northeast Pacific which is the largest, high resource-grade deposit of its kind on Earth. To properly gauge potential impacts of seabed mining operations, and thus to be able to apply adequate management practices, the environmental baseline needs to be established. Moreover, during and post-mining, potential impacts on ecosystems need to be monitored. Ideally, relevant indicators should be measurable in a relatively fast and standardized manner.

Previous morphology-based metazoan meiobenthos (<32 µm) studies, focusing on the dominant phylum of Nematoda in the GSR exploration contract area (eastern CCFZ), showed no significant differences in diversity and composition between (1) distant but environmentally similar nodulebearing sites, and (2) nodule-free and nodule-bearing sediments. However, these identifications were performed at genus-level and species-level for a single nematode genus. To accurately assess biodiversity, identifications at the highest taxonomic resolution are needed. However, Nematode taxa are speciose and not always morphologically distinct, rendering morphological identification a tedious task requiring considerable taxonomic expertise. Therefore, only a subset of the nematodes present in a sample are typically identified.

Here, we present metabarcoding data (18S v1-v2 Amplicon Sequence Variants) obtained from the same locations as the morphological samples, which should yield more reliable and comprehensive biodiversity estimates as, unlike morphological assessments, (1) the entire community is considered, (2) these data also provide phylogenetic insights. We will investigate whether the patterns revealed by the morphological data are corroborated by metabarcoding and thus whether this technique can serve as a reliable tool for deep-sea meiobenthos monitoring.

- Biodiversity, biogeography, and connectivity in the world's largest marine minerals exploration frontier

Eva CD Stewart, Guadalupe Bribiesca-Contreras, Thomas Dahlgren, Helena Wiklund, Sergi Taboada, Erik Simon-Lledo, Daniel O B Jones, Muriel Rabone, Craig R Smith, Adrian Glover

The Clarion-Clipperton Zone (CCZ), equatorial Pacific Ocean, has become an area of commercial importance owing to the growing interest in mining high-grade polymetallic nodules at the seafloor. Nodule mining is expected to have a significant impact on the vulnerable and diverse abyssal fauna found in the CCZ. However, spatial patterns of faunal diversity and community composition are still largely unknown. Here, a DNA taxonomy approach is used to investigate patterns of taxonomic and phylogenetic alpha and beta diversity, and genetic connectivity, of polychaetes (Annelida) across the abyssal seafloor. A combination of phylogenetic and taxonomic alpha and beta diversity metrics were used to analyse patterns of biodiversity. Connectivity analyses was based on haplotype distribution data for a subset of the studied taxa. DNA taxonomy identified 280 – 289 polychaete species from the COI and 16S datasets respectively, with remarkably high alpha diversity across the CCZ. Both taxonomic and phylogenetic beta diversity were high between sites, and were mostly explained by lineage turnover. Comparison against a null model found that over half of pairwise comparisons were more phylogenetically distinct than expected based on their taxonomic diversity. The connectivity analyses indicate absence of population structuring at the spatial scale studied. These results suggest that environmental filtering, rather than dispersal limitation, plays a greater role in regulating spatial patterns of biodiversity in the CCZ, highlighting the importance of considering the biogeochemical representativeness of designated protected areas if they are to succeed in preserving the CCZ fauna in the event of nodule mining. This is of particular relevance to APEI-6, which showed significant shifts in community structure when compared to all examined nodule exploration areas.

- Abundance, biodiversity and community structure of deep-sea benthic metazoan meiofauna in the polymetallic nodule fields of the Clarion-Clipperton Fracture Zone, eastern Pacific Ocean

Samantha Jia Wen Tong, Bin Qi Gan, Koh Siang Tan

The sea floor of the Clarion-Clipperton Fracture Zone (CCFZ) in the Pacific Ocean is expected to be a commercially important polymetallic nodule mining area in the coming years. It is crucial to understand the distribution and abundance of deep-sea biodiversity and their communities, so that nodule mining can be designed to minimize deleterious impacts on marine life. In February 2015, Ocean Mineral Singapore (OMS) and United Kingdom Seabed Resources Limited (UKSRL) set out on a joint research expedition—Abyssal Baseline Project 2015 (ABYSSLINE 02/AB02). Twenty-one papers that included biological data found in the OMS area were published so far, but our overall understanding of biodiversity is still missing a crucial component—the metazoan meiofauna. We provide here the first quantitative findings of metazoan benthic animals ≥ 40 µm in the 30 × 30 km area survey stratum in the OMS contract area. A total of 88 867 individuals were identified from 23 major taxa based on multiple corer samples at 12 randomly sampled stations. Even in our small surveyed area, the community structure was different at our sites, confirming that the CCFZ deep sea floor is very diverse. Our results suggested that shear strength contributed to the difference in meiofaunal community, whereby stations with lower shear strength found higher meiofaunal abundances and vice versa. Although nodule surface area and nodule volume were negatively correlated with meiofaunal abundance, these parameters did not affect the meiofaunal community structure at the major taxon level. The mean meiofaunal abundance (235.73 ind/10cm2) was higher at our sites when compared to previous studies elsewhere in the CCFZ, confirming the westward decrease in meiofaunal abundance across the CCFZ.

- Application of scientific criteria for identifying hydrothermal ecosystems in need of protection

Sabine Gollner, Ana Colaço, Andrey Gebruk, Patrick Halpin, Nick Higgs, Elisabetta Menini, Nélia C. Mestre, Pei-Yuan Qian, Jozee Sarrazin, Kamil Szafranski, **Cindy Lee Van Dover**

Hydrothermally active vent fields in the deep sea are globally rare (abundant in numbers, but extremely small in area) and are rich in extraordinary life based on chemosynthesis rather than photosynthesis. Vent fields are also sources of polymetallic sulfides rich in copper and other metals. Mineral resources of the seabed beyond national jurisdictions are administered by the International Seabed Authority (ISA), which has mandates to manage mineral resource-related activities and to ensure effective protection of the marine environment from harmful effects that may arise from such activities. To date, the ISA has approved 3 contracts for mineral exploration on the northern Mid-Atlantic Ridge (nMAR). A Regional Environmental Management Plan (REMP) for the nMAR is in development, including application of area-based management tools to mitigate potential impacts of mining activities and protect vulnerable ecosystems. Several inter-governmental organizations have developed criteria to identify vulnerable ecosystems in need of protection. Here we use criteria developed by FAO for Vulnerable Marine

Ecosystems (VME), by the Convention on Biological Diversity for Ecologically or Biologically Significant Areas (EBSAs), and by the International Maritime Organization (IMO) for Particularly Sensitive Sea Areas (PSSAs) to assess whether the 11 confirmed vent fields on the nMAR may meet these criteria based on published scientific literature and expert knowledge. Our assessment indicates that 10 of 11 active vent fields within the management area meet all criteria and one vent field meets multiple criteria.

- Spatial Diversity and Connectivity of Microbial Communities in Clarion-Clipperton Fracture Zone (Northesat Equatorail Pacific Ocean)
  Batuhan Cagri-Yapan, Massimiliano Molrai, Julia Maren Otte, Felix Janssen, Frank Wenzhofer, Matthias Haeckel, Antje Boetius

Microbes constitute an important part of diversity and biomass in deep-sea sediments. Yet, our knowledge on microbial diversity and microbially-mediated processes is very limited. The potential mining of polymetallic nodules in abyssal plains makes it more urgent to elucidate microbial diversity and its spatial patterns before deep-sea ecosystems will lose their pristine state. A more comprehensive knowledge of deep-sea ecosystems is of vital importance to mitigate negative impacts of mining activities. In this study , in order to disclose diversity and study connectivity of benthic bacterial and archeal communities in polymetallic nodule fields we have taken samples form surface sediments, nodules and bottom water in Clarioin-Clipperton Fracture Zone, an important potential mining area. Samples were collected in two contract areas (BGR and GSR), approximately 1000 km distance, and at spatial scales from hundreds of meters to kilometres in each claim. Microbial diversity was investigated by 16S rRNA gene tag sequencing, and 16 rRNA transcript data is analysed to reveal active taxa. In addition to extend the spatial analysis of benthic microbial diversity at oceanic basin scale and at different trophic condition, our results were compared with those of previous study (Vonnahme et al., 2020) carried out in the nodule fields of Peru Basin (South-Central Pacific Ocean). Preliminary data analysis suggests significant clustering of microbial assemblages according to substrate type and sampling region. Further analysis on alpha diversity and beta diversity will reveal diversity patterns of microbial communities within and between regions, and help to explain the drivers of these patterns. Our study provide crucial information to fill up the knowledge gap on benthic microbial diversity and connectivity of the Central Pacific Ocean, Understanding the factors shaping structure of microbial assemblages have an important potential for developing policies to mitigate negative impacts of deep-sea mining.

General & Special Sessions 2 Biodiversity and ecosystem functioning from microbes to megafauna (biodiversity patterns, species distribution, function, food webs)

General session

- Complete mitogenomes of two black corals (Hexacorallia: Antipatharia: Antipathidae) from Rapa Nui (Easter Island)
  Cynthia Asorey, Javier Sellanes, Daniel Wagner, Erin Easton

Antipatharians, commonly known as black corals, consist mostly of deep-water species that occur in all oceans from tropical to polar regions. During benthic surveys off Rapa Nui (Easter Island), whip corals were observed at 60-240 m and two black whip coral specimens were collected using a Commander MK2 remotely operated vehicle (Mariscope Meerestechnik, Kiel, Germany), stored in 95% ethanol, and deposited at the Universidad Catolica del Norte, Chile. DNA was extracted and submitted to the Biopolymers Facility at Harvard Medical School for next-generation sequencing. Trimmed reads were assembled de novo with SPAdes and mapped to the resulting reference sequence to generate a consensus sequence. Genes were annotated by manually adjusting Stichopathes luetkeni (NC018377) annotations mapped to the consensus sequence. Both mitogenomes presented the classic pattern expected for Hexacorallia: 13 protein-coding genes, 2 rRNA genes, and 2 tRNA genes (tRNA-met and tRNA-trp). Although whip corals from Rapa Nui have historically been identified as Stichopathes sp. based on morphological characters, we assigned the collected specimens as Pseudocirrhipathes sp. (SCBUCN 8849 collected at 120-180 m) and Stichopathes sp. (SCBUCN 8850 collected at 180 m) based on our more detailed morphological analyses and phylogenetic reconstructions using ITS1 rDNA. The complete mitogenome of Pseudocirrhipathes sp. was 20,389 bp (29.0% A, 15.2% C, 19.9% G, and 35.9% T) and Stichopathes sp. was 20,463 bp (29.0% A, 15.3% C, 19.9% G, and 35.8% T). These two complete genomes add important new information to our knowledge on black corals, a group that is poorly known because most species inhabit deep-water environments (>50 m), which are logistically challenging to study. Funding: FONDECYT 1181153, NM ESMOI, Conservation International, and Oceana Chile.

- The theory of Hydrothermal Vent biogeography
  Brunner Otis, Chong Chen, Thomas Giguere, Shinsuke Kawagucci, Yuka

Suzuki, Verena Tunnicliffe, Hiromi Watanabe, Satoshi Mitarai

Hydrothermal vent ecosystems are discrete 'oases' of high biological productivity and endemicity in the deep sea supported by chemosynthetic primary production. Local populations of vent-endemic species are spatially isolated but can be demographically linked to one another through planktonic larval dispersal forming an interconnected network. Understanding connectivity is important as it supports higher levels of local biodiversity while maintaining regional ecosystem stability, which are targets of conservation management. Here, methods developed from network theory were used with species presence/absence data at vent sites in the North-West Pacific to assess the role of each site in maintaining connectivity across the region. Two complementary networks were generated: a bipartite network of species nodes with links to the vent site nodes at which they are present, and a similarity network where vent site nodes are linked by edges weighted based on the pairwise similarity between their communities. Results from analysing these networks suggested the presence of three distinct subregions, and two outlying sites, within the North-West Pacific. Both networks indicated that a small number of vent sites play a disproportionately important role in maintaining regional connectivity while the bipartite network also identified key vent sites for maintaining connectivity within their respective sub-regions. In addition to distinct advantages in the detection of biogeographic boundaries, when compared to more commonly used hierarchical clustering approaches, these methods are also informative in that they can compare the role of each vent site in driving regional and local connectivity. Our results will be particularly valuable when selecting priority sites for conservation and estimating multi-vent scale impacts from proposed deep-sea mining in the North-West Pacific.

- ## Coral Communities on the Corner Rise Seamounts

  Harold Carlson, Rhian Waller, and all participants in the telepresence program for EX2104

The North Atlantic Stepping Stones: New England and Corner Rise Seamounts expedition in July 2021 visited seamount areas with the Deep Discoverer ROV system onboard the NOAA Ship Okeanos Explorer (EX2104). This expedition was part of the Atlantic Seafloor Partnership for Integrated Research and Exploration (ASPIRE), a major multiyear, multinational collaborative field program focused on raising collective knowledge and understanding of the North Atlantic. This expedition was telepresence enabled, allowing participation from scientists located from across the globe through real time ship to shore video and communications. This expedition took high resolution video imagery from seamount targets in the New England and Corner Rise seamount chains, as well as biological and geological collections. All data from this cruise is freely and publicly available. This poster presents images collected from the Corner Rise Seamount chain and a basic comparative community level analysis of scleractinian and octocoral communities from new sites in this understudied region of the seafloor. Previous research has shown that assemblages of these benthic fauna correlate with longitude, temperature, substrate and depth (Lapointe et al. 2020). Here we will determine whether a cross-seamount comparison of benthic communities reveals similar environmental correlations with diversity

Reference:

Lapointe, A.E., Watling, L., France, S.C., Auster, P.J., 2020. Megabenthic assemblages in the lower bathyal (700–3000 m) on the New England and Corner Rise Seamounts, Northwest Atlantic. DeepSea research. Part I, Oceanographic research papers. 165, 10336

- ## New deep-sea glass sponges (Porifera, Hexactinellida) of the tropical Atlantic seamounts

  Celso Domingos, Daniel Kersken, Astrid Schuster, Katharine Hendry, Joana R. Xavier

Remote and poorly investigated deep seamount environments are increasingly threatened by anthropogenic activities such as bottom fishing, oil and gas exploitation, and climate change. This has resulted in an increased global interest to protect these ecosystems. Glass sponges (Porifera, Hexactinellida) constitute an important and dominant component of the deep-sea megabenthic communities and play key ecological roles, often forming structural habitats in the deep-sea. Currently, there are 143 species of hexactinellids reported for the Atlantic Ocean, the vast majority of which occur in the Northern Atlantic. This study uses an integrative taxonomic approach to identify glass sponges collected on several seamounts (Carter, Knipovich, Vayda) and the Vema fracture zone, located in Areas Beyond National Jurisdiction (ABNJ) across the tropical Atlantic. In total, 28 specimens were analysed and assigned to 19 species, distributed across 15 genera and 6 families. Of these, 12 species are new to science and are currently being described and illustrated. Phylogenetic reconstructions (mtDNA 16S and rRNA 28S) confirm our taxonomic identifications and support previous results on the monophyly of these hexactinellid families. The discovery of such a high number of new species highlights the low exploration and research efforts in the Tropical and South Atlantic, where much deep-sea diversity is yet to be unravelled. The results of this work are particularly relevant in the context of the United Nation's agreement on the conservation and sustainable use of marine biological diversity in ABNJ, setting the baseline for future protection strategies of these vulnerable deep-sea species.

- ## Salas y Gómez Ridge Benthic Habitat and Community Assessment of Seamounts and Oceanic Islands

  Kara Eckley, Javier Sellanes, Dhugal Lindsay, Erin E. Easton,

Seamounts are essential benthic habitats. They provide habitat for organisms and can function as stepping stones for dispersal and possible refugia. In addition to being ecologically important, seamounts are also economically valuable, supporting deep-sea fisheries and potential mineral mining activities The Salas y Gómez Ridge in the southeast Pacific Ocean longitudinally extends ~2,900 km across the South Pacific Subtropical Gyre. The western extent experiences ultraoligotrophic and highoxygen conditions, whereas the eastern extent experiences eutrophic and low-oxygen conditions where it coincides with Eastern South Pacific Oxygen Minimum Zone. These conditions and the distance between seamounts have led to high levels of endemism along this ridge. However, there have been few studies in this region because of its remoteness, and most of the studies were clustered around the islands and in the mesophotic zone. To better understand the biodiversity along this ridge, five seamounts and two oceanic islands were surveyed during the EPIC Cruise (MR18-06-03) by JAMSTEC's R/V Mirai to assess the communities and describe the benthic habitats and megafauna. At each site, the benthic community (from ~900 to 200-400 m) was surveyed by a towed camera and environmental data were collected. Benthic habitat and community characterization based on analysis of the videos and environmental data are underway. Subsequent analyses of the relationships between environmental data and the habitat and communities will follow. Here we report, preliminary geographic and bathymetric ranges for select taxa, habitat characterizations, and environmental data distributions. Funding provided by JAMSTEC, Fondecyt 1181153, and MN ESMOI.

Megafauna communities from abyssal sites along the Gloria Fracture Zone (NE Atlantic)

Teresa C. Ferreira, Christian Hensen, Pedro Terrinha, Mark Schmidt, Thomas Müller, Kasia Sroczynska, Sofia P. Ramalho, Helena Adão

Fracture zones are areas of poorly known abyssal landscapes and benthic faunal communities. During the R/V Meteor M162 cruise several imagery surveys were performed using a TV-CTD guided camera system along four main areas of the Gloria fault system, between the Terceira ridge and the Madeira Tore Rise. Based on these records, we were able to characterize - for the first time - the megafaunal composition, their abundance and diversity along the sub-basin of the Gloria fault at depths between 3500 and 4500m. Quantitative annotations of the observed fauna, as well as evidence of animal traces on the seafloor were explored in relation to topography, substrate type, and geochemical data acquired during surveys. Preliminary observations revealed a total of 121 morphospecies, of which Holothuroidea is the most diverse group, with 12 morphospecies. Deepest transects carried out along the main trace of Gloria Fault system showed the highest similarity among dives, predominantly characterised by soft sediment areas with Elpidiidae holothurians frequently observed. In contrast, the survey carried out at the Terceira ridge showed more diverse communities, which is likely due to a larger variability in substrate and topography. Specifically, soft-sediment sections showed a higher proportion of holothurians, ophiuroids and acorn worms, while unique Anthozoan and Porifera morphospecies were observed in areas with presence of hard substrates. The findings of this study provide unique knowledge of abyssal fauna associated with the Gloria Fault System, including areas inside of national jurisdiction and of relevance for management and conservation actions.

Deep Forests – Assessing the relative vulnerability of South African potential VME indicator taxa

Mari-Lise Franken, Kerry Sink, Lara Atkinson, Natasha Karenyi

Vulnerable Marine Ecosystems (VMEs) are considered hotspots of biodiversity and ecosystem functioning but are sensitive to demersal fishing impacts. VMEs are characterised by five criteria defined by the Food and Agricultural Organization guidelines for management of deep-sea fisheries. Efforts to designate South African VMEs have lagged due to inadequate data and taxonomic expertise. VMEs are commonly identified based on the occurrence of indicator taxa. Although tailored lists of VME indicator taxa have been developed elsewhere, South African efforts have relied on international lists and expert judgment to date, lacking any robust and repeatable method. This study aimed to systematically assess potential South African VME indicator taxa in terms of their alignment to the recognised criteria for VMEs and map their distribution. An existing scoring matrix was adapted and applied to 22 potential indicator taxa, using the species level where possible. Drawing from literature, taxa were scored for uniqueness and rarity, functional significance, fragility, life history and structural complexity criteria on a scale of 1 – 5. An integrated VME indicator score was calculated for each of the taxa using the quadratic mean of all criteria. Individual VME indicator scores ranged from 2.14 (Astrocladus euryale) to 4.56 (Solenosmilia c.f. variabilis and Goniocorella dumosa) with reef building corals having the highest scores across the five categories. Tabulating relative measures across multiple criteria provided an indication of the position for each indicator taxa on the continuum from more resilient taxa through to the most vulnerable. Indicator taxa of eight potential VME habitat types were mapped drawing from available museum records, research trawl invertebrate bycatch data and visual survey records. This study serves as a useful guideline to formalise the list of indicator taxa for monitoring and mapping of VMEs within national jurisdiction to support research and management efforts of South Africa's fragile deep forests.

Acquisition of symbiotic partners: modalities and consequences on establishment, distribution and ecology of vent species

Marion Guéganton, Lucile Durand, Johanne Aubé, Valérie Cueff-Gauchard, Marie-Anne Cambon-Bonavita, Florence Pradillon

In deep-sea hydrothermal ecosystems where light does not penetrate, the food web is sustained by chemoautotrophic microbial production. Symbioses between animals and microbial communities are there a commonality. This is the case of the emblematic shrimps Rimicaris exoculata and R. chacei on the Mid-Atlantic Ridge (MAR). These two species co-occur in active vent areas, but exhibit widely different population densities, distribution patterns at small scale, and diet, as well as differences in post-settlement morphological modifications leading to the adult stage. Despite these contrasting biological traits, both species harbour similar -in terms of composition- bacterial communities in their cephalothoracic cavity and digestive tract at the adult stage. Bacterial proliferation through juvenile growth, after settlement and until the fully metamorphosed adult, may,at least partly, explain the ecological differences observed between these two species. The acquisition of the symbiotic partners in juveniles may thus be an important mechanism of their recruitment dynamics, and may explain their colonisation patterns.

The objective of my study is to better characterize symbiont acquisition in R. exoculata and R. chacei throughout their life cycle, focusing here on their post-settlement stages collected during the HERMINE (2017) and BICOSE 2 (2018) cruises at TAG and Snake Pit vent fields.

I used both metabarcode sequencing and FISH (Fluorescent in situ hybridization) imaging approaches to characterize microbial communities at each investigated life stage of each species at each site. In this presentation, I will focus mainly on the FISH results that illustrate well the changes in the distribution and abundance of the main symbiotic lineages through the life cycle of each host species.

- ### Effects of Energy Availability and Wood Type on Deep-Sea Wood Fall Community Assemblages in the Northern Gulf of Mexico

  Granger Hanks, S. River D. Bryant, Craig R. McClain

Wood in the deep-sea serves as substantial food sources in an otherwise barren environment, forming specialized and diverse community assemblages and adding to diversity in the deep-sea. Little information is known of how wood fall community assemblages differ between wood types (species) and carbon availability. Forty three logs composed of eleven species and four distinct log masses (2, 4, 6, and 8 kg) were deployed in 2017 in the northern Gulf of Mexico along the continental slope at approximately 2,000 meters depth. Wood fall communities were analyzed after recovery in 2019 in efforts to identify the effects of wood type and carbon availability on Gulf of Mexico wood fall community assemblages. Three main conclusions can be drawn from this study: (1) Species abundance, richness, and diversity were found to increase with increasing wood mass in softwood communities; (2) species abundance, richness, and diversity were found to be highest in softwood when compared to hardwood, and (3) Gulf of Mexico wood fall community assemblages were found to be significantly more rich in species than wood fall communities off the coast of northern California. Our findings here suggest that natural variations in wood-falls, including wood type and size, may have a great impact on terrestrial carbon driven communities in the deep-sea.

- ### The Role of Cephalopods in the Azorean Pelagic Food Web

  Nis Hansen, Miguel Guerreiro, Dr. Marco Scotti, Dr. Henk-Jan Hoving

Cephalopods are carnivorous mollusks that occur worldwide from coastal areas to the deep sea, where they often occupy mid-trophic level positions and attain high biomasses. Due to their typically single reproductive cycle cephalopods display very fast population turnover rates. Their importance as prey is significant as their beaks are found regularly in the stomachs of apex predators, such as cetaceans, sharks, and seabirds. Although cephalopods are key players in energy transfer from lower to higher trophic levels, their role in mesopelagic food webs is still unresolved for most oceanic regions. Therefore, this study aims to characterize the role of cephalopods in the pelagic food web of the Azores. We hypothesize that cephalopods occupy mid-trophic level positions in the Azorean pelagic food web and that they act as major links for energy circulation, emphasizing the importance of cephalopods in the Azores and possibly also in other regions. To test this hypothesis, we constructed a trophic interaction network of over 800 unique interactions obtained from already published and newly acquired dietary data of organisms occurring at the Azores. Then, we applied the dominator tree algorithm to identify the main pathways for energy circulation in the trophic network. Our first preliminary results show that seabird´s diet comprises 40% of total cephalopod species-richness and is significantly more diverse ($p < 0.05$, $H' = 4.51 \pm 0.003$) than the diet of sharks ($H' = 4.46 \pm 0.003$), cetaceans ($H' = 3.56 \pm 0.006$), and cephalopods ($H' = 4.04 \pm 0.004$). Relatively low error (0.023) and attack (0.042) sensitivities, assessed by a preliminary filtered (Numerical Frequency >10%) dominator tree calculation, indicate a potentially robust food web. This study contributes to a better understanding of the potential role of cephalopods in pelagic food webs as major links for energy circulation.

- ### Abyssal megafauna communities respond at short time scales to changing food supply

  Christine Huffard, Linda Kuhnz, Larissa Lemon, Alana Sherman, Paul McGill, Rich Henthorn, Daniel Fabian, Victoria Assad, Ken Smith

Deep-sea megafauna behaviour and population density fluctuate with changes in food supply. This understanding comes from short-term observations of experimental food enrichments, and longterm studies, typically conducted at seasonal or annual intervals. By contrast, little is known about how rapidly megafauna community composition may change in response to natural food pulses reaching the sea floor. Here we followed hourly changes in megafauna densities at Station M (NE Pacific, 4000 m) over a 12-month period, using time-lapse photo-imagery. We assessed the timing and nature of changes in residence time (a proxy for food-searching behaviour), community structure, and species richness associated with natural, high-magnitude depositions of phytodetritus that occurred during the observational period. As expected, deposit-feeders, predators and scavengers responded differently to changes in this food supply.

- ### Estimating the community structure of deep-sea amphipods among seamounts

  Eri Ikeuchi, Akira Iguchi, Hiroyuki Yokooka, Hideki Sugishima, Kazumasa Ikeda, Ryuichi Miwa, Miyuki Nishijima, Nozomu Iwasaki, Yuichiro Tanaka, Taiga Kunishima, Shogo Kato, Junpei Minatoya, Nobuyuki Okamoto, Atsushi Suzuki

The aim of this study was to assess the differences in biodiversity between seamount with cobalt-rich ferromanganese crusts with a focus on deep-sea amphipods. In the Arnold and Scripps seamounts off Minami-Torishima Island (JA03 and JA17 seamounts) in the North Pacific Ocean, we we mounted a custom-made cylinder-type baited trap on a free-fall deep-sea camera lander known as “Edokko Mark I” and tried to collect deep-sea amphipods, which are well diversified group in deep-sea area. We succeeded in collecting a large number of amphipod samples, which may include several species with different life characters. With these amphipod specimens and those previously collected from Xufu Seamount (JA06 Seamount), were subjected to community analysis based on COI DNA barcoding and molecularly operational taxonomic units (MOTUs). We detected 24 MOTUs from total of 385 amphipods. Cluster analysis based on the MOTUs showed that the clusters were divided between the base and the flat-top of the seamount, and that JA03, JA06 and JA17 formed separate clusters on the flat-top. Our trial with DNA barcoding around the cobalt-rich ferromanganese crusts demonstrates their potentials for facilitating environmental baseline studies and impact assessments in consideration of future deep-sea mining projects.

