# ABSTRACTS
# Deep-Sea Biology Symposium 2018
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# Advances in taxonomy and phylogenetics - TALKS

TALK - Advances in taxonomy and phylogenetics - ABSTRACT 174
TUESDAY Midday • 13:15 • San Carlos Room

## The impact of intragenomic variation on alpha-diversity estimations in metabarcoding studies: A case study based on 18S rRNA amplicon data from marine nematodes

Tiago Jose Pereira, Holly Bik
University of California, Riverside

Although intragenomic variation has been recognized as a common phenomenon amongst eukaryote taxa, its effects on diversity estimations (i.e. under or over estimates) in metabarcoding studies have not been fully addressed. To avoid or reduce over estimations due to PCR and sequencing errors, a number of steps including chimera detection, removal of singletons, different clustering thresholds are often applied to datasets prior to any downstream analyses (e.g. alpha and beta diversity comparisons). On the other hand, these same procedures can also remove variation caused by real intra-genomic and intra-specific diversity. In order to evaluate the existence and the potential effects of intragenomic variation on diversity estimations, we explored an rRNA amplicon dataset (i.e. V1-V2 regions of 18S rRNA) obtained from single marine nematode specimens collected from coastal and deep-sea sites. Prior to DNA extraction and high-throughput sequencing using the Illumina MiSeq platform, nematode specimens were morphologically identified (i.e. assigned to genus and/or putative species) using light microscopy, covering a wide range of nematode groups and thus allowing us to assess how frequent is intragenomic variation in marine nematodes. Specifically, we evaluate different metrics per nematode specimen (e.g., number of OTUs, relative abundance of each OTU, variation on the taxonomic assignment of OTUs, genetic divergence among OTUs, and the frequency of base changes in the stem and loop regions of the 18S rRNA) to depict common patterns (e.g. low or high intragenomic variation, broadly or restricted among marine nematode taxa). Finally, our findings are discussed in the context of species delimitation, especially in biodiversity/ecological studies based solely on metabarcoding approaches, where genetic diversity cannot always be linked to an individual and/or species.

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TUESDAY Midday • 13:30 • San Carlos Room

## Eastern Pacific scaleworms (Polynoidae, Annelida) from seeps, vents and whalefalls.

Gregory Rouse, Avery Hiley, Sigrid Katz, Johanna Lindgren
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Sampling across deep sea habitats ranging from methane seeps (Oregon, California, Mexico Costa Rica), whale falls (California) and hydrothermal vents (Juan de Fuca, Gulf of California, EPR, Galapagos) has resulted in a remarkable diversity of undescribed polynoid scaleworms. We demonstrate this via DNA sequencing and morphology with respect to the range of already described eastern Pacific polynoids. However, a series of taxonomic problems cannot be solved until specimens from their respective type localities are also sequenced. We highlight some resolved taxonomic issues, and new species, with respect to Bathykurila, Branchipolynoe and Peinaleopolynoe. While many of the scaleworm species show wide geographic ranges across thousands of kilometers, others were also only found at one site. While many were found at both seeps and whale fall habitats, very few were found to live across both seeps and vents.

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TUESDAY Midday • 13:45 • San Carlos Room

## Bathyal slope to hadal trench: diversity and biogeography of Solenogastres (Mollusca) in the Northwest Pacific

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Several recent joint German-Russian research cruises investigated the deep-sea benthos in the Northwest Pacific with the aim to identify biogeographic links or isolating factors between the semi-enclosed Sea of

Okhotsk and the open Pacific. Solenogastres are a clade of shell-less, worm shaped molluscs and a frequent albeit not overly abundant component of the collected deep-sea fauna. Due to their inaccessibility and complex taxonomy, Solenogastres are generally understudied and underestimated – the latter at least in regard to their diversity, which is estimated to be at least ten-fold above the currently known 300 species. Many of these species are based on single findings and as a consequence vertical and horizontal distribution ranges of the group are poorly explored. We studied approximately 150 specimens of Solenogastres, collected from the bathyal slope and basin of the Sea of Okhotsk, the abyssal plain of the Northwest Pacific, and hadal depths of the Kuril-Kamchatka Trench. We used an integrative taxonomic approach combining multiple mitochondrial markers, 3D-microanatomy based on histology, and scanning electron microscopy to delimitate different lineages and investigate their bathymetric and biogeographic distribution ranges. In total, we discovered more than 40 species in the region, largely new to science and by far exceeding the previously known solenogaster diversity in the area. Solenogastres have rarely been reported from hadal depths, but we discovered several lineages at 9,500 m. Overall there is a unique solenogaster fauna in each of the sampled regions with few lineages present on both sides of the Kuril-Kamchatka Trench, which we think might act as a barrier to their dispersal. This is the first comprehensive study evaluating phylogenetic relationships, population genetic patterns and distribution ranges in Solenogastres on a regional scale. It provides a reliable barcoding library for easier identification in future faunistic surveys and therein a first baseline for beta-biodiversity comparisons.

## Multi-locus phylogenetic analysis of Amphipoda supports monophyly of the pelagic suborder Hyperiidea

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Hyperiidea (Peracarida; Amphipoda) is an exclusively pelagic crustacean suborder, possessing a wide range of unique adaptations to life in the dim, open expanse of the oceanic midwater. The group exhibits such diversity that no common morphological synapomorphy unites the approximately 350 described species. Hyperiid amphipods are defined only by their pelagic existence, despite the presence of holopelagic representatives in several other amphipod groups. Previous morphological and molecular analyses have led to uncertainty in the monophyly of Hyperiidea and in their relationship to other amphipods, raising the possibility of convergent evolution of their pelagic lifestyle. Here we present results of a multi-locus phylogenetic analysis of publicly available amphipod sequences for 3 nuclear (18S, 28S, H3) and 2 mitochondrial loci (COI and 16S). This is the largest analysis, to date, aimed at addressing the question of hyperiid monophyly and includes approximately 500 amphipod genera, 40 of which are hyperiids. We recover strong support for a monophyletic Hyperiidea, as well as reciprocally monophyletic hyperiid infraorders Physocephalata and Physosomata, with the enigmatic genera Cystisoma and Paraphronima more closely related to the Physosomata. We also identify two clades of benthic, commensal amphipods as potential sister groups of Hyperiidea. These taxa have not previously been considered close hyperiid relatives and include the genera Amphilochus, Colomastix, Anamixis, Paranamixis, and Leucothoe. Our results are a first step toward resolving the phylogenetic placement of the suborder Hyperiidea within Amphipoda and are being used to inform taxon sampling for an on-going transcriptome-based phylogenomic study.

## Genetic connectivity and adaptive evolution in the squat lobsters *Shinkaia crosnieri* inhabiting both hydrothermal vent and cold seep habitats

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Institute of Oceanology, Chinese Academy of Sciences

Deep-sea hydrothermal vents and cold seeps are two types of extreme habitat for marine organisms. The differences between the ecosystems of hydrothermal vents and cold seeps may facilitate the genetic heterogeneity and local adaptation of the species in both environments. Here, we combined restriction-site associated DNA (RAD) and comparative transcriptome analysis to evaluate the extent of genetic differentiation and the pattern of selection in the dominant species, Shinkaia crosnieri Baba & Williams, 1998, inhabiting both environments. Using RAD technique, we identified 21,182 single nucleotide polymorphisms (SNPs) for 30 S. crosnieri specimens. In lined with mitochondrial DNA results, structural and phylogenetic topology analyses based on SNPs showed clear genetic differentiation between the vent and seep populations. Local adaptation of populations was tested by searching for increased population divergence using FST-based outlier tests, which resulted in 710 potentially locally selected SNPs. To obtain further insights into the driving force of divergence in S. crosnieri, we followed the method of comparative transcriptomic analysis to identify one-to-one orthologs. A total of 5347 orthologous unigene pairs was identified between vent and seep samples, among which 938 and 302 genes were found to undergo purifying and positive selection, respectively. The functional enrichment results indicated that these positively selected genes covered diverse functional categories, including sulfur metabolism, detoxification, anti-oxidative stress and immune defense, suggesting that abiotic and biotic stresses were important selective pressures in the adaptation of S. crosnieri to different deep-sea chemosynthetic environments. These results provide evidence for genetic divergence and adaptive differentiation of S. crosnieri inhabiting hydrothermal vent and cold seep habitats and shed insights into the adaptation process to deep-sea extreme environments in marcoorganisms.

## New Species of Narcomedusae (Hydrozoa, Trachylina) Collected by NOAA Okeanos from the Musician Seamounts, Pacific Ocean

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The first medusa collected by NOAA Okeanos was found in association with, and apparently feeding on, an octocoral at 1,762 M depth on Paganini Seamount, part of the Musician Seamounts, northwest of the main Hawaiian Islands. Multiple individuals – readily identified to the hydrozoan order Narcomedusae by tentacles arising above the margin of the bell – were observed by ROV clinging to Iridogorgia magnispiralis with their mouths enveloping individual zooids of the octocoral. Upon collection of a large fragment of the octocoral, most individuals of the medusa were dislodged but a single animal was retained, photographed live, and subsequently fixed in formalin, with a tentacle subsampled into ethanol. The systematics of Narcomedusae, a relatively low diversity taxon including 43 accepted species, is in a state of flux, with recent analyses showing families, genera, and sometimes even species to be non-monophyletic. The corallivorous species described here has red pigmentation, a bell diameter of roughly one cm, and four primary interradial tentacles associated with peronia, broadly reminiscent of species that until recently were lumped under the name Aegina citrea. However, this species has four hollow secondary tentacles, flanked by free

hanging statocysts, more similar to Bathykorus bouilloni and Sigiweddellia benthopelagica. Morphological and molecular evidence are used to place this species within the emerging systematics of Narcomedusae. Similar medusae to the one described here have been observed on octocorals by the NOAA Okeanos Explorer and other deep-sea expeditions.

## Clarifying the Pacific glass squids: Who are the cranchiids in your neighbourhood?

Aaron Boyd Evans, Kat Bolstad
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A recent revision of the ecologically important squid family Cranchiidae ('glass' squids) in the Pacific Ocean has revealed the presence of additional taxa in several genera; in total, 31 species were encountered, of which at least six appear to be new to science. Several new species of Taonius were identified, a genus which has historically been considered (relatively) systematically stable in the Pacific Ocean. For previously known taxa, this research aimed to provide further description and illustration to aid in the future identification and differentiation at a species level, since members of this family are notoriously challenging to identify. Many cranchiids undergo significant morphological changes with ontogeny, and descend to greater depths with age, suggesting complex trophic roles, which can be more accurately assessed now that these taxa have been recognised and reported.

## Evolution and ecology of Macellicephalinae scale worms (Polynoidae, Annelida)

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Smithsonian National Museum of Natural History

Scale worms (Aphroditiformia) are one of the most successful annelid radiations and are easily recognizable by their paired dorsal covering of segmental scales. Within Aphroditiformia, family Polynoidae is the largest and most diverse group, having colonized all marine habitats and ecological extremes. Among polynoids strictly bound to the deep sea, Macellicephalinae are most abundant, prevalent among abyssal muds, whale falls, chemosynthetic vents/seeps, and are one of the few annelid groups known from hadal depths. Due to restricted access to material, few studies have assessed their evolution into (or origin within) these habitats. As a result, longstanding uncertainties persist in the interpretation of macellicephalinid evolution due to lack of phylogenetic resolution and representation. However, we recently managed to include two cave genera of Macellicephalinae (Pelagomacellicephala and Gesiella) from caves of different age, geology and opposing sides of the Atlantic, in a phylogenetic study on scale worms. For the first time, we showcase these rare cave genera, recovering them in a sister relationship and nested within a strictly deep-sea inhabiting clade. Divergence estimates suggest a single colonization into subterranean environments from the deep sea during late stage opening of the Atlantic. Phylogenetic comparative methods and ancestral character reconstructions further explored this deep sea-cave connection, examining behavioral and morphological traits between extreme and non-extreme scale worm taxa. Our results indicate that deep sea and cave taxa have similar morphological specializations, including eye loss and elongated sensory structures that evolved after initial colonization of the deep sea from a shallow water ancestor, becoming more pronounced in taxa occupying caves and the pelagic realm. Resourcefulness however continues to be discovered within Macellicephalinae as we report the first record of enteropneust

commensalism. Together, systematic relationships and adaptations will inevitably help guide our phylogenomic investigations into the underlying functional and molecular mechanisms of adaptation in extreme environments.