- ### The impact of seafloor variance on biodiversity of deep-sea coral and sponge habitats

  Yumna Ismail, Arline Camilo Hernandez, Kayla Cannon, Franchesca Gonzales, Ryan Bohen, Joseph Cartwright, Xavier Delcid, Jack Donaldson, Austin Feasley, Lydia Fregosi, Gagan Kaur, Hannah Lehman, Hailey Niles, Jillian Quay, Nima Sherpa, Jimin Son, Jacob Stern, Maddie Tetreault, Skyler Virginia, Brett Woodworth, Mackenzie Gerringer

Deep-sea coral ecosystems are hotspots of biodiversity, home to many unique species and associate fauna. In shallow-water communities, rugosity generated by coral reefs and rock formations creates a diverse and complex habitat that supports high biodiversity. However, little is known about how rugosity affects deep-sea coral communities. As part of an undergraduate Marine Biology course and undergraduate research experience at SUNY Geneseo, we analyzed rugosity effects on deep-sea coral ecosystems in ROV video collected by NOAA's Okeanos Explorer off Jarvis Island at depths up to 820 meters in the Pacific Remote Islands Marine National Monument (EX1705_Dive05). The rugosity of the seafloor was appraised using a range of 0-4 with increasing complexity; 0 represented flat seafloor and 4 represented complex seafloor. We observed at least 70 unique organism types across seven phyla. Our species accumulation analysis predicted that there were approximately 106 different morphotypes in this sampling site off Jarvis Island. We found no significant difference in community biodiversity between each rugosity level. Benthic and sessile organisms had a similar number of observations at different rugosities, while pelagic and mobile organisms had more variance. However, we did find that certain phyla were more prevalent at higher rugosity levels. As rugosity increased, sponge abundance also increased, indicating a positive correlation between complex seafloor topography and sponge populations. There may be additional factors affecting deep-sea coral community biodiversity, including temperature, presence of predators, food availability, and interspecies relationships. Understanding how small changes in seafloor topography impact ecosystem diversity in deep-sea coral ecosystems could inform management of these habitats that are especially vulnerable due to their slow growth rates and long life-spans.

- ### Molecular confirmation of the bolitaenin genera

  Heather Judkins, Amanda Sosnowski, Michael Vecchione

The pelagic octopod family Amphitretidae includes the subfamily Bolitaeninae, comprised of two phenotypically similar species in separate monospecific genera, Bolitaena pygmaea (Verrill 1884) and Japetella diaphana (Hoyle 1885). These species are extremely difficult to identify, except as mature adults, unless specimens of similar sizes for both species are side-by-side. Until the terminal mature stage, the main characters that separate the two species are relative length of the optic stalk between the eye and the brain, and the relative sizes of the eyes. Misidentifications of juveniles are very common. Due to their many similarities, we hypothesized that these should be collapsed into one genus rather than being considered separate genera. The Deep Pelagic Nekton Dynamics of the Gulf of Mexico Consortium (DEEPEND) has been conducting midwater sampling in the Gulf of Mexico since 2015, collecting many deep-sea cephalopods including Japetella diaphana and Bolitaena pygmaea. One of DEEPEND's goals is to create a DNA barcode database for the Gulf of Mexico midwater fauna, including the use of molecular tools to confirm species identifications and better understand intraspecies genetic variation. Molecular analyses of Japetella diaphana and Bolitaena pygmaea DEEPEND samples included COI and 16S rRNA sequencing that yielded 39 COI and 23 16S rRNA sequences. The sequences revealed two distinct clades, sharing only 92% and 95% pairwise identity in the COI and 16S rRNA trees, respectively. Despite their morphological similarity, these two species are sufficiently different genetically to be considered separate genera, supporting the current accepted phylogenetic relationships of Bolitaeninae.

- ### Can Whale-Fall Studies Inform Human Forensics?

  Brett D. Jameson, Fiona Juniper, **S. Kim Juniper**, Craig R. Smith & Lynne S. Bell

Experimental knowledge of human body decomposition in the deep ocean is very limited, partly due to the logistical challenges of deep-sea research. The literature on ecological responses to the arrival of naturally sunk and implanted whale carcasses on the seafloor represents a potential source of information relevant to questions of human body survival and recovery in the deep ocean. Whale falls trigger the formation of complex, localized, and dense biological communities that have become a point of interest for marine biologists for the past 2-3 decades. Researchers have documented whale falls by whale type, size, geographic location, water depth and water chemistry, and there have been some comparative analyses of decomposition rates and faunal presence on carcasses. We undertook a review and meta-analysis of the whale-fall literature to identify and statistically model trends relevant to human forensics. Results from studies using deep-sea cameras baited with pig carcasses and simulated carrion provided further validation of noted trends. The stages of whale carcass decomposition most relevant to human forensics are those characterised by mobile scavengers that strip the soft tissues from carcasses, and to a lesser degree, other biota that degrade skeletal material. Our statistical models used the number of faunal taxa attracted to the whale carcasses as a measure of the ecological response and the potential rate of decomposition. Negative binomial models identified significant influences of carcass age and dissolved oxygen concentration on the ecological response (taxon numbers). The strongest environmental effects were identified in data from experimental studies that implanted whale carcasses across a broad range of dissolved-oxygen conditions. We propose directions for further experimental research to refine models of environmental controls on decomposition in the deep sea. Our results also highlight the potential use of publicly available global databases on environmental conditions in the deep ocean for informing body scavenging activity and thus body survival. Applying a forensic lens to whale-fall studies provides a window into an otherwise unseen world from the standpoint of human forensic taphonomy.

- ### Species delimitation of Hexacorallia and Octocorallia around Iceland using nuclear

and mitochondrial DNA and proteome fingerprinting

Severin Korfhage, Sven Rossel, Saskia Brix, Steinunn Hilma Ólafsdóttir, Pedro Martínez Arbizu

Cold-water corals build up reef structures or coral gardens and play an important role for many organisms in the deep sea. Climate change, deep-sea mining, and bottom trawling are severely compromising these ecosystems, making it all the more important to document the diversity, distribution, and impacts of corals. This goes hand in hand with species identification, which is morphologically and genetically non-trivial for Hexa- and Octocorallia. Morphological variation and slowly evolving molecular markers are part of the difficulty in species identification. In this study, a fast and cheap species delimitation tool for Octocorallia, and Scleractinia of the Northeast Atlantic was tested based on 53 specimens. Therefore, two nuclear markers (ITS2 and 28S) and two mitochondrial markers (COI and MutS) were tested. The sequences formed the basis for a reference library to compare the results with the proteomic analysis of the MALDI-TOF MS. The genetic methods were able to distinguish 17 of 18 presumed species. The MALDI-TOF MS method, which here was first introduced in Scleractinia and Octocorallia, was able to distinguish seven species. The undistinguished species still achieved good signals but were not represented by enough specimens to compare them with each other. Therefore, it is predicted that with an extensive reference library of spectra of Scleractinia and Octocorallia, MALDI-TOF MS may provide a rapid and costeffective alternative for species discrimination in corals.

- ### The importance of chemosynthesis in the pelagic realm of Santos Basin, Southwestern Atlantic Ocean

Deborah S. Kutner, Flávia M. P. Saldanha-Corrêa, Mateus G. Chuqui, Pedro M. Tura, Daniel L. Moreira, Frederico P. Brandini, Camila N. Signori

The distribution of chemosynthetic rates in the pelagic zones and their participation in the carbon cycle, especially when compared to photosynthetic rates, are still unclear. The goal of this study was to measure chemosynthetic productivity and analyse its spatial distribution and relative contribution to photosynthesis in the Santos Basin, Southwestern Atlantic Ocean. Within the scope of the Santos Project "Chemical and biological characterization of Santos Basin", coordinated by PETROBRAS/CENPES, samples were collected for chemosynthesis experiments throughout the water column, from the surface, deep chlorophyll maximum (DCM), 250 m, 900 m, 1200 m to 2300 m, and were incubated with 14C-bicarbonate in the dark for a period of 9-12 h. Samples for photosynthesis experiments were incubated for 5-8 h in eight different light levels, simulating in situ conditions. Chemosynthetic rates were analysed using statistical tests to verify spatial differences between groups of samples. In addition, chemo- and photosynthetic rates were integrated from the surface to the DCM and compared at the same stations to determine the relative contribution of each process. The chemosynthetic and photosynthetic rates were, on average, 0.97 ± 1.22 mgC.m-3 .h-1 (considering all depths) and 2.30 ± 2.10 mgC.m-3 .h-1 (considering surface and DCM, without outliers), respectively. Statistical tests showed significant differences ($p<0.05$) in chemosynthetic rates only when considered between radials from southwest to northeast across the basin. On average, chemosynthesis represented 31% of the total primary productivity. Of an overall of 13 stations analysed, five showed higher chemosynthetic rates than photosynthetic, representing 52-88% of total productivity. They were apparently favoured by oceanographic features, as the occurrence of vortices and an upwelling. Therefore, chemosynthesis may play a significant role in the carbon cycle in the pelagic realm of the Southwestern Atlantic. Further investigation will shed light on the influence of abiotic factors and oceanographic phenomena on chemosynthesis.

- ### Determining Dietary Specialization in Siphonophores Using Remotely Operated Vehicle Data

Alex Lapides

Although the open-ocean midwater represents the largest habitat on the planet, we still have much to learn about the trophic connections that structure the midwater food web. Siphonophores are colonial gelatinous predators, highly abundant and diverse in the open ocean, that play a central role in this ecosystem. With the advent of submersible technologies it is increasingly feasible to observe both siphonophores and their potential prey in situ, allowing us to make high-quality predictions about their abundance and distribution. Using MBARI's Video Annotation and Reference System database, we built generalized additive models of 15 different siphonophore species as well as their potential prey and quantified the predicted spatial-temporal overlap between each pair. We then compared these overlap measurements with observed feeding events to determine prey selectivity and specialization of various siphonophores. We also investigated the relationship between specialization and selectivity, and selectivity and depth. Finally, we compared trophic niche overlap with spatiotemporal overlap to determine whether competitive niche segregation was occurring. We found a strong relationship between total selectivity and specialization (Shannon-Wiener's H) and no evidence of competitive niche segregation. Understanding these trophic links enhances our understanding of midwater food webs and allows us to make predictions about how the system may respond in the future.

- ### The Influence of Steep Submarine Canyon Bathymetry on the Behavior and Distribution of the Deep Pelagic Community

Astrid Brigitta Leitner, Rob Sherlock, Kim Reisenbichler, Bruce Robison

Submarine canyons are ubiquitous features of continental shelves globally. Canyons are well documented biological hotspots linking deep sea and nearshore communities. Their impacts on the coastal ecosystem and local economies are disproportionate to their areal extents, and the oceanographic and ecological mechanisms responsible for this phenomenon is an active area of research. Here we investigate whether topographic blocking of deep pelagic vertical migrators on the rim of the Monterey Canyon is a mechanism that regularly aggregates deep-sea migrating midwater prey. By combining active acoustic surveys and bathymetrically oreinted midwater remotely operated vehicle (ROV) transects, we report the frequency of occurrence of topographic blocking at our focus site and relate our observations to oceanographic drivers such as local current velocity. We describe how topographic blocking manifests at the canyon shelf break and which midwater community members are affected. Finally, we discuss possible implications to bentho-pelagic coupling and ecological canyon dynamics. Our unique approach allows for greater spatial and temporal coverage while still providing the high degree of taxonomic resolution required for understanding the role of abrupt bathymetry in influencing the behaviors and distributions of the deep pelagic community.

- ### A Year in the Life of a Deep Sea Coral Community

  Amanda Gannon, **Steven Y. Litvin**, Chris Lovera, Alana Sherman, Paul McGill, Dale Graves, Rich Henthorn, Aaron Schnittger, Jim Barry

Cold water corals are an important component of canyon, ridge, seamount and other deep sea systems throughout the world. These corals provide habitat complexity and support a wide range of fish and invertebrate species, resulting in “hot spots” of biodiversity. However, deep water corals are long lived and generally exhibit slow growth rates, making them vulnerable to disturbance and making recovery times lengthy. Thus, while there is a vital need for additional studies on the ecology of deep water corals and their associated communities, approaches must avoid significant damage or extraction of the corals themselves. Toward this goal, remotely operated vehicles (ROV) have been widely used to study the distribution, abundance and population structure of deep sea corals or to repeatedly survey specific coral communities, usually annually or less often. Fewer studies have focused on the dynamics of deep sea coral communities on shorter time scales. To address this need, scientists and engineers developed a time-lapse camera system as part of the Monterey Bay Aquarium Research Institute’s Deep Sea Coral and Sponge Observatory (DiSCO) project. The timelapse camera is comprised of a digital SLR camera, a custom low-power controller, and two custom 200 W-sec strobes. In addition, this time-lapse system is designed with a tilt motor and the ability to communicate via wet-mateable connectors to a ROV, enabling users aboard the ship to set tilt angle and camera parameters before initiating a long-term deployment. The system can collect one image per hour during a yearlong deployment (~9000 images). It was first deployed from March 2020- March 2021 at 1213m depth at Sur Ridge, a system rich in deep sea corals located off the coast of central CA, USA. We present our initial analyses from this unique time series.

- ### Biodiversity of mesopelagic fish community on the slope of the Bay of Biscay

  Liz Loutrage, Jérôme Spitz, Anik Brind’Amour

The mesopelagic zone, also called the twilight zone, lies between 200 m and 1 000 m depth and is one of the least well-known ecosystems in the world ocean. Acoustic surveys suggest that estimation of biomass could hold up to 90% of the fish biomass in the planet, representing a huge potential for exploitation. However, the mesopelagic community plays a considerable role in global biogeochemical cycling, biological carbon pump and provides an important food sources for large pelagic predators like tuna and marine mammals. Increased knowledge of this community is therefore essential to estimate the ecosystem services provided by mesopelagic organisms. The objective of this study is to provide a first quantitative description of the taxonomic and functional structure of mesopelagic fish community in the Bay of Biscay where data are particularly lacking. For this, we used the data collected by opportunistic pelagic trawling on the slope during the EVHOE scientific surveys since 2002. The fish community included 95 different species belonging to 30 families, the Myctophids being the most diverse family with 23 different species recorded. In terms of density, 95% of the specimens captured belonged to only 15 different species. The dominant species of fish were some myctophids (Benthosema glaciale, Ceratoscopelus maderensis, Notoscopelus kroeyeri and Myctophum punctatum), an alepocephalid (Xenodermichthys copei) and a paralepidid (Arctozenus risso). Species richness reaches highest values in depth ranging between 1200 and 1600 m. Thus, in order to identify environmental characteristics shaping the distribution of the mesopelagic communities under study topographic, physico-chemical, and density-dependence variables are being tested. The next step will be to understand the trophic relationships among these species that occupy a key link between primary consumers and higher trophic levels in oceanic ecosystems.

- ### Mitogenomics of Vestimentifera: New Mitochondrial Genomes and Biogeographical Implications

  Marina McCowin, Greg Rouse

Deep-sea tubeworms within Siboglinidae (commonly referred to as Vestimentifera) are well known for their abundance at chemosynthetic environments. These annelids' endosymbiotic relationship with chemoautotrophic bacteria allows them to thrive at hydrothermal vents, cold seeps, and organic falls, and their tendency to grow in dense aggregations creates essential habitat for other organisms. Recent phylogenetic studies of this clade have demonstrated the utility of mitogenomic data in resolving relationships among its members (e.g. Li et al., 2015; Sun et al., 2018). However, these phylogenies of Vestimentifera are still missing some key taxa, including two genera: Alaysia Southward, 1991 and Arcovestia Southward & Galkin, 1997. The placement of these two lineages within Vestimentifera is largely unknown, with only two phylogenetic studies involving either lineage to date, neither of which revealed any well-supported relationships of Alaysia or Arcovestia to other taxa within Vestimentifera. In addition, preliminary data have shown these lineages may be paraphyletic. We complete the mitogenomic sampling of Vestimentifera by sequencing the mitochondrial genomes of Alaysia and Arcovestia species, and add further new mitogenomic data to the Vestimentiferan phylogeny with the sequencing of additional Lamellibrachia and Escarpia species that are currently missing from existing mitogenomic datasets. We utilize Maximum Likelihood and Bayesian approaches to resolve the placement of Alaysia and Arcovestia and consider the implications of this more complete mitogenomic phylogeny for the biogeography and habitat evolution of Vestimentifera.

- ### Does trophic specialization drive the remarkable diversity of deep pelagic dragonfishes?

  Ryan McGonagle, Tracey Sutton

Dragonfishes (Stomiidae) are the most speciose family of mesopelagic fishes, with the subfamily Melanostomiinae (scaleless black dragonfishes) contributing 220 of the 317 described species. The relationship between diversity (both systematic and morphological) and feeding of the subfamily

Melanostomiinae has not been previously examined, primarily due to sample size limitation. Here the diet and morphology of 16 species of melanostomiine dragonfishes in the Gulf of Mexico were examined to ascertain whether the remarkable speciation in this fish clade was and/or is driven by prey specialization, as is the case with many other speciose fish families. Gut content analysis revealed three feeding guilds by major prey taxon, with most species grouped into a primarily piscivorous guild and two much smaller guilds selecting for cephalopod prey. Piscivorous dragonfishes were further categorized into feeding groups by prey fish family, where four feeding groups were identified. Within this feeding guild, the majority of piscivorous dragonfishes were grouped into a myctophid-eating cluster, with three small clusters including predation upon bristlemouths (Family Gonostomatidae), oceanic basslets (Family Howellidae), bigscales (Family Melamphaidae), and other dragonfishes. Regarding functional morphology, five morphotypical groups were identified, with dissimilarity driven mostly by barbel length, vertical oral gape, and horizontal maxillary oral gape. There were no robust morphological-dietary relationships amongst melanostomiines, with dietary diversity much lower than morphological diversity. These results suggest that other factors, perhaps species-specific bioluminescence, attuned visual physiology, and sexual selection, may be primary drivers of hyperspeciation in an otherwise homogeneous environment such as the midwater domain.

Trophic ecology, diet and feeding behaviour of three bathyal sea anemones (Actiniaria: Cnidaria) in the Northwest Atlantic

Jiamin Sun, Jean-François Hamel, Violaine Shikon, Edison F. Cossignani, **Annie Mercier**

Sea anemones are often presented as a major component of benthic communities and described as ecologically important in benthic food webs. However, studies on the trophic ecology of deep-sea species are rare. Here, the feeding habits and dietary sources of three species of bathyal sea anemones (Actinostola callosa, Actinauge cristata, Urticina sp.) from the Northwest Atlantic were studied in a multi-faceted approach including stable isotopes, gastrovascular contents, lipid and fatty acids analysis and observations in a mesocosm. Stable isotope analysis showed that A. callosa sits at a slightly lower trophic level than A. cristata and Urticina sp. and that the two latter species rely on different carbon sources at roughly the same trophic level. The gastrovascular cavity contents and mesocosm study revealed that all three species ingest a variety of food items, from inorganic materials to a diversity of metazoans, including whole large prey. Total lipid content varied across species and was highest in Urictina sp. Phospholipids constituted the main lipid class in all three species, with consistently high levels of wax ester storage lipids. All sea anemones were also characterized by high proportions of mono and polyunsaturated fatty acids (MUFA and PUFA) as well as ω3 and ω9 FAs, and strikingly low proportions of 20:4ω6 (ARA). High values of 20:5ω3 (EPA), 20:1ω9 and 22:1ω11(13) evoke a diet centered on zooplankton, with notable particularities. For instance, Urticina sp. had the highest PUFA to saturated fatty acids ratio, indicative of carnivory. Overall, results suggest that the three sea anemone species occupy different niches in the spectrum of opportunistic polyphagous predation/feeding, with Urticina sp. relying chiefly on more energetic and larger prey and A. cristata targeting smaller zooplankton, foraminifera and particulate food, highlighting that large actinians play diverse roles in benthic food webs.

Building up DeepIso - A global open database of stable isotope ratios and elemental contents for deep-sea ecosystems

Loïc N. Michel, James B. Bell, Stanislas F. Dubois, Gilles Lepoint, Karine Olu, William D. K. Reid, Jozée Sarrazin, Gauthier Schaal, Brian Hayden

Stable isotopes have been instrumental to many key-findings about deep-sea ecosystem functioning, particularly in chemosynthesis-based habitats (hydrothermal vents, cold seeps). However, constraining sampling logistics commonly limit the scope, extent, and therefore insights drawn from isotope-based deep-sea studies. Overall, much is left to discover about factors globally influencing food web structure in deep-sea ecosystems. In this context, it is crucial that all generated data are easily discoverable, available, and reusable. DeepIso is a collaborative effort to produce a global compilation of stable isotope ratios and elemental contents in organisms from deep-sea ecosystems. In doing so, it aims to provide the deep-sea community with an open data analysis tool that can be used in the context of future ecological research, and to help deep-sea researchers to use stable isotope markers at their full efficiency.

The database, accessible under CC-BY licence at https://doi.org/10.17882/76595, currently contains 18677 fully documented measurements. Archived parameters include δ13C (n = 4587), δ15N (n = 4388), δ34S (n = 951), %C (n = 2740), %N (n = 2741), %S (n = 752) and C/N ratio (n = 2518). Those measurements pertain to 4378 distinct samples belonging to 493 taxa, plus sediments, suspended particulate organic matter, plankton and detritus. Samples were taken between 1989 and 2018 in multiple environments (hydrothermal vents, cold seeps, cold water coral reefs, and other benthic or pelagic environments) and at depths ranging up to 5209 meters.

To maximise the scope of the project, we are looking to integrate more data, either underlying published articles, from grey literature, or even unpublished. We'll be happy to assist in data formatting and publication. If you are willing to contribute, or simply if you have feedback about the database, please get in touch via mailto:loicnmichel@gmail.com

Amino acid stable isotope composition of sinking and suspended particles in the North Pacific reveals their importance for abyssal food web dynamics

Elizabeth Miller, Sonia Romero-Romero, , Kenneth L. Smith, Christine L. Huffard, Brian N. Popp, Jeffrey C. Drazen

Organisms living on the abyssal plain are dependent on particulate organic material sinking from surface waters, which raises questions of how this nutrient-poor material might fuel complex abyssal food webs. The δ15N and δ13C values of individual amino acids can provide information about origins, composition, and extent of microbial alteration of detrital particles and allows for identification of the material that forms the base of a food web. Previous δ15N and δ13C values of individual amino acids at Station ALOHA (North Pacific Subtropics) showed that particles undergo significant microbial breakdown as they settle through the water column, and that small, suspended particles (53 µm) particles at Station ALOHA and at Station M (off the California coast) to abyssal depths. We aim to determine which particle types are utilized by various abyssal organisms at these sites. We found that the stable isotope composition of particles varies considerably with size, season, depth, and location. At both sites, small and large particles collected using large volume in situ pumps from 50 meters above bottom have distinct amino acid δ15N and δ13C values reflective of their different origins and states of microbial alteration and abyssal fauna vary in their dependence on different particle sizes. At Station M particles undergo less isotopic change before reaching the abyssal plain, with seasonal pulses of detritus delivering larger amounts of fresh material utilized by deposit feeders. Microbial pathways may have more of an impact on benthic metazoans in oligotrophic areas like Station ALOHA, where we find extensive evidence of microbial reworking of particles forming the base of the abyssal food web.

Myctophid Ecology in the Gulf of Mexico: 2011 - 2017

Rosanna J. Milligan, Tracey Sutton

Lanternfishes (Myctophidae) are a highly diverse and globally-important family of fishes that form a ubiquitous part of the deep-pelagic micronekton. The majority of lanternfish species conduct diel vertical migrations (DVMs) from the mesopelagic (200 – 1000 m) to the epipelagic (0 – 200 m) where they feed at night. As voracious zooplanktivores and an important food source for commerciallyimportant fishes, seabirds, and deep-living predators, myctophids play a key role in the biological pump and are an important intermediate trophic group, linking coastal, upper-ocean and deep-ocean ecosystems. Nonetheless, relatively little is known about the variability of myctophid biodiversity, assemblage structure and species distribution patterns, or of their DVM behaviours over spatial and temporal scales. In this study, we present a synthesis of recent research findings examining the community composition and distribution patterns of a high-diversity myctophid assemblage in the northern Gulf of Mexico in relation to environmental variability in the years following the Deepwater Horizon oil spill of 2010. We present spatially and temporally-explicit analyses from depth-stratified data (0 – 1500 m) collected between 2011 and 2017 across a 200 x 700 km survey area. Analyses indicate that the lanternfish assemblage is weakly structured, with individual species showing stronger and more predictable responses to mesoscale environmental conditions, primarily driven by changes in their vertical distributions and migratory behaviours. Our findings to date suggest that the overall assemblage is comprised of a highly-dispersed, well-mixed suite of individual populations, each of which respond independently to environmental cues. We discuss the implications of these findings for ecosystem structuring and carbon transfer between the surface and deep oceans.

Comparison of environmental DNA and imaging methods for monitoring deep-sea fishes on a seamount

Miyuki Nishijima, Akira Iguchi, Eri Ikeuchi, Hiroyuki Yokooka, Hideki Sugishima, Kazumasa Ikeda, Ryuichi Miwa, Yoshiro Sekido, Nozomu Iwasaki, Masahiro Suzumura, Ayumi Tsukasaki, Yuichiro Tanaka, Shogo Kato, Junpei Minatoya, Nobuyuki Okamoto, Taiga Kunishima, Yuji Ise, Atsushi Suzuki

To efficiently evaluate fish biodiversity around a seamount with cobalt-rich ferromanganese crusts, we compared environmental DNA (eDNA) methods using seawater and sponge samples and imaging methods using a remotely operated vehicle (ROV) and a free-fall deep sea camera lander called the Edokko Mark I on the Takuyo-Daigo Seamount in the northwestern Pacific Ocean. We detected 16 fish families. The patterns of detection differed significantly between eDNA and imaging methods. This difference is attributed to the difference in the powers of detection of some fish groups between methods. The difference in fish composition was not significant between seawater and sponge eDNA methods, but was significant between Edokko Mark I and ROV methods. The latter difference may be attributed to different sensitivities of some fish groups to ROVs. Although eDNA analysis requires more improvements such as better sampling, combining eDNA and imaging methods enables us to grasp deep-sea fish biodiversity more comprehensively. Our trial with eDNA analyses using seawater and sponge samples around cobalt-rich ferromanganese crusts demonstrates the potential for facilitating environmental baseline surveys and impact assessments around mineraliferous seamounts.

Observations of deep-sea cirrate octopods off southeast Brazil using a manned submersible

Jose Angel Alvarez Perez, Paulo Yukio Gomes Sumida, Yoshihiro Fujiwara, Richard Schwarz

Cirrate or “dumbo” octopods are a representative cephalopod taxon found in deep-sea habitats all over the world. However, cirrate records are very rare in the South-western Atlantic. The animals are vulnerable to trawl catches, but are highly damaged when captured hampering proper preservation of the animals for posterior studies and display in museum collections. Over the last three decades, in situ observations using remotely (ROV) or human occupied vehicles (HOV) provided new insights on the behaviour and distribution records of these animals. The Brazil-Japan joint expedition ‘IatáPiúna’ (JAMSTEC – IOUSP – CPRM consortium), conducted during April-May 2013, surveyed deep water areas of the São Paulo Ridge and São Paulo Plateau off the Southeast Brazil, using the manned submersible Shinkai 6500, and resulted in the first in situ observations of deep-sea cirrate octopods in the region. A total of eight animals were observed between depths of 2,532 and 4,099 m, where bottom water temperatures ranged from 0.5 to 3.0 °C under the influence of Atlantic deep-water masses: Antarctic Bottom Water and North Atlantic Deep Water. Observed octopod taxa included specimens of the genus Grimpoteuthis spp. and Cirrothauma cf. magna displaying different swimming behaviour, body orientation and locomotion activities. Large specimens (~1000 mm TL) of Cirrothauma cf. magna were observed hovering over the muddy seafloor of the São Paulo Plateau. Two animals, a maturing specimen of Grimpoteuthis cf. discoveryi with a total length (TL) of 144 mm and a young individual of Cirrothauma cf. murrayi (166 mm TL) were collected using a slurp gun and preserved on-board. Our results provide the most accurate depth records of cirrate octopods hitherto in the South-western Atlantic and increase the knowledge of the distribution range for the observed species.

- ### The effect of hydrography on the benthos of a submarine canyon: the study case of the South African Cape Canyon

Eleonora Puccinelli, Zoleka Filander, Tarron Lamont, Marcel van den Berg, Gavin Tutt, Laurenne Snyders, Leon Jacobs, Mfundo Lombi

Submarine canyons are heterogeneous environments known to support a variety of benthic organisms, being considered biodiversity hotspot. The peculiar hydrographic conditions that characterize these systems including the high level of organic matter accumulation and transport, as well as disturbance events, can lead to intense resuspension that can influence the food available to the benthos. The Cape Canyon is the largest South African canyon located off the west coast of the country. It has an unique structure, that connects the coastline to deep-sea environments, and it is also extremely productive being under the influence of upwelling water, and due its ecological functions, has been classified as a Vulnerable Marine Ecosystem (VME). Here we aim to characterize the role of hydrography in influencing the food availability to the benthos, comparing sites within the Cape Canyon and of adjacent areas. Samples were collected during three oceanographic cruises in 2016, 2017 and 2018. Information were acquired to describe the physical environment (temperature, salinity, oxygen), and benthic invertebrate specimens were collected for stable isotope analyses. Benthic organisms were assigned to different trophic groups based on their diet and feeding habits. The results indicated that unconsolidated benthic communities, including echinoderms, molluscs, and crustaceans dominated within the canyon, where bottom temperatures were much lower than the surrounding waters, indicating recent fuelling of upwelled water. Suspension and deposit feeders had the lowest stable isotope compositions and trophic levels, while predators the highest. However, there was a higher range of feeding modes and level of niche overlap in the canyon compared to the non-canyon sites, suggesting a higher degree of plasticity of specimens within the canyon. This information increase our understanding of the ecological function of the benthos in the Cape Canyon, which is essential for a proper management of this VME.

- ### Body size, vertical migration, and depth of occurrence explain variation in the stable isotope signatures of a diverse, low latitude micronekton assemblage

Travis M. Richards, Tracey T. Sutton, R.J. David Wells

Stable isotope analysis (SIA) can be used to delineate trophic structure and highlight energy pathways in deep-pelagic ecosystems. However, interpreting SIA data is difficult due to multiple sources of variation influencing isotope values that are unrelated to a consumer's trophic status. Understanding to what extent biological and environmental factors explain variation in SIA allows for an enhanced understanding of deep-pelagic trophic structure. Here, we use multiple linear regression on δ 13C and δ15N data from 57 deep-pelagic species to examine to what extent intrinsic and extrinsic factors (vertical migration, body size, diet, depth of occurrence, capture location, etc.) explain isotopic variation within the Gulf of Mexico micronekton assemblage. Results of multiple regression on δ13C values differed between migratory and non-migratory species, with nighttime depth of occurrence, body size, and water depth identified as the most important explanatory variables for non-migrators (R2 = 0.33), while body size and water depth were the most important variables for migrators (R2 = 0.25). Multiple regression on δ15N values indicated depth of occurrence and body size were the most important variables for non-migrators (R2 = 0.41), while body size was the most important explanatory variable for vertical migrators (R2 = 40). Within non-migrators, the significant positive relationship between δ15N and depth of occurrence, combined with a nonsignificant relationship between body size and depth of occurrence, suggests variation in δ15N values is explained by species inhabiting lower meso- and bathypelagic depths increasingly feeding within food webs with elevated baseline δ15N values. Alternatively, because migratory species feed largely within the confines of the epi- and upper mesopelagic where baseline δ15N values are similar, trophic structure is primarily dictated by body size. These results demonstrate that the factors influencing isotope values of micronekton can vary within assemblages and should be considered when interpreting SIA data collected in deep-pelagic systems.

- ### Modelling the distribution of the sea pen Kophobelemnon stelliferum

Jasmine Rix, Kerry Howell, Amelia Bridges, Kyran Graves

Kophobelemnon stelliferum is a deep-living species of sea pen that is known to form aggregations in the North-East Atlantic. Aggregations of sea pens are currently classed as threatened and/or declining habitats under the OSPAR Convention, and as Vulnerable Marine Ecosystems (VME) under UNGA 61/105. Understanding their distribution is therefore important to marine spatial management. In this study, habitat suitability modelling is used to model the distribution of K. stelliferum in the UK and Irish EEZ, N.E. Atlantic in order to identify areas that are likely to support VME. Presence and absence data for K. stelliferum were collected by analysis of HD ROV video from three research cruises in 2017, 2018 & 2019, on the Irish continental margin. Maximum Entropy modelling is used with preselection of environmental variables by generalized additive modelling. Models are validated using repeated 70/30 train/test data splits using AUC and threshold-dependent assessment methods. Predicted distribution maps are created to visualise modelled K. stelliferum occurrence. Temperature (7.72%), BBPI (2.95%) and FBPI (1.33%) were the most important variables in predicting the distribution of K.stelliferum. Model performance (AUC) is rated as fair (0.7-0.8) suggesting the environmental variables used are not the most important drivers of the sea pen's distribution at the resolution used. It is likely that K. stelliferum distribution is driven by other key environmental variables including substrate type and current speed, and/or variables operating at a finer scale than that available for use in this study. Suitable habitat was predicted in canyon areas along the slopes of the Irish continental margin, the Rockall Bank and the Porcupine Bank supporting earlier suggestions of a possible association between this species and canyon habitats.

- ### Machine learning facilitates study of Benthocodon pedunculata population variability in the benthic boundary layer at Station M over > 30 years

Giovanna Sainz, Krish Mehta, Eric

Orenstein, Christine Huffard, Kakani Katija, Ken Smith

Understanding the ecological variability of deep-sea organisms is critical for the preservation and protection of deep-sea ecosystems. Many animals, including gelatinous zooplankton, are commonly found within the benthic boundary layer (BBL), an important region in the water column that is essential for pelagic-benthic coupling processes (e.g. carbon and nutrient cycling). BBL processes, and changes in animal communities, have been studied at Station M (~ 4,000 m deep in Northeast Pacific) since 1989. In this present study we ask: how does animal abundance change in the BBL in relation to time and environmental factors? With its distinct identification features and observed high densities at Station M, the gelatinous hydrozoan, Benthocodon pedunculata, makes an ideal study candidate. Specifically, we tested for seasonality in the abundance of these hydromedusae, whether some years experienced higher densities, and whether those variations could be explained by environmental factors. To achieve this, we leveraged 30 years of visual data collection at Station M, which includes remotely operated vehicle (ROV) video transects, and still images from time lapse cameras and a seafloor-transiting benthic rover. To analyze this high volume of imagery, we applied machine learning (ML) by (1) training a multi-object benthic classifier on FathomNet data; (2) deployed the classifier on the image data to generate proposals for classifications and localizations; (3) reviewed the ML proposals of B. pedunculata using the vars-gridview tool; and (4) compared the labeled observational data with the synchronized environmental data. Preliminary results indicate that variations in abundance are correlated with current speed and temperature. Applying these ML workflows to other members of the benthic community will significantly streamline studies to understand pelagic-benthic coupling using large image archives from multiple sources.

- ### Biogeography of deep-sea octocoral communities in the North Atlantic

Emma Saso, Andrea M Quattrini, Steven R Auscavitch, Louise A Allcock, Erik E Cordes, Catherine S McFadden

The deep ocean is magnificent in scale, yet our understanding of deep-sea faunal biogeography is constrained by scarce observations skewed towards megafaunal communities. Deep-sea octocorals (Anthozoa) are globally distributed across an expansive bathymetric range, where they inhabit seamounts, submarine canyons and hard-bottom reefs. These long-lived and phenotypically diverse ecosystem-engineers build complex heterogenous structures hosting diverse faunal assemblages, and engage in symbioses with fish and invertebrate species. Despite their importance to ecosystem functioning, octocorals have been the focus of relatively few biogeographical studies. While technological advances have facilitated sampling of deep benthos, questions of octocoral biogeography and species endemicity are complicated still by cryptic species and unresolved taxonomy. Recent studies have found species distributions to be more strongly influenced by depth and water mass than geographic distance, yet this pattern has not been corroborated for octocorals throughout the deep North Atlantic nor across ocean basins to date. Here, we determine biogeographic patterns of phylogenetic species diversity and composition across spatial scales using environmental and species presence data from several expeditions in the western Atlantic off the U.S. eastern seaboard, the eastern Atlantic off Ireland, the Gulf of Mexico and the Caribbean Sea. Octocoral specimens were collected during ROV and HOV Alvin dives from 312 to 2800 m water depth. 28S and mtMutS genes were sequenced to delimit molecular operational taxonomic units and determine species relatedness in phylogenetic diversity analyses. We investigated the roles of specific depth-related abiotic variables (i.e. water mass, temperature) and habitat features on distribution and community composition within a phylogenetic framework. The slow growing and highly adapted nature of octocorals makes them extremely susceptible to disturbances and changing ocean conditions. Awareness of the environmental gradients impacting connectivity is key to informing successful management strategies to conserve these foundation species across the North Atlantic Ocean basin.

- ### Deep-sea tardigrades of the North-Western Pacific: diversity, morphology and distribution

Anastasia Saulenko, Anastassya Maiorova, Vladimir Mordukhovich

Tardigrades are represented within meiofaunal communities in all oceans, from intertidal zone to hadal depths. Despite the wide occurrence of deep-sea tardigrades, information on their diversity, ecology, and distribution remains scarce with many regions remaining wholly unstudied. Thus far, only 1 tardigrade species – Angursa seisuimaruae – have been recorded from the deep-sea NW Pacific (Fujimoto & Hansen, 2019). Four German-Russian joint deep-sea expeditions have been conducted to the NW Pacific during 2010-2016. These expeditions allowed us to collect extensive material for meiofauna study, including the diversity and distribution features of Tardigrada. Tardigrades were found at 21 out of 45 stations (frequency of occurrence 46.7%) at depths from 1473 to 9539 m. The abundance varied from 0.02 individuals/10 cm2 to 1.52 individuals/10 cm2 . We identified the representatives of three genera: Angursa, Moebjergarctus and Coronarctus. Study of anatomy and morphology of the collected specimens has been done using light microscopy and different techniques of scanning electron microscopy. Representatives of the genera Moebjergarctus and Coronarctus are new species to science. This study was funded by a grant of the Ministry of Science and Higher Education of the Russian Federation (agreement number 075-15-2020-796, grant number 13.1902.21.0012).

- ### A faunal inventory of methane seeps on the Pacific margin of Costa Rica

Charlotte Seid, Avery Hatch, Marina McCowin, José Carvajal, Harim Cha, Shane Ahyong, Oliver Ashford, Odalisca Breedy, Douglas Eernisse, Shana Goffredi, Michel Hendrickx, Kevin Kocot, Christopher Mah, Allison Miller, Nicolás Mongiardino Koch, Rich Mooi, Tim O'Hara, Estefanía Rodriguez, Josefin Stiller, Ekin Tilic, Paul Valentich-Scott, Anders Warén, Mary Wicksten, Nerida Wilson, Erik Cordes, Lisa Levin, Jorge Cortés Nuñez, Greg Rouse

The methane seeps on the Pacific margin of Costa Rica support notable animal diversity and offer insights into deep-sea biogeography and phylogeography. Located approximately 50 km offshore at depths of 400-3600 m, these seeps span vertical hydrogeographic gradients and are characterized by authigenic carbonates, vestimentiferan tubeworm bushes, mussel and clam beds, and microbial mats. These seeps also intersect with other chemosynthesis-based habitats: wood and bone falls and the "hydrothermal seep" site at Jaco Scar, where water temperatures up to 3 °C above ambient support certain vent-affiliated fauna. During five cruises in 2009-2019, we conducted intensive faunal sampling via 79 submersible dives to 11 localities. Based on these expeditions and published literature, we synthesize voucher specimens, images, and DNA sequences to present a taxonomic inventory of macrofaunal and megafaunal diversity, with a focus on invertebrates. We report >450 taxa, including 109 described species and at least 46 undescribed species. Of the described species, 27 are known only from the Costa Rica seeps. Others reveal new biogeographic and ecological connections. We report range extensions for species known from California, Mexico, the Galápagos seamounts, and Chile; new depth records; and the first seep records for species associated with vents and/or organic falls. In synthesizing these examples, we note that no single evolutionary narrative explains the patterns of biodiversity at these seeps. For instance, Costa Rica seep species can have sister taxa in the eastern Pacific, western Pacific, or western Atlantic, reflecting complex connectivity and a history of pre-Isthmian gene flow. Even morphologically indistinguishable species can have distinct biogeographic and depth restrictions. We emphasize the value of careful molecular taxonomy and comprehensive specimen-based inventories for assessing cryptic species, endemism, connectivity, habitat requirements, and other ecological baselines important for conservation and research.

Functional diversity patterns of deep-sea organic-fall benthic assemblages in an experiment along the SW Atlantic

Bruno H.M. Souza, Gilberto Bergamo, Joan M. Alfaro-Lucas, Maurício Shimabukuro, Paulo Y.G. Sumida

The comprehension of the patterns of different biodiversity facets and their drivers is of paramount importance for ecology, but it is a particularly difficult endeavour in the deep sea due to technical issues and elevated research costs. In this environment, organic falls (wood and whale carcasses) create unique habitats colonized by a suit of specialist and generalist taxa. These organic falls are ideal laboratories to perform colonizing and manipulative experiments to comprehend biodiversity patterns and their causes. This study is based on the benthic assemblages associated to sizestandardized whale bones and woods artificially implanted along SW Atlantic at five sites at 1500m and 3300m depth for 23 months, under the influence of different water. We aimed to determinate the patterns of taxonomic and functional diversity and their relationships between depths in both organic substrates. Organisms were classified to the lowest taxonomic level possible and functional traits (i.e., adult mobility, size, feeding behaviour and strategy) were assigned to each taxon to create a pool of functional entities (taxa that shares the same functional characteristics) to estimate the functional richness, diversity, dispersion, redundancy and evenness. Preliminary results suggested that functional richness was defined specially by organic falls specialist groups. Even though species diversity contrasted significantly in every site, the functional diversity slightly differed between depths and water masses. Functional space tended to be maximized and conserved while differing in its inner occupancy along localities, suggesting a partial independence between species richness and their functional identities. More studies including additional data, refining functional traits and applying other analyses should be carried out to verify the patterns obtained in this preliminary work and obtain further results. This work may help to understand the diversity in deep-sea habitats and the need of conservation measures in these yet poorly known environments that sustain a unique fauna.

Deep seafloor imagery from the Weddell Sea document natural food falls and octopod diversity and distribution

Julian B. Stauffer, Richard Schwarz, Autun Purser, Laura Hehemann, Henk-Jan T. Hoving

Food falls are carcasses of pelagic organisms that reach the deep-sea floor and provide localised pulses of energy to benthic scavenging communities. Such events could help explain measurement discrepancies between energy supply and consumption by benthic communities, but observations of natural food falls are scarce, hampering quantification of their contribution to local carbon cycles. Our goal here was twofold: 1) document natural food falls in the Southern Ocean and 2) identify benthic octopods, which represent the dominant cephalopod group in the Southern Ocean and one that has shown to increase in abundance in areas of overexploitation and environmental change. We analysed 7900 seafloor images from the Weddell Sea between 400m and 2200m, captured with the Ocean Floor Observation and Bathymetry System (OFOBS) during the expedition PS118 to the Antarctic Peninsula in March 2019. Three imaging transects were analysed for this project. Six carcasses were found, including one baleen whale, one penguin, and four fish at depths of 647m, 613m, 647m, 2137m, 2165m, and 2112m, respectively. These food falls varied in their decomposition stages and assemblages of scavenging fauna. The whale fall was completely skeletonised whereas other carcasses showed soft tissue remains. Additionally, we annotated around 500 octopods between 400m and 2200m, resulting in the largest dataset of Southern Ocean octopods in situ observations. Observed octopod taxa included Cirroctopus glacialis and the genera Muusoctopus, Graneledone, Thaumeledone, Pareledone, and Adelieledone. This dataset will allow us to assess behavioural observations and associations as well as the precise distribution and vertical zonation of these octopods. Preliminary results indicate depth records for at least one taxon, probably because trawling data is often limited to shallower depths. The data shows the scarcity of natural food falls and the abundance of octopods in the waters proximate to the Antarctic peninsula, an environment subject to rapid climate change.

First ecological characterization of whip corals (Hexacorallia: Antipatharia) assemblages in the Easter Island Ecoregion, southeastern Pacific

Jan Tapia-Guerra, Cynthia Asorey, Erin Easton, Daniel Wagner, Matthias Gorny, Javier Sellanes

One of the main priorities of current marine research is to promote biodiversity conservation and management. In this context, the identification of key and potentially fragile habitat-forming species, such as whip corals, is crucial. Despite their ecological importance, whip corals in the order Antipatharia remain poorly studied around the world, and especially in the southeastern Pacific. During recent expeditions to explore mesophotic and deep benthic habitats of Rapa Nui (Easter Island) and nearby seamounts in the Easter Island Ecoregion (EIE), assemblages of whip corals were observed. We report the first a detailed description of the distribution and abundance of these corals and provide some insight into associated fauna and habitat. These descriptions were based on analysis of video surveys collected on 67 ROV dives conducted between 2014 and 2019 at three sites within the EIE (Pukao seamount, Apolo peak, and Rapa Nui island shelf and slope) at depths from ~ 60 to 280 m. At least four morphotypes were observed: yellow (Pseudocirrhipathes sp.), red (Stichopathes sp.), white/orange (unidentified), and red-small (unidentified). Our data shows that extensive fields of whip corals were present at 28 sites, with densities up to 13.2 ± 0.8 colonies m-2, from 60 to 245 m depth and that red and yellow morphotype were the predominant morphotypes/species. Corals were observed on rocky, coarse sand, and rhodolith bed bottom habitats. Numerous faunal associations were observed, mainly with ophiuroids, echinoids, and undescribed as well as commercially important fishes. Our observations of this keystone group should be considered in management decisions and future conservation efforts on Rapa Nui, where a Multi-Use Marine Protected Area was established in 2018. Funding: Fondecyt 1181153; NM ESMOI, Chile; Conservation International; and Oceana Chile.

- ### Ecological niche modelling in three dimensions and ecomorphology of a widespread midwater Narcomedusan genus

  Gerlien Verhaegen, Mehul Sangekar, Henk-Jan Hoving, Dhugal Lindsay

The midwater, the oceans' pelagic zone located under the euphotic zone and above the seafloor, is the largest continuous biome for multicellular organisms on our planet. Despite the technological advances in survey techniques over the last 30 years, and pelagic ecosystems being widely acknowledged for their relevance in ecosystem services, less than 1% of this vast and hard to reach habitat has been sampled. These methodological challenges in studying midwater ecosystems can be overcome to some extent by using ecological niche modelling (ENM) techniques in three dimensions (3D). As gelatinous zooplankton are important members of midwater food webs, in this study we used 3D ENM to investigate the ecology and distribution of a widespread Narcomedusan genus: Solmissus – the dinner plate jellyfish. Occurrence records for Solmissus spp. that had accompanying depth data were harvested from a variety of sources, including unpublished data from cruises, published literature, and online deep-sea databases provided by a range of stakeholders (e.g., JAMSTEC, MBARI, ONC, and SOI). Most video or photographic records were of a quality where approximate tentacle number was the only morphological character analyzable for the majority of records. We found morphotype clusters, with those having less than 28 tentacles occurring at a median depth of 516 m, whereas morphotypes with 28 or more tentacles were found in much deeper waters of 935 m. We then further explored the distribution and associated environmental variables for these different morphotypes. Because Narcomedusae are specialised in feeding on other gelatinous prey, from predators to filter feeders, and therefore play a key role in maintaining a well-balanced midwater ecosystem, our study provided important ecological insights on these topdown regulators. Furthermore, it illustrated the value of online databases including imagery and videography records for studying midwater organisms, and highlighted regions of interests for planning of future midwater expeditions.

- ### Megafauna Assemblage on Mineral-rich Hardgrounds in the Southern California Borderland

  Devin Vlach, Lisa Levin, Kira Mizell

The Southern California Borderland is an active tectonic area, comprised of a series of seamounts, escarpments, banks and ridges. The underwater currents and low-oxygen conditions allow iron, manganese, other metals and phosphorite to precipitate out of seawater onto these features. Although mineral exploitation has not yet occurred in the deep sea, phosphorite and ferromanganese crusts pose a commercial interest as mineral resources. To provide baseline information for megafauna associated with phosphorite and ferromanganese hardgrounds, we conducted 38 100-m long video transects at eight sites in the Southern California Borderland ranging from depths of 250m to 1700m. Megafauna assemblages varied at each site based on oxygen and depth, as well as exhibiting notable differences at inshore vs offshore sites. The base of escarpments were typically sediment covered, with the predominant taxa consisting of sea cucumbers (Scotoplanes), sea pens (Halipteris and Anthoptilum), cnidarians (Umbellula), and brittle stars. Hardgrounds contained a variety of taxa, including urchins (Araesoma and Asthenosoma), corals (Paragorgia, Anthomastus, and Swiftia), sponges (Hyalonema, Mycale, Farrea, Abestopluma, Heterochone), fish (Scorpaenodes and Sebastolobus) among others. The sites occurred above, within and below a pronounced oxygen minimum zone. Dense bands of brittle stars were found at depths of 560m and oxygen concentrations of 5.8 µM, reflecting possible oxygen minimum zone edge effects.

A key goal is to identify VME indicators such as large colonies of coral or sponges that could provide potential habitat for fish species or other features that may merit protection. The primary substrate from each transect will be identified to explore megafaunal affinities for phosphorite and ferromanganese crust substrates.

- ### Ecosystem modeling in the oceanic zone: A Gulf of Mexico case study

  Matthew S. Woodstock, Tracey T. Sutton, Tamara Frank, Yuying Zhang

Ecosystem-based modeling is rapidly becoming an established technique to investigate the health and stability of ecosystems. Ecosystem models have been applied to many neritic systems, but less focus has been placed on the oceanic domain. The absence of this effort in the oceanic zone is attributed to a paucity of data in the oceanic zone, particularly concerning the deep ocean. Since 2011, severe population declines have been observed in many micronekton groups that occupy the mesopelagic zone (200 – 1000 m depth). Here we present an ecosystem model for the oceanic northern Gulf of Mexico for the year 2011, simulate that model according to micronekton trends through 2018, and quantify the top-down and bottom-up impacts that each functional group has on one another. These trends were examined to determine whether interactions between the two groups have changed directionally over time. In 2011, zooplankton occupied greater than one-third of the total metazoan biomass, and also 40% of the total energy throughput ascended to higher trophic levels in the system.

Of the 1849 possible functional group interactions (most of which are indirect), approximately 27% showed significant changes between 2011 and 2018, which were related to shifts in biomass and diet throughout the simulation. Direct top-down interactions changed more frequently than other types of trophic relationships, a result of prey switching by apex predators in response to a depleted mesopelagic prey field. Moving beyond the Gulf of Mexico, systems that have population abundance estimates and diet information for key species are candidates for ecosystem modelling efforts. Other life history information (e.g., growth, reproduction) would improve the efficacy of models but may also be transferrable across localities. When a sufficient amount of data exists, ecosystem models are an effective tool to assess trophic structure shifts and monitor ecosystem functioning of mesopelagic realms.

- How does Alvinella pompejana acquire carbon from chemoautotrophic bacteria?

  Magali Zbinden, Philippe Compère, Gilles Lepoint, Bruce Shillito, Loïc N. Michel

Like many deep-sea hydrothermal organisms, the tube-dwelling polychaete Alvinella pompejana depends on chemosynthesis for its nutrition. While trophic markers (stable isotopes, lipids) suggest this species primarily feeds on chemoautotrophic bacteria, the way in which it acquires energy is still an open question. The worm is believed to be a deposit-feeder which can use its retractile tentacles to pick up bacteria and ingest them, but direct in situ evidence of the feeding behavior are scarce. Since A. pompejana spends most of its time in its tube, it was also proposed to forage on bacterial mats that grow on the inner tube surface. Finally, the worms, that harbor a dense epibiotic microflora on its dorsal tegument, could derive carbon from this ectosymbiosis. Metabolites released by the chemoautotrophic bacteria associated with the worms have indeed been hypothesized to be directly transferred to underlying tissues, through a thin and highly vascularized tegument. In this study, we used ex situ 13C incubations in pressurized aquaria to test the latter hypothesis. Significant incorporation of carbon was detected in the dorsal epibionts when incubated in presence of thiosulphate, suggesting the assemblage indeed contains some chemoautotrophs. However, no carbon incorporation was detected in the underlying dorsal epithelium, nor in other worm tissues (ventral epithelium, muscle). Methodological considerations (e.g. incubation time and/or temperature) put aside, those results could point out that metabolite transfer from epibionts does not seem to be a major carbon acquisition pathway in A. pompejana. These results markedly differ from those obtained in other hydrothermal species with external symbioses, such as the shrimp Rimicaris exoculata. While these findings should be replicated in other experimental conditions, they highlight the important diversity of feeding strategies displayed by hydrothermal organisms.

Special session Extra2a#

- Diversity of deep-sea scale-worms (Polynoidae) in the Clarion-Clipperton Fracture Zone

  Paulo Bonifácio, Lénaïck Menot, Lenka Neal

The polymetallic nodules lying on the seafloor of the Clarion-Clipperton Fracture Zone (CCFZ) represent over 30 billion metric tons of manganese. Whereas one mining operation is expected to directly impact 100 km2 per year of the seabed, the biodiversity and functioning of the benthodemersal ecosystem remain poorly understood. Recent studies point out the strong influence of the northward and eastward gradients of decreasing primary productivity driving variations in macrofaunal community structure. Oligotrophic waters and barrier to dispersal are suggested to drive the composition structure and turnover of sedentary assemblage sampled using box corer. This study examines Polynoidae, a diverse family of mobile polychaetes, most sampled with epibenthic sledge (EBS) within the eastern CCFZ where five areas (BGR, IOM, GSR, Ifremer and APEI no. 3) were visited under the influence of the sea surface productivity gradient. Specimens were identified using morphology and DNA (i) to provide an account of regional polynoid diversity, and (ii) to assess the factors driving species turnover, in particular the dispersal ability. The patterns of species composition of polynoid assemblages were attributed to organic carbon fluxes at regional scale which explained 40 % of total variance (PCA) validating recent studies based on box corer sampling. Although rarefaction curves have not reached the asymptote, the patterns of diversity assessed by classic and phylogenetic methods agreed that polynoid assemblages at APEI no. 3 are the most diverse. These results clearly diverge of similar recent studies showing very low density and diversity at APEI no. 3. The main hypotheses emerging to explain such unexpected results is the diversification of Macellicephalinae. Macellicephalins seem being able to evolve under extremely low food supply thought adoption of a semipelagic mode of life which enabled them to explore the less exploited available niches and lead to their radiation at great depth.

- Arctic Megafaunal Assemblages of Disko Bay, West Greenland

  Emmeline Broad, Diana Krawczyk, Martin Blicher, Nanette Hammeken, David Blockley, Chris Yesson

We have limited knowledge of the distribution and processes structuring Arctic benthic habitats. In Greenland, there has been a recent impetus to examine some of these habitats, a number of which may be impacted by continued demersal trawl fisheries.

Between 2017 – 2020, a research consortium consisting of Greenland Institute of Natural Resources (GINR, Greenland), Geological Survey of Denmark and Greenland (GEUS, Denmark), National Institute of Aquatic Resources (DTU Aqua, Denmark) and Institute of Zoology (IoZ, United Kingdom) developed a protocol for habitat mapping areas of the Greenland shelf. Data collection was focused within South West Disko Bay due to its complex geomorphology, strong seasonal hydrographic regime, and pre-existing knowledge of marine diversity.

In 2020, 36 benthic imaging transects were conducted in Disko Bay between 152 m to 696 m to ground-truth broad-scale observations of rocky substrate derived from multibeam echosounder data. Using a low-cost photographic and video platform, information on the benthic community composition, density, and habitat type were collected. Here we present preliminary results from imagery extracted from this survey.

A high degree of habitat heterogeneity was observed, which was significant in driving changes in epibenthic megafaunal community structure. Soft sediments support a mixed community dominated by filter feeders. Highly sloped rocky habitats supported a distinct mix of suspension and filter feeders, some of which are classified as Vulnerable Marine

Ecosystem (VME) indicator species. Fan shaped sponges (Axinellidae) were observed along with Cauliflower corals (Nephtheidae), Primnoa sp. (Primnoidae) along with the most northern occurrence of Paragorgia arborea (Paragorgiidae) in Greenland waters.

These preliminary observations expose the diversity of epibenthic fauna in the region. They also stand to contribute towards the conservation of vulnerable habitats, by informing fisheries in Marine Stewardship Council sustainability schemes and policy makers for the effective management of marine resources within Disko Bay.

• Assessing Mesophotic and Deep Benthic Communities and Their Habitats For Restoration Following the Deepwater Horizon Oil Spill Using an Ecosystem-based Approach

Randy Clark, Stacey Harter, Amanda Demopoulos, Kris Benson

Mesophotic and deep benthic communities (MDBC) are vast and complex environments that provide essential ecosystem services to the Gulf of Mexico (GOM) . Over 770 square miles of deep-sea habitat and 4 square miles of mesophotic habitat were injured by the Deepwater Horizon (DWH) oil spill.