# Advances in taxonomy and phylogenetics - POSTERS

## From Hansen report to IceAGE program – a century of the research of small peracarids around Iceland

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Tanaidacea belong to the smallest peracarid crustaceans (body length usually >2 mm) with great and underestimated diversity in deep waters. They represent demersal organisms which inhabit the surface or upper layers of the sediment. The history of the deep sea (<200 m) Tanaidacea around Iceland and Greenland goes back to over 100 years ago when Hansen (1913) summarised the current knowledge. That list which included over 30 rare tanaidacean taxa was supplemented subsequently by the results of the next scientific expedition exploring waters around Iceland (e.g. BIOICE, BIOGAS). During two IceAGE expeditions a large collection of Tanaidacea was gathered from the shelf down to the slope (213-2750 m) in six areas off Iceland – the Irminger Basin, the Iceland Basin, the Norwegian Sea, the Denmark Strait, the Iceland-Faroe Ridge and the Norwegian Channel. The current list of Tanaidacea known from vicinity of Iceland includes almost a hundred of taxa found in 40 samples collected with different gear (e.g. EBS, VVG. GKG). The most diverse family was Typhlotanaidae with over thirty species, while most numerous was family Pseudotanaidae which constituted a quarter of all tanaid individuals. Where possible, a reversal taxonomy was applied. For the first time highly dimorphic males ('swimming') were assigned to species. Applying morphometric methods a cryptic complex was identified. Based on current data and literature records similarity among fauna of Pseudotanaidae was assessed with applying Bray–Curtis formula. As result, potential zoogeographic regions in the North Atlantic have been distinguished.The study was completed thanks to funding provided by the National Science Centre, Poland (grant no. 2014/13/B/NZ8/04702).

## Mitogenomics and phylogeny of Northeast Atlantic Pennatulacea

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Pennatulaceans were collected from RV Celtic Explorer using ROV Holland I between 2013 to 2016, and from collaborators from surveys in UK, Greenland, and France. Indexed libraries were prepared using a TruSeq Kit (Illumina) and sequenced on an Illumina MiSeq. Mitogenomes and the nuclear rDNA (18S, ITS1, 5.8S, ITS2, 28S) were assembled and annotated following standard protocols. We present the first mitogenomes of deep-sea and Northeast Atlantic Pennatulacea, representing nine genera and eight families. These include one species of each of the deep-sea genera Halipteris, Protoptilum and  Distichoptilum,  four species each of Umbellula and Pennatula, three species of Kophobelemnon and two species of Anthoptilum, as well as one species of each of the shallow-water genera Funiculina and Virgularia. Seventeen circular genomes

ranged from 18,513 bp (Halipteris finmarchica) to 19,171 bp (Distichoptilum gracils). The mitogenome of Umbellula sp.1 was recovered as two separate contigs (~13 k bp and ~5 k bp). We found at least three different gene orders in Pennatulacea, the ancestral gene order, the same gene order as the bamboo coral Acanella eburnea, and a novel gene order from Umbellula sp.3. Maximum Likelihood phylogenies constructed separately from whole mitogenomes and nuclear rDNA recovered similar topologies. The included Kophobelemnidae were recovered as a well-supported monophyletic group. Distichoptilum appears to be nested within Pennatula, with Protoptilum sister taxon to this clade. Umbellula and Anthoptilum were recovered as a well-supported sister group in the tree based on nuclear rDNA. This grouping also appears in the tree built from mitogenomes, but a fourth species of Umbellula, for which rDNA genes could not be assembled, falls in a separate clade apparently rendering Umbellula polyphyletic.   A tree based on 28S only, which could be assembled for the fourth Umbellula species, also found Umbellula to be polyphyletic.

## The mitochondrial genomic characters of an ancient hadal amphipod from Mariana 10,908 m trench

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The Challenger Deep in the southernmost Mariana Trench is the deepest point on the Earth with 10,920 m below sea level. It is known that Hirondellea gigas was the absolutely dominant species living in it. However, recently another amphipod (Amphipoda sp.) was collected from the Challenger Deep with similar density with H. gigas. Moreover, Amphipoda sp. was only observed in the Challenger Deep at positions deeper than 10,000 m that was different from H. gigas living from around 7000-11,000 m. Phylogenetic analysis indicated that Amphipoda sp. formed a separated clade from other available amphipods with mitogenomic information, and the genetic distance to other clades are large enough to a family or superfamily level. The molecular dating results suggested the divergence time for the superfamily represented by Amphipoda sp. was the most ancient compared with other lineages with around 109 Mya during the Cretaceous, revealing this species could be an ancient one that have got through the Mass Extinctions in the Late Cretaceous/Early Palaeocene and the Late Palaeocene/Early Eocene, while H. gigas was much younger with the divergence time of around 58Mya near the boundary of Palaeocene and Eocene. Our analysis showed that the special large scale of gene inversions, altered transcriptional polarity and reversed strand bias in the base composition of PCGs and tRNAs were main characters of Amphipoda sp. mitogenome. Moreover, there are more non-polar amino acids in mitochondrial PCGs for the hadal species compared with the amphipods in other habitats. The analysis of dN/dS indicated the amphipods in hadal ecosystems were under strong purifying selections. The strong purifying selections and the postulated mitochondrial gene recombinations are regarded as two survival strategies for the hadal amphipods to counteract effects of Muller's Ratchet which could bring about the extinction of the mitogenomes by gradually accumulating minor deleterious mutations.

## Polychaetes from Australia's Eastern Abyss

Laetitia Gunton, Pat Hutchings, Robin Wilson, Anna Murray, Hannelore Paxton, Ingo Burghardt, Tim O'Hara
Australian Museum

The abyssal environment makes up around 30% of Australia's marine territory and off the east coast the shelf break usually occurs within only 15 km of the shoreline, despite this, very few studies have investigated the Australian abyssal environment. The 31-day expedition 'Sampling the Abyss' on board the Marine National Facility research vessel Investigator, led by Museums Victoria and supported by CSIRO and NESP Marine Biodiversity Hub in 2017, was the first Australian research cruise focused on investigating the abyssal environment from Tasmania to southern Queensland. Forty-nine beam trawl samples were collected from 13 sites. These trawl samples were conducted at both lower bathyal (~ 2500 m) and abyssal depths (~ 4000 m). A total of about 600 polychaetes from 24 families were recorded, with Ampharetidae, Maldanidae, Onuphidae, and Serpulidae being the most abundant polychaete families. Further investigation into these families revealed new species and interesting patterns in species abundance and distribution between sample sites and sample depths. This project will contribute to the understanding of polychaete abundance, diversity and connectivity in the poorly-sampled deep-sea environment off the coast of Australia.

## Biodiversity Exploration and Phylogeny of Cocculinidae (Gastropoda: Cocculiniformia)

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The Cocculinidae is the family consisting of small, white bathyal gastropods that live primarily on sunken woods. Due to their limited size, rareness, and sampling difficulties, this family is one of the least-studied families of the Gastropoda. Many questions on the systematics of the family Cocculinidae, including their species diversity, geographical and ecological distributions, and evolutionary relationships, remain largely unanswered. Herein, we conduct a comprehensive investigation to explore the diversity and to infer the phylogeny of cocculinids in the Indo-West Pacific (IWP). 489 cocculinid samples are collected from 182 IWP localities during several expeditions under the Tropical Deep-Sea Benthos program. The collected samples are examined using both molecular and morphological methods. Three gene markers are used for species delimitation (cox1, and 28S) and phylogeny reconstruction (cox1, 28S, and H3); six key morphological characters are further explored for the purposes of taxonomic practices including identification of species and genus. In the present study, more than 60 putative IWP species are identified based on the combination of molecular, morphological, and ecological evidences whereas the number of currently recognized IWP species is only 24. Our result reveals an exceptional cryptic diversity and the existence of many undescribed species within the Cocculinidae. At higher taxonomic level, the result from phylogenetic analyses and morphological examinations allow us to identify nine main clades within the Cocculinidae. Five of them may be attributed to existing genera; the others should be assigned to new genera that remain to be described.

## Progress on the research of fish systematics and evolution through the Tropical Deep-Sea Benthos program

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March 22, 1976, the research vessel Vauban catches the "living fossil" mud lobster Neoglyphea inopinata in deep water off Lubang Island, in the Philippines, exactly from where the Albatross had collected the first specimen in 1908. This spectacular rediscovery becomes the birthmark of the "Musorstom campaigns" which in 1999 became the Tropical Deep-Sea Benthos (TDSB) expeditions. With Neoglyphea came a cornucopia of all kinds of benthic biota which Jacques Forest and Alain Crosnier, the initiators of the program, farmed out to a worldwide network of specialists. Taiwanese partners jointed this program since 2000 and the cooperative

activities of both countries became important thanks to the bilateral cooperation research project from MOST and ANR entitled "Taiwan France marine diversity exploration and evolution of deep-sea fauna (TFDeepEvo)" conducted between 2013 and 2016. In 2016, forty years later, the TDSB expeditions have made over 5,000 dredge and trawls hauls for the biodiversity explorations. Here, I present some progress on the research of fish systematics and evolution through the TDSB. By combining our exploration strategy with some hypothesis-driven studies, we provided a better access to the taxonomic knowledge of the deep-sea fishes, especially with help of modern molecular tools, and better understandings of causes of the pattern of diversity and evolution of the deep-sea fauna.

## First records of *Nicella* coral garden epibionts of the Brazilian continental margin

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UNIVERSIDADE FEDERAL RURAL DE PERNAMBUCO

Octocoral species may serve as biogenic substrate for epifaunal communities,especially on the continental slope, where consolidated substrates are scarce. In this study we record, for the first time in Brazil, the genus Nicella forming a coral garden (with three different species), describe the diversity of Cnidarian taxa epibiont in these octocorals. This is also the first record of the species Nicella spicula and Nicella gracilis for the Southern Hemisphere. Specimens were sampled in the Potiguar Basin (Brazil) at 108 m depth. Sea anemones (Amphianthus sp. nov.), scleractinians (Madracis myriaster and Astrangia solitaria) and nine species of hydroids (Halopteris carinata, Antenella sp, Monostaechas quadridens, Aglaophenia rhynchocarpa, Gymnangium sp., Sertularia distans, Sertularella rugosa, Hincksella formosa, Synthecium tubithecum) of families Halopterididae, Aglaopheniidae, Sertulariidae and Syntheciidae were found. All colonial cnidarians were fixed onto the base of the octocoral, whereas the anemones demonstrated preference for terminal branches. Despite few studies exploring octocorals as biogenic substrate, it is known that such substrate is used mainly by suspension feeders, such as the cnidarians found in this study. The first record of Nicella garden in South Atlantic is important because it indicates the role of these species as constructors of frameworks that serve as a hábitat for several organisms. This kind of ecological information is essential and will contribute to the development of continental slope's habitat management and fishery politicies.