Funding acquired from the Natural Resource Damage Assessment is supporting the following projects to restore MDBC: mapping, ground-truthing and predictive habitat modeling; habitat assessment and evaluation; coral propagation technique development; and active management and protection. Project goals include:

● restore mesophotic and deep benthic communities and species injured by the spill;

● actively manage these communities to protect against threats and provide a framework for monitoring, education, and outreach;

● improve understanding of MDBC to inform management and ensure habitat resilience

This presentation will describe the planning and implementation activities for the habitat assessment and evaluation project. Using an ecosystem-based approach, the project will identify and fill data gaps for benthic life histories, diversity, population and community structure, and trophic connectivity in concert with characterizing the associated environmental conditions within soft sediment and coral habitats. This information will help establish baseline conditions and characterize communities at injured and reference sites, and identify the environmental drivers of species, population, and community-level patterns and interactions. Surveys and discrete collections will also support determinations of ages, growth rates, and reproductive potential of mesophotic and deepwater corals, as well as their health and condition. In addition, the project will maximize the effectiveness of MDBC restoration and protection efforts through the use of population genetics and predictive modeling.

Project results will fill critical gaps in our understanding of the biology, ecology, health, biodiversity, recovery, and resilience of mesophotic and deep-sea habitats (corals and soft sediments) and will support and inform restoration planning and implementation for MDBC.

• First insights into biodiversity of deep-sea peracarids (Crustacea, Peracarida) from New Caledonia

Inmaculada Frutos, Laure Corbari, Magdalena Błażewicz

The central Indo-Pacific is a global hotspot of marine biodiversity and center of endemism where most marine families have their greatest concentration of species in a comparatively small triangle located in the heart of this area: The Coral Triangle. Located close to its center, New Caledonia is considered as a unique place of high diversity and endemism where the lack of knowledge on Peracarids is critical. The peracarids comprise a superorder of crustaceans divided into 12 orders, mainly represented by Amphipods, Isopods, Tanaidaceans, Cumaceans and Mysids. With about 25000 known species, Peracarida is considered a hyper-diversified group with many more species yet to be discovered. So far, only a few hundred of deep-sea peracarids are known from New Caledonia. Through the deep-sea cruise KANADEEP 2 (September 2019), on board R/V l'Atalante several sampling methods were performed in order to provide new taxonomic data for filling the gaps of knowledge in Peracarids and question biodiversity patterns, endemism and connectivity in deep-sea environments of New Caledonia.

The implementation of complementary sampling gears (sledge, beam trawl, dredge and ROV) allowed the collection of 5191 specimens of peracarids in a depth range from 314 to 3226 m; where 71% of individuals were sampled by sledging, suggesting its efficiency for small-sized and fragile fauna. Main taxonomic groups are represented by Isopods (2096 individuals, 40% of the total peracarids; 21 families) and Amphipods (1551 ind., 30 % of the total peracarids; 40 families). First taxonomical approach already suggests a high potential of species new to science. Diversity and composition of peracarids will be analysed and compared according to sampling gears, environmental parameters as well as habitats. This New Caledonian fauna will be also recontextualised in the global knowledge of Southwestern Pacific Peracarids from previous cruises of Tropical Deep-Sea Benthos program led by MNHN.

• Sexual dimorphism on deep-sea weaponry: the case of the Costa Rican yeti crab Kiwa puravida Thurber, W.J. Jones & Schnabel, 2011 (Decapoda: Anomura: Kiwaidae)

Juan Carlos Azofeifa-Solano, Olivia Pereira, Erik Cordes, Lisa Ann Levin, Shana Goffredi, **Jorge Cortés**

The occurrence of sexual selection in a species often promotes sexual dimorphism over traits that favor access to mating partners such as weaponry. However, in crustaceans, the "female-guarding" behavior is a common type of mating system where males are usually larger than females and bear defensive mechanisms to fight against rival males and guard the females. The family of yeti crabs Kiwaidae includes four species exclusively in deep-sea chemosynthetic ecosystems, but little is known about the reproductive biology of these species. Kiwa puravida is a yeti crab endemic to the Costa Rica margin methane seeps at depths of ~1000 m, and forms aggregations known for their 'dancing' (claw waving) behavior on carbonate rocks subject to active seepage. We aimed to test, for Kiwa purivida of Mound 12, Costa Rica, if the chelae, suspected to be under sexual selection, display sexual dimorphism, and to discuss possible implications of this obscure mating system of this deep-sea crustacean. In addition, we searched for sexual dimorphism in the carpus of the second walking leg (notsuspected under sexual selection). We found that the slope of the relation claws' length and width with the carapace length is steeper in males than in females, while there were no differences between sex regarding the length of the carpus of the second walking leg, as expected. Thus, males' claws are probably under sexual selection, which can be the result of male-male competition and/or female choice, suggesting that K. puravida possibly has a mating system of the "female-guarding" type. This is the first attempt to study the reproductive biology of K. puravida, and additional observations will be necessary to shed more light on this matter.

Deep-sea Enteropneust Fauna of the Bering Sea

Olga V. Ezhova, Anastasiya I. Lukinykh, Elena M. Krylova, Sergey V. Galkin, Andrey V. Gebruk

We present the first report on deep-sea enteropneust fauna in the Bering Sea. Three species were recorded: Torquaratorid-1 and Torquaratorid-2 from Torquaratoridae, and *Saxipendium* sp. from Harrimaniidae. It is the northernmost locality in the Pacific for torquaratorids and the first record of *Saxipendium* beyond the East Pacific. Torquaratorid-1 is a bathyal epibenthic species found on the Volcanologists Massif slope. It dominated the soft-sediment community at depths 1830–2290 m, but also was found on hard substrate. Its faecal trails were mainly meandering or rarely a combination of meandering and switchback patterns. Torquaratorid-2 is an abyssal species known from the Volcanologist Massif and Komandorsky Graben with a spiral counter-clockwise pattern of trails. It is common on soft sediments at depths 3334–4277 m, but did not reach high densities. Our results suggest that the taxon specificity may be the main factor shaping the pattern of trails, meandering or spiral, in torquaratorids

Saxipendium sp. is a bathyal-abyssal species occurring on the Volcanologists Massif slope (1930 m) and north-west of the Volcanologists Massif (3334–3931 m). Animals were often recorded with their posterior parts buried in sediment between rocks and with anterior parts exposed on the substratum.

Morpho-anatomical analysis of Torquaratorid-1 allows clarifying the diagnosis of Torquaratoridae. It demonstrates several new features: collar coelomoducts, axial complex with pericardial coelom and a stalk skeleton comprising two plates. One character in Torquaratorid-1 – the opening of the collar coelomopores directly into the exterior – is shared with other class of Hemichordata, Graptolithoidea. This morphological condition makes Torquaratorid-1 an important link for understanding the evolution of Hemichordata and Deuterostomia.

Funding: The work was supported by Russian Science Foundation (pr.no. 18-74-10025) and by Ministry of Science and Higher Education, Russian Federation (grant 13.1902.21.0012, contr.no. 075- 15-2020-796).

Distribution of Pheronema carpenteri (Porifera) in relation to oceanographic variability and other environmental drivers in the Porcupine Seabight, NE Atlantic

Kyran Graves, Amelia Bridges, Prof Kerry Howell

Deep-sea sponge aggregations are classified as Vulnerable Marine Ecosystems (VMEs). Understanding drivers of their distribution and density is critical for the successful mapping and protection of this VME. Current literature suggests a link between internal waves and other regions of enhanced currents with sponge aggregations, via an increase in suspended organic material associated with such oceanographic processes. The aim of this research was to investigate the role of internal wave activity and other environmental drivers in determining the distribution and density of Pheronema carpenteri aggregations within the Porcupine Seabight, NE Atlantic. A presence/absence P. carpenteri dataset was obtained through collating historical datasets collected by trawl and ROV, whilst an additional density dataset was acquired through re-analysis of archived ROV video transects. Environmental data were obtained at 200x200m grid resolution, including topographical and oceanographic variables, with a particular focus on temperature variability (at monthly, seasonal and annual temporal scales) as a proxy for internal wave activity. Generalised additive models (GAMs) were fitted to the presence/absence dataset to characterise the relationship with each environmental variable, and a multivariable GAM constructed. Linear models and GAMs were also fitted to the density dataset to explore the relationship with environmental variables. All individual variables were statistically significant when GAMs were fitted to the presence/absence datasets, with mean annual temperature variability being the most important variable when a full multivariable GAM was constructed. A statistically significant negative linear relationship between mean temperature variability and P. carpenteri density was identified, but only at specific temporal periods – September, January, autumn and winter. These results suggest mean temperature variability, a proxy for internal wave activity, is an important driver of P. carpenteri distribution, with P. carpenteri occupying regions of intermediate variability. These preliminary results will be used to inform the development of high resolution P. carpenteri habitat suitability models.

Paleo-hydrothermal vent bivalve records on the Mid-Atlantic Ridge (MAR) with implications for modern biogeography

Elena M. Krylova, Tina N. Molodtsova, Sergey V. Galkin, Kirill V. Minin, Irina G. Dobretsova, Andrey V. Gebruk, Georgy A. Cherkashov

Accumulations of fossil bivalves were discovered on the Mid-Atlantic Ridge within the Russian Exploration Area during Cruises 37 and 39 of RV *Professor Logatchev* in 2015 and 2018 at the following three sites: 13°48'N, Logatchev-4 (~14°43'N) and Pobeda (17°09'N) hydrothermal fields. The composition of fossil bivalves was the same at all sites and included the three species: *Bathymodiolus puteoserpentis* (Bathymodiolinae), *Thyasira southwardae* (Thyasiridae) and '*Archivesica*' cf. *puertodeseadoi* (Pliocardiinae). Shells of the latter species from the Logatchev-4 field were dated to ~40 kyr; condition of shells of two other species and the character of shell depositions suggested that the shells could be approximately of the same age. Previously only one paleo-hydrothermal vent community on the MAR was described - in the vicinity of Rainbow (36˚13'N) with assemblages of shells of *Thyasira* aff. *southwardae* and '*Phreagena*' sp. (='Archivesica' cf. *puertodeseadoi*) dated to 24-27 kyr. All examined MAR fossil communities were associated with ultramafic rocks covered by sediments and located at bathyal depths ~2000-2500m.

Paleo-data are considered in the context of understanding colonization pathways of patchily distributed ephemeral habitats and factors shaping the distribution patterns of extant species. Among the fossil bivalves recorded on the MAR, only the species '*Archivesica'* cf. puertodeseadoi is absent in extant MAR communities. Closely related (or the same) species currently lives in the Scotia and Argentine Seas, at 852-2204 m. A fossil species quite probably representing the same lineage, dated to ~18 kyr, was reported from the Gakkel Ridge, Arctic. Forty-twenty thousand years ago, the MAR might have been a conduit for the dispersal of chemosymbiotic bathyal fauna between the Antarctic and Arctic. Recent *Bathyomodiolus puteoserpentis* and T. *southwardae* are presently found only below 3000 m. The meaning of the records of these species in extinct communities at the shallower depths -about 2000 m, are discussed.

Demosponges (Porifera) of abyssal nodule fields in the Clarion- Clipperton Zone

Swee-Cheng Lim, Koh-Siang Tan

The Demospongiae is the largest and most diverse class of Porifera with over 7000 species described mostly from coastal waters worldwide. However, less than 100 Demospongiae species are known from the abyssal plains, which represent the largest habitat on earth encompassing 50% of the seafloor surface. At the Clarion-Clipperton zone in the eastern Pacific Ocean, we demonstrate that demosponges attached to polymetallic nodules are highly diverse, comprising more than 25 species from 14 genera belonging to some 10 families and 6 orders. Many of these demosponges are small, with a simple or degenerate skeletal structure made up of only a few types of spicules. In many cases, it is impossible to determine their identities using morphological characters, and even assignment to family is fraught with uncertainty. The difficulties of classifying these sponges and determining their phylogenetic relationships are further compounded by their seemingly incongruent genetic data. Are they products of evolutionary legacy and ecological processes unique to the abyssal plain, or are they actually relict fauna that have taken refuge in the stable, unchanging abyssal environment? The problematic taxonomy of these "reduced" abyssal nodule demosponges are described and discussed.

Amathillopsidae (Amphipoda, Crustacea) reveal new species and a clinging lifestyle in the deep sea worldwide

Anne-Nina Lörz, Tammy Horton, Rachael Peart

During recent expeditions to the North Atlantic and South West Pacific, charismatic specimens of amathillopsid amphipods were filmed by Remote Operated Vehicles and then sampled for further study. The species were new to science and even though sampled on opposite sides of our planet showed remarkable morphological similarities. Further investigations of photographic and video records revealed the genus *Amathillopsis* to be more widely distributed, both geographically and bathymetrically, than indicated by current literature records. This deep-sea family occurs at abyssal depths in all oceans. Specimens of *Amathillopsis* are reported clinging to a variety of different organisms, such as polychaete and sponge tubes, whose erect structures provide the means to raise these rarely documented deep-sea predators above the seafloor facilitating feeding opportunities. Stills and video camera technology have developed in recent years to a level that enables high resolution images at bathyal and abyssal depths. Until now, the habits of species of *Amathillopsis* could only be postulated, on the basis of their possession of posterior pereopods adapted to a clinging lifestyle. Based on their morphology we assume *Amathillopsis* species to be predators, capturing their prey, such as zooplankton or small suprabenthic crustaceans from the water column. We have also provided an analysis of the many photographic records that have been collected in recent years, documenting the deepest known (unconfirmed) records of *Amathillopsis* from the Clarion Clipperton Fracture Zone in the abyssal Pacific Ocean, where explorations are currently taking place for deep-sea mining.

The diversity of calcaxonian octocorals from the Irish margin

Declan Morrissey, Candice Untiedt, & Louise Allcock

Deep-water octocorals are prevalent on the Atlantic margin but tend not to be identified to species due to a global deficit in taxonomic skills. Our aim was to determine how many species of the suborder Calcaxonia (families Chrysogorgiidae, Primnoidae, and Isididae) are present in Irish waters. We collected tissue samples and morphology vouchers from 74 Isididae (bamboo corals), 22 Primnoidae, and 20 Chrysogorgiidae colonies during two expeditions of RV Celtic Explorer to the Irish slope. We extracted DNA and sequenced four mitochondrial gene regions: MutS, COI +igr1, 16s-nad2, and igr4. Using a concatenated 3389 bp sequence, we built haplotype networks and a phylogenetic tree. We discovered 25 haplotypes of Isididae, nine haplotypes of Primnoidae, and five haplotypes of Chrysogorgiidae. Some haplotypes contained more than one distinct morphotype. For every morphotype within every haplotype, we compared gross colony morphology using in situ and ex situ photographs. We also examined polyp morphology using light microscopy, and sclerite morphology using scanning electron microscopy.

We were able to confidently assign species names to most of the Primnoidae. Genus names were assigned to all chrysogorgiids and the remaining primnoids. For the Isididae, species names could be assigned to a haplotype from the subfamily Isidinae. However, no genus names, bar Acanella, were assigned to haplotypes within the subfamily Keratoisidinae due to the large morphological variation present both within and between haplotypes.

We concluded that no species had more than one molecular haplotype but that multiple species may share a single haplotype. Finally, more robust taxonomic characters are needed for use in tandem with genetic characteristics to accurately describe the biodiversity of bamboo corals.

Advancing Habitat Suitability Models for Vulnerable Marine Ecosystem indicator taxa in the South Pacific: have we reached the limit for presence-only models?

Fabrice Stephenson, Ashley A. Rowden, Owen F. Anderson, C. Roland Pitcher, Matt H. Pinkerton, Grady Petersen, David A. Bowden

Vulnerable marine ecosystems (VMEs) are typically fragile and slow to recover, making them likely to be substantially altered by disturbance. In the High Seas, regional fishery management organizations (RFMOs) are required to implement measures to prevent significant adverse impacts on VMEs. The objectives of the present study were to: update distribution models of VME indicator taxa in the South Pacific RFMO Convention Area; evaluate these against newly-collated independent field data to test the reliability of the presence-only habitat suitability models; and assess how well the updated models were able to predict into unsampled space. Ensemble habitat suitability models of 10 VME indicator taxa performed well using the newly collated data (AUC > 0.95; TSS > 0.76 and RMSE < 0.34). There were no obvious patterns of decreasing model performance with decreasing environmental coverage; areas with few samples underpinning model predictions still had AUC > 0.93; TSS > 0.71 and RMSE < 0.43. Despite these encouraging results, we also identify some important inherent issues with presence-only models that have profound implications for their use in management of VMEs. Future modelling efforts for VME management purposes should be based ideally on the use of survey presence-absence data and, preferably, abundance data.

- ### An integrative analysis on the benthos of Astrid Ridge and Maud Rise, Southern Ocean

  Anne Helene S. Tandberg, Luis Martell, Francisca Correia de Carvalho, Jon A. Kongsrud, Anne K. Sveistrup, Joan J. Soto Àngel, Tone Ulvatn, Aino Hosia

The benthic fauna of the Kong Haakon VII Sea, the sea north of Dronning Maud Land, is far less explored compared with adjacent parts of the Southern Ocean. The Norwegian 2019 cruise with R/V Kronprins Haakon is part of the effort to build further knowledge about this area. The benthic diversity of the Astrid Ridge (67-69° S, 12° E, 2000 - 1200 m) and Maud Rise (65° S, 2° E, 1750-1200 m) was assessed using a combination of beam trawl, epibenthic sled and ROV with HD-video and manipulators for physical sampling (ROV Ægir6000). This study constitutes the first diversity assessment for the benthos at Astrid Ridge and the second ever of benthic fauna in the Maud Rise.

The collected material of 900 curated vouchers and 36 hours of video is analysed both to evaluate the extent of Vulnerable Marine Ecosystem (VME) indicating taxa, and to describe the faunistic assemblages. Preliminary results indicate high diversity, presence of rare species, and high abundance of few megafauna taxa. We observe clear differences between the faunal composition between the Astrid Ridge and the Maud Rise.

An extensive voucher-linked reference library of DNA-barcodes and other genetic markers (COI, 16S, MtMutS) is built based on the material collected during this cruise, with specific vouchers being linked to the video footage.

The results from this study will be used to support the Norwegian contribution to the CCAMLR ongoing MPA process for the Weddel Sea, (CCAMLR Domain 4).

- ### Adding pieces to the puzzle: insights into diversity and distribution patterns of Cumacea (Crustacea: Peracarida) from the deep North Atlantic to the Arctic Ocean

  Carolin Uhlir, Martin Schwentner, Kenneth Meland, Jon Anders Kongsrud, Henrik Glenner, Angelika Brandt, Ralf Thiel, Jörundur Svavarsson, Anne-Nina Loerz, Saskia Brix

The Nordic Seas have one of the highest water-mass diversity in the world, yet large knowledge gaps exist in biodiversity structure and biogeographical distribution patterns of the deep macrobenthic fauna. This study focuses on the marine bottom-dwelling peracarid crustacean taxon Cumacea from northern waters, using a combined approach of morphological and molecular techniques to present a first insight into genetic variability of this taxon. In total, 947 specimens were assigned to 77 morphologically differing species, representing all seven known families. Out of these, 131 specimens were successfully included in 16S rRNA gene amplification and subsequent analyses. For 60 species, morphological and molecular-genetic delimitation was fully congruent, highlighting the overall success and high quality of both approaches. Differences were due to eight instances resulting in either morphologically variable species or morphologically cryptic species, uncovering hidden diversity. An interspecific genetic distance of at least 8 % was observed as a realistic distance with a clear barcoding gap for molecular delimitation of cumacean species. Data from public databases and specimens collected during different international expeditions revealed a change in the composition of taxa from a Northern Atlantic-boreal to an Arctic community. The relative dominance of cumacean taxa at family level corresponded well with the Greenland-Iceland-Scotland Ridge (GIS-Ridge) as a geographical barrier and/or with predominating water masses. A closer investigation on species level revealed occurrences across multiple ecoregions or patchy distributions within defined ecoregions.

Special session 2a#: Biodiversity and ecology of the deep-sea and polar benthos - Presentations in honour of Prof Craig R. Smith of the University of Hawaii.pdf – Sweetman et al.

- ### Range extensions for 9 species of Osedax boneworms

  Gabriella H. Berman, B. Johnson, Greg W. Rouse

Osedax boneworms, first discovered in 2004 off California, are now known from many of the world's oceans and their diversity continues to rise. Currently, little is known about species ranges, with most descriptions from single localities. However, a few taxa have very large ranges, though species delimitation issues have arisen. Based on extensive sampling in the eastern Pacific from Oregon to Costa Rica's Pacific coast and available GenBank data from off Japan and Brazil, we used cytochrome oxidase subunit I (COI) sequences as a basis for nine haplotype networks for *Osedax docricketts, O. frankpressi, O. knutei, O. packardorum, O. priapus, O. randyi, O. roseus, O. talkovici, and O. westernflyer. O. docricketts, O. randyi, O. roseus* and *O. westernflyer* range from California to Japan, though *O. docricketts* may be a species complex. *Osedax packardorum, O. priapus and O. talkovici* were found from California to Oregon. Osedax frankpressi occurred from California, Costa Rica, Oregon, and possibly Brazil, since species delimitation issues also arise for the latter site. Osedax knutei ranges from California to Costa Rica. *O. frankpressi, O. packardorum, O. priapus, O. roseus* and *O. talkovici* had a dominant COI haplotype shared by individuals at multiple localities, suggesting that they are experiencing gene flow throughout some or all their ranges. This study greatly expands the ranges for these nine species most of which previously were only known from single localities

- ### Seascape Ecology of a Blake Ridge Cold Seep
  Kellie Johnson, Avery Taylor, Annika Socha, Ellie Barksoumb, Cindy Lee Van Dover

Blake Ridge is a region of the western Atlantic ocean with notable chemosynthetic cold seep activity. Chemosynthetic are extremely vulnerable to human influence, and thus characterizing the seascape ecology of cold seeps can prove useful when divising environmental management measures. This is especially relevant given the recent rise of deep-sea disturbances caused by mining, drilling, and bottom trawling. In this study, a photo survey was conducted by AUV *Sentry* of an approximately 400x400m area at the Blake Ridge South site with roughly equal coverage of seep and non-seep terrain. These photos were used to assess community structure and faunal associations. To characterize faunal associations, pairwise probabilistic co-occurrence matrices were generated for 29 morphotypes. Biotic interactions were explored using a network approach both in the seep vicinity and non-seep areas. To assess the influence of environemental variables such as redox potential (Eh), salinity, depth and temperature on morphotype distribution, principal components analysis was used. The co-occurrence matrices revealed 7 positive and 6 negative significant associations between taxa and seep indicator morphotypes (mussels, clams, bacterial mat, tubeworms, and/or authigenic carbonates). Xenophyophores, shrimp, octopods and squat lobsters were among the positively associated species, while brittlestars had a particularly strong negative association with seep indicators. Preliminary network analysis indicates that morphotype interactions are more numerous and complex in areas of seep activity. A pending principal components analysis will test the hypothesis that there are significant associations between environmental factors and morphotype abundance. These results contributes to the growing understanding of Blake Ridge seascape ecology, particularly which morphotypes interact with one another and the seep environment and which are negatively associated with seep activity.

- ### Deposit feeders are secondary consumers of detritus in an abyssal food web
  Sonia Romero-Romero, Elizabeth C. Miller, Jesse A. Black, Brian N. Popp, Jeffrey C. Drazen

Trophic ecology of abyssal food webs is still poorly understood. These food-poor ecosystems depend on detritus, with deposit feeders dominating megafaunal communities, which cope with food scarcity by employing an array of feeding and digestive strategies. In this sense, microbial gut communities might increase their efficiency to exploit the limited resources. Also gut microbes can be a nutritional source, but it is unkown to what extent they might be an important component of abyssal food webs. We used compound-specific nitrogen isotope ratios of amino acids to estimate the trophic position of three abundant species of deposit feeders (*Oneirophanta mutabilis, Scotoplanes globosa* and *Echinocrepis rostrata*), their gut contents and the surrounding sediments all collected from the abyssal plain of the Northeast Pacific (Station M; ~ 4000 m depth). On the abyssal plain, detritus forms the base of the food web and deposit feeders are secondary consumers of that detritus. Our results suggest that gut contents of deposit feeders have a trophic position consistent with primary consumers and are largely composed of a living biomass of heterotrophic prokaryotes. Based on δ 13C values of essential amino acids, we found that gut contents are distinct from the surrounding surface detritus and form a unique food source, which was assimilated by the deposit feeders primarily in periods of low food supply. Overall, our results show that the guts of deposit feeders constitute hotspots of organic matter on the abyssal plain that occupy one trophic level, increasing the food-chain length in this detritus-based ecosystem. Moreover, the role of prokaryotes as primary consumers might be crucial in providing stability to the food web.

Special session 2b#: The deepest places on Earth - Bringing light in Hadal zones.pdf – Shimabukuro et al.

- ### Effect of high hydrostatic pressure on copepod carcass degradation
  Belén Franco-Cisterna, John Paul Balmonte, Clemens Schauberger, Torkel G. Nielsen, Peter Stief, Ronnie N. Glud

Sinking copepod carcasses are a prevalent source of labile compounds for pelagic microbes in marine ecosystems. At low temperatures, sinking copepod carcasses are slowly degraded, increasing their potential to export carbon to the deep sea. High hydrostatic pressure may also decrease carcass degradation rates, as demonstrated for other fast-sinking particles; however, its effect on degradation dynamics of copepod carcasses is little understood. Here, we investigated the effect of hydrostatic pressure on carcass degradation of the small, cosmopolitan copepod Acartia tonsa, and the large, Arctic copepod Calanus sp. We measured aerobic microbial respiration in oxic incubations exposed to pressure levels of 0.1, 20, and 60 MPa in rotating pressure tanks. Preliminary results from 1-day incubations showed that aerobic microbial respiration rates were negatively correlated with hydrostatic pressure. For both types of carcasses, the highest and lowest microbial respiration rates were observed at 0.1 MPa and 60 MPa, respectively. Our results suggest that high hydrostatic pressure slows down the degradation of copepod carcasses, increasing their potential for being a food source to deep-sea communities. Pressure-related preservation of organic matter may be particularly important in environments dominated by large copepods, such as Calanus sp., whose fast-sinking carcasses exceed velocities of 180 m d-1. Future research focused on incubations over longer time scales and higher pressure levels, aswell as the characterization of microbial community composition and enzymatic activities associated with sinking copepod carcasses, will further advance the current results.

Coastal upwelling as a source of C and N for the deep ocean ecosystem in the southeast Pacific: evidence from isotopes analysis of zooplankton

Carolina E. González, Ruben Escribano

The Deep ocean ecosystem in the southeast Pacific reaches its maximal expression in the Atacama Trench (>8000 m) extending for near 6000 km, limiting the offshore boundary of the continental shelf along the South American coast. Extreme conditions in this ecosystem (low temperature, lack of light and limited food), suggest that external sources of C and N support its fauna. In the southeast Pacific, the highly productive upwelling zone may provide inputs of C and N to the ultra-deep Atacama Trench, although the mechanisms promoting the import of organic matter are unclear. This study suggests that drifting plankton from the upwelling zone, being advected offshore, may be a major source of C and N for the deep-water ecosystem, including the Atacama Trench. During the MOPEX (Mesoscale Ocean Processes and Experiments) cruise in September 2016, epipelagic and mesopelagic zooplankton were sampled at onshore (upwelling zone) and off-shore stations over a cross-shelf section in Central Chile (27-33 °S). The community structure of size-fractioned zooplankton (5 size classes) was assessed along with their isotope composition of C and N (δ15N and δ 13C). The analysis of δ15N and δ13C, the trophic positions, the isotopic niches and the taxonomic composition of the 5 size classes of zooplankton showed that in onshore stations, diatoms mostly supported the primary production and the food sources of small-sized zooplankton. Small zooplankton is then advected off-shore by zonal currents, as revealed by intense mesoscale activity, where they become predated by large-sized, carnivorous zooplankton, which prevail in the off-shore region. At offshore, active transport, passive sinking and a trophic ladder may promote the input of C and N, originally produced in the upwelling zone, downward to the deep-water ecosystem.