## Evolutionary shifts in habitat depths of bamboo worms (Annelida: Maldanidae)

Genki Kobayashi, Ryutaro Goto, Tsuyoshi Takano, Shigeaki Kojima
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Many marine benthic taxa have speciated along depth gradients despite no apparent dispersal barriers. Thus, understanding evolutionary shifts of habitat depths has been one of the central themes in deep-sea biology. The Maldanidae (bamboo worms) comprise more than 280 species of 40 genera and six subfamilies that occur in various environments from the intertidal to hadal zones. They can provide a suitable opportunity for studying evolutionary shifts in bathymetric zones and speciation along depth gradients. Phylogenetic relationships within the family, however, remain largely undetermined based on molecular data. In this study, we reconstructed a molecular phylogeny of more than 50 maldanid species from six subfamilies based on two nuclear (18S rDNA and 28S rDNA) and

two mitochondrial gene (16S rDNA and COI) sequences. Mapping habitat depths on the phylogenetic tree suggested that habitat shifts among bathymetric zones occurred multiple times; four lineages contain abyssal and/or hadal species. Although Praxillella gracilis has been recorded from depths of 4–1,600 m and thus considered to be an eurybathic species, we detected great genetic deviations among three individuals of P. gracilis that are morphologically indiscriminable but inhabit different bathymetric zones. We also discuss statuses of intra-familial taxonomic groups and morphological evolution of tube-capping plates on a head and tail, which were lost at least three and one times, respectively, despite their protective benefit. The losses may reflect changes in maldanids' behavior and habitat.

## From shallow to deep: phylogeny and evolutionary radiation of marine mussels (Bivalvia: Mytilidae)

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Marine mussels are bivalves that are distributed in the oceans worldwide and occupy various habitats, including one special group (subfamily Bathymodiolinae) inhabiting hydrothermal vents, cold seeps, and sunken woods/whale falls. However, their taxonomy and phylogeny remain unclear from genus to family levels due to equivocal morphological and/or anatomical characters. In the present study, we aimed to revisit the deep phylogenetic relationships among extant marine mussels (family Mytilidae) and test evolutionary hypotheses. To this end, we inferred phylogenetic relationships among 42 mytiloid species, 19 genera and five subfamilies by using two mitochondrial (COI and 16S rRNA) and three nuclear (18S and 28S rRNA, and histone H3) genes. Phylogeny was reconstructed with a combination of five genes using Bayesian inference (BI) and maximum likelihood (ML) method, and then divergence time was estimated for the major nodes using a relaxed clock model with three fossil calibrations. Identical tree topologies were obtained by BI and ML methods, and two major clades (Clades 1 and 2) were revealed with strong support. In Clade 1, the deep sea mussels (subfamily Bathymodiolinae) were sister to subfamily Modiolinae (represented by Modiolus), and then was clustered with Leiosolenus (subfamily Lithophaginae). Clade 2 comprised Lithophaga (subfamily Lithophaginae) and subfamily Mytilinae. Additionally, a Modiolus species and Musculus senhousia (subfamily Crenellinae) were positioned within the subfamily Mytilinae. The phylogenetic results strongly indicate monophyly of Mytilidae and Bathymodiolinae, polyphyly of Modiolinae and Lithophaginae, and paraphyly of Mytilinae. Divergence time estimation showed an ancient and gradual divergence in most mussel groups, whereas the deep-sea mussels originated recently from shallow to deep waters and diverged rapidly during Paleogene. This work provides the most comprehensive molecular phylogenetic analyses of the Mytilidae mussels, and will support their taxonomic revision. The findings will shed light on the evolutionary history of this important bivalve group.

## Phylogeny and biogeography of deep-sea wood boring Xylophagainae (Mollusca, Bivalvia)

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Deep-sea wood falls lying on the seafloor may constitute patchy organic resources that sustain diverse fauna. Microbial activity around and inside

the decaying wood substrate can result in a sulfide-rich habitat that can be colonized by specialized invertebrates, including taxa shared with other chemosynthetic habitats. Among the first colonizers able to digest wood and open up the wood falls are the bivalve mollusks, Xylopagaidae. More than 50 named species of xylophagaid bivalves are known worldwide, however very little is known about species distribution, genetic diversity or overall phylogeny. We collected and analyzed wood-boring bivalves from 19 sites (500-2500 m depth): eleven in the Atlantic and the Mediterranean, six in the Pacific and two in the Indian Ocean. The aim was to combine morphological and molecular analyses to identify wood-boring deep-sea bivalves of the three xylophagaid genera Xylophaga, Xyloredo and Xylopholas and to document their phylogeny and biogeography. We used mitochondrial and nuclear markers (cytochrome c oxidase subunit I, 18S and 28S rRNA) to identify the specimens and to examine their phylogenetic relationships along with representatives of the closely related taxa; Pholadidae and Teredinidae. The combined analysis of the genetic markers provided consistent topologies model-based phylogenetic methods. We identified a total of 19 clades of Xylophagainae: seven in the Atlantic including one potential new species closely related to Xylophaga atlantica, nine in the Eastern Pacific and two in the Indian Ocean. Xylophaga atlantica and X. dorsalis were the species shared by most of the Atlantic-Mediterranean sites, while X. washingtonia, X. oregona and X. cf. siabenalleri were widely distributed among the Pacific ones. COI haplotype networks showed limited connectivity between the Mediterranean and the Atlantic sites for X. brava and X. atlantica. Our study provides the first detailed study on the phylogeny of Xylophagainae and the results suggest that further research and a revision of their taxonomy are needed.

## *Chiridota heheva* - the cosmopolitan holothurian

Elin Thomas
University of Southampton

Hydrothermal vents are renowned as hotspots of species discovery. With the advent of deep-sea mining, there is an urgent need for greater knowledge of hydrothermal vent fauna. The 67th voyage of RRS James Cook to the Longqi hydrothermal vent field on the South West Indian Ridge (SWIR) culminated in the collection of 21 different taxa, including holothurian specimens initially proposed to belong to the genus Chiridota. This project employs morphological and molecular analyses, including scanning electron microscopy and phylogenetic marker sequencing, to explore the taxonomic affinity of the SWIR holothurians and to determine whether or not they represent a new species. Whilst phylogenetic analyses confirm the affinity of the SWIR holothurians within Family Chiridotidae, the genus Chiridota is not recovered as a monophyletic clade and Bayesian inference posterior probability values are too low to discern the exact phylogenetic relationship of Chiridota spp. To date, Chiridota hydrothermica represents the single holothurian species described from hydrothermal vent habitats. However, morphologically, the SWIR holothurians are identified as Chiridota heheva, with key distinguishing features including six-spoked wheel-shaped body wall spicules, non-perforated calcareous ring, and twelve radially symmetrical peltato-digitate tentacles with conspicuous finger-like digits arranged along the margin. This is a significant and rare discovery, as C. heheva may now be added to the limited collection of deep-sea species described from hydrothermal vents, cold seeps, and ephemeral organically-enriched habitats. Furthermore, the novel results of this project, along with existing evidence collated from previous studies, suggest that C. heheva and C. hydrothermica may be synonymous, representing a single widespread species displaying environmentally-mediated phenotypic plasticity. This project outlines the first step in investigating the nature and relationship of holothurians endemic to chemosynthetic and organically-enriched environments, and highlights the need for phylogenetic study of multiple specimens when inferring future taxonomic status.

## Three Siphonostomatoid Copepods (Dirivultidae) from a Deep-sea Hydrothermal Vent Field in the Central Indian Ridge

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Three species of copepods belonging to the family Dirivultidae (Siphonostomatoida) are collected from a deep sea hydrothermal vent field on the Central Indian Ridge in the Indian Ocean during the conduct the deep sea research cruse (July 28 – August 16 2017) by R/V ISABU of Korea Institute of Ocean Science and Technology (KIOST), and reported. They consist of Aphotopontius limulatus Humes previously known from vent fields in the East Pacific and two new species, as follows: Aphotopontius n. sp. and Stygiopontius n. sp. Aphotopontius n. sp. is characterized by the presence of the inner coxal seta in the first to third legs, not in the fourth leg, 2.86 times as long as wide of the caudal ramus in the female, and the lateral margin with an angular apex in the genital double-somite. Stygiopontius n. sp. is easily distinguishable from the congeners by possessing the only three setae on the inner lobe in the maxillule, and a large tubercle on the first endopodal segment and two spinules-tipped distal spines on the second endopodal segment in the antenna. This is the first record on copepods living in vent fields of the Indian Ocean.

## Different, different but same? Extreme morphological plasticity in deep-sea limpets

Chong Chen, Hiromi K. Watanabe, Yukiko Nagai, Takashi Toyofuku, Kei Sato, Robert G. Jenkins, Ting Xu, Jin Sun, Jian-Wen Qiu, Ken Takai, Katsunori Fujikura, Takenori Sasaki
JAMSTEC

Chemosynthetic ecosystems harbour rich megafaunal communities, of which gastropod molluscs comprise a major component and have received considerable taxonomic efforts. Pectinodontid limpets, characterised by a white shell with cancellate sculpture and a radula with a single trifurcating lateral teeth on each side, are a common constituent of vents and seeps in the western Pacific. Thus far, two genera (Bathyacmaea and Serradonta) totalling eight species have been described based on shell and radula characteristics, usually with disjunct distribution ranges. However, no data on their intraspecific morphological variation or population genetics have been published. In the present study, numerous pectinodontid specimens from Sagami Bay seeps, Okinawa Trough vents, and South China Sea seeps were investigated morphologically, revealing great disparity in both shell and radula within each locality, rendering existing species and even genera boundaries questionable. Morphological plasticity in shell form according to the substrate shape was confirmed through live-rearing in a controlled aquarium. Furthermore, phylogenetic and population genetic analyses of these Bathyacmaea and Serradonta specimens clearly demonstrated that they belong to a single molecular operational taxonomic unit regardless of their shell form, shell sculpture, or radula characteristics. Altogether, these results strongly suggest that the currently described vent and seep pectinodontids ranging from Sagami Bay to South China Sea are actually all forms of a single extremely morphologically plastic species. An additional population from the southeastern Mariana Forearc proved to be genetically distinct, and electron microscopy showed that this population was distinct from other aforementioned populations in terms of shell microstructure, indicating that this may serve as a reliable taxonomic

character in pectinodontid limpets. As a case study, the present research serves to raise awareness against interpreting taxonomy and ecology of both living and fossil species solely based on hard part morphology without carefully assessing the reliability of characteristics used.

# Autecology - TALKS

## *Hi! Lights*: Bioluminescent communication of a mesopelagic lanternfish

José Paitio, Shiro Takei, Masakazu Iwasaka, Fanny de Busserolles, Justin Marshall and Yuichi Oba
Chubu University

Lanternfish species (Myctophidae) have diverse light organs with proposed specific ecological purposes. The head photophores may be used to illuminate prey and the surrounding environment, and/or startle predators, while lateral body photophores may be used for intraspecific communication, and the ventral body photophores for counterillumination. Their eyes also possess several adaptations to increase sensitivity (e.g. pure rod retina, tapeta lucida) and allow vision in dim light conditions and for viewing bioluminescence.The functional structure of the myctophids' photophores has received little attention to date, and it is still unclear if the hypothesized differences in ecological uses of their light organs are also reflected at the structural level, and how it all fit with their visual system. To answer these questions, we analysed into details the photophores and eyes of Diaphus watasei collected in Mimase and Katahara harbours in Japan, using histology, spectrometry and photophore chemistry. Results show that the internal structure of head and lateral body photophores allows a wider lateral light emission than the ventral body photophores. Moreover, the head photophores have a silver reflection and high coelenterazine content while the body photophores present a blue reflection and a lower coelenterazine amount. These structural properties correlate well with the proposed ecological use of the different luminous tissues: the lateral body photophores may allow a dim intraspecific communication, the ventral photophores an accurate counterillumination camouflage, and head photophores a bright illumination. Furthermore, the tapetum lucidum reflection of D. watasei was found to be limited to the blue-green part of the visible light spectrum, allowing a better perception of the bioluminescent signals of conspecifics as well as the common blue-green bioluminescent signals of other organisms (prey and predators). This work was supported by JST CREST Grant Number JPMJCR16N1, Japan.

## The curious tale of *Astomonema* in the deep sea – a chemosynthetic worm feeling at home in high-deposition heterotrophic sediments

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Astomonema is a nematode genus characterized by endosymbiotic chemo-autotrophic bacteria inside the body. Their dependence on these prokaryote symbionts as an energy source is evident since they lack a mouth and their pharynx is vestigial, precluding food uptake via the mouth. Until 2012, astomenematines had never been observed beyond shelf seas. Here we report the presence of Astomonema s.l. in six different deep-sea canyon systems in the Atlantic and the Mediterranean. Their sample abundances range from one individual to being the dominant component in meiofauna assemblages. Astomonema abundance generally increases with increasing sediment depth, supporting their known association with reduced sediments in shallow-water habitats. We try to answer the question "Why are these nematodes doing well in deep-sea canyon systems?" We present evidence on the environmental conditions that can support the astomonematine life style in the deep sea. Nematode results of a time series (2006, 2010, 2014) from a Whittard Canyon site dominated by Astomonema are discussed in the context of organic enrichment and high deposition rates in canyon systems. We also explore the potential of deep community analyses of benthic assemblages in revealing more widespread occurrence of chemosynthetic pathways supporting the traditional detritus-based, heterotrophic food web found in canyons.

## Buoyancy, migration, and foraging in the abyss: How do deep-sea fishes balance the energy budget?

Imants G. Priede
University oif Aberdeen, Hellenic Centre for Marine Research

It is axiomatic that in an extreme food-limited environment such as the deep sea, actively swimming animals such as fishes should optimise their energy expenditure so as to maintain positive balance enabling them to grow and reproduce. Theory indicates that to minimise energy cost fishes should swim at the optimum Uopt or maximum range speed that varies between 0.7 and 5.0 body lengths per second (L.s-1) depending on species (Videler, 1993). However, tracking of abyssal grenadiers (Coryphaenoides armatus) shows that they swim at an average speed of 0.2 L.s-1; much slower the predicted optimum. Optimum swimming speed theory contains an implicit fallacy that early arrival at an appointment (e.g. spawning) is advantageous. If there is no time schedule and the fish is neutrally buoyant, swimming at slow speeds requires very little energy. At a speed of 0.1 m.s-1, an abyssal grenadier can travel over 3000 km per year with a negligible (1%) increase in metabolic rate above resting. For dense-bodied fish that are negatively buoyant, slow swimming is very costly. They incur a cost of take-off which means they must swim at a relatively high speed (Uopt) to achieve minimum energy cost. However, neutral buoyancy can also entail energy costs such as in sequestering low density oils or inflation of a gas bladder. This study evaluates the energy cost of different adaptive options.

## Recruitment and growth of Arctic deep-sea invertebrates in a long-term experiment

Kirstin Meyer, Melanie Bergmann, Thomas Soltwedel
Woods Hole Oceanographic Institution

The early life-history stages of deep-sea invertebrates are understudied, particularly in polar regions. It is especially difficult to estimate growth rates in situ for species that may grow just millimeters per year. A long-term (1999 – 2017) experiment in the Arctic HAUSGARTEN observatory provides valuable insights into the recruitment and growth of polar deep-sea invertebrates, and how these processes are influenced by environmental factors. After 18 years on the Svalbard continental slope (79⁰ N, 2500 m depth), panels were colonized by 13 metazoan species as well as calcareous and agglutinating foraminiferans. There were significant differences in the community composition and abundance of recruits on panels made from different materials, at different altitudes off bottom, and at different angles to the predominant bottom current, revealing species-specific microhabitat preferences of the recruits. We calculated maximum growth rates for two common species, the crinoid Bathycrinus carpenterii and the sponge Cladorhiza gelida, and used these rates to calculate the

ages for the recruits. In years with higher estimated recruitment, there was a westerly bottom current (average bearing 270 – 280º). This indicates that a densely-populated rocky reef located to the east of the experiment location may have served as a source population.

## A first glimpse into the physiology and metabolism of Indian Ocean vent gastropod holobionts
Julia Sigwart, Chong Chen, Ken Takai
Queen's University Belfast & University of California, Berkeley
Physiological traits are the foundation of an organism's success in a dynamic environment; the ability to metabolize oxygen can determine an animal species'fitness, spatial distribution, and its capacity to adapt to changing conditions. We measured routine metabolism (oxygen uptake) in two hydrothermal vent gastropods, Alviniconcha marisindica and the Scaly-foot Gastropod Chrysomallon squamiferum, from Kairei and Edmond vent fields on the Central Indian Ridge (23-25° S). Both host chemosymbiotic endosymbionts; chemoautotrophy is very demanding of oxygen and we predict that these holobionts would have high oxygen demand. A previous study reported a measurement of oxygen demand in Alviniconcha hessleri, from the Mariana Back-arc Basin, indicating that Alviniconcha has a very high metabolism and one of the most efficient symbioses among hydrothermal vent endemic metazoans. No previous studies have measured routine metabolism in any Indian Ocean vent animals. Our previous research on the anatomy of Chrysomallon indicated it has very enlarged respiratory and circulatory systems, which we interpreted as adaptations to provide oxygen to the endosymbionts in its esophageal gland. Thus we predicted that the routine metabolism and oxygen demand of Chrysomallon may be even higher than that of Alviniconcha. Oxygen demand of Alviniconcha from the two vent fields did not differ in laboratory experiments. Surprisingly, oxygen consumption of Chrysomallon was not higher than in Alviniconcha per unit tissue mass; however, Chrysomallon maintained a steady metabolic demand in experiments over a wide thermal range. While these two large gastropod species co-occur at Kairei, differences in their oxygen consumption may reflect the separate niches they occupy in the vent ecosystem.

## Pacific flatnose *Antimora microlepis* and blue hake *A. rostrata* (Moridae, Gadiformes): global overwiew of ecology, inter- and intra-species relationships, and chemical compositions
Alexei M. Orlov (1,2,3,4,5), Svetlana Yu. Orlova (1), Alexandr M. Sytov (1), Elena V. Vedishcheva (1), Pavel K. Afanasiev (6), Ilya I. Gordeev (1,7), Roman V. Artemov (1), Valeria V. Gershunskaya (1), Igor V. Grigorov (1), Nikolai B. Korostelev (2), Natalia I. Lazareva (1)
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The genus Antimora (Moridae, Gadiformes) is represented by two species, Pacific flatnose A. microlepis and blue antimora A. rostrata, widely distributed mainly in deep temperate and cold waters (Pacific flatnose in the North Pacific and blue antimora in the rest global ocean). Published data on their ecology, inter- and intra-species relationships, and chemical compositions are very limited. Here we overview the data on their distributions; age and growth; size, weight and shape of otoliths; genetic diversity based on the analysis of mtDNA gene CO1; chemical compositions of muscle tissues and liver. Haplotypic composition was studied based on samples of blue hake from Southern Ocean, Eastern Australia, New Zealand, Indian Ocean, SW Greenland, Flemish Cap, Bay of Biscay and Pacific flatnose from Emperor Seamounts, SE Sakhalin, US and Canada West coasts (Alaska to California). The most frequent haplotypes were H3 and H4 in blue antimora samples while haplotypes H1, H2 and H13 were most frequently observed in Pacific flatnose samples. Haplotypes H4 and H13 were common for both species. Attempt was made to evaluate population relationships based on comparison of relative size, weigth, and shape of otoliths analysis using samples of A. rostrata from the NW Atlantic, SW Atlantic and Antarctic and A. microlepis from the NW and NE Pacific. Statistically significant differences were found in otolith shape between both species as well as between the NW Atlantic and Antarctic A. rostrata samples. Data on age and growth is presented for blue hake from SW Greenland and Wedell Sea and for Pacific flatnose from US and Canada West coasts. Chemical compositions of muscle tissues and liver are presented for blue hake from NW Atlantic and for Pacific flatnose from British Columbia and SW Sakhalin (Sea of Okhotsk).This research was supported by the Russian Fund of Basic Research (grant 16-04-00516).

# Autecology - POSTERS

## Visual signaling by a group-forming squid in the deep sea
B.P. Burford, Robison, B.H.
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Several species of squid inhabiting the mesopelagic zone of the deep sea display repertoires of visual behaviors comparable to or exceeding those performed by their shallow-water counterparts. However, it largely remains unknown for what the deep-water species, which spend the majority of their lives in a dimly-lit or totally dark environment, use their remarkable visual displays. In the mesopelagic of the California Current System, we used cameras mounted on Remotely Operated Vehicles to document the Humboldt squid, Dosidicus gigas, to predictably display unique postures, colors, and locomotion within foraging and conspecific density categories. The patterns of subcutaneous photophore density and size in D. gigas muscle tissue align with the color-changing displays we identified as important for communication and foraging. Our results not only support the hypothesis that inter- and intraspecific communication are potential explanations for the evolution and maintenance of diverse visual behaviors in deep-sea cephalopods, but also imply a potential mechanism by which complex visual behaviors are relevant in the darkness of the deep sea.

## Discovery of a colossal slickhead (Alepocephaliformes: Alepocephalidae): An active-swimming top predator in Suruga Bay, Japan
YOSHIHIRO FUJIWARA, M. Kawato, J. Y. Poulsen, S. Tsuchida, H. IIda, Y. Chikaraishi, N. Ohkouchi, K. Oguri, S. Goto, G. Ozawa, S. Tanaka, M. Miya, T. Sado, K. Kimoto, T. Toyofuku, K. Fujikura
JAMSTEC, Australian Museum, Kitasato University, Hokkaido University, Tokyo University of Marine Science and Technology, TechnoSuruga Laboratory, Tokai University, Natural History Museum and Institute, Chiba,

To understand the roles of top predators in deep-sea ecosystems, we are currently working on an ecosystem model. In 2016, we conducted bottom longline surveys and in situ camera observations in Suruga Bay, Japan, with the aim of obtaining information on the faunal diversity and trophic interactions of deep-sea predatory fishes at depths between 200 and 2,500 m. Unexpectedly, an unidentified fish of the family Alepocephalidae (slickheads) was collected at depths greater than 2,171 m in Suruga Bay. Compared with other alepocephalid slickheads, which never exceed 5 kg in weight, this species is colossal in size (reaching ca. 140 cm in total length and 25 kg in body weight), and shows a unique combination of morphological characters, including no overlap between the dorsal and anal fin bases, large dentitions, elongated lateral line scales, and small eyes. Mitogenomic analyses also supported the novelty of this large deep-sea slickhead. Whereas most slickheads are benthopelagic or mesopelagic feeders of gelatinous zooplankton, behavioral observations and dietary analyses indicated that the new species is piscivorous. In addition, stable nitrogen isotopic analysis of specific amino acids showed that this slickhead occupies the highest trophic position recorded in Suruga Bay to date. Video footage recorded using a baited camera deployed at a depth of 2,572 m in the mouth of Suruga Bay revealed the active swimming behavior of this slickhead. The scavenging ability and broad gape of the fish might be correlated with its colossal body size and relatively high trophic position.