Morphological and molecular evidence for a new isopod species at the abyssal and hadal transition

Stefanie Kaiser, Bente Stransky, Robert M. Jennings, Terue Cristina Kihara, Saskia Brix

Hadal trenches are perceived as a unique deep-sea ecosystem with fundamentally different communities compared to the nearby abyss. So far, however, scarce information exists about the connectedness of species and populations at the abyssal-hadal transition, especially in the size class of less than 1 cm. Here, we present the morphological and molecular-genetic characterization of specimens within the isopod genus Austroniscus Vanhöffen, 1914 (family Nannoniscidae) obtained from abyssal and hadal depths of the Puerto Rico Trench (PRT), NW Atlantic. Samples were collected as part of the Vema TRANSIT expedition onboard RV Sonne in January 2015. Morphological examination using traditional light microscopy and Confocal Laser Scanning Microscopy (CLSM) is combined with molecular analysis based on mtDNA (COI and 16S) to examine Austroniscus specimens occurring over a large depth range (4,552 to 8,338 m). Aside from the question of genetic structuring and the number of species present in the samples, our data definitely lead to description(s) of species new to science.

Comparative biogeography of benthic foraminiferal communities among western Pacific hadal trenches

Hiroshi Kitazato, H., Ohkawara, N., Gooday, A.J.

Benthic foraminifera are one of major biota at hadal trenches. We have long been worked deep sea benthic foraminiferal communities at the Western Pacific since 1990th . We analysed more than ten localities of the western Pacific deep-sea. Benthic foraminiferal community consists of monothalamous soft-shelled forms, agglutinated forms, porcelaneous forms, hyaline forms and large xenophyophores from morphological taxonomic points of view. In the shallow deep-sea such as abyssal depths, agglutinated foraminifers are rich. In contrast, hadal trenches such as Challenger deep of the Marianas Trench or Horizon deep of the Tonga Trench are characterized by the low concentration of agglutinated forms. The tendency suggests that agglutinated foraminifera prefer to distribute at abyssal depths than hadal depths.

We compare populations between Challenger deep (10899m) and Horizon deep (10810m) of the western Pacific hadal trenches, where differences of the depth show less than 100m each other. Foraminiferal population at the Horizon Deep shows much higher concentrations of agglutinated forms. How can we explain populational differences between two deeps?

We compare populations between Challenger deep (10899m) and Horizon deep (10810m) of the western Pacific hadal trenches, where differences of the depth show less than 100m each other. Foraminiferal population at the Horizon Deep shows much higher concentrations of agglutinated forms. How can we explain populational differences between two deeps?

A new species of Thermanemertes from Kairei hydrothermal vent field, Central Indian Ridge

Xu Liu, Chong Chen, Jin Sun, Shichun Sun

Over 500 endemic animal species have been discovered from deep-sea hydrothermal vents, but only one free-living nemertean has been formally described – Thermanemertes valens from the Eastern Pacific. Although another nemertean has been reported from the Kairei vent field in Indian Ocean, 17,000 kilometers away from Juan de Fuca hydrothermal vent field where T. valens was described from, but no further studies has been done on it for over 20 years and its relationship with T. valens has been unclear. Here, we studied this Indian Ocean vent nemertean based on recently collected material. From morphological analyses, we confirmed this species within the same genus as T. valens since they both possess well-developed dorsoventral muscles. However, it differs from T. valens in possessing neither cerebral organs nor a cephalic furrow and is an undescribed species. Phylogenetic analysis based on 16S rRNA, 18S rRNA, 28S rRNA, and COI genes indicates that Thermanemertes nests within Oerstediidae, instead of Emplectonematidae where it is currently placed. We found that our new species possesses cerebral vessels protruding into the rhynchocoel where they pass through the cerebral ring, which is a characteristic of Oerstediina, supporting our phylogenetic analysis. We therefore recommend Thermanemertes to be transferred from Emlectonemertidae to Oerstediidae. The presence of two Thermanemertes species a great distance apart shows that this genus is likely present in other hydrothermal systems in-between, and highlights that nemerteans have been largely neglected in vent biology. Additional work on vent nemertean samples from other vents around the world are required to shed light on the evolution and adaptation of this particular phylum in vents.

Special session 2c#: NW Pacific and Arctic biodiversity.pdf – Saeedi & Brandt

- ### Exploring the role of gelatinous zooplankton in Tomorrow's Arctic Ocean

  Charlotte Havermans, Annkathrin Dischereit, Ayla Murray, Andrea Eschbach, Madlen Friedrich, Véronique Merten, Gerlien Verhaegen, Henk-Jan Hoving, Dmitrii Pantiukhin,

Gelatinous zooplankton or "jellies" (ctenophores, cnidarians, tunicates) are known to be major drivers of ecosystem changes. Increases in jelly biomass, referred to as "jellification", have been observed in several marine ecosystems, causing, amongst others, the collapse of major fisheries. For the Arctic region, abundance data on jellies are virtually non-existent, impeding our ability to detect changes of a similar magnitude. To better understand the role of jellies in the Arctic seas, the Helmholtz Young Investigator Group ARJEL aims to combine the most recent technologies in optics, acoustics, and environmental DNA (eDNA) analyses. Based on data collected during recent international campaigns, we attempt to link distributional patterns of jellies to oceanographic features and sea ice. Furthermore, we apply species distribution models to a broad set of archived data to understand observed species and community patterns and to predict changes under future climate-change scenarios. The role of jellies in the Arctic food web and their importance as prey for planktonic predators and fish is assessed with molecular diet studies, which will improve food web models currently neglecting jellies as major predators and prey. We also explore the genetic connectivity of dominant jelly species across the Arctic Ocean and its adjacent seas. An overview of the project's goals, methods and first results will be given. Our ongoing research foci include: 1. the comparison of species composition and abundances of ctenophores and cnidarians in Arctic vs. Atlantic-influenced Svalbard fjords to better understand the impact of the ongoing Atlantification of the Arctic; and 2. the comparison between optical methods, net catches and eDNA for assessing jelly diversity and abundances.

- ### Not so cosmopolitan: isolation and speciation in the midwater

  Shannon B. Johnson, Jacob R. Winnikoff, Darrin T. Schultz, Lynne M. Christianson, Wyatt L. Patry, Claudia E. Mills, and Steven H.D. Haddock

Often population genetic studies are focused on environments where there are obvious boundaries to gene flow. By focusing on disjunct environments, we underestimate biodiversity of places like the midwater zone of the ocean, which is the most voluminous habitat in the world. Comb jellies (phylum Ctenophora) are common occupants of the midwater for which many species are thought to have a worldwide distribution. We examined global population structure within and between species of the lobate ctenophore Bolinopsis using mitochondrial and nuclear loci. Genomic data provided us a rare opportunity to explore the evolution of a pelagic species. Sequencing efforts revealed numerous cryptic species despite high fecundity and seemingly endless dispersal capabilities, and illuminated subdivisions within Bolinopsis species. In addition, for one species from the eastern Pacific Ocean we found evidence of a secondary contact zone of previously isolated populations along the coast of California. Our results showed that despite the lack of obvious oceanographic boundaries, pelagic ctenophores are clearly subject to barriers such as ocean currents, which are typically thought to aid in dispersal rather than restrict it.

- ### Methane seep communities on the Koryak slope of the Bering Sea

  Elena Rybakova, Elena Krylova, Vladimir Mordukhovich, Sergey Galkin, Inna Alalykina, Igor Smirnov, Nadezhda Sanamyan, Georgy Vinogradov, Vladimir Shilov

Methane seeps and associated communities on the Koryak slope of the Bering Sea were discovered in 2018 during the 82nd cruise of the RV Akademik M.A. Lavrentyev using ROV Comanche 18. Seep fields found between 400 and 700 m depth are the northernmost chemosynthetic habitats (~61°N) known to date in the Pacific. We investigated species composition and macrofaunal community structure of methane seeps and background benthic communities from the following three depth horizons: 400-402 m, 417-429 m and 647-695 m.

A total of 324 macrofaunal species were identified from all studied sites. Cluster analysis based on quantitative data showed significant difference between the deepest communities and those from shallower depths. The deepest methane seep community was dominated by the thiosymbiotroph pliocardiine Calyptogena pacica. The species richness in this community was the highest (254 species) exceeding the number of species in the background by more than three times (70). This difference might be from a higher sampling effort at seeps but we can expect the numbers reflect the general trend. The seep community was characterized by relatively high evenness and large variations in the composition and structure related to heterogeneity of the substrate type.

In contrast, shallower-water seep communities were dominated by background species with only single specimens of C. pacica present. Seepages at 400–402 m depth were marked by bacterial mats with rare background actiniarian Sagartiogeton cf. californicus. Seep community at 417-429 m was dominated by the echinoid Brisaster latifrons. The density of echinoids on the bacterial mat was four times higher than in the background. The seep communities at shallower depths were characterized by low species richness (~30 species versus ~70 in the background), relatively low evenness and diversity of macrofaunal community structure.

The reported study was partly funded by RFBR 19-04-00281-a and the Ministry of Science and Higher Education, Russian Federation (grant 13.1902.21.0012 for ID, contract No 075-15-2020-796).

Special session 2d#: Marine bioluminescence.pdf – Martini

- ### Etmopterus Lantern Sharks Use Coelenterazine as the Substrate for Their Luciferin-luciferase Bioluminescence System
  Gaku Mizuno, Daichi Yano, José Paitio, Hiromitsu Endo, Yuichi Oba

The lantern shark genus Etmopterus (Squaliformes, Etmopteridae) is one of the most diverse groups of sharks, with approximately 40 species currently recognized. They emit blue light mainly from the ventral body surface, and the primary biological function is considered to be for camouflage by counterillumination. It has been reported that their bioluminescence systems are intrinsic (not symbiotic), but the reaction mechanism has not been elucidated. Coelenterazine is a compound used as luciferin of specific luciferase or chromophore of photoproteins in wide range of bioluminescent organisms living in the sea, such as jellyfish and crustaceans. It has also been suggested to be a luciferin in many marine luminescent fishes, but little is known about their luciferases. In this study, we detected both coelenterazine and its luciferase activity in tissues containing the ventral photophore of genus Etmopterus. The presense of coelenterazine was examined by HPLC separation of methanol extract and mass spectrometry. The retention time, detected mass, and fragment ion peaks were consistent with the authentic coelenterazine. We also confirmed that the luciferase activity was eluted as single peak by gel filtration. These results suggested that bioluminescence in lantern sharks is produced using coelenterazine as the substrate for the luciferin-luciferase reaction. Considering its higher trophic level, lantern shark will obtain coelenterazine through predation of the deep-sea luminouse teleosts and shrimps. Now we are trying to purify the luciferase protein by using various chromatographic techniques to determine the responsible gene.

- ### Identification of coelenterazine-type luciferases in bony fishes
  Daichi Yano, José Paitio, Teerapong Seesamut, Gaku Mizuno, Hinano Imai, Manabu Bessho-Uehara, Masakazu Iwasaka, Yuichi Oba

Lanternfishes (Myctophidae, Myctophiformes) are worldwide distributed with high abundance and species diversity1 . Stomiiformes (e.g., hatchetfishes, dragonfishes) have additional luminous structures such as barbels and red and blue suborbital photophores2 . Luciferase of lanternfishes and Stomiiformes fishes have been shown to luminescence using coelenterazine as a substrate3 . There are many coelenterazine-based luminescent fish in the ocean, but the corresponding gene has never been determined yet. To understand the frequent evolution of coelenterazine-type luciferase in marine bony fishes, we are trying to determine the luciferase from various fish species collected at fishery harbours in Japan.

We collected lanternfishes in Mimase and Siina harbours of Kochi Prefecture, and Owase harbour of Mie Prefecture, Japan. Other fishes were provided from Suruga Bay and by the National Research Institute of Fisheries Science of Japan. Luciferase from lanternfish Diaphus watasei photophores was extracted and purified by anion exchange chromatography, hydrophobic chromatography, and gel filtration purification. In vitro spectrum maximum was 454 nm and half band width 61 nm. The SDS-PAGE result showed that the molecular weight of the luciferase is approximately 50,000. This band was excised from gel and were performed by LC-MS/MS.

We also analysed the luciferase of the blackchin (Nescopelidae, Myctophiformes) Neoscopelus microchir and the pearlside (Sternoptychidae, Stomiiformes) Maurolicus japonicus. We estimated the molecular weight of Myctophiformes and Stomiiformes luciferases by gel filtration purification and compared the enzymes between different species of the two fish orders.

References for paper

[1] V. Catul, M. Gauns, P. K. Karuppasamy, A review on mesopelagic fishes belonging to family Myctophidae, Rev Fish Biol Fisheries (2011) 21:339-354. DOI :10.1007/s11160-010-9176-4.

[2] P. J. Herring, C. Cope, Red bioluminescence in fishes: on the suborbital photophores of Malacosteus, Pachystomias and Aristostomias, Marine Biology (2005) 148: 383–394. DOI: 10.1007/s00227-005-0085-3.

[3] O. Shimomura, S. Inoue, F. H. Johnson, Y. Haneda, Widespread occurrence of coelenterazine in marine bioluminescence, Comp Biochem Physiol (1980) 65B: 435–437. DOI: https://doi.org/10.1016/0305-0491(80)90044-9

Special session 2e#: Deep-sea microbial diversity and ecology - overview of micro eukaryotic and prokaryotic biota.pdf – Velez

- ### Health screening of the reef forming scleractinian cold-water corals Lophelia pertusa and Madrepora oculata in a remote submarine canyon on the European continental margin, NE Atlantic
  Appah J. K. M., Lynch, S. A., Lim, A., O' Riordan R., O'Reilly L., de Oliveira L., Wheeler A. J.,

Environmental stressors such as temperature and sedimentation can increase the virulence of pathogens and expedite their ability to cause diseases in deep-sea environments. The present research employed a combination of histology/microscopy and polymerase chain reaction diagnostic techniques to investigate whether Vibrio spp. and other potential pathogens were present in the cold-water scleractinian corals Lophelia pertusa and Madrepora oculata in the Porcupine Bank Canyon (PBC), NE Atlantic in May 2019. Vibrio spp. are common in the environment and most species are problematic pathogens. A total of 75 intact coral polyp tissues were screened for pathogens. No potential pathogen or unidentified cells were observed in the Madrepora samples possibly due to the different feeding strategies between the two scleractinian corals. Neither histology nor standard PCR detected Vibrio spp. in the coral samples, although using Illumina technology, Vibrio shilonii was observed in a couple of L. pertusa samples in low abundances (0.22%). Also, other unidentified organisms were observed in the histological samples, including a Rickettsiales-like organisms (RLOs), which occurred at an overall prevalence of 8.0% and at a low infection intensity of 1 - 4. The framework-forming coral, L. pertusa, showed a few RLOs infection from the PBC canyon head (2.7%) with more coral infections observed in the south branch of the PBC (5.3%). Similarly, unidentified cells observed in L. pertusa tissues from the south branch (4.0%) were more common than those found in the canyon head (1.3%) with an overall prevalence of 5.3%. Although the route of pathogen infection is unclear, a likely mode of entry could be associated with particulate availability and the feeding strategies of the scleractinian corals. This suggest that this slow growing coral, away from human impacts, invests energy into an enhanced immune function and reduced susceptibility to global pathogens despite a changing ocean environment.

- ### The fungal niche at deep-sea methane seeps: Distribution of fungi and Actinobacteria across the Cascadia Margin

  Lila Ardor Bellucci, Susie Cummings, Sarah Seabrook, Kerry McPhail, Amanda Demopoulos, Tamara Baumberger, Nicole Raineault, Andrew Thurber

Marine fungi and Actinobacteria play a key role in carbon cycling through remineralizing refractory and complex carbon in a multitude of environments. Although seemingly ubiquitous, the distribution of these taxa and their roles in deep-sea processes remain poorly understood, particularly in methane seep habitats. We posit that methane seeps, through combining both highly labile in situ with refractory ex situ (detrital matter) production will present a novel environment where the “fungal niche” may be both divergent and important to overall ecosystem function. Here we explore the distribution and community composition of fungi and actinobacteria within seep sediments of the US Cascadia Margin, combining ITS1 and 16S rRNA gene sequencing from 20 sites within 7 distinct regions of the margin. Overall, both taxonomic richness and average relative abundance of actinobacteria increased with proximity to seep habitat, with the highest values in clam beds and reduced sediments. Actinobacterial community composition was characterized by high variability, both within and between sites. We identified 52 families and 66 genera of actinobacteria, dominated by the order Actinomarinales, which had an average relative abundance of approximately 60%. Multiple seep cores contained Streptomycetes and Actinomycetes, rare orders of particular interest for bioprospecting of marine genetic resources. These groups expand the niches present in seep sediments, adding to the overall biodiversity of the deep sea and further contributing to the physical and biogeochemical footprint of the myriad processes that occur in reducing habitats.

- ### Microbial functional diversity at methane seeps of the Cascadia Margin

  Susie Cummings, Sarah Seabrook, Lila Ardor Bellucci, Kerry McPhail, Tamara Baumberger, Amanda Demopoulos, Andrew R Thurber

Methane seeps are ubiquitous habitats of the deep ocean, and they host unique chemosynthetic, methane-consuming microbial communities. Though we have increasing data on the makeup of the microbial communities at seeps, the functional diversity of these microbes, especially the Archaeal members, remains underexplored. We seek to examine the microbial functions present at methane seeps, and how they vary across the physical, geochemical, and biological gradients of the deep ocean. Here, we analyze the functional gene profiles from seven sites along the Cascadia Margin, from over 50 sediment cores collected on five research cruises between 2016 and 2020. Through combined predictive functional algorithm analysis of the 16S rRNA gene and metagenomic sequencing, we aim to advance our understanding of ecosystem function beyond the methane cycle. We found that metabolic profiles are distinct among seep habitats (microbial mat, Calyptogena clam beds, and ampharetid beds). These communities show clear gradients with increasing distance from active seepage in the abundance of genes responsible for sulfur, iron, and nitrogen metabolisms. This expands our understanding of the role that seeps play in biogeochemical cycling, as well as their hand within diverse ecosystem processes and services. Through our proposed functional analysis, we facilitate a greater understanding of community ecology at seeps: from foundational shifts in dominant metabolism, to microbial inter-communication, and chemosynthetic processes.

- ### Spatial and temporal dynamics of microbial communities in active hydrothermal chimneys

  David X. François, Erwan G. Roussel, Françoise Lesongeur, Ewan Peller, Sandrine Cheron, Xavier Philippon, **Anne Godfroy**

Hydrothermal chimneys are mineral structures resulting from the precipitation of various chemical species during the mixing between the hot, reduced hydrothermal fluid and the cold, oxygenated seawater. The structure and mineral composition of the chimneys is heterogeneous and evolves over the time as porous sulphates are progressively replaced by massive sulphides. These mineral structures and the hydrothermal plume represent various microhabitats hosting a high diversity of microorganisms that transfer carbon to the upper trophic levels of this unique chemosynthetic ecosystem.

To investigate the spatial and temporal dynamics of microbial communities from deep-sea hydrothermal vents, we collected more than 50 chimneys and proximal plume samples at the Lucky Strike hydrothermal vent field between 2008 and 2019. X-ray diffraction analyses were carried out to determine the mineral composition and the growth stage of the chimneys. The diversity of archaeal and bacterial communities was studied using a metabarcoding approach, and has shown important differences between the microbial communities of chimneys and plume, and also an increase of the diversity over the growth of the chimneys. A focus was realized on the culturable microbial communities from four chimneys samples, representative of sulphates- and sulphides-dominated chimneys. MPN enrichments were performed in various conditions in order to determine the concentration of viable microorganisms. Also, the autotrophic and heterotrophic microbial biomass production rates were measured using radiolabelled substrates on the same samples. The culturable cells concentration and the microbial biomass production were the highest at the lower incubation temperature (30 °C), and decreased with the increase of temperature. In addition, we have shown some quantitative and taxonomic differences in the microbial communities inhabiting the different types of chimneys (sulphates/sulphides). For example, the microbial communities of young sulphate chimneys are dominated by mesophilic and autotrophic members of the genus *Sulfurimonas*.

- ### Fungal diversity in a minimum oxygen zone of the Tropical Pacific Ocean revealed by Illumina sequencing
  Judith Posadas, Patricia Velez, Silvia Pajares, Laura Espinosa, Jaime Gasca

The oxygen minimum zone (OMZ) of the Pacific Ocean is the largest in the world. Such deficientoxygen environment can increase the production of nitrous oxide (N2O), a potent greenhouse gas that contributes to global warming. Fungi have a denitrification pathway that predominantly produces N2O, so that evaluating their diversity has a relevant impact from an environmental, ecological and economic point of view. Despite the above, the fungal diversity of the OMZ of the Pacific Ocean still remains little explored, particularly for the area of Mexico there are no studies. Using a metabarcoding approach, we analyzed fungal diversity and community composition in sediment samples collected in four locations across a transect from the coastal to the open sea with bathymetric gradient (32 – 705 m) in the OMZ of the Mexican Tropical Pacific. Our results revealed the presence of 518 fungal amplicon sequence variants. Ascomycota represented the most abundant phylum with Sordariomycetes constituting the dominant class, followed by the Basidiomycota with dominant class Agaricales, and finally the basal clade Rozellomycota. Additionally, the shallow near-shore sites were more diverse than the deep-sea sites in the open ocean, this may be due to extreme deep-sea conditions. The abundance and prevalence of fungal DNA reported in this work in a transect from the coast to the open sea provide data on biodiversity, marine fungal distribution and suggests that they may be performing relevant ecological and biogeochemical functions in the sediments of the OMZ of the Mexican Tropical Pacific.

- ### Persephonella atlantica sp nov.: How to adapt to physico-chemical gradients in high temperature hydrothermal habitats
  David X. François, Anne Godfroy, Clémentine Mathien, Johanne Aubé, Cécile Cathalot, Françoise Lesongeur, Stéphane L'Haridon, Xavier Philippon, **Erwan G. Roussel**

Persephonella atlantica MO1340T represents a new species within the bacterial genus Persephonella within the order Hydrogenothermales. As for the three other species of the genus, P. atlantica is a thermophilic and autotrophic Bacteria, and was isolated from a deep-sea hydrothermal chimney. A characterization of this strain was carried out as well as a detailed study of its metabolic capacities, using gas and ion chromatography. We demonstrated that strain MO1340T could oxidise hydrogen, elemental sulphur or thiosulphate using oxygen as electron acceptor. Anaerobic nitrate reduction using hydrogen could also be performed.

Each catabolic reaction had a different optimal growth temperature (65 to 75◦C) and an optimal dissolved oxygen concentration (11.4 to 119.7 µM at 70◦C for aerobic reactions) that varied according to the electron donors utilised. Because the optimal growth temperature and oxygen concentration are inversely correlated, these experimental results are consistent with the physico-chemical gradients resulting from the mixing between the hot, reduced hydrothermal fluid and the cold, oxygenated seawater. This is also in accordance with the distribution of these catabolic substrates along the temperature gradient observed in active hydrothermal systems. These experimental results strongly suggest that this adaptive strategy could confer a selective advantage for strain MO1340T in the dynamic part of the ecosystem.

- ### Hydrothermal vent fileds in the southern Gulf of California as fungal hotspots
  Patricia Velez, Diana L. Salcedo, Laura Espinosa-Asuar, Jaime Gasca-Pineda, Abril Hernandez-Monroy, Luis A. Soto

Deep-sea hydrothermal vent fields have been regarded as oases of life in oceans. Since their discovery in 1977, many endemic species of chemo-lithoautotrophic prokaryotes and emblematic macrofauna have been described. These unique biotic assemblages are adapted to extreme environmental conditions of temperature, darkness, high hydrostatic pressure, and toxicity, where hydrothermal fluids sustain life. However, this biome remains as one of the least studied because of its remoteness and the technological challenges for its investigation. In past years, microbial eukaryotes at deep-sea hydrothermal vents have been pointed out from molecular microbial ecology studies. In this sense, very few studies have been carried out on fungal communities, representing an enormous gap in knowledge. These organisms are considered key elements in terrestrial biogeochemical cycles, due to their ability to degrade organic matter. In recent years, new vent systems were discovered at 3,800 m depth in the Pescadero Basin, Alarcón Rise, and Pescadero Transform Fault, in the Southern Gulf of California, Mexico, at the northernmost segments of the East Pacific Rise. So, the objective of this work was to examine microfungal diversity and community structure from these hydrothermal vent fields in the Southern Gulf of California, using a ITS gene amplicon Illumina sequencing approach. Our results evidenced a rich and diverse fungal community characterized by both, filamentous and yeasts forms; and dominated by Ascomycota members, including cosmopolitan taxa such as Alternaria, Aspergillus, Cladosporium, and the extremophiles such as Naganishia. This work represents an important step towards understanding fungal diversity, abundance and function in deep-sea hydrothermal vents.

Special session 2f#: Biology of deep-sea microorganisms.pdf – Cario et al.

- ### Study of marine iron-rich microbial mats from Lucky Strike: influence of environmental variations
  Aina Astorch Cardona, Mathilde Guerre, Valérie Chavagnac, Céline Rommevaux

Although oceans are considered to be mainly oxygenated and depleted in Fe(II), there are different areas in which these conditions are not met, such as hydrothermal vents1 . In these environments, superheated reduced vent fluids enriched in Fe(II) flow into cold oxygenated seawater, creating redox gradients which allow the development of unique ecosystems based on chemolithoautotrophy1,2. While a great number of microorganisms are able to thrive in these habitats2 , there is a particular interest in a group of bacteria which use dissolved Fe(II) or Fe0 as their main energy source: marine iron-oxidizing bacteria (FeOB)1–3 .

FeOB are considered to be primary producers in such ecosystems, forming centimetre-thick orangecoloured iron-rich microbial mats3 . Although several studies have been carried out on FeOB, any of them has so far examined neither their relationships with the other microorganisms present in these mats, nor how these communities evolve over time and in response to environmental variations.

This project focuses on analysing the structure and composition of the microbial communities present in iron-rich microbial mats collected annually since 2016 at two vent sites (Eiffel Tower and Capelinhos) of the Lucky Strike hydrothermal field. Besides, it aims to assess the role of FeOB within the mats and how these communities adjust to any variations of physico-chemical conditions.

The analysis of the phylogenetic diversity of the mats based on 16S rRNA genes sequencing is presented, as well as the comparison of the microbial communities present in the mats depending on the differences between sites and on the temporal modifications of the environmental conditions, as recorded by the EMSO-Azores observatory.

1. Emerson, D. et al. PLoS One 2, (2007).

2. Rommevaux, C. et al. Geochemistry, Geophys. Geosystems 20, 3065–3089 (2019).

3. Scott, J. J., Breier, J. A., Luther, G. W. & Emerson, D. PLoS One 10, 1–19 (2015).

Deep sea microbial community: diversity and activities under in situ condition

Marc Garel, Christian Tamburini

Most of the ocean is deep with most of its volume (> 80%) lying under a depth higher than 1000 m and is poorly sampled (< 0.01%). It is characterized by high hydrostatic pressure, low temperature, high inorganic nutrients, and low organic carbon concentrations. Carbon input is mainly supplied as particulate and dissolved organic forms by physical and biological processes. Bioavailable dissolved organic carbon (DOC) is mainly consumed in surface water by prokaryotes, while most of DOC in the deep ocean is recalcitrant, more difficulted to degrade. To study deep-sea prokaryotes under in situ conditions, we have a ready-to-use pressure-retaining sampler, which can be adapted to use on a CTD-carouselsampler and able to collect, to transfer and to incubate sample under in situ conditions (high hydrostatic pressure and temperature).

According to the hydrological conditions, deep-sea microbial communities are composed by either autochthonous adapted microbes or a mix of autochthonous and allochthonous microbes. Hence, to study degradation of DOC in a real condition, maintaining in situ condition is the best way to study the ability of deep-sea microbes to utilize recalcitrant dissolved organic matter (Garel et al., 2021). Secondly, through an experimentation with deep-sea samples collected and incubated under in situ condition and decompressed we have shown that the composition of the prokaryotic community is influenced by sampling methods. In fact, into sample maintained at in situ conditions piezophilic taxa like Colwelliaceae family are maintained while under decompressed condition microbial community are dominated by Alteromonadaceae (Garel et al., 2019). With our last two studies, we can conclude that to study the diversity and metabolic activities of the microbial community at depth, an adequate sampler is necessary.