## Inferred post-spawning reproductive system morphology in female *Octopoteuthis sicula* Rüppell, 1844 (Cephalopoda: Octopoteuthidae)

Jesse T. Kelly
Institute for Applied Ecology New Zealand, Auckland University of Technology

Octopoteuthid squids remain a poorly studied group owing to the historic taxonomic disarray of the family, with little known about their biology or ecology. During a recently completed global revision of the family, opportunistic observations were made on variation in the morphology of the reproductive system in female Octopoteuthis sicula. Maturity stages of 75 female O. sicula were assessed and initially categorised into three stages: immature, maturing, and mature; interpretation midway resulted in the proposition of a fourth stage, resting. Size-at-stage for immature individuals was ML 9.5–92 mm; ML 70–142 mm for maturing; ML 152–206* mm for mature; and ML 151–201 mm for resting specimens. Detailed examinations of the reproductive organs of 22 mature or resting females (ML 142*–206* mm) showed two distinct morphologies among individuals of overlapping size. Mature individuals had large, developed nidamental (length 40–53% ML) and oviducal (length 14–22% ML) glands; oviducts were filled with ovulated ova; ovaries contained additional ova as well as ooctyes in various stages of development. Resting individuals had considerably reduced nidamental (length 15–24% ML) and oviducal (length 7% ML) glands; oviducts were empty; ovaries contained only undeveloped oocytes. At present, differences in appearance of the reproductive glands differentiate resting from maturing individuals; additional analyses including histology are forthcoming. Preliminary evidence suggests O. sicula may employ a polycyclic spawning strategy. Alternatively, the resting stage as proposed for O. sicula may instead represent spent morphology among octopoteuthids, which would contrast that found in other oegopsid families (e.g., Gonatidae, Onychoteuthidae).

## Flow characteristics of deep sea coral and sponge communities

Frank Parrish, Thomas Oliver
Pacific Islands Fisheries Science Center NOAA

Eighteen instruments placed by submersibles were used to measure and monitor the flow direction, speed, and tidal spectra of the seafloor water movement through patches of deep sea corals at three topographically different sites. Collecting data for 7 to 30 months, the instruments identified similar average flow rates at two of the coral patches (12.7-13.6 cm/sec) and a much lower rate at the third (4.5 cm/sec). Tidal extremes pushed max flow speeds to as high as 95.3 cm/sec, but high speed did not guarantee a patch would have higher density or diversity of deep sea corals. The low flow patch and one high flow patch showed higher diversity (15-28 taxa) and average number (0.9-7.13 colonies/meter traveled) than the patch where the max flow was recorded (11 taxa and 0.20 colonies/meter traveled). The data from the placement of multiple instruments within a patch showed variability consistent with topographic influences on flow rates (e.g., ridges versus sheltered substrate). Notable patterns in the coral community include the sites with higher average flow having more Acanthogorgia sp., Coraliidae, Lepidisis olapa, Primnoidae, and Thouarella hilgendorfi, and the two sites with the lower flow had more Kulamanamana haumeaae and Plexauridae. Sponges (e.g., Characella sp. Hexactinelida sp. Regadrella sp.) were seen only at the two high flow sites. Finally, comparison of the tidal spectra at the three locations shows obvious differences among the 3 patches and is an important factor in understanding colonization patterns of deep coral and sponge communities.

## Reproductive ecology of dragonfishes (Stomiiformes: Stomiidae) in the Gulf of Mexico

April Cook, Alex Marks, Tracey Sutton
Nova Southeastern University

Meso- and bathypelagic fishes play an important role in deep-sea food webs by mediating energy flow from surface waters to great depth. Of these fishes, the most speciose taxon is the dragonfish family Stomiidae, the numerically dominant fish predators of the global mesopelagic zone. Despite this biodiversity and ecological predominance, their reproductive ecology is poorly known. Larger, sexually mature stomiid adults are rarely caught in research surveys, impeding reproductive ecology studies. A large-scale survey was conducted in the Gulf of Mexico using both a research-sized, opening/closing trawl (10-m2 MOCNESS) and a large, commercial-sized trawl (HSRT). Size-distribution analysis of stomiids collected by each gear type revealed: 1) the HSRT caught more specimens per species than the MOCNESS, and 2) the HSRT caught significantly larger specimens, while the MOCNESS sampled more juveniles. Thus, samples from the two gear types provided an unprecedented opportunity to address stomiid reproductive ecology. Gonads were dissected from 714 individuals belonging to 47 species. Histological assessment of gonads indicated that stomiids are gonochoristic (not a given, since hermaphroditism is established in a sister taxon), and that both males and females are iteroparous, spawning multiple times throughout their lifespan. A total of 11 of the 12 dominant species had sex ratios that did not significantly differ from a 1:1 male:female ratio (P < 0.05). Histological analysis indicated that females become mature at larger sizes than males. The information presented will shape modeling usage of publically available length-frequency data, particularly with respect to size at first reproduction and interpretation of size-frequency distribution peaks as a function of sexual maturity of the separate sexes. Given the lack of age and growth data for this taxon, these data are critical for estimating stomiid production rates, a key element for quantifying the role of stomiids in the global biological pump.

## Reproductive biology and ecology of Pacific hagfish (*Eptatretus stoutii*) and Black hagfish (*Eptatretus deani*)

Aharon Fleury
Neptune and Co, Inc

Hagfish are one of the more lucrative commercial opportunities in the world with fisheries harvesting them specifically for food and for their skin for leather-based products. In 2013 a three year experimental fishery opened off the west coast of Vancouver Island, British Columbia in order to determine the sustainability of a Pacific hagfish (Eptatretus stoutii) and Black hagfish (Eptatretus deani) fishery. In this study, I examined the reproductive biology of both species including: length-weight relationships, sex ratios, fecundity, and size-at-gonadal development. This study corroborates previous suggestions that Pacific hagfish are juvenile protogynous hermaphrodites while black hagfish are likely to be dioecious with an unknown juvenile stage. Sexual dimorphism appears in both species of hagfish, which is likely the result of inter- and intraspecific morphological differences. For both species fecundity decreases throughout developmental stages, and the average fecundity is very low (27-32 eggs per female). Additionally, in both species females commence gonadal development prior to males. Furthermore, both species exhibited extreme female: male sex ratios across length-classes, however, in opposite directions. The reproductive biology of Pacific and Black hagfish models that of a k-selected species, which is a species that tends to live long and has a slow growth rate, low fecundity, and late maturity. As a result there are a variety of concerns that should be addressed when developing a sustainable hagfish fishery to prevent collapses observed in previous hagfisheries.

POSTER 20 ⚡ Autecology
TUESDAY Lightning Talks • 08:30 • Serra Room

## A CRISPR focus on *Ridgeia piscesae* endosymbiont population structure

Maeva Perez, Bernard Angers, Kim Juniper
Université de Montréal

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) are DNA sequences that constitute a historical record of the viral infections suffered by bacteria that possess the CRISPR-cas immunity. As such, they may be used to discriminate between different lineages or strains of otherwise indistinguishable bacteria and to resolve the structure of their population at unprecedented scales.Several CRISPR-cas operons were recently discovered in the representative genomes of Candidatus Endoriftia persephone; the sulfide-oxidizing bacterial symbiont associated with the vestimentiferans Riftia pachyptila, Tevnia jerichonana, Oasisia alvinae and Ridgeia piscesae. These horizontally transmitted endosymbionts are essential to the survival of the tubeworms but unfortunately, they are hard to study because they have so far escaped in-vitro cultivation and free-livings have not been sampled in the environment. Inside the housing organ of their host however, the symbionts are very abundant and metagenomic data suggest that a single host may house multiple strains of highly homogeneous symbionts. Here, we used CRISPR and other polymorphic DNA sequences to look at the genetic diversity of Ca. Endoriftia persephone within and across individual R.piscesae hosts that were sampled in contrasting environments along the Juan de Fuca ridge. Understanding the biogeographic distributions of the symbiont populations is important to understanding their evolution and predicting resilience of their host populations to changing environmental conditions.

POSTER 21 - Autecology
TUESDAY Evening • 17:45 • Serra Ballroom

## Response of sea urchin fitness traits to environmental gradients across the

## southern California oxygen minimum zone

Kirk N Sato, Andreas J. Andersson ; James M.D. Day ; Jennifer R.A. Taylor ; Michael B. Frank ; Jae-Young Jung ; Joanna McKittrick ; Lisa A. Levin
Okinawa Institute of Science and Technology ; Scripps Institution of Oceanography

The pink fragile sea urchin, Strongylocentrotus (formerly Allocentrotus) fragilis, is distributed across natural gradients in temperature, salinity, oxygen, and pH, which provides an ideal system to evaluate potential effects of multiple climate variables on carbonate structures in situ. We assess fitness trait variability across four distinct climatic zones in a natural experiment to simulate species-specific implications of oxygen minimum zone (OMZ) expansion, deoxygenation and ocean acidification. We determine from S. fragilis adults collected across multiple depth zones that urchin size and potential reproductive fitness (gonad index) are considerably reduced in the OMZ core (450-900 m) relative to adjacent zones. We also conclude that observed increases in porosity and mean pore size coupled with decreases in mechanical nanohardness and stiffness of calcitic endoskeletons in individuals collected from environments characterized by reduced pH[Total] (7.57-7.59) and reduced dissolved oxygen (13-42 $\mu$mol kg-1) suggest that S. fragilis may be vulnerable to crushing predators if these conditions become more widespread in the future. In addition, elemental composition determined using inductively coupled plasma-mass spectrometry (ICP-MS) indicates that S. fragilis has an endoskeleton composed of the low Mg-calcite mineral phase of calcium carbonate (mean Mg/Ca= 0.02 mol mol-1), the lowest Mg/Ca values measured in sea urchins known to date. Although S. fragilis was previously identified as a climate change-tolerant species, these collective results suggest that ongoing declines in oxygen and pH will likely affect the ecology and fitness of this dominant echinoid on the California margin.

POSTER 22 - Autecology
TUESDAY Evening • 17:45 • Serra Ballroom

## Clade-based differences in deep-sea wood-boring bivalves potentially impact associated animals

Janet R Voight, Raymond W Lee
Field Museum

Wood falls, like other organic falls in the deep sea are recognized as centers of increased animal diversity. However, the diversity among different wood falls can differ dramatically, potentially depending on the clade of the xylophagaids that bore the wood. The northeast Pacific Ocean hosts Xylophaga oregona and X. washingtona, members of the Xylophaga dorsalis clade. They all share the characters of dense settlement, and a short excurrent siphon with positive allometry that deposits a conspicuous fecal chimney around the bivalve's siphon inside the borehole. The fecal chimneys, according to Electron Dispersive X-ray Spectroscopy (EDS), are composed mainly of carbon and oxygen, with the elements sulfur and calcium being minor constituents (<2.5%). Isotopically, the fecal chimneys differ only slightly in δ13C from the wood into which the bivalves had bored, and the fecal chimneys have a higher N content than does the wood. However, the animal tissue is clearly more positive than is the wood (especially in X. dorsalis). No bacterial colonies can be detected in the fecal chimneys examined. The fine-grained lining of the chimneys is consistent with mucus – which can moderate diffusion of small ions. The fecal chimneys, as masses of organic material, fill the bivalve's boreholes, functionally reducing the surface area of even heavily bored wood. Chemically, their rich organic composition likely consumes oxygen and increases the anoxic zone around the wood fall, contributing to a larger, longer lived sulfide-rich habitat. Between the reduced habitat surface area and the more challenging chemical environment, the chimneys may result in lower diversity of the wood fall assemblage.

# Biodiversity and ecosystem functioning - TALKS

## Biodiversity and Process Gradients in an Area of Deep-water Convection and Acidification

David Coté, Sheena Roul, Kristin Heggland, Evan Edinger
Fisheries and Oceans Canada

Canada has committed to protecting 10% of its marine and coastal areas by 2020 as part of its commitment to achieve international (the Convention on Biological Diversity 2011 20 Strategic Plan for Biodiversity's Aichi Targets) biodiversity conservation goals and targets. Achieving these goals will likely include Marine Protected Areas (MPAs) in large offshore ocean areas. A 150,000 km2 offshore portion of the Labrador Sea (2,000-3,800 m depth) is being investigated as a potential candidate large offshore ocean area. Despite being an area of global significance for deep-water convection and carbon capture, the scientific knowledge regarding this frontier ecosystem is limited for biological elements, as the depths extend well beyond the range typically monitored by Canadian stock assessment surveys. A biodiversity (demersal and pelagic fish, marine mammals and benthos) and oceanography (sedimentation, currents, colonization) research program (2017-2019) is now underway to establish shelf to abyssal gradients and to evaluate the effects of deep-water convection and ocean acidification on biological communities. To date surveys have established the presence of deep-water corals and sponges and a variety of demersal fish species. While the dominant fish species in this study area are common to other deep-sea areas in the Atlantic, specimens of blue hake showed a high prevalence of mature or maturing individuals, which have not been reported elsewhere, suggestive that the study area serves as the first known spawning ground for this species.

## Deep-sea bioregions based on network analyses

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The definition of bioregions based on assemblages of species or communities is fundamental in ecology and biogeography but also in evolution and conservation biology where conservation policies often imply spatially based measures such as protected areas. Hence, spatial units should be biologically and ecologically relevant. In the deep sea, the definition of bioregions faces different constraints and limits. First, only a small percentage of the biggest realm on Earth has been explored. Second, species description rates are continuously increasing, highlighting the scarcity of our knowledge on deep-sea marine species. Here, we aimed at delineating bioregions of the Indo-Pacific region, based on two major (and well documented) taxa of the deep sea benthos: the Galatheids and the Ophiuroids. To cope with data of limited quantity and variable spatial coverage, we first tested aggregating of occurrence data at multiple scale to investigate the impact of the scale used for bioregion delimitation and chose the optimal scale. Then, we applied an innovative method to find bioregions based on bipartite networks. This method allows identifying bioregions but also biodiversity hotspots and transitional zones, which represent an interesting and challenging concept in the open marine environment. We compared our results to existing marine regions classifications (shallow, pelagic or deep-sea ones). Finally, we discuss our

results under the perspective of the opportunities and caveats of museum data for such applications.

## Using metabolic theory to assess structure and function in the deep-sea benthos, including microbial and metazoan dominance.

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Constraining seafloor carbon stocks and flows, and their links to biodiversity, remains a major global challenge, particularly in the deep ocean. We examine the density, biomass, respiration, and species richness size spectra of polychaetes from a time-series study (1991-2011) in the abyssal NE Pacific (Station M, 35° N 123° W, 4050 m water depth). The spectra met the predictions of the metabolic theory of ecology (MTE), and were consistent with Damuth's rule of energetic equivalence. When combined via MTE, resource supply rate and habitat temperature have valuable predictive power for seafloor standing stocks. Intra-annual comparisons suggested seasonally variable resource acquisition rates and metabolism, consistent with the scope for specific dynamic action in polychaetes. Accepting and applying the assumptions of MTE, Damuth's rule, and 3/4-power mass-scaling of metabolism to the entire benthos, then two thirds of carbon remineralised at the seafloor might be attributable to metazoan invertebrates. This is contrary to the common finding of microbial dominance, but may be resolved by considering (1) that only a fraction of microbial biomass may be metabolically active, and (2) that the metabolism of the largest members of the benthos could only be assessed at physical scales much greater than are usually examined.

## Using species area relationships to improve deep-sea sampling strategies

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Recent advances in technology have resulted in substantial increases in the quality and quantity of data collected from deep-sea ecosystems, particularly high-definition video and image data. However, the transect length and sampling effort required to accurately document species richness in deep-sea habitats remains elusive. Species-Area Relationships (SARs) describe the cumulative number of species encountered as a greater area of habitat is surveyed. SARs have been applied to many aspects of ecology, including estimating species richness, but their use has typically been restricted to terrestrial systems. Here, we use SARs to estimate species richness and sampling frequency of video transects along deep-sea soft sediments. We analysed high-definition video data collected at Rockall Bank in the North-East Atlantic. Replicate 750m-long transects were collected at 1200m depth and frame-grabs were extracted at 20-second and 1-minute intervals for the duration of the transect (277 and 94 images/transect, respectively). Images were reviewed and megafaunal morphospecies >1cm diameter were identified and quantified. EstimateS V9.1.0 was used to produce rarefaction curves over 100 randomised iterations for both datasets, and these rarefaction curves were extrapolated. Both extrapolated curves approximated asymptotes close to a sample number of 850, indicating analysis of 850 images is required to adequately assess species richness for that particular substrate. Interestingly, there was no significant difference in the number of species recorded when the transect was sampled more frequently at 20-second intervals compared to 1-minute intervals, demonstrating that sampling

images at a higher frequency along transects of soft sediment does not significantly increase the number of species documented. Thus, to ensure common and rare species are encountered, particularly when species density is low, longer transects are necessary (2.25km) to adequately sample (850 images) the substrate. These results are important in informing all future survey design and monitoring strategies for deep-sea soft sediment epibenthic megafaunal species.

## Do biodiversity – ecosystem functioning relationships shift across methane seepage gradients?

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Because deep-sea biodiversity is coming under increasing pressure from anthropogenic activities, it is crucial to understand the relationship between biodiversity and ecosystem functioning (BEF). The form of this relationship has important implications for the vulnerability of ecosystem functioning to biodiversity loss.Here we investigate BEF relationships in methane seeps. We test a theory that the relationship between biodiversity (independent variable) and ecosystem functioning (dependent variable) takes a positive and sinusoidal form, consisting of accelerating, linear and saturating portions expressed in that order. The dominance of each of these portions is modulated by the 'interaction frequency' of organisms contributing to an ecosystem function, this reflecting a balance between facilitative and competitive interactions. Methane seeps provide an interesting natural system in which to investigate BEF relationships because they consist of areas of elevated food availability in proximity to typical deep-sea benthic environments. We analyze macrobenthic push core assemblages collected by HOV Alvin from Pacific continental slopes off Costa Rica. Samples were collected from gradients of active seepage, through seep transition zones, to background sediments. To characterize biodiversity, we investigated both functional and taxonomic metrics of assemblage diversity. To measure ecosystem functioning, we investigated proxies for carbon storage, bioturbation activity, and trophic structure (considering carbon and nitrogen isotope values). Preliminary results show assemblage density to decrease, but diversity and evenness to increase, and community composition to change with increasing distance from seepage. We test the hypothesis that BEF relationships in high-density macrofaunal assemblages collected from areas of active seepage will rapidly saturate, suggesting a dominance of competitive forces. Under these circumstances, we predict ecosystem functioning to be relatively robust to biodiversity loss. Further, we hypothesize that BEF relationships in lower-density assemblages collected from background sediments will be non-saturating in form, suggesting an importance of facilitative interactions. Under these conditions, we predict ecosystem functioning to be highly vulnerable to biodiversity loss.

## Factors affecting trophic patterns of offshore benthic invertebrates at a Sub Antarctic archipelago

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Food availability is a key regulator of the distribution, metabolism and success of benthic populations. In deep sea ecosystems, hydrodynamics and depth play fundamental roles in determining benthic food resources. Recent studies suggest that the Southern Ocean Sub-Antarctic Front is shifting southwards, with implications for primary production and food availability around the Sub-Antarctic Islands embedded in the Antarctic Circumpolar Current. We used fatty acid (FA) and stable isotope (SI) analyses to investigate variability of suspended particulate matter (SPM) and the diet of benthic invertebrates at three Depths (shallow-100m, middle-300m and deep-600m) in three Hydrographic Regions with different flow and productivity regimes around the Southern Ocean Prince Edward Islands. Region and Depth both affected the SI values of SPM, while feeding guild was the key factor influencing consumer trophic pattern. Depth affected the δ15N of all trophic groups and the FA signatures of suspension feeders. Deeper samples showed higher δ15N values and a greater proportion of mono- and saturated fatty acids than shallower specimens, reflecting greater remineralization of SPM and food reaching the seafloor. Region affected the δ13C value and FA signatures of SPM, suspension feeders and deposit feeder/scavengers, with differences between the interisland and open ocean regions. This was probably linked to the retention of nutrients and phytoplankton between the islands. Critically, the effects of Depth and Region were taxon-specific, indicating that long-term responses to environmental change may have complex consequences for the feeding ecology and viability of benthic populations, with implications for the higher trophic levels that these populations support.

## Submarine canyons as centres of bioturbation activity and distinct ecosystem functioning

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The deep-sea benthos occupies more than three quarters of the planet's surface, yet our knowledge of how benthic communities contribute to ecosystem processes is still in infancy. Submarine canyons are known as conduits of organic matter and sediments from shelf to abyssal plains and are often associated with distinct macrobenthic communities, enhanced diversity and standing stocks compared to neighbouring slope environments. However, whole community canyon system studies assessing how these communities function and contribute to important deep-sea sedimentary ecosystem processes are lacking. To investigate how environmental conditions within canyons can alter ecosystem function, this study examined the functional differences between two canyons and adjacent slopes macrofaunal communities in the Mid-Atlantic Bight region in the western north Atlantic. A total of 49 trait modalities across 10 biological traits were used and showed that higher functional richness was present within upper and middle canyon communities compared to slope communities across the studied depth gradient. Lower canyon communities (800-900 m) were less functionally rich, a feature attributed to substantial biomass contribution of opportunistic and dominant taxa that benefited from organically-enriched sediment in the canyons. Bioturbation potential was higher in the canyons than adjacent slope, especially within Baltimore Canyon, and was attributed to the high affinities for surface and subsurface sediment modifiers and sediment ingestion or filter-feeding bioturbators. The trait affinities within canyons showed propensity for sediment reworking to greater depths, suggesting that canyon communities may enhance nutrient fluxes and burial of accumulated organic matter. The findings confirm that enhanced macrofaunal community ecosystem function and higher bioturbation occurred within the canyons compared to the adjacent slopes and provides new insight into the distinct functional roles found within canyon and slope macrofauna.

## Estimating the abundance, distribution, and diversity of deep seafloor life through

## surveying, macro-ecological analysis, and modelling

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CeNCOOS, MBARI, NOC

Results from in situ surveying, macro-ecological analyses, and modelling are revising the understanding of standing stocks of biomass, diversity, how biomass is distributed spatially, and how it might change in relation to climate change. For example, there are robust macro ecological relationships between resources, the body size of individual organisms, their abundance and diversity in the deep sea. At large basin scales surface productivity, depth and temperature are critical factors in determining ecological patterns. At finer spatiotemporal scales the shape and composition of the seafloor play increasing roles in defining such patterns, as do life history traits in addition to body size. Here we examine ecological and biogeochemical data in a variety of quantitative frameworks in spatial and temporal domains, including models based directly on the Metabolic Theory of Ecology (MTE), models that reproduce indirectly the basic features of MTE, and likelihood based linear inverse models. We found that the observed macro-ecological patterns provide practical ways to examine microbial and metazoan biomass beyond any single sampling or surveying approach. The quantitative frameworks enable clear ways to examine the balance of ecosystem function across a very wide range of body sizes. Multiple model approaches looking into the potential impacts of climate change suggest that there may be substantial shifts in abundance and body size distributions on the deep seafloor. Together the results to date pose new questions about where climate change may have its most intense effects and the roles of microbial vs. metazoan life in key ecosystem functions like remineralization of organic carbon at the seafloor.