References

Garel, M., Bonin, P., Martini, S., Guasco, S., Roumagnac, M., Bhairy, N., Armougom, F., Tamburini, C., 2019. Pressure-Retaining Sampler and HighPressure Systems to Study Deep-Sea Microbes Under in situ Conditions. Front. Microbiol. 10, 453. https://doi.org/10.3389/fmicb.2019.00453

Garel, M., Panagiotopoulos, C., Boutrif, M., Repeta, D., Sempéré, R., Santinelli, C., Charrière, B., Nerini, D., Poggiale, J.-C., Tamburini, C., 2021. Contrasting degradation rates of natural dissolved organic carbon by deep-sea prokaryotes under stratified water masses and deep-water convection conditions in the NW Mediterranean Sea. Mar. Chem. 231, 103932. https://doi.org/10.1016/j.marchem.2021.103932

High-pressure transparent micro and millifluidics reactors: new tools for investigating the deep-sea biosphere at lab scale:

A. Cario, E. Vidal, C. Lecoutre, O. Nguyen, **S. Marre**

Conventional cultivation and analysis techniques used for the deep-sea biosphere studies offer limited optical access, thus slowing down the speed at which characterizations and exploration can be conducted. This results in narrowing the ability to investigate deep-sea microbial communities, in particular at lab scale.

The use of transparent high-pressure multiscale reactors could contribute to address part of these limitations, providing ways for in situ investigations under pressure and fast screening capabilities. Specifically, thanks to the development of high-pressure micro and millireactors [1], the deep-sea microbiology community could benefit from approaches, which have greatly advanced the (micro)biology field, in particular for epipelagic microorganisms [2]. The advantages concern the fast screening capabilities, the implementation of in situ analyses, the reproducibility and the low consumption of samples. Hence, HP microfluidics appears particularly well adapted to the investigation of microbiology under extreme conditions such as deep-sea microorganisms.

In this presentation, we will first detail the interest of both transparent micro- and millifluidics technologies and the different strategies developed to manufacture and use them. Then, we will present the use of milli- and microfluidic biocompatible high-pressure microreactors for the culture and the study of microorganisms living in deep environments, along with examples of HP microfluidics approaches for the fast phenotyping (determination of the optimal conditions) of a model deep-sea vents microorganism. After summarizing the advantages of these experimental approaches compared to traditional instrumentation, we will give some perspectives concerning other future applications such as the study and use of extremophile microorganisms.

New microbial colonizer sampling the physico-chemical gradient: first results

Céline Rommevaux, Valérie CHAVAGNAC, Alain CASTILLO, Pascal GISQUET

Hydrothermal systems, hosted on the seafloor or in the sediments affected by hydrothermal circulation around, are suitable environment for the development of a wide variety of microorganisms1 . They take advantage of the great temperature and chemical gradient created by the mixing between cold oxygenated seawater and hot reduced hydrothermal fluids. To better understand the colonization process of a natural mineral substrate according to the environmental conditions, we have developed a new patented 3D geomicrobiological colonization device named BIOLUCKY2 , allowing in-situ recording of temperature gradient at centimetre scale. Each end of the colonisers is equipped with temperature sensors that continuously record the evolution of the temperature gradient over the duration of the deployment.

For the first time, the BIOLUCKY device was deployed for one year at the interface between seawater and hydrothermal sediments at the White Castle vent site located at the Lucky Strike hydrothermal site. Mixing of seawater and hydrothermal fluids occurs within sediments at the foot of the chimney, creating a thermal gradient between 4 and over 100°C within a 5 cm thick sediment deposit.The colonizers were filled with natural basaltic glass. Here, we present the comparison of the microbial community composition present in the different colonizers according to the temperature gradient.

• Microbial Strategies for Survival in the Glass Sponge Vazella pourtalesii

Kristina Bayer, Kathrin Busch, Ellen Kenchington, Lindsay Beazley, Sören Franzenburg, Jan Michels, Ute Hentschel, **Beate Slaby**

We investigated the microbial community of the glass sponge (Hexactinellida) Vazella pourtalesii that forms globally unique, monospecific sponge grounds under low-oxygen conditions on the Scotian Shelf, where it plays a key role in its vulnerable ecosystem. To elucidate the microbiome composition and the functional strategies of the main symbionts, we combined microscopic approaches with metagenome-guided microbial genome reconstruction and amplicon community profiling.

In microscopic images, host and microbial cells appeared within dense biomass patches, presumably syncytial tissue aggregates. Based on abundances in amplicon libraries and metagenomic data, SAR324 bacteria, *Crenarchaeota*, Patescibacteria, and *Nanoarchaeota* were selected for in-depth genomic analysis. The V. *pourtalesii* symbionts had very small genome sizes (0.5-2.2 Mb) and low GC contents, even below those of seawater relatives. Based on functional analyses of metagenomeassembled genomes (MAGs), we propose two major microbial strategies:

- The ‘givers,’ namely *Crenarchaeota* and SAR324, heterotrophs and facultative anaerobes, produce and partly secrete all required amino acids and vitamins.
- The ‘takers,’ *Nanoarchaeota* and Patescibacteria, are anaerobes with reduced genomes that tap into the microbial community for resources, e.g., lipids and DNA, likely using pilus-like structures.

We posit that the existence of microbial cells in sponge syncytia together with the low-oxygen conditions in the seawater environment are factors that shape the unique compositional and functional properties of the microbial community associated with V. *pourtalesii*.

• Combined high-pressure technologies for studying and isolating methanogen strains at lab scale without decompression

Emeline Vidal, Karyn L. Rogers, Anaïs Cario, Carole Lecoutre, Olivier Nguyen, Anthony Ranchou-Peyruse, Samuel Marre

Deep ocean exploration has revealed a broad diversity of microbes, especially around hydrothermal vents [1]. The main factor that has limited a better understanding of these subsurface ecosystems is technical, as high-pressure experiments requires a certain expertise to perform.

Understanding subsurface microbial activities requires maintaining high pressures throughout all experimental steps, which is the aim of the DEEP project (PI K. Rogers). Sampling devices have been designed and enabled the collection of samples while maintaining in situ pressure, even directly in the experimental site [2]. Several microbial species have been isolated from deep-sea vents, like methanogens which play an important role in the geobiochemical carbon cycle. The chase for new methanogens strains accelerating CO2 conversion to methane can find obvious opportunities in hydrothermal vents environments. Many are hyperthermophilic and may have higher metabolic reaction rates than their mesophilic homologous. The impact of these indigenous extreme microbes has not yet been considered within a CO2 geological storage context. Thus, the BIGMAC project (PI S. Marre) aims at understanding the impact of CO2 injection in deep saline aquifers at the pore scale, in order to validate and quantify the capture of CO2 by endemic methanogens.

In a recent expedition to the Mid-Cayman Rise, we combined several technologies to maintain in situ pressures (up to ~500bar) in hydrothermal fluids throughout sample retrieval, transfer, enrichment, and filtration (DEEP project). This presentation will present the Fulbright collaborative project (ICMCB/RPI) that will combine advanced technologies to isolate and study new methanogens from the deepest vent known so far. This laboratory exploration could potentially bring proof of concept of the feasibility of the CO2 recycling potential.

References :

1. Jebbar et al, Extremophiles, 2015, 19, 721-740

2. Garel et al, Front. Microbiol., 2019, 10, 753

• Metagenomic analysis revealed a wide distribution of phototrophic bacteria in hydrothermal vent on the ultraslow-spreading Southwest Indian Ridge

Long-Fei Wu, Hong Chen, Denghui Li, Aijun Jiang, Jianwei Chen, Xue-Gong Li, Wei-Jia Zhang, Shanshan Liu

Deep sea hydrothermal vents emit light that could potentially drive photosynthesis in vent ecosystems. Metagenomic studies sporadically reported occurrence of phototrophic populations such as cyanobacteria in hydrothermal vent samples. To answer the question how geographically and taxonomically widespread are phototrophs in the deep-sea hydrothermal vents we collected samples from three niches in a hydrothermal vent on the Southwest Indian Ridge and carried out an integrated metagenomic analysis. We observed typical community structure of microorganisms found in active venting fields, and identified all populations of known potential chorophototrophs and retinalophototrophs. Complete chlorophyll synthetic pathways were identified in all samples. In contrast, proteorhodopsins were only found in the active beehive smoker diffuser. Taxonomic groups with potential phototrophy, dependent of semiconductors present in hydrothermal vents, were also found in these samples. This systematic comparative metagenomic study shows a wide spread distribution of phototrophic bacteria in the hydrothermal vent fields and support the hypothesis that the ocean is a seed bank of diverse microorganisms.

General Session 3 Life-history traits and population connectivity (reproductive ecology, larval development and dispersal, and population connectivity)

- ### Goniocorella dumosa are brooders! Opportunistic observations of larval behaviour, settlement, and corallite development of a New Zealand deep-sea stony coral

  Jenny Beaumont, Di Tracey,Graeme Moss, Vonda Cummings, Malcolm Clark, Rhian Waller

Little is known of the reproductive traits and dispersal potential of deep-sea stony corals. Spawning events have been observed for only a few species of azooxanthellate stony corals globally and most deep sea corals have been thought to broadcast spawn gametes into the water column (Waller 2005).

In September 2020, we documented a larval release event of *Goniocorella dumosa*, a habitat-forming deep-sea scleractinian stony coral found in the New Zealand region. This was the first observation of a spawning event for any deep-sea coral in New Zealand waters.

Colonies of G. *dumosa*, held in an in-aquaria environment, released large (approx. 1.1 mm x 0.8 mm) free-swimming larvae. Over a 3 month period we documented the behaviour and settlement of larvae and the development and calcification of corallites. Further investigation showed that this species is a brooder, with up to 10 mature larvae found in single mature polyps.

A small previous study had suggested G. *dumosa* were broadcast spawners, with fertilisation likely to occur in late April or May (Burgess & Babcock 2005). Our results change this understanding with respect to both spawning mode and seasonality. The more limited dispersal potential of brooders, compared to broadcast spawners, has significant implications for population connectivity, and for potential recovery from human induced disturbance activities. This in turn could influence the management and protection of G. dumosa habitat within the region.

References cited:

Burgess, S., Babcock, R. (eds). (2005). Reproductive ecology of three reef-forming, deep-sea corals in the New Zealand region. Cold-water corals and ecosystems. Springer-Verlag, Berlin. 701-713 p.

Waller, R.G. (ed.) (2005). Deep-water Scleractinia (Cnidaria: Anthozoa): current knowledge of reproductive processes. Cold-Water corals and ecosystems. Springer-Verlag, Berlin. 691-700 p.

- ### Does larval food availability explain the retention of seasonal breeding in bathyal echinoids? An experimental test of Crisp's Rule

  Avery Calhoun, Lauren Rice, Caitlin Plowman, Matt DePaolis, Carmen Reddick, Larry Basch, Craig M. Young

Seasonal breeding is a common strategy amongst shallow-water marine invertebrates where proximate seasonal and periodic cues such as temperature, lunar period, day length, and sunlight intensity synchronize spawning and gametogenic cycles. Crisp's Rule is a long-standing hypothesis that invokes seasonal availability of larval food as the ultimate factor that drove the evolution of seasonal reproduction. Even though deep-sea animals have no access to the seasonal proximate cues found in the euphotic zone, many deep-sea animals whose ancestors came from shallow water still reproduce seasonally. Does Crisp's Rule explain this surprising retention of seasonal breeding in the deep sea? Strongylocentrotus fragilis, a seasonally spawning deep-sea urchin on the Oregon shelf, inhabits a depth range of 100 m – 1200m, with the largest individuals found at 200m. We tested Crisp's Rule experimentally by determining whether larvae are more successful during the spring phytoplankton bloom than during the winter months. We spawned captive adult S. fragilis in May and December of 2020 and cultured the larvae on a diet of wild-caught phytoplankton collected from the mouth of the Coos Bay estuary on the incoming high tide. Larvae were tracked and measured through development and settlement in stirred cultures. Despite a 2-month lag in settlement time, S. fragilis plutei developed and settled when fed naturally lower concentrations of phytoplankton six months out of phase with their typical spring spawning season. Our findings show that Crisp's Rule does not fully explain the retention of seasonal breeding in the life cycle of this bathyal echinoid, though slower development in the winter months would expose larvae to the hazards of planktonic development for a longer period of time.

- ### First insights on the reproductive traits of the vent crab Segonzacia mesatlantica (Guinot, 1989) from the Mid-Atlantic Ridge

  Mariana Cruz, Nadine Le Bris, Ana Colaço

Characteristics on the life-history biology of hydrothermal vent species are a prerequisite to understand the dispersal, population connectivity and ecology of these insular populations. The vent crab Segonzacia mesatlantica (Guinot, 1989; Brachyuran: Bythograeidae) is one of the most dominant indigenous predators at deep-sea hydrothermal vents along the Mid-Atlantic Ridge (MAR). However, the biological life-history characteristics remain poorly understood for this specie. Thus, the objective of this study was to increase the knowledge on the reproductive ecology of S. mesatlantica from the Broken Spur vent field by providing information regarding its gametogenesis (histological analysis), fecundity (manual by hand counter), embryonic and larvae development and the behaviour of brooding females at vent fields (video analysis). According with histological analysis, the oogonia develop into previtellogenic oocytes, and when they grow to a size of 70 µm, vitellogenesis begins. The presence of oocytes at all stages of development in both individuals analysed, suggested a continuous gametogenesis. Brooding females of S. mesatlantica were observed at the vent periphery. Furthermore, a sequence of four behaviours was observed within brooding females, suggesting that they might be providing oxygen to their embryo mass, that is composed by embryos in different stages of embryonic development. Females produce a large number of relatively small eggs, with the release of a prezoea larvae that undergoes through at least four stages of development, which implies a planktotrophic development. This study highlights relevant characteristics on the life- history biology of S. mesatlantica, contributing to a better understanding on its reproductive ecology and the importance for the maintenance of healthy populations.

Evaluating the use of polyp counts to assess size structure trends of a sea pen (Cnidaria: Pennatulacea) from in situ imagery

Bárbara de Moura Neves, Peter Lawton

The use of seafloor imagery in benthic biodiversity studies has increased in recent decades, as imagery is often less invasive than other types of sampling gear, and it can provide data on in situ morphology and behavior. However, it remains challenging to determine the size of organisms that form erect structures, such as sea pens (order Pennatulacea). Sea pens are the focus of conservation objectives in several conservation areas in Canadian waters. Here we used in situ digital still imagery obtained with a downward-looking drop camera system to examine the use of polyp counts as a proxy for size in the sea pen Kophobelemnon sp. in the Laurentian Channel (Northwest Atlantic) Marine Protected Area (MPA). We developed five scores (very low to very high) to assess confidence of polyp counts to assess potential bias. Video annotation included scanning imagery for the presence of colonies along 2-3 parallel transects per station (N = 19 stations), from depths of 341-466 m. Polyps were counted in 611 colonies. However, their number significantly increased with confidence score, which might indicate an underestimation in number of polyps when confidence is not high. We also found a trend of number of polyps decreasing with image field of view (FOV) area. Therefore, only images between 2-4 m2 and colonies for which confidence level was rated as highvery high were retained (N = 120). Number of polyps per colony ranged 2-37 and followed a slightly right-skewed distribution. This study indicates that using polyp counts to estimate Kophobelemnon’s size trends in the Laurentian Channel MPA is possible, although time-consuming. However, employing confidence metrics and focusing on comparable FOV areas early in the video annotation can accelerate the process. Finally, data based on physical specimens are needed to investigate the potential existence of bias due to colony behaviour.

A 16,000 km connection under the sea? Tracing the spread and adaptation of a deep-sea weed: the chemosymbiotic siboglinid Sclerolinum contortum

Magdalena Georgieva, Ana Riesgo, Sergio Taboada, Nathan Kenny, Mari Eilertsen, Hans Tore Rapp, Maria Belen Arias, Nadezda Rimskaya-Korsakova, Adrian Glover

The siboglinid tubeworm *Sclerolinum contortum* is renowned for its ability to colonise a variety of deep-sea habitats where reduced chemicals dominate, such as hydrothermal vents and cold seeps, as well as for its remarkable range, which spans the Arctic to the Antarctic. It apparently achieves this through characteristics typical of weeds, such as broad habitat preferences, tolerances, and wide dispersal capability. However, the ability to colonise such a vast range is highly unusual, even in an environment as seemingly continuous as the deep ocean. Here, we apply population genomic, transcriptomic, and microbiome analyses in S. contortum and the closely-related species *S. brattstromi*, to explore in greater resolution the connectivity of *S. contortum* populations, and how individuals from various reduced environments have adapted to diverse settings. Our findings indicate a lack of gene flow between the two polar oceans, with Southern Ocean S. contortum individuals being distinct to others, but found greater support for connectivity between the Gulf of Mexico and the Arctic. Our results also suggest a retention of similar adaptive traits despite separation by distance, and irrespective of habitat type, further supported by selection of the same endosymbiont despite geographic location or chemosynthetic habitat type in *S.* contortum. Transcriptomic data indicate that adaptation to local habitat conditions likely occurs through the activation of key genes involved in responding to environmental characteristics at the different sites, such as the heat response, nitrate assimilation, and denitrification processes. Our findings represent one of the most comprehensive investigations into a widespread deep-sea taxon, and suggest that pre-adaptation as well as adaptive plasticity are key weedy/invasive characteristics that favour the successful colonisation of new habitats for S. *contortum.*

Diversity of western pacific back-arc basins invertebrates reevaluated through a barcode approach – Results on decapods and polychaetes

Ambre Chabert, Valérie Cueff-Gauchard, Marie-Anne Cambon, **Stéphane Hourdez**

Western-Pacific hydrothermal thermal vent communities form an apparently homogeneous biogeographic province. The CHUBACARC cruise (May-June 2019) sampled different communities in the Futuna volcanic area, and the Manus, Woodlark, North Fiji, and Lau Basins. It aimed at investigating the connectivity within and between basins to determine whether a finer-grain structure existed. Based on morphology, some species are indeed reported from all Western Pacific back-arc basins and this has implications in the management and conservation of these unique ecosystems. The recent push towards the exploitation of deep-sea mineral resources has brought the scientific community to identify and target knowledge gaps in our understanding of species distributions, discovery of cryptic species, and connectivity studies. Our current knowledge on mid-oceanic ridges already points to great differences depending on spreading speeds, and chemistry of the vent fluid. The back-arc basins however, form a complex situation, potentially limiting larval exchange. In addition, most of the earlier studies were focused on emblematic or very abundant taxa, with very few or no studies on less abundant taxa. These studies have already pointed to major differences in species distribution depending on the considered taxon, pointing to the need for more case-by-case studies. We studied decapods and polychaetes, and sequenced the mitochondrial barcode marker COI for a total of over 600 specimens from different sites in all 5 areas visited during CHUBACARC. We show that some morpho-species actually correspond to complexes of species (i.e. cryptic species). Some of the species studied have distributions that are limited to a single basin, while others are found in multiple basins in the area. When the number of individuals sequenced was sufficient, we used population genetics analyses and found that all species considered exhibited evidence of a passed demographic bottleneck followed by population expansion

Comparative reproductive biology of deep-sea ophiuroids inhabiting polymetallic-nodule fields in the Clarion-Clipperton Fracture Zone

Sven R Laming, Magdalini Christodoulou, Pedro Martinez Arbizu, Ana Hilário

Deep-sea mining in the Pacific Clarion-Clipperton Fracture Zone (CCZ), a low-energy sedimentary habitat with polymetallic nodules, is expected to have considerable and longlasting environmental impact. The CCZ hosts extraordinarily high species diversity across representatives from all Domains of Life. Data on species biology and ecology remain scarce, however. The current study describes the reproductive biology of two ophiuroids frequently found in the CCZ, *Ophiosphalma glabrum* (Ophiosphalmidae) and *Ophiacantha cosmica* (Ophiacanthidae), collected in 2015 and 2019 from four contract areas. Size-class frequencies (disc diameter and oocytes feret diameters), sex ratios, gametogenic status, putative reproductive mode and a simple proxy for fecundity are presented. While *Ophiosphalma glabrum* is epibenthic, occurring as single individuals, Ophiacantha cosmica often form size-stratified groups living on stalked sponges, suggesting gregarious settlement or retention of offspring (though no brooding individuals were found). In both species, individuals were at various stages of gametogenic maturity, but no ripe females were identified. While *O. glabrum* is likely gonochoric, reproductive mode was less conclusive for Ophiacantha cosmica. Both species are presumptively lecithotrophic, with vitellogenicoocyte feret diameters exceeding 250 µm. Oocyte feret diameters at times exceeded 400 µm in *Ophiosphalma glabrum*, indicating substantial yolk reserves. Estimates of instantaneous fecundity (vitellogenic specimens of O. *glabrum* only) were confounded by interindividual variability in gonad characteristics. Well-furnished lecithotrophic larvae of O. glabrum would be capable of dispersing even under food-impoverished conditions. The current study examines ophiuroid reproductive biology over multiple localities in the CCZ concurrently for the first time, at sites characterised by differing productivity regimes. The reproductive biology of each species is thus discussed with reference to past evolutionary (habitat stability), contemporary (food supply) and future environmental drivers (potential impacts of deep-sea mining.

Development of a shipboard high-pressure plankton observatory (HIPPO) for investigating swimming behaviors of deep-sea larvae

Lauren Mullineaux, Stéphane Hourdez, Helen Fredricks, Susan Mills, Lauren Dykman, Michelle DiBenedetto, Shawn Arellano, Ahna Van Gaest, Caitlin Plowman

Swimming behavioural responses of deep-sea plankton reveal important insights into their ecology, including interactions with the environment, feeding, and response to predators. Many species from deeper than 1500 m, however, cease swimming when brought to surface pressure. We have developed a high-pressure system (HIPPO) that allows for shipboard observation of swimming behaviours at ambient deep-sea pressure. The system comprises a pressure chamber originally designed for physiological studies and a pump with tubing, valves, gauges, and fittings designed for high-pressure liquid chromatography (HPLC), combined with a high-resolution Basler digital video camera and an IR light source. Critical design criteria include keeping the plankton alive, active, and in the field of view, orienting the lighting to reveal details of the plankter morphology, and recording sufficient numbers of plankter tracks to analyse swimming metrics. We tested the system aboard the R/V Roger Revelle during a cruise in March/April 2021 to deep-sea hydrothermal vents near 9°N on the East Pacific Rise. We recovered plankton from near vents (2500 m depth) in a high-volume McLane pump, brought to the surface in an insulated filter chamber, and immediately placed in chilled seawater in an environmental chamber at 4°C. Motile larvae of benthic vent species were transferred into the pressure chamber, along with 10-15 fast-moving copepods that were useful for optimizing the video image, and brought up to pressure over 30-60 minutes. Video images recorded in the dark with IR illumination showed many swimming tracks of copepods, a few extended tracks of helically swimming vent polychaete larvae, and short bursts of a *Bythograea microps* megalopa. We are in the process of categorizing and quantifying these behaviours using image analysis code in Matlab, and further optimizing the design of the chamber and lighting for future experiments.

Did the experimental seafloor disturbance affect deep-sea nematode biological traits patterns? An example from the Clarion Clipperton Fracture Zone (CCFZ) (subequatorial NE Pacific)

Teresa Radziejewska, Valentina Galtsova,

Joanna Rokicka-Praxmajer, Kamila
Mianowicz

Biological traits of metazoans reflect the extent of functional differences among taxa in a community and are indicative of resource use complementarity, thus providing a link between biodiversity and ecosystem functioning. Biological Traits Analysis (BTA) aims to describe functional aspects based on features expressed by specific traits and explores the occurrence of these traits over assemblages. It uses multivariate ordination techniques to describe patterns of trait occurrence and frequency in assemblages. We applied BTA to assemblages of deep-sea nematodes, a major component of the metazoan meiofauna on the abyssal seafloor to address the following questions: 1) was the high genus-level taxonomic diversity of the abyssal nematode assemblages reflected in their functional complexity? 2) did the experimental sediment disturbance affect the BTA patterns immediately and after disturbance? and 3) did a temporal shift in resource availability affect the functional structure of the assemblages? In our analysis, the traits assumed as representative of different functions included buccal cavity structure, tail shape, adult size, adult shape, and life history strategy. The nematode assemblages analysed were sampled from 4200-4300 m depth in the eastern part of the Clarion-Clipperton Fracture Zone (CCFZ) (subequatorial NE Pacific), an area known as an extensive polymetallic nodule field. The samples were collected from a nodule-free patch of the seafloor prior to an experimental seafloor disturbance as well as immediately and 22 months post-disturbance. The analysis demonstrated the functional diversity of the taxonomically complex (a total of about 230 genera) assemblages to be relatively low, the assemblages showing a fairly stable set of persistent traits. The trait set was found to be more sensitive to a change in environmental conditions represented by phytodetritus sedimentation than to the effect of the seafloor disturbance produced.

We acknowledge the support of the Polish National Science Centre grant No. 2014/13/B/ST10/02996.

Comparisons of Reproductive Output and Isotopic Signatures in a Facultative Hyper-epibiotic Polychaete from Methane Seeps in the Gulf of Mexico

Lauren N. Rice, Oregon Institute of
Marine Biology, University of Oregon
(United States), lnr@uoregon.du Craig M.
Young

Biodiversity in siboglinid tubeworm aggregations is well understood to increase over time, with late stage bushes of the siboglinid worm Lamellibrachia luymesi becoming encrusted with hydroids, sponges, serpulid polychates, and other epibotic species. At several cold seep systems within the Gulf of Mexico, an undescribed sabellid polychaete has been observed within both the authigenic carbonate and the valves of the epibiotic Acesta oophaga file clam. As the two settlement locations exhibited by the unknown sabellid are different in height and settlement substrate within the seep communities, this facultative hyper-epibiont provides a unique opportunity to investigate whether epibiosis confers advantages in reproductive output. Specimens were collected from the cold seep systems at Bring Pool NR-1, Bush Hill, and Green Canyon 234 within the Gulf of Mexico using HOV Alvin and the ROV Jason in February 2020 and June 2021. We used histological technique and δ 13C and δ 15N isotopic analysis to examine and compare aspects of the reproductive biology and nutrient sources between epibiotic and free-living individuals of the unidentified sabellid. Preliminary isotopic results indicate slight differences in δ 13C between seep sites and some significant differences in δ 15N between epibiotic and free-living individuals within site locations. A stronger chemosynthetic signal was detected in specimens collected from Brine Pool NR-1 while individuals from Bush Hill seemed to have a stronger photosynthetic signal. Initially observed specimens were gonochoristic and early reproductive data have shown an average oocyte size of 92.5 µm with an observed maximum of 238 µm. This study seeks to provide a detailed look at inter- and intra-site variability in reproductive output and nutrient sources to quantitatively determine how epibiotic organisms alter their lifehistory strategies to accommodate life on biological substrata.

Bioenergetic modelling of a deep-sea bivalve, Christineconcha regab

Marine Vandenberghe, Sylvie Marylène
Gaudron, Gonçalo Montairo Marques,
Ann Andersen, Karine Olu, Carole
Decker, Sébastien Duperron

Christineconcha regab, *Cosel* & *Olu* 2009 (Mollusca, Bivalvia, Vesicomyidae) has been discovered and named from the Regab pockmark deep-sea cold seeps located in the Gulf of Guinea, along the Congo continental margin. Cold seeps are extreme environment with the release of chemically reduced compounds. Striving for life in those extreme conditions and to take advantage of this chemical energy, *C. regab*, like the dominant bivalves in deep-sea cold seeps and other chemosynthetic habitats, evolved to live with symbiotic autotrophic bacteria providing nutrients to their hosts. The bacterial symbiont of *C. regab* is a thiotroph (sulfur-oxidizer) and is maternally transmitted to offspring as has been shown for other species of the vesicomyid family. When adults, vesicomyids are strictly symbiotrophic and have a reduced digestive tract. Up to now, there are only very few Dynamic Energy Budget (DEB) models in the Add-my-Pet database available for deep-sea benthic invertebrates, and no DEB model on strictly deep-sea symbiotrophic species. We aim to use the *C. regab* symbiotic relationship to develop a DEB model suitable for symbiotic organisms from chemosynthetic ecosystems in order to gain insights into dispersal, growth, lifespan, maximum body size and generation of offspring of deep-sea organisms like Vesicomyidae. Preliminary results based on the conceptual model will be presented here.

Biogeography of deep-sea hydrothermal vent copepods on the Izu Bonin Arc, northwestern Pacific

Hiromi Kayama WATANABE, Daisuke
UYENO, Kento KAWATANI, Tomo
KITAHASHI, Hidetaka NOMAKI, Chong
CHEN, Motohiro SHIMANAGA

Copepods are abundant as plankton, benthos, and symbiont in marine ecosystems. Their community dynamics are thought to be correlated with environmental conditions, and are thus often used as indicator taxa. In the deep ocean, however, much remains to be learned about the distribution range of each species and how much closely related species vary in their dispersal ecology. Hydrothermal vent is an island-like habitat type in the deep seafloor characterized by high productivity and patchy distribution. Vent copepod communities are mixtures of vent-specific and deep-sea generalistspecies, and studying vent-specific copepods in various sites within a biogeographic region can provide key knowledge on the connectivity and dispersal capabilities of deep-sea copepods. Here, we present an updated distribution of vent copepods in the western Pacific and discuss the differences in dispersal capabilities among species based on the mitochondrial COI gene, with a focus on the vent-specific family Dirivultidae. We found high interspecific sequence divergences of over 80/560 bp (14 % or 0.166 in Kimura 2-parameter distance) in the family, while the intraspecific divergences were below 10/560 bp (2 % or 0.018 in Kimura 2-parameter distance); demonstrating a clear barcoding gap among species. These results allowed us to assess their larval dispersal potentials and the barcodes also enabled us to identify different life stages of the same species. Furthermore, phylogenetic reconstruction based on the same gene indicated that some genera defined on morphological basis may be non-monophyletic. Further sampling is required to fill the spatial gaps to elucidate the biogeography and evolution of dirivultids and other copepods in the global deep ocean.

- ### Divergence population genetics of bacterial symbionts of hydrothermal vent mussels

  Sook-Jin Jang, Yujin Chung, **Yong-Jin Won**

Geographical connectivity of vent species (especially benthic invertebrates) is determined by both biotic factors (life historical characteristics related to larval dispersibility) of the species and abiotic factors (e.g. ocean flow, lateral offset, temporal stability of vents) acting at various geographical scales. Notwithstanding long studies of vent animals, population diverging processes of their symbiotic bacteria remains largely unexplored at a regional scale. In this study, we targeted dominant symbionts in gill-associated bacterial community of hydrothermal vent mussel, sulfuroxidizing bacteria, and obtained sequence data of multi-locus using species-specific DNA primers. The goal of our study is to investigate diverging processes of symbiont populations based on genetic structure observed in different spatial scales. We studied from local and regional scales in the Central Indian Ridge (CIR) to global scale by comparing the results of the CIR and the East Pacific Rise (EPR). In the CIR, DNA sequences of six protein-coding genes of symbiont populations exhibited Isolationby-distance pattern between pairwise nucleotide differences (Dxy) and geographical distance. Isolation with Migration analyses (IMa3), a kind of genetic model for diverging populations, supported the phylogeny with the northern Onnuri Vent Field population as a remote sister to the southern Solitaire and Kairei populations, which was consistent in both host species and symbiotic bacteria. Especially, the estimated pattern of gene flow among bacterial populations accorded with deep-ocean currents flowing northward below 2,500 m depth near the central ridge. At a global scale, estimates of Dxy between vent fields were much greater in the CIR than the EPR, which suggests that the geological settings in the ridge systems affect population dynamics of bacterial symbionts as well as vent animals.

General & Special Sessions 4

Adaptations of deep-sea organisms (from molecules to organisms: how life adapt to extreme conditions)

General session

- ### A second scaly snail: Hard dermal sclerites of the vent gastropod Ifremeria nautilei

  Chong CHEN, Satoshi OKADA, Hiromi Kayama WATANABE, Katsuyuki UEMATSU, Noriyuki ISOBE

Deep-sea hydrothermal vents are ‘extreme’ habitats that require adaptive novelties for animals to conquer successfully, most notably endosymbiosis with chemoautotrophic bacteria. The vent provannid snail *Ifremeria nautilei* hosts a sulfur-oxidising bacteria in gill bacteriocytes, and is also known for brooding a unique larval form named the “Warén’s larva” – two aspects of its biology that have attracted considerable attention. A much overlooked yet striking morphological feature of *Ifremeria* is the numerous ‘warts’ on the surface of its foot, only briefly mentioned in the literature and its exact nature has not been examined. Here, we show that these ‘warts’ are in fact chitinous dermal sclerites and a novel hard structure specific to this species. Dissection, sectioning, and micro- computed tomography revealed each ‘wart’ to be a bundle of several narrow sclerites, connected by occasional bridge-like structures. The base of each sclerite contains a core filled with soft pedal tissue that probably carries out secretion. Periodic acid Schiff (PAS) staining indicated the sclerites are mostly made from polysaccharides, identified as chitin by microscopic FT-IR (transmission Fourier- transform infrared) spectroscopy. This makes I. *nautilei* the second living gastropod species secreting dermal sclerites, after the phylogenetically distant peltospirid Scaly-foot Snail *Chrysomallon squamiferum* which is also vent-endemic and relies on endosymbiosis. Sclerites in the Scaly-foot Snail have been shown to act as sites of detoxification by excreting sulfur waste and the presence of a similar, yet clearly analogous, structure in *I. nautilei* is suggestive of similar function. The discovery of a second living gastropod lineage with convergent dermal sclerites highlights the capacity of molluscs, and lophotrochozoan animals in general, to rapidly evolve novel hard parts for various reasons – cautioning against the use of scleritome as evidence for homology in the interpretation of scaly Cambrian fossils such as *Wiwaxia* and *Sinosachites*.

- ### Anatomical studies of Desmosomatidae (Isopoda) using X-ray microtomography

reveal functional adaptations to abyssal environments

Patricia Esquete, Marina R. Cunha

Biological adaptations of faunal species are related to ecological aspects of their benthic lifestyle. In abyssal plains where resources are scarce, the presence of sensory organs, mobility, and the capacity to store and mobilize key chemical elements are particularly relevant traits for species survival and reproduction.

Here, we studied the internal and external anatomy of isopods of the family Desmosomatide using 3D and 2D images obtained by means of micro-CT imaging as a tool for unveiling the biology of deepsea species from a manganese nodules area of the Clarion-Clipperton fracture zone . The ethanolpreserved specimens were scanned after treatment with hexamethyldisilazane, and then stained with iodine in order to obtain a higher definition of the least electrodense tissues. Variations in density throughout the exoskeleton and internal organs were enhanced using pseudo color filters. EDX microscopy and ICP analyses provided further details on the presence of chemical elements in selected structures.

Observed density variations in the exoskeleton corresponded with the functionality of the various areas of the body: the cuticle appeared visibly demineralized in areas with sensory organs, genital openings, or along walking limbs, while calcium deposits were located in the inner face of the pereonites. On the other hand, the digestive, nervous and circulatory systems were well visible in 2D and 3D images and showed genus-specific morphologies of the hepatopancreas, guts, and brain. Chemical analyses of the digestive glands revealed inorganic elements accumulation. These results demonstrate the relevance of the study of the anatomy of deep-sea organisms for a better understanding of their biology and to infer their role in the ecosystem and potential responses to environmental changes.

- ### Glutamate optimizes enzymatic activity under high hydrostatic pressure in Desulfovibrio species: effects on the ubiquitous thioredoxin system

Hélène Gaussier, Matthieu Nouailler, Marc Garel, Christian Tamburini, Alain Dolla, Nathalie Pradel

In piezophilic microorganisms, enzymes are optimized to perform under high hydrostatic pressure. The two major reported mechanisms responsible for such adaptation in bacterial species are changes in amino acids in the protein structure, favoring their activity and stability under high-pressure conditions, and the possible accumulation of micromolecular co-solutes in the cytoplasm. Recently, the accumulation of glutamate in the cytoplasm of piezophilic *Desulfovibrio* species has been reported. Analysis of the effect of glutamate on the enzymatic activity of the thioredoxin reductase/thioredoxin enzymatic complex of either a piezosensitive or a piezophilic microorganism confirms its role as a protective co-solute. Analysis of the thioredoxin structures suggests an adaptation both to the presence of glutamate and to high hydrostatic pressure in the enzyme from the piezophilic strain. Indeed, the presence of large surface pockets could counterbalance the overall compression that occurs at high hydrostatic pressure to maintain enzymatic activity. A lower isoelectric point and a greater dipolar moment than that of thioredoxin from the piezosensitive strain would allow the protein from the piezophilic strain to compensate for the presence of the charged amino acid glutamate to interact with its partner.

- ### Relationship status – it's complicated: Vent fluid chemistries constrain host-endosymbiont dynamics in Alviniconcha hessleri

Nova B. Hanson, Suzanne C. Dufour, Amanda E. Bates

Hydrothermal vents occur across geologically distinct settings resulting in hydrothermal fluid chemistries that can vary spatially and temporally. Even vents in close proximity can present different fluid profiles and thus different environments for invertebrate communities. Many species that span across multiple vents and fluid profiles host nutritional bacterial symbionts that depend upon the reduced chemicals in vent fluids. Thus, vent systems provide an opportunity to understand how hydrothermal fluid chemistry can determine host-endosymbiont dynamics. The energetic inputs from the symbiont to the host are constrained by the fluid chemistry, which dictates both the productivity of the symbiosis and the energetic costs to the host living in a highly variable and often hostile environment. Therefore, species that occur across vents which vary markedly in fluid chemistry may exhibit different fitness outcomes. To investigate this, we focused on *Alviniconcha hessleri sensu stricto*, Hessler's Punk-rock Snail, a species restricted to hydrothermal vent fields located along the Mariana Back-arc. This back-arc experiences differences in spreading rate across its length, resulting in hydrothermal vents with effluents that range widely in temperature, pH and metal concentrations. *Alviniconcha hessleri sensu stricto* relies on the energy provided by chemoautotrophic endosymbionts, which inhabit their enlarged gill tissues. We predict a relationship between vent fluid chemistry, population characteristics and reproductive allocation based on energetic trade-offs. To assess spatial variation in energy allocation to reproduction, we examined population size structure, gonad morphology and gametogenesis in *A. hessleri s.s.* collected from five hydrothermal vents along the Mariana Back-arc. Overall, histological sections and size-structure data indicate that *A. hessleri s.s.* exhibits hermaphroditism with continuous reproduction despite apparent periodic recruitment. Our findings suggest that the energetic cost of living in more stressful vent fluids may limit the productivity of the symbiosis and allocation to reproduction by imposing high physiological or maintenance costs.

- ### Rainbow bodies: revisiting the diversity of coelomocytes and aggregates across subtidal and deep-sea echinoderms

Sara Jobson, Jean-François Hamel, Annie Mercier

The innate immunity of echinoderms has consistently provided ever deeper knowledge of its complexity and evolutionary aspects. The basal elements of the echinoderm immune system are coelomocytes, which are diverse cells capable of responding in a variety of ways, including via movement, phagocytosis, aggregation, and encapsulation. However, features of cellular immunity have never been compared in echinoderms from phylogenetic and distributional perspectives, to provide insight into ecological and evolutionary patterns. Particularly challenging is the inclusion of deep-sea echinoderms to create a comprehensive survey of immune agents in species living in extreme environments. The present study catalyzed and characterized the formation of coelomocyte aggregates in all five extant classes of echinoderms using a standard method, including nine deep-sea species. The morphological characteristics (shape, texture, size) and major cellular components of the aggregates were described. Coelomocyte presence (in free and aggregated forms) was compared across deep-sea and subtidal species. The diversity of these cells was determined to be the highest in Holothuroidea and the lowest in Crinoidea. The colors of coelomocyte aggregates appeared to be more closely linked to phylogeny rather than geographic range, with Asteroidea, Crinoidea and Ophiuroidea displaying colors from transparent to green and red aggregates, while Echinoidea and Holothuroidea demonstrated purple and red variants. The findings show coelomocyte aggregate formation is a conserved innate immune response across echinoderms and across depths, with important variations in the complexity, shape and size of implicated cells.

• Exploring Chemical Peptide Diversity from the mucus of the Deep Sea Scavenger Parborlasia corrugatus

Quentin Laborde, Erik Jacobsson, Håkan Andersson, Ulf Göransson

Parborlasia corrugatus (McIntosh, 1876) is a marine worm from the Nemertea phylum known to be a source of peptide and protein toxins. This marine ribbon worm can live in environment down to 3 500 meters below sea level and can be found mostly in cold southern oceans. Life in such environments raises challenges for marine organisms both as prey and predator. Therefore, P. corrugatus survives by being a scavenger, a top predator and non-palatable to other known predators. The most likely explanation for its success is the presence of mucus secretions surrounding *P. corrugatus* epidermis. Previous investigations have permitted to detect presence of 10 kDa cytolysins named parabolysins in *P. corrugatus* mucus epidermis secretions. Parabolysins, larger neurotoxic peptides and smaller cysteine knot containing peptide toxins have also been found in other species of Nemertea (Lineus longissiumus & Cerebratulus lacteus), however, no recent study has been performed on the two latest for *P. corrugatus*. Discovery and characterization of potential peptide toxins among *P. corrugatus* mucus would help to decipher its successful survival in deep-sea environment giving better understanding about its interactions within the ecosystem. Here, will be presented the intended workflow allowing chemical investigation of peptide toxins in *P. corrugatus* mucus epidermis secretions.

• Hemoglobins are a keystone adaptation for deep-sea hydrothermal vent scaleworms

Victor Le Layec, Stéphane Hourdez

Deep-sea hydrothermal vents are characterised by extreme and chaotic thermal and chemical conditions. In these environments, the cold and highly oxygenated deep-seawater mix with the hot, anoxic and hydrothermal fluid that also contains toxic compounds. This creates niches where the oxygen availability is very low and where the temperature fluctuates from 250°C to 4°C over a 10-cm distance, although metazoa only occupy the lower range up to temperatures of about 50˚C. Many annelid species living in those particular environments have developed specific adaptations that set them apart from their close relatives from other marine environments and allow them to survive and thrive in hypoxic conditions or even in temporary anoxia. Thisstudy isfocused on differentscaleworms species (Annelida, Polynoidae) which are endemic to deep-sea hydrothermal vents and have shallow water relatives that we used as references. Although living under chronic hypoxia, hydrothermal vent species have consumption rates similar to temperate species. To meet this demand, vent species have developed specific adaptations, including the presence of gills in some species while shallow water species are devoid of them and presence of circulating hemoglobin, lacking in allshallow waterspecies. Vent species also exhibit a capacity to oxyregulate while shallow-water species oxyconform. This capacity is not linked to the presence of gills but the presence of circulating hemoglobins is necessary. The sheer presence of hemoglobin can allow the individuals to withstand periods of complete anoxia.

• Genomic adaptations of cold-water corals to low calcium carbonate saturation

Michelle L. Neitzey, Kate R. Castellano, Timothy M. Shank, Rachel J. O'Neill

Low calcium carbonate saturation is a unique constraint of the deep sea. Because of increased hydrostatic pressure and low temperatures, the solubility of calcium carbonate increases with ocean depth, making it harder for corals to build their skeletons. It is known that some corals (order Scleractinia) are able to overcome this low saturation by using ATPase pumps to create a high pH internal environment, and others (subclass Octocorallia) utilize calcite, the more stable polymorph of calcium carbonate. Cold-water corals represent 65% of coral species, provide habitat for other animals, and are highly impacted by anthropogenic activities. However, the effects of low calcium carbonate saturation on deep-sea corals have yet to be investigated at the genomic level. To enable comparative genomics studies, we have developed the first deep-sea coral genome from the Primnoidae family using short and long-read sequencing technologies. Primnoid species exhibit one of the greatest depth ranges for calcifying coral families, making them an excellent candidate for comparing genomic adaptations across pressure, temperature, and alkalinity with depth. Assembly pipeline, correlative transcriptome data analyses, and preliminary comparative analysis of biomineralization toolkits between shallow and deep corals will be presented. Future research will focus on comparative analysis with a shallow primnoid genome to minimize evolutionary distance as a confounding variable, and comparison of non-coding regions.

• How do hydrothermal vent shrimp cope with extreme temperature fluctuations?

Juliette Ravaux, Nelly Léger, Gérard Hamel, Bruce Shillito

The deep-sea hydrothermal vents host species that must cope not only with extreme temperatures, but also with a thermal environment that has the highest variability among all aquatic habitats. The vent shrimp Rimicaris exoculata, an emblematic species of the Mid-Atlantic Ridge sites, thrives in the chaotic mixing zone of warm hydrothermal fluids with cold abyssal seawater, with large amplitude temperature variations over short spatial and temporal scales. This species must therefore have evolved molecular mechanisms and/or behavioral strategies to cope with extreme temperature fluctuations, as well as the constant threat of exposure to deleterious temperatures.

We assessed the shrimp thermal tolerance using a compilation of multiple parameters such as species thermal limits, thermal behavior, as well as molecular response to thermal stress. While the thermal limits of R. exoculata define this species as neither a heat specialist nor a thermophilic species, the molecular response thresholds clearly reflect a high thermotolerance in this species. However, this heat stress response was found to be rarely triggered in natural populations, which would be due to thermoregulatory behavior of shrimp swarms. We were thus able to highlight the complementarity of strategies involved in the response of this species to heat stress at scales ranging from the molecular to the population level.

- Removal mechanisms of embedded ribonucleotides in DNA from deep-sea archaeal microorganisms

Maurane Reveil, Lucie Chapel, Blandine Vourc'h, Pierre Raia, Ludovic Sauguet, Yann Moalic, Mohamed Jebbar, Ghislaine Henneke

Ribonucleotides (rNMPs) are the main non-canonical nucleotides into genomic DNA. Indeed, rNMPs can be incorporated into DNA by DNA polymerases of the three domains of life during DNA synthesis. Embedded rNMPs in DNA can be used as positive signals (e.g. mating-type switching in yeast, nascent strand recognition during the mismatch repair). However, if rNMPs are not removed from the DNA they can cause genomic instabilities. Ribonucleotides removal mechanisms are well documented in eukaryotes and bacteria but are still unclear in archaea. We aim to study the removal mechanisms of embedded rNMPs in archaeal DNA. First, replicative DNA Polymerases possess several mechanisms to avoid rNMP incorporation during DNA synthesis: a steric gate allowing the discrimination between rNTPs and dNTPs and a proofreading exonuclease activity that corrects mismatches. The exonuclease activity of some eukaryotic DNA Polymerases can also excise misincorporated rNMPs. Our model, the deep-sea euryarchaea Pyrococcus abyssi, possesses 2 replicative DNA Polymerases: a family B DNA polymerase (PolB) and a family D DNA polymerase (PolD). We assessed the ability of euryarchaeal exonuclease activity of these two DNA Polymerases to correct rNMPs. To study the contribution of proofreading exonuclease activity on rNMP processing, we compared the ability of wild type and exonuclease-deficient PolD and PolB to remove rNMPs into DNA. The results indicate that the exonuclease activity of PolD is more efficient than PolB in editing newly inserted rNMP at terminal primers. According to our structural data, this difference cannot be accounted by physical constraint of rNMP into the exonuclease active site. Secondly, we studied the Ribonucleotide Excision Repair (RER) pathway in vitro in euryarchaea. The RER pathway was reconstituted with both PolB and PolD to assess their involvement in this pathway. Preliminary results show that RER pathway seems more efficient with PolB than PolD, suggesting a conserved mechanism in deep-sea archaea.

- Lipidome variations of deep-sea vent shrimps acclimated to atmospheric pressure: A homeoviscous response?

Bruce Shillito, Céline Desurmont, Dominique Barthélémy, Dominique Farabos, Gaëtan Després, Juliette Ravaux, Magali Zbinden, Antonin Lamazière

Comparison between deep and shallow marine species point at a number of biological features which respond to pressure conditions, and the molecular composition of biological membranes is one of them. During the AbyssBox project at the Océanopolis aquarium, deep-sea vent shrimps (Mirocaris fortunata) originating from 1800m depth were acclimated for several months at their natural pressure (18 MPa). Remarkably, these animals also proved capable of acclimation at atmospheric pressure. The present work questions the ability of these shrimps to modulate the molecular composition of their membrane lipids, as a function of acclimation pressure. In particular, it is shown that shrimps exposed to atmospheric pressure exhibit a significantly lower level of the mono-unsaturated fatty acid, vaccenic acid (C18:1n-7), compared to those maintained at natural pressure. The observed fatty acid variations are consistent with a homeoviscous response, i.e. a modulation of the lipidome composition, in response to physical constraints, in order to balance the effects of pressure on membrane order. Additionally, supervised multivariate data analysis was performed for complex lipids and revealed an increase in levels of sterols, sphingomyelins, and etherphosphatidylethanolamine lipids for animals exposed to atmospheric pressure. These observations strongly suggest that lipidic domains (so-called « rafts ») are involved in the shrimp's response to experimental conditions, and thereby support the emerging view that the homeoviscous response is probably more complex than described up to now, and that it is not only a matter of fatty acid composition. Overall, the observed lipidomic response undoubtedly illustrates an acclimation process, and the phenotypic plasticity of these organisms regarding environmental variations.

- Brain morphology and sensory specialisations in lanternfishes

Jasper Stead, Kara Yopak, Justin Marshall, Fanny de Busserolles

Due to limited access, resources, and the difficulty in performing in-situ experiments, the behavior and ecology of most deep-sea organisms remains a mystery. In many cases, the study of sensory systems can be used to inform the behavior of these animals. In teleosts, the size and complexity of major brain areas is often used as a proxy for sensory specialisation and behavior. Myctophidae (lanternfish) is one of the most abundant families of mesopelagic fishes. Recently, their visual system was investigated in detail and results showed a great interspecific variability in eye designs at all levels, suggesting that some species might rely more on vision than others. To confirm this and predict the relative importance of other sensory systems in lanternfishes, we assessed the diversity in brain morphology in ~ 50 species of lanternfishes, representing more than 50% of the currently recognised genera. For each species, the volume of the optic tectum, olfactory bulbs, octavolateralis area, and facial/vagal lobes, which receive primary afferents relating to vision, smell, audition/lateral line, and gustation, respectively, were measured. Two key sensory integration areas, the telencephalon and the cerebellum, were also analysed. Similar to the visual system, preliminary results show a great diversity in brain morphology and size between species, even at the genus level. Based on relative development of major brain regions, some species appear to be clear visual specialists, while others likely rely more on their lateral line/auditory systems and/or gustation. Using phylogenetic comparative analyses, relationships between patterns of brain organization and ecological parameters (i.e. depth and migration pattern, bioluminescence, sexual dimorphism) will also be assessed, considering the evolutionary history of the family. This study will shed some light on the ecology and behavior of the lanternfish family as well as expand our knowledge about the evolution of sensory systems in the deep-sea environment.

Morphological investigations into the calceoli of selected Amphipoda (Crustacea)

Roxana Timm, Alexandra Kerbl, Anne-Nina Lörz

Although calceoli have been known for almost 200 years and an otherwise comprehensive understanding of the sensory organs of crustaceans exists, their function is still unclear. Calceoli occur in limnic, marine and subterranean amphipods. They are mainly found on the antennae of male animals. For this reason, previous studies suggested a chemosensory function mainly related to reproduction. In later studies, the theory was put forward that the calceoli could be vibro-sensors, as none of the previous studies were able to detect any innervation. To further develop the vibrosensor theory, the calceoli were examined in this study using a combination of microscopic techniques. Thereby a detailed overview of the structure of the calceoli for *Gammarus locusta* (Linnaeus, 1758) and *Oediceroides calmani* Walker, 1906 was provided for the first time. In addition, nerves underneath the calceoli were found, further supporing the vibrosensor theory.

Special session 4a#: Vision in the deep ocean.pdf – Stenvers

The rod-like cone retina of mesopelagic fish larvae suggests a new visual developmental pathway in vertebrates

Lily Fogg, Fabio Cortesi, Stamatina Isari, Justin Marshall, Fanny de Busserolles

Most vertebrates have two types of retinal photoreceptors, rods for dim-light (scotopic) vision and cones for bright-light (photopic) vision. During development, most vertebrates start with a cone-dominated retina, well suited to photopic conditions, with rods added separately at a later stage. This aligns well with the ecology of most marine fishes, which start their lives in the brightly lit upper pelagic ocean. However, mesopelagic fish larvae inhabit slightly deeper waters and experience intermediate (mesopic) light conditions that usually require both rods and cones, before migrating to the scotopic deep-sea environment during development. Whether they deviate from the typical vertebrate devolopmental trajectory to permit mesopic vision from early stages is largely unknown. To investigate this, we studied visual gene expression and retinal morphology in larvae and adults of three mesopelagic species: *Vinciguerria mabahiss*, *Maurolicus mucronatus* and *Benthosema pterotum*. Results show that larval *V. mabahiss* exclusively expressed the green-sensitive cone opsin, RH2, while adults only expressed the rod opsin, RH1. However, at the ultrastructural level, all photoreceptors had rod-like features, irrespective of developmental stage. This implies that instead of having "true" rods or cones that are well suited to scotopic and photopic conditions, respectively, larval *V. mabahiss* combine the characteristics of both cell types into a single rod-like cone, likely to optimise vision in mesopic conditions. Adults, on the other hand, only have "true" rods, adapted for scotopic conditions. Similar results were found in *B. pterotum* and *M. mucronatus* but with less extreme changes over development. Therefore, the visual systems of mesopelagic fishes are well suited to their respective environments at all stages, with larvae deviating from the classical developmental pathway to achieve this. These findings challenge our understanding of vertebrate visual development and suggest that mesopelagic fishes may have evolved a unique developmental pathway for life in dimmer waters

Visual gene expression reveals a cone to rod developmental progression in deep-sea fishes

Nik Lupše, Fabio Cortesi, Marko Freese, Lasse Marohn, Jan-Dag Pohlmann, Klaus Wysujack, Reinhold Hanel, Zuzana Musilova

Many deep-sea fishes use only rod cells in retina in their visual system. Both rod and cone genes are, however, preserved in their genome. As deep-sea fish larvae start their lives in the shallow, well-lit epipelagic zone, they have to cope with diverse environmental conditions during ontogeny. Using a comparative transcriptomic approach in 20 deep-sea species from eight teleost orders, we report on a developmental cone-to-rod switch and we show that while adults mostly rely on rod opsin (RH1) for vision in dim light, larvae almost exclusively express mid-wavelength-sensitive cone opsins (RH2) in their retinas. The phototransduction cascade genes follow a similar ontogenetic pattern of conefollowed by rod-specific gene expression in most orders, except for the pearleye and sabretooth (Aulopiformes), in which the cone cascade remains dominant throughout development. Our findings provide molecular support for a conserved vertebrate pattern whereby cone photoreceptors develop first and rod photoreceptors are added only at later developmental stages.

One species, two habitats: Shinkaia crosnieri inhabits in both hydrothermal vents and cold seeps in the Pacific Ocean

Yao XIAO, Ting Xu, Jin Sun, Yan Wang, Wai Chuen Wong, Yick Hang Kwan, Chong Chen, Jian-Wen Qiu and Pei-Yuan Qian

Shinkaia crosnieri is a dominate species of squat lobster in deep-sea chemosynthetic ecosystems in the Western Pacific Ocean. Previous studies comparing S. crosnieri living in deep-sea hydrothermal vent and methane seep communities have suffered from methodological and/or sample size limits. Therefore, by using transcriptome-wide single nucleotide polymorphisms (SNPs) markers in this study, we reveal the extent of genetic connectivity between these two habitats, as well as their signatures of local adaptation. A total of 44 individuals of S. crosnieri were adopted, and 20 individuals from a methane seep in the South China Sea with other 24 individuals from a hydrothermal vent population in the Okinawa Trough. Differentially expressed genes (DEGs) analysis between these two populations and population-specific genes (PSGs) analysis revealed that plenty of unigenes showed opposite expression patterns between these two populations. Population genetic analyses based on both entire and outlier SNP datasets revealed a clear genetic differentiation between these two populations with an Fst value of 0.07 and 0.43 ($p < 0.0005$), respectively. Physical oceanographic modelling of the ocean currents in middle and deep layers also suggests a weak connection within these two sites. Further functional analysis of outlier SNPs revealed unigenes potentially under positive selection. Overall, exploring the population structure of S. crosnieri using transcriptome-wide SNP markers resulted in an improved understanding of its molecular adaptation and expression plasticity in vent and seep ecosystems.