## Macrofaunal community structure and ecosystem function of organic-rich habitats on the Washington-Oregon margin

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While it is accepted that organic-rich habitats such as whale-bones and wood-falls contribute to biodiversity and ecosystem function in the deep sea, existing studies of organic-fall community structure across bathymetric gradients and differing geographical locations have been largely qualitative. We are using a comparative-experimental approach involving the deployment and quantitative recovery of organic-rich substrates along the Washington-Oregon margin to address several key hypotheses: (1) The community structure of macrofaunal colonisers in whale-bone and wood-fall habitats varies between depths, locations and substrate types along the WA-OR margin, and (2) Wood degradation rates, and the abundance and diversity of the infaunal wood-fall community, are directly related to the abundance of wood-boring xylophagaid bivalves. Four identical benthic landers holding replicate wood, bone and inorganic hard substrates were deployed for 15 months to depths of 1500 and 3000 m, spaced ~400 km along the WA-OR margin. Multivariate analyses revealed that epifaunal community structure varied predominantly with depth, followed by location and finally by substrate type. The abundance of xylophagaid bivalves (genus Xylophaga) was greatest in wood blocks deployed to 1500 m and was responsible for up to 92% of wood mass loss. The abundance of xylophagaid bivalves in wood blocks was positively correlated with infaunal abundance and species richness, but negatively with species evenness, caused by increased dominance by dorvilleid polychaetes in the most heavily degraded wood blocks. This study allows us to quantitatively assess the role of wood-boring bivalves as key ecosystem engineers at deep-sea organic-fall habitats.

## Arctic benthic size spectra, biomass and production (Fram Strait)

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We present bathymetric patterns in benthic community structure and functioning at the Long-term Ecological Research observatory HAUSGARTEN in the Fram Strait. Meiofauna, macrofauna, and sediments were sampled at 15 stations along a bathymetric gradient from Spitsbergen coastal waters (100-300m) across the Vestnesa Ridge (1000m) down to the Molloy Hole (5561m). Benthic organisms were identified, enumerated and measured to obtain individual dimensions, biovolume, and biomass. Secondary production, respiration, and carbon demand were estimated based on individual biomass. Benthic size spectra were constructed by plotting the biomass against the log2-transformed size classes. Benthic standing stocks, production, and carbon demand declined with depth alongside the decline in food quantity and quality (as indicated by POC and chlorophyll a content in sediments). Bathymetric declines were stronger for macrofauna than for meiofauna and a transition towards a system dominated by smaller organisms in deeper ocean zones was documented. Meiofauna:macrofauna biomass and production ratios increased from 0.1 and 0.6 in coastal waters to 0.3 and 1.9 on the rise (4042-5102m). The benthic biomass size spectra were bimodal in shape, the width of size spectra declined with increasing depth (from 32 to 23 classes). A reduction of number of size classes was stronger in macrofaunal part of the spectra. The largest and the smallest size classes and the peak in biomass for macrofauna were shifted towards smaller sizes in deeper zones. Fragmented size spectra observed at the two stations (including the Molloy Hole) could be interpreted as effects of physical sediment disturbance (by currents or bioturbation) and resulted in dramatic increase in meiofauna:macrofauna ratio in biomass (0.8) and production (6.5) in the Molloy Hole. The presented patterns are likely to be modified by on-going regional changes in ice coverage, productivity and food supply to the deep sea in the course of the climate warming.

## Biodiversity–ecosystem functioning relationships in long-term time series and palaeoecological records: deep sea as a test bed

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The link between biodiversity and ecosystem functioning (BEF) over long temporalscales is poorly understood. Here, we investigate biological monitoringand palaeoecological records on decadal, centennial and millennial time scales from a BEF framework by using deep sea, soft-sediment environments as a testbed. Results generally show positive BEF relationships, in agreement with BEF studies based on present-day spatial analyses and short-term manipulative experiments. However, the deep-sea BEF relationship is much noisier across longer time scales compared with modern observational studies. We also demonstrate with palaeoecological time-series data that a larger species pool does not enhance ecosystem stability through time, whereas higher abundance as an indicator of higher ecosystem functioning may enhance ecosystem stability. These results suggest that BEF relationships are potentially timescale-dependent. Environmental impacts on biodiversity and ecosystem functioning may be much stronger than biodiversity impacts on ecosystem functioning at long, decadal–millennial, time scales. Longer time scale perspectives, including

palaeoecological and ecosystem monitoring data, are critical for predicting future BEF relationships on a rapidly changing planet.

## Biodiversity and vulnerability of the Ligurian deep circalittoral megabenthic communities

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The Ligurian Sea is among the most studied Mediterranean basins due to the numerous research groups that, since the beginning of the last century, have characterized the benthic and pelagic biota, mainly thanks to SCUBA diving and trawl surveys. Nevertheless, a large knowledge gap still exists for deep circalittoral communities, which thrive in the deepest part of the continental shelf and upper slope. Recent reviews, however, suggest that this bathymetric zone may host the deepest extension of the shallow-water animal forest as well as a diverse deep circalittoral assemblage that constitutes the so-called roche du large community. Considering that hard grounds found at relatively short distances from the coastline attract a substantial amount of professional and recreational fishermen, it became very important to carry out an extensive investigation in this area.Four years of ROV surveys (2012, 2015, 2016, and 2017) were performed along the Ligurian continental shelf and shelf break at depths of 50 to 220 m in order to characterize the main megabenthic biocoenoses and quantify the anthropogenic disturbance. More than 70 ROV dives were thoroughly examined to identify variations in substrate type, depth and slope, together with all megabenthic species and traces of human impact and lost litter. A comprehensive community analysis was then carried out to identify the main benthic assemblages and the most relevant environmental parameters that explain the patterns observed. A well-preserved deep circalittoral environment was found, with representatives of gorgonian and black coral forests, horny sponge grounds, Dendrophyllia cornigera aggregations as well as soft-bottom meadows of sabellids and alcyonaceans.A georeferenced database has also been created, where community maps were overlapped with areas of high impact in order to identify a potential network of sensitive habitats that may constitute the basis to identify future Marine Protected Areas (MPAs).

## Abyssal ecosystems and biogeochemical cycles revealed by in-situ experiments

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JAMSTEC

Abyssal plains dominate more than 50% of Earth surface and thus play important roles on biogeochemical cycles. Sinking organic matter (OM) flux, derived from ocean surface to the seafloor, is believed to play a crucial role in the abyssal plain benthic ecosystems. However, the biogeochemical cycles starting from the sinking OM and their functions, are poorly understood at abyssal plains. To investigate both heterotrophic and autotrophic activities of the abyssal benthic ecosystems and corresponding carbon and nitrogen cycles, samplings of surface sediment and organism, as well as in-situ experiments, were performed at western Pacific stations (39º00'N, 146º01'E, 5260 m; 12º00'N, 154º00'E, 5940 m; 1º15'N, 163º15'E, 4280 m) under different surface productivities (net primary production: 323.7, 42.8, and 106.1 gC m-2 yr-1, respectively). The results suggest that the OM fluxes affect both sediment geochemistry and organisms; 8.7 times higher sedimentation rates, 21.1 times higher

concentration of phytopigments, 106, 27.5, 3.5, and 1.3 times higher abundances of mega-, macro-, meiofauna, and prokaryotes, respectively, at 39ºN than 1ºN. Higher viral abundances and viral production rates at 39ºN than 1ºN suggest that prokaryote turnover is much higher at 39ºN than 1ºN, even though the prokaryotic abundances were similar each other. Consequently, oxygen consumption rates at 39ºN was 3.2 times higher than 1ºN. Experimental addition of labeled algae, diatom, and cyanobacteria, further confirmed intense consumptions of labeled algae at 39ºN. Interestingly, the faunal responses to algal OM were different between diatom and cyanobacteria additions. Autotrophic microbial productions were almost negligible at both sites, supporting the importance of sinking OM originated from ocean surface through water column to the abyssal benthic ecosystems.

## Abyssal bioluminescence

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Abyssal seafloor is considered to extend from 2000 to 6000m, it is a cold dark place (0 to 4°C no sunlight), it represents more than 70% of the ocean and about 50% of the total planet surface. This vast territory was virtually unknown a century ago and it is only quite recently that during 10 years a systematic exploration was conducted by one international consortium called CeDEMar (Census of the Diversity of Abyssal Marine Life). An astonishing biodiversity was found and the researchers aimed to describe 500 commonly found species. It is believed that only 1% of this biotope has been sampled and a huge number of organisms remain unknown. Rarely sampled, the abyssal benthic fauna capability to produce light is virtually unknown. Few reports were produced using highly sensitive camera mounted on an autonomous lander send to the seafloor. Abyssal luminous organisms were either not recognized or could not be identified at specific level but most of them belong the following taxa: Cnidaria, Ctenophora, Copepods and Echinoderms. During a recent expedition on the East coasts of Australia, systematic surveys of abyssal plains from Hobart to the Great Barrier Reef were realized using bottom beam trawls. These brought back at the surface specimens that were observed in a cold dark room enabling us to document for the first time some bioluminescent display of rarely seen organisms using sensitive camera, video recordings, luminometer and microspectrophotometer. Images and data from benthic abyssal organisms revealed the diversity of abyssal bioluminescence. Tissue were frozen and fixed for further analysis, work is in progress to describe this fauna. Deep down animals shine light but for what purpose, this remains a mystery, new expeditions will be necessary to better understand abyssal bioluminescence.

## Patch dynamics of beta diversity across multiple spatial scales in the deep Gulf of Mexico macrofauna communities

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Arguably one of the most influential ideas about deep-sea diversity, the patch-mosaic hypothesis, (J. Frederick Grassle & Howard L. Sanders, Life histories and the role of disturbance, Deep Sea Research and Oceanographic Abstracts, Volume 20, Issue 7, 1973, Pages 643-659): "In species with highly specialized microhabitat preferences, patchiness may develop on a much smaller scale than would be expected in shallow water." The 'patch-mosaic model' has been invoked multiple times in discussions of deep-sea diversity. A variety of factors can create a landscape of distinct (micro)habitats including spatially localized and seasonally pulsed imports of food, ecosystem engineering through biogenic structures and bioturbation, and disturbance and sediment sorting

from currents. However, results from both manipulative experiments and precision sampling to test the patch-mosaic model of Grassle & Sanders (1973) have varied, leading some authors to suggest that patch dynamics may be unimportant in explaining high deep-sea biodiversity.We utilized a remotely operated vehicle and a spatial sampling protocol that documents patterning at scales of centimeters, 100's of meters, and 100's of kilometers over an isobath to document patterns of beta-diversity and patchiness in macrofauna of the Gulf of Mexico. All cores were subsampled for analysis of sediment grain size and carbon content, both hypothesized drivers of species diversity within deep-sea sediments. We document extreme variation in species composition from cores at all levels of spatial scale. Part of this biological patchiness appears to reflect underlying microhabitat patchiness in environmental characteristics. The remaining unexplained variation is potentially related to neutral processes related to random draws of recruits from a regional pool. Overall, our findings support the patch-mosaic model and suggest that the deep sea, and its high biodiversity, may be unique in patch persistence and density

## Habitat use and associations of demersal fish in the vicinity of the Sub-Antarctic Prince Edward Islands.

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South African Environmental Observation Network, South African Institute for Aquatic Biodiversity

The properties of unconsolidated benthic habitats, including their biogenic structures, are increasingly recognized as determinants of demersal fish assemblage composition. We present the results of the visual surveys of demersal fishes and their habitat offshore of the Prince Edward Islands (PEI), Southern Ocean. Photographic surveys were conducted over three austral autumn expeditions to survey the island's outer shelf and slope habitats. Physical habitat characteristics and epibenthic invertebrate fauna were quantified alongside the identification of fishes. Multivariate statistics were used to test for effects of epibenthic invertebrate assemblages and habitat characteristics on the distribution of fishes. The richness of ichthyofauna was low with 10 species recorded. The most abundant of these was, by a large margin, Lepidonotothen larseni, followed by L. squamifrons and Gobinotothen marionensis. Habitats with emergent filamentous biogenic structures were found to influence the distribution and abundance of most species but certain taxa including flatfishes were almost exclusively observed in areas with little to no biogenic structure. Results are the first indication of patterns of habitat usage for these fishes at the islands.

## Deep-reef fish assemblages of the Great Barrier Reef shelf-edge (Australia)

Tiffany Sih, Michael J. Kingsford, Mike Cappo
James Cook University, AIMS@JCU partnership with the Australian Institute of Marine Science, ARC Centre of Excellence for Coral Reef Studies

Underwater video has great utility to study harder to sample areas such as deeper reefs. Baited Remote Underwater Video Stations (BRUVS) and multi-beam bathymetry were used to investigate deep-reef fish communities off the continental slope in the Great Barrier Reef, Australia. BRUVS were deployed between 50-300m and fish species richness and diversity were recorded using Australian Institute of Marine Science (AIMS) software. There were significant differences in fish assemblages across depths, with different dominant families and groups of species characterising broad depth categories. For the particular reefs studied, multi-beam habitat derivatives such as depth, rugosity and slope were correlated with higher species diversity and greater abundance. This study resulted in novel records for fish species recorded elsewhere in the Indo-

Pacific at similar depths and also identified potential new species. BRUVS have proved useful as a fishery-independent method to survey fish communities, to identify potential "hot-spots" of biological diversity and new species, and to explore surprisingly diverse deep reefs.

## Functional morphology of deep-sea fishes from micro-computed tomography

Mackenzie Gerringer, Abigail A. von Hagel, Adam P. Summers
University of Washington

The deep sea is home to a stunning array of adaptations driven by high pressure, low light levels, limited food availability, cold temperatures, and more. Although there has been extensive research on the functional morphology of fishes, the difficulty and cost of collecting deep-sea specimens has limited most studies to shallow-living species. Representative taxa of the bathyal, abyssal, and hadal fish communities were chosen for an investigation of feeding mode across depth and habitat, including members of the families Liparidae, Macrouridae, Synaphobranchidae, Zoarcidae, and Ophidiidae. Skeletons of deep-sea fishes from recent collections and museum collections were imaged using micro-computed tomography (micro-CT, Bruker SkyScan 1173). Morphometrics and relative densities of skeletal elements involved in feeding were analyzed and compared across phylogeny and collection depth. Mechanical advantage of the jaw was calculated. The majority of data collected from this study focused on skeletal morphology, however, select specimens were stained with iodine to assess jaw musculature and calculate suction-feeding index. Suction feeding index and mechanical advantage provided insight into the species' reliance on manipulative feeding versus suction feeding. Hadal fishes rely primarily on suction feeding, while abyssal species displayed more diverse feeding modes. Differences in feeding mode in fishes in the abyssal and hadal zones could be due to the increased biomass of small crustaceans in hadal trenches caused by funneling of organic matter. Although overall skeletal density was lower in deeper-living fishes, well-ossified pharyngeal jaws were found in even the deepest-living species. All micro-CT data from this research are made publicly available through the online database MorphoSource for open use in teaching, outreach, and research, facilitating multiple studies where collection opportunities are limited and serving as a digital archive of morphological biodiversity in the deep sea.

## Functional biodiversity of New Zealand's marine fishes across depth.

Elisabeth Myers, Marti Anderson, David Eme, Libby Liggins, Clive Roberts, Euan Harvey
Massey University

Changes in the composition of species assemblages have long been studied using taxonomic diversity alone. To better understand and predict ecological processes, ecosystem services, and resilience, it is important to also study functional biodiversity. Decreases in light, temperature, and trophic resources, along with increases in pressure that occur with greater depth, renders the deep sea one of the most constraining environments for supporting life. However, little is known about how biodiversity, and especially functional biodiversity, changes along the depth gradient. This work aims to fill this gap by assessing how fish traits associated with the structure, locomotion, and feeding of fishes, reflect functional adaptations to the extreme environment of the deep sea. Fish community composition and functional trait measurements were obtained from unique stereo-baited remote underwater video (stereo-BRUV) footage of fishes in 7 locations from subtropical to subantarctic New Zealand waters, spanning 21 degrees of latitude. The video footage is drawn from a structured, stratified replicated sampling design including 7 depth strata (50m, 100m,

300m, 500m, 700m, 900m, and 1200m), with 144 fish accurately identified to species level. Trait measurements were taken from this stereo-video footage as well as direct measurements of preserved specimens held in museum collections. These trait measurements included several which capture the functional changes predicted to be important across the depth gradient for fishes (i.e. oral gape shape, eye size and position, body transversal shape, and caudal peduncle throttling). Eye size was found to peak at intermediate depths of 500-700m, potentially indicating a strategy maximizing the paucity of light still present, whereas oral gape shape consistently increases and is largest in the deepest stratum (1200m), suggesting increased generalization of feeding behavior. I will present these results and our on-going analyses exploring trait relationships of New Zealand fishes across the depth gradient using multivariate functional diversity measures.

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TUESDAY Afternoon • 17:30 • San Carlos Room
## Changes in reef fish communities from the altiphotic to the rariphotic
Paris Stefanoudis, Lucy Woodall, Alex Rogers
Nekton Foundation, UK, University of Oxford, UK
Shallow ('altiphotic', <30 m), warm-water coral reef habitats are on the decline worldwide due to a suite of anthropogenic pressures including overfishing, pollution and the effects of climate change. As commercial exploitation of the oceans (e.g. fishing) moves gradually into greater depths, providing baseline information for fish communities from deeper reef habitats in the mesophotic (30-150 m) and the rariphotic (150-300 m) remains as timely as ever, especially since it has been suggested that they could act as refuge for shallow-water populations. With that in mind, in 2016 we conducted diver and submersible video surveys on the Bermudian slope and flank of Plantagenet Bank to investigate patterns of fish assemblages between 15-300 m. Our results demonstrated a decline in fish abundance and biomass with increasing depth, although diversity peaked at the transition from the altiphotic to the mesophotic. Fish communities were primarily depth-stratified with unique faunas inhabiting the mesophotic and rariphotic zones, while location, substratum composition and benthic cover (hard corals, macroalgae) also played a significant role in shaping fish assemblages. The unique nature of the deeper fish communities reported here, highlights the inherent vulnerability of deep reefs to targeted fishing pressures and should be taken into account in future coral reef conservation and management planning.

# Biodiversity and ecosystem functioning - POSTERS

POSTER 23 ⚡ Biodiversity and ecosystem functioning
TUESDAY Lightning Talks • 08:30 • Serra Room
## The biodiversity of bivalves and gastropods north and south of the Greenland-Iceland-Faroe ridge
Hronn Egilsdottir, Niall McGinty, Gudmundur Gudmundsson
Marine and Freshwater Research Institute, Iceland ; Mathematics and Computer Science, Mount Allison University, Canada ; Icelandic Institute of Natural History, Iceland
Lack of data on benthic diversity in the deeper parts of the marine realm A) limits understanding of general patterns and processes shaping phylogenetic- and functional diversity in the deep sea and B) hinders understanding of how rapid environmental changes will alter benthic communities within this century and beyond. We address this knowledge gap by describing and comparing the diversity of bivalves and gastropods along the bathymetric gradient north and south of the Greenland-Iceland-Faroe (GIF) topographic ridge which separates the Nordic Seas from the bulk of the North Atlantic. Patterns of alpha-diversity were estimated as

E(S20). Regional and depth related beta-diversity was analysed and the additive contribution of turnover (species replacement) and nestedness (species loss/gain) to beta-diversity was calculated. This study sheds new light on deep sea diversity patterns of bivalves and gastropods in the high latitude North Atlantic and provides baseline data on species occurrences, data of importance for understanding the impacts of ocean warming and acidification on benthic molluscs throughout the region.

POSTER 24 + Biodiversity and ecosystem functioning
TUESDAY Evening • 17:45 • Serra Ballroom
## Deep-water macrofauna diversity and functional traits at Gulf of Mexico central coast: General patterns associated to depth and temporal variation
Ivan Hernandez-Avila, Daniel Pech
Laboratorio de Biodiversidad Marina y Cambio Climático (BIOMARCCA), ECOSUR, Campeche, México.
Deep-water benthic environment from the Perdido area, Gulf of Mexico is currently threatened by the undergoing oil industry. Although the increasing concerns about the risks and vulnerability of deep-water benthic, many gaps persist, including general patterns of diversity. The aim of this study is determinate the patterns of species and functional-trait diversity of benthic macrofauna at the Perdido area, their variation in function of the depth range (40-3500 m depth) and time (2016-2017). Four oceanographic cruises (two per year) were performed on the B/O Justo Sierra, collecting sediment samples using a Hessler-Sandia dredge (N= 316 pseudoreplicates). Samples were systematically collected at continental shelf (< 200 m), slope (200-2000 m) and bathyal range (2000-3500 m depth) in all cruises. The estimated accumulative species diversity (total: 427.1±16.9 spp, extrapolated to 475 samples) increased slightly from the continental shelf to the slope and decrease at bathyal depths. Assemblages were dominated by polychaets, peracarid crustaceans, and copepods. Significant changes in species assemblages were associated with combination of depth ranges and cruises. Shelf and slope shown different patterns of temporal variation, meanwhile temporal variation at bathyal depth was not detected. Assemblages, based on functional traits, show consistent pattern of species assemblages change in function of depth and time. Species variation and shifts are discussed according the hypotheses of organic carbon input to deep-waters. Changes in species and functional traits related with environmental conditions, including those potentially generated by oil industry, are discussed.

POSTER 25 ⚡ Biodiversity and ecosystem functioning
TUESDAY Lightning Talks • 08:30 • Serra Room
## Deep-water Holothuroids from the West Coast of Baja California, Mexico: Taxonomy and some Ecological Aspects.
Ana K. Luna-Cruz, Michel E. Hendrickx
Postgrado en Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México. Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México
Until recently deep-ocean research off western Mexico was extremely scarce and the knowledge of communities and environmental conditions in these ecosystems was very limited. The present study is a contribution to the updating of the systematic list of deep-sea species of the class Holothuroidea (Echinodermata) occurring off the west coast of the Baja California Peninsula, Mexico. A total of 45 deep-water samples were obtained during two oceanographic campaigns (TALUD XV, July-August 2012; TALUD XVI-B, May-June 2014) on board the R/V El Puma, UNAM and 1223 specimens were collected in 23 stations in a bathymetrical range from 530-625 to 2075-2090 m. At each station, environmental data (salinity, temperature, dissolved oxygen, sediments type and composition) were recorded and used to characterize the area. The new data provide information on the geographical and bathymetric distributions of 15

species. The holothuroids community that was sampled occur below the Oxygen Minimum Zone (OMZ), with 38% of the samples obtained in stations with dissolved oxygen values <0.5 ml O2/l. The three dominant species were: Pannychia mosseleyi (up to 1136.22 orgs/ha), Abyssocucumis albatrossi (up to 504.18 orgs/ha) and Synallactes virgulasolida (up to 170.32 orgs/ha). Presence of a wide OMZ in the area generate hypoxic