General & Special Sessions 5 Access to the deep sea (technological and methodological advances to access and investigate deep-sea life, including observatories and cutting edge technologies –e.g. A.I. and omics)

General session

Evolution of pressurized devices for deep-sea fauna study

Louis Amand, Magali Zbinden, Juliette Ravaux, Nelly Léger, Bruce Shillito

Animal Biology studies have always benefited from the achievement of experiments on live animals, which obviously provide data on dynamic aspects of physiology. When it comes to deep-sea fauna, in vivo experiments are impaired, and in some cases impossible, due to the severe and often lethal decompression effects during the sampling process. Addressing these issues requires that target species be captured at depth, recovered and submitted to *in vivo* investigations at natural pressure. Accordingly, our group (AMEX) designed a pressurized recovery device named PERISCOP (“Projet d’Enceinte de Récolte Isobare Servant à la Capture d’Organismes Profonds”), which has allowed the successful capture and recovery of live animals throughout 90 dives, from depths reaching 3000m. Once collected, deep-sea fauna may be maintained alive and in good condition thanks to a specific pressurized aquarium also designed by our team, the IPOCAMP (“Incubateur Pressurisé pour l’Observation et la Culture d’Animaux Marins Profonds”), which restores environmental conditions prevailing at depth *in situ*.

We here describe the up-to-date evolutions of these two pressure devices. For PERISCOP the main upgrade is the addition of a passive pressure compensator that allows maintaining 90% of the maximal pressure during the ascendant phase of the shuttle device. We also improved its buoyancy, thermal insulation and ease-of-use by underwater vehicles. For IPOCAMP, we designed and installed a 5cm diameter viewport on the top of the incubator allowing direct observations and HD recordings. We also added a dedicated lock allowing feeding without decompression, in order to conduct long-term experiments.

Exploration of Deepwater Seamount-Associated Chondrichthyans of the Southern Indian Ocean Using Genetic barcoding, eDNA, and Deepwater Cameras

Paul J Clerkin and Jan R McDowell

Chondrichthyans (sharks, rays, and chimaeras) are top predators in almost every environment they inhabit and thus are important to overall ocean health. However, the biology of Indian Ocean deep-sea chondrichthyans is poorly understood; these species are difficult to monitor and assess due to misidentification by inexperienced observers, a high incidence of cryptic species, and limited accessibility to remote sites. These constraints can be overcome by combining traditional taxonomy and life history methods with advanced technologies.

For this project we will work with commercial vessels deep-sea fishing along seamounts from the Madagascar Ridge east to the 90 East Ridge and south to Heard Island Sound (an area of >5,000,000 square miles) at depths up to 2 km, to explore the chondrichthyan fauna of the Southern Indian Ocean using a combination of methods: 1) cataloging species complete with life history information and including an associated genetic barcode for each species encountered, 2) collection of eDNA samples from each seamount to estimate species richness and relative abundance, 3) use of gear-mounted deep-water cameras to observe species and bottom conditions.

The findings from this study will contribute to our currently limited knowledge of the deep-sea chondrichthyan species in the Southern Indian Ocean. The results will include a database of life history, distribution, habitat information, and other biological information that can be used as a baseline to monitor seamount health and prioritize conservation management.

FISH, a new tool to fix in situ motile fauna in deep-sea environments for symbiosis studies

Cueff-Gauchard Valérie, AUBE Johanne, LAGADEC Jean-Romain, BIGNON Laurent, IFREMER, LAFONTAINE Jean-Pierre, HERNANDEZ-AVILA Ivan, SHILLITO Bruce, AMAND Louis, ROUSSEL Erwan, CAMBON Marie-Anne

Deep-sea hydrothermal environments are light-deprived ecosystems where chemolithoautotrophic microorganisms are the main primary producers. There, most of the dominant fauna nutrition is fuelled by bacterial symbiosis. To better understand the functioning of these symbioses according to geochemical conditions, the analysis of symbiont metabolism is essential. As their cultivation is highly complicated, another approach is to analyse their metatranscriptomes. However, one of the main limitation of our studies lies in the collection methods in the deep-sea and the delays of onboard recovery, as messenger RNA is very labile, yet preventing a precise picture of *in situ* activities. Several hours spent outside the hydrothermal context generate a loss of RNA but also significant physico-chemical variations (pressure, temperature, redox potential) leading to metabolic modifications, mRNA rearrangments and even cell death.

We present here the development of a new collection tool implemented on submersibles allowing to: (i) capture mobile fauna, (ii) inject a fixative of active molecules such as RNA later or formaldehyde, (iii) homogenise the sample to facilitate tissue impregnation. The FISH (Fixer In-situ of Homogenised Substrates) sampler collected different species of shrimp. On *Rimicaris* exoculata specimens, we compared this method of sampling to two other methods: the usual suction sampler and the PERISCOP© enclosure which allows pressurised recovery. For this purpose, RNA extractions were performed on symbionts from the cephalothoracic cavity and metatranscriptomic analyses were conducted. This approach revealed better preservation of mRNAs as well as different profiles according to the sampling method.

- ### A target-enrichment bait set for assessing environmental change in deep-water octocorals

Sriram Ramamurthy, Ariane Buckenmeyer, **Danielle M. DeLeo**, Andrea M. Quattrini

Evolutionary processes that generate diversity in the deep sea remain poorly understood, though it has been hypothesized that environmental factors, including depth, serve as strong selective pressures driving adaptation and speciation in the deep sea. Octocorals (Anthozoa: Octocorallia) are common residents of deep-sea ecosystems, yet little is known about their biology, especially how they respond to environmental stressors. As the majority of recent genomic efforts for Anthozoa have largely focused on Hexacorallia and shallow-water anthozoans, there is a large knowledge gap with regard to the genomic makeup of deep-sea corals. Target enrichment hybrid capture is an effective means of recovering and sequencing loci from Anthozoa, including museum specimens and samples not intentionally preserved for genomics. As adaptive divergence with depth may be driving diversification in octocorals, including the ecologically-important genus Paramuricea, target-capture baits were designed to explore adaptations among putative environmental response genes. Using previously published transcriptome data for three deep-sea taxa, Callogorgia delta, Paramuricea biscaya, and Paramuricea type b3, we designed baits for target-enrichment hybrid capture by targeting protein coding genes associated with maximizing survival under rapid environmental change, including those related to immunity, cellular repair and survival, and gamete recognition. Our final target bait set captures 1,704 loci across our three focal taxa. These bait sequences will ultimately be tested on Paramuricea spp. to identify genes under potential selection within this genus, possibly lending to speciation across depth. Additional genomic efforts using these baits on various species of octocorals will improve our understanding of how deep-sea corals respond to external stressors, and to assess deep-sea ecosystem health and resilience in a changing environment.

- ### Improving biodiversity inventories of the deep sea using Capture by Hybridisation

Babett Günther, Sophie Marre, Pierre Peyret, Sophie Arnaud-Haond

The metabarcoding of environmental DNA (eDNA) opened large prospects for the future biomonitoring of marine environments. Yet, Metabarcoding still relies on Polymerase chain reaction (PCR) of relatively short fragments, mostly through the use of “universal” primers. Small fragment size limits both the accuracy of taxonomic assignment and the reconstruction of robust phylogenies. Direct sequencing (such as shotgun sequencing) may solve these limitations through the reconstruction of longer fragments, yet metagenomes are usually dominated by DNA from microorganisms and do not allow a good coverage of metazoans genomes. Here we present an intermediate, less expensive option using capture by hybridization (CBH) for inventorying biodiversity in deep-sea sediment samples. First studies revealed a broader spectrum of prokaryotic, eukaryotic, and particularly metazoan communities than metabarcoding using “universal” primers, and allowed reconstructing full-length barcode regions (up to 1900bp). We built on this first steps and designed new probes to still improve the detection of a broader range of metazoans, and tested them on mock communities. In the current work, we also added the mitochondrial COI barcode region and increased the sequencing depth to improve taxonomic identification. The aim is to better describe unknown taxa (and possibly) phyla, to overcome major gaps of the reference system through better phylogenetic reconstruction and enhanced taxonomic resolution. This works show the promise of CBH in environments still largely underrepresented in public databases and is a valuable addition to current eDNA based marine biomonitoring approaches.

- ### A biological approach on CTD data along with EBS tracks to assign water masses to marine benthic species distribution data

Vivien Hartmann, Saskia Brix, Simon Tewes, Maik Wilsenack, Mia Schumacher

During the IceAGE3 (SO276 MerMet17-06) expedition “Depth transects and connectivity along gradients in the North Atlantic and Nordic Seas in the frame of the IceAGE project (Icelandic marine Animals: Genetics and Ecology)” in summer 2020, we aimed to do oceanographic measurements to assign specific water masses to our biological working areas supporting our biological findings with abiotic measurements. Different gear equipped with a conductivity, temperature, and depth sensor (CTD) were deployed. Usually, oceanographic data are acquired by a Seabird 911 CTD mounted to a rosette sampler. The rosette sampler, however, is never fully lowered on the seafloor, resulting in a lack of data directly above (less than 1m) and on the bottom. To cover this blind spot, we used a Seaguard RCM9 in conjunction with an Epibenthic sledge (EBS), which is lowered completely to the ground and dragged over the seafloor for a certain distance. Through analysis and evaluation of the two datasets, we concluded that data provided by the two sensors are comparable. Through this research we noticed that the data of the Seaguard RCM9 showed a slight shift in temperature when the EBS wasSüdstrand 40, 26382 Wilhelmshaven dragged over ground. We want to discuss possible hypotheses that could explain this effect: First, it might be a matter of mechanical friction, produced by the sledge while dragged on the ground, which could produce small amounts of heat which are captured by the sensitive sensor. Second, temperature increase might be due to bioturbation in the deep-sea floor, producing heat. Due to their distinct mustache-like form, we named these plots the "Dalí-effect", inspired by the famous artist Salvador Dalí. We would like to show and explain this effect as well as the observed water masses.

- Video Analysis: a valuable tool to gather data about deep-sea associations?
  Alexa Parimbelli, Charlie Keeney, Joana R. Xavier, Louise Allcock, Claire Laguionie Marchais

In the deep sea, several species develop associations with other organisms. These associations are mostly studied when the specimens can be collected. However, more and more information about deep-water organisms comes from videos. Video analysis is not a widespread tool for the study of deep-sea associations, as it comes with important limitations, such as the impossibility to identify some organisms to a low taxonomic level, or to determine the nature of the observed relationship. Our aim was to investigate the possibility of raising new knowledge about deep-sea associations just from the use of videos.

In 2018, we collected about 110 hours of high-definition ROV videos from a variety of deep-water habitats, including submarine canyons, on the Irish Continental Margin, from 816 to 2700 m. Here we present the most recurring associations observed with Porifera and Cnidaria, along with an analysis of the influence of host taxon, and environmental factors such as depth and substrate composition.

From videos, we were able to report new and poorly investigated deep-sea associations. We also demonstrated that factors such as the taxon of the host, depth and, to a lesser degree, substrate influence both the presence of associations and the phyla of the associates.

Given the current threatsthat the deep sea is currently facing, gathering information about interactions between deep-sea species is becoming more and more urgent. Inaction could result in the loss of host species, which could be critical for the survival of the associated organisms.

Therefore, all data should be exploited, and we advocate that video analysis is a valuable tool for the collection of new data on the deep-sea, and that implementation of such analyses will have important implications for deep-sea research and conservation management.

Special session 5a#: Deep-sea ecosystem dynamics - long-term observations and evolving approaches.pdf – *Matabos et al*

- Stories Told by Animals and Argo-floats: Long-Term Observations of Offshore Currents
  Cherisse Du Preez, Tetjana Ross, Debby Ianson

There was an Argo float circling SGaan Kinghlas-Bowie (SK-B) Seamount for three months in late 2020/early 2021. Although this single float does not provide conclusive evidence, it supports the long-standing supposition that a Taylor cone circulation or that seamount-attached eddies may be present (helping to retain larvae and increase productivity over this uniquely shallow seamount). In a Marine Protected Area focused on the conservation of cold-water corals and sponges, it begs the question "can we link this physical oceanographic process to the benthic biological systems?" We provide a new perspective on the flow around SK-B seamount using a combination of nearly 20-years of trajectory and hydrographic data from Argo floats that passed near SK-B seamount, satellite altimetry data, and remotely operated vehicle imagery of sessile organisms. Some remarkably longlived coral species provide natural long-term current meters. They are known to orient across the mean-flow direction—like catcher's mitts—and the degree of curvature across the organism is related to the flow strength. Tall, stiff, fan-like corals integrate the flow over many years, while flexible organisms indicate the instantaneous flow direction allowing biological assessment of current across multiple time scales. The medium timescales can be filled in with the Argo-floats' Lagragian and geostrophic views of flow around SK-B seamount to paint a surprising picture.

- BathyBot – a deep-sea crawler to see the unseen in the NW Mediterranean Sea
  Séverine Martini, Christian Tamburini, Carl Gojak, Jacopo Aguzzi, Aurélien Arnaubec, Laury Barnes-Davin, Karim Bernardet,Olivier Bocquet, Bruno Bombled, Vincent Bertin, Pierre Chevaldonné, Paschal Coyle, Viorel Ciausu, Elodie Rouanet, Christian Grenz, Zouhir Hafidi, Patrick Lamare, Céline Laus, Dominique Lefèvre, Nadine Lebris, Karim Mahiouz, Simone Marini, Marjolaine Matabos, Cécile Militon, David Nerini, Thierry Perez, Marc Picheral, Romain Piasco, Christophe Rabouille, Jozée Sarrazin, Delphine Thibault, Laurenz Thomsen

The deep sea remains one of the less known environments on earth and is characterized by its high pressure, low organic matter availability and its darkness. While there are still numerous discoveries concerning the capabilities of deep-sea organisms, this ecosystem is under an increasing pressure due to anthropogenic stressors such as temperature change, deep-sea fishing, mineral mining, human pollution (microplastics), oil and gas extraction. How these changes will affect biodiversity and ecosystem functioning is one question of major importance for the future. In the darkness of the oceans, most organisms have the capability to emit light: called bioluminescence. Recent studies quantified that as much as 75% of pelagic and about 40% of benthic organisms are known to be bioluminescent. In this framework, we present a new deep-sea crawler, BathyBot, to be dedicated to long-term exploration, biological and-geochemical survey. BathyBot will be deployed in 2020 in the Mediterranean Sea, at the MEUST-NUMerEnv/KM3NeT site, to strength the ecological-based monitoring capability of the European Multidisciplinary Seafloor and water column Observatory (EMSO ERIC) network. BathyBot will be able to explore the sea at 2500m depth and will be devoted to 1) explore relationships between deep-sea organisms, biogeochemical (carbon, oxygen) and environmental variables (temperature, salinity, current) in the context of global changes and their effects on the deep ocean, 2) better define the role of bioluminescence in situ (increasing the dataset of bioluminescence records), 3) observe and monitor deep-sea pelagic and benthic organisms and 4) investigate benthic biogeochemical processes through the use of oxygen microprofiling in sediment porewaters.

- A Strategy to Map, Explore, and Characterize the U.S. EEZ.
  Mark Mueller, Amanda Demopoulos, Stacy Aguilera-Peterson, Chrissy Hayes, Lucila Houttuijn Bloemendaal, Max Showalter, Caitlin Adams

A vast expanse of the deep sea is unmapped, unexplored, and uncharacterized, representing a fundamental knowledge gap and incomplete baseline information needed for meaningful long-term ocean observations. In 2020, the United States government released an innovative policy framework for mapping, characterizing, and exploring the Nation's Exclusive Economic Zone. The National Ocean Mapping, Exploration, and Characterization (NOMEC) Strategy sets out ambitious goals and actions to address these needs, including mapping the seafloor in all U.S. waters deeper than 40 m by 2030 and exploring and characterizing identified priority areas. The new Federal NOMEC Council and interagency working groups of the Ocean Policy Committee are establishing data and protocol standards, identifying strategic priorities, developing and maturing new technologies, systematically sharing data, and inspiring and involving the public. We will discuss this evolving, collaborative approach to better coordinate the U.S. mapping, exploration, and characterization enterprise and generate opportunities for developing sustained public-private partnerships. Successfully mapping, exploring, and characterizing the world's oceans relies on robust multisector engagement and can contribute directly to U.S. and international endeavors such as Seabed 2030, 30x30, and the United Nations Decade of Ocean Science for Sustainable Development.

These efforts aim to inform decision-making on challenges both national and global, from coastal resilience to sustainable resource management. For example, improving the available baseline information needed to detect and characterize long-term trends of concern such as changes in water chemistry would benefit from technological advancements and cost reductions in ocean instrumentation. Cutting-edge moored vertical profilers capable of measuring shifts in the aragonite saturation horizon and other carbonate chemistry associated with ocean acidification could reveal trends with significant implications, considering the valuable ecosystem services provided by some deep-sea organisms. Cost-effectively siting such condition-characterizing instruments in ideal locations is dependent on their first being appropriately mapped and explored.

- Insight into the Ecology and Hydrography of Mesopelagic Monterey Bay through MBARI's Midwater Time Series
  Rob E Sherlock, Kim R Reisenbichler, Astrid B Leitner, Monique Messié, Bruce H Robison

The long-term Midwater Time Series at the Monterey Bay Aquarium Research Institute has quantified mesopelagic animals for more than two decades in order to better understand their abundance, seasonality, and depth distributions. These video data are collected alongside CTDO (conductivity, temperature, depth and oxygen) data by remotely operated and autonomous underwater vehicles (ROVs and AUVs). The Midwater One study site is located approximately 15 km from shore, over a deep submarine canyon, and is in a region comprised by strong upwelling and dynamic environmental conditions. Oceanographic data are collected at a nearby mooring and, together with the ancillary ROV and AUV data, allow us to link patterns in animal distribution to the changing hydrography. Understanding the population dynamics of mesopelagic animals is a first step toward predicting how they might respond to changing ocean conditions.

Special session 5b#: The use of the A.I. for biodiversity studies in the deep sea.pdf – *Zeppilli et al.*

- 2D convolutional neural networks for benthic fauna identification
  Khawla Ben Gaied, Abdesslam Benzinou, Abdul Qayyum, Kamal Nasreddine, Catherine Borremans, Valentin Foulon, Terue Kihara, Pedro Martinez Arbizu, Daniela Zeppilli

The rapid increase of anthropogenic pressures on marine ecosystems presents an urgent need for analyzing their impact on these ecosystems. This requires improving the knowledge and mapping of species to measure changes and losses in biodiversity. Benthic fauna are animals living in the sediments of the seabed which are the best marine bioindicator available to assess these environmental changes.

Visually benthic species identification is time consuming and requires years of taxonomic experience. That is why we need a fast and precise species identification system. So, we are updating our knowledge to keep pace with the latest technologies and advances in the field of artificial intelligence (AI). Here we present 2D classification model to identify benthic species. We use deep learning networks based on convolutional neural networks. In fact, deep learning network applications are everywhere these days, but we do not see them applied in the deep sea domain.

What makes our deep learning based model, so powerful is the way it can learn features from data. It automatically extracts the features and processes information from digital samples. This will allow a precise automated classification to identify which organisms belong to which taxonomic categories. We present different architectures (VGG, AlexNet…) trained from scratch or by pretrained models (fine-tuning and transfer learning techniques). Results are very promising and demonstrating that AI concept has strong potential for automatic benthic fauna identification.

Fish Species Recognition in Unconstrained Underwater Environment Using Convolutional Neural Networks

Bentamou Abdelouahid, BENZINOU Abdesslam, NASREDDINE Kamal

Recently, marine biologists use more and more underwater videos to study species diversity and fish abundance. These techniques generate a large amount of visual data. Automatic analysis using image processing is therefore necessary, since manual processing is time-consuming and labor-intensive. However, there are numerous challenges to implement automatic processing of underwater images: for example, high luminosity variation, limited visibility, complex background, and the high diversity of species.

n this work, we are interested in fish detection and species classification in underwater video images. Fish have very variable shapes, sizes, colors and textures. They move in three dimensions and can hide behind algae and rocks or overlap with other fish. These factors make the task of fish species recognition difficult with current traditional image processing techniques.

For the fish localization task, a robust approach is proposed. It consists of efficiently combining the feature spaces of two CNN streams to fuse the appearance and movement information of fish. This approach significantly improves the fish detection performance compared to a single-stream approach.

For species classification, three CNN-based approaches are developed to improve the accuracy of fish species identification. For this purpose, we use transfer learning with different CNN architectures. These approaches are validated on two public benchmark datasets of fish images in unconstrained underwater environment.

Biodiversity underestimation in our bLUe planEt: artificial intelligence (AI) REVOLUTION in benthic taxonomy (BLUEREVOLUTION)

Catherine Borremans, Daniela Zeppilli, Abdesslam Benzinou, Kamal Nasreddine, Valentin Foulon

The Earth's Ocean is the largest three-dimensional living space on our Planet. It is crucial to life as we know it, yet we know less about the entire seafloor than we do of the surface of the moon. Infaunal benthic communities comprise some of the most diverse groups of organisms on Earth, and only a very small amount of this diversity has been described by science. Despite our partial exploration of this vast domain, all marine habitats, including the deepest trenches, experience direct or indirect human impacts. Thus, the scientific community faces the need for fast and accurate monitoring studies and building baseline datasets to measure future changes and biodiversity losses. The introduction of DNA taxonomy and metabarcoding initiated the development of fast fingerprinting methods to address this growing need. However, molecular identities (OTUs) are in themselves not valuable if not linked to species obtained through thorough taxonomic identification and for which we have biological and ecological information.

Inspired by the pioneering project "Tara Oceans" merging expertise in taxonomy, ecology, molecular biology and bioinformatics to conduct a large-scale inventory of plankton diversity, the BLUEREVOLUTION project aims at developing in- and ex-situ methods using automatic imaging techniques (holographic microscopy and 3D-fluorescence imaging) linked with taxonomic classification tools (AI) for high throughput analysis of benthic diversity. This will ultimately allow for quantitative, genetic and functional data of benthic communities being generated at speeds unseen before and will produce a standardized method for building open-access reference databases together with fast and reliable tools for impact assessments and biodiversity surveys. The project will also contribute to the training of the next generation of benthic integrated taxonomists and ecologists with skills in species identification and the ability to employ cutting-edge techniques to revolutionize the way we discover and monitor our Ocean's seafloor.

FathomNet: An open underwater image database for training AI

Kakani Katija, Brian Schlining, Lonny Lundsten,Kevin Barnard, Giovanna Sainz, Eric Orenstein, Oceane Boulais, Benjamin Woodward, Katy Croff Bell

Ocean-going platforms are integrating high-resolution, multi-camera feeds for observation and navigation, producing a deluge of visual data. The volume and rate of this data collection can rapidly outpace researchers' abilities to process and analyze them. Recent advances in machine learning enable fast, sophisticated analysis of visual data, but have had limited success in the oceanographic world due to lack of dataset standardization, sparse annotation tools, and insufficient formatting and aggregation of existing, expertly curated imagery for use by data scientists. To address this need, we are building FathomNet, a public platform that makes use of existing (and future), expertly curated data. Initial efforts have leveraged MBARI's Video Annotation and Reference System and annotated deep sea video database, which has more than 6M annotations, 1M framegrabs, and 4k terms in the knowledgebase, with additional contributions by National Geographic Society and NOAA-OER anticipated in 2021. FathomNet now has over 100k localizations of 1k midwater and benthic classes, with plans for the database and portal (www.fathomnet.org) to be released this year. We will demonstrate how machine learning models trained on FathomNet data can be applied to other institutional video data, (e.g., National Geographic Society's DropCam and NOAA's ROV Deep Discoverer), and enable automated acquisition and tracking of midwater animals by underwater vehicles. As FathomNet continues to develop and incorporate more image data from other oceanographic community members, we hope that this effort will ultimately enable scientists, explorers, policymakers, storytellers, and the public to understand and care for our ocean.

Deep Learning and Deep Arctic Jellies: a case study pipelining real- time ROV video annotations, post-cruise analysis, data

dissemination and production of machine-learning training sets

Dhugal Lindsay, Mitsuko Hidaka, Mehul Sangekar, Takashi Hosono, Daisuke Matsuoka, Daisuke Sugiyama, Ariell Friedman, Russell Hopcroft

The deep sea, in spite of its remoteness, is increasingly coming under a variety of pressures, from resource exploitation such as fishing and/or mining, pollution (eg. plastic wastes), to the effects of climate change. A bottleneck exists with respect to the gathering of baseline data and its analysis, in order to enable assessments of intrinsic variability versus the possible effects from outside forcing. We describe an integrated system, built upon the Squidle+ annotation platform, that includes extensions for realtime and post-processing analysis to acquire and annotate video data streams from remotely-operated vehicles (ROVs) with their associated metadata at sea, through to supplying data repositories with the survey results. Annotations use the Aphia ID/WoRMS vocabulary with extensions based on other standard vocabularies (eg. VARS Knowledge Base terms). Rapid reannotation back in the land-based lab is facilitated by using realtime annotations logged in the field to index into relevant parts the video files, based on field observation timestamps, using a custom video player. Such post-cruise annotations for the production of a cruise report can be kept sandboxed from more methodical linear re-annotations through a multi-user login permissions and management system. Organism occurrence data can be exported to DarwinCore format for ingest into the Ocean Biogeographic Information System (OBIS), while localized image annotations can be output to produce training sets for machine-learning applications (eg. COCO format). Tags applied to annotations identify multiple annotations of single organisms to enable both quantitative analyses and the export via restful APIs of within-image object location data for linking with external tracking algorithms.

This system was tested using the multi-camera output from the ROV Global Explorer acquired during Cruise HLY1601 of the Icebreaker Healy in the Chukchi Sea, in Arctic summer 2016. This presentation describes both the workflow and results of these analyses of the 4K video, concentrating on the gelatinous midwater fauna. Some experiments on this dataset using deeplearning algorithms are also introduced.

Seafloor classification with optimized texture convolutional neural network: application to complex benthic habitats on seamount and volcanic island slopes

Thibault Napoléon, Melissa HANAFI-PORTIER, Clémence CARCOPINO, Camille DUGARD, Simon GOURDON, Catherine BORREMANS, Karine OLU

Seafloor heterogeneity is a key parameter structuring seamount biodiversity at multiple spatial scales. However, substrates characterization at very small (meter) scale from manual processing of optical images is time-consuming and difficult to be objectively applied on a large dataset. Consequently, quantification of several substrate types per image is usually lacking.

To automize seafloor classification, we proposed to use a supervised machine learning algorithm. First, a substrates dataset with 772 annotations composed of four classes was produced (volcanic, carbonate, gravel, and soft) and splitted randomly into two parts: 90% for training, 10% for validation. A biogenic class was also extracted but set aside because of its small size towards others. Note that several annotations refinements were made to respect computer vision standards.

To classify theses substrates, we used a texture specialized convolutional neural network based on wavelets [1]. For the training step we used a pretrained VGG19 network as basis and we applied a transfer learning approach to tune our network for our substrates dataset. We artificially increased the number of annotations by applying a data augmentation technique. The wavelets network was improved, and we obtained a classification rate close to 85% on validation set. Finally, due to the seafloor heterogeneity, an image segmentation process based on sliding windows was applied to extract statistics over tests images with a 224x224 patch size.

This substrate classification algorithm was used to assess percent cover of the four substrate classes per image from nine towed camera surveys (i.e. 9000 images) on seven seamounts and volcanic island slopes along the Mozambique Channel. From this dataset, the variability of substrate composition along and among these seamounts was tested as structuring factors of benthic megafaunal assemblages (Hanafi-Portier et al., this meeting).

[1] Shin Fujieda, Kohei Takayama, Toshiya Hachisuka. "Wavelet Convolutional Neural Networks for Texture Classification." (2017)

Dataset takes part of the project PAMELA (Passive Margin Exploration Laboratories):

Pamela-Moz01 cruise : https://doi.org/10.17600/14001000

Pamela-Moz04 cruise : https://doi.org/10.17600/15000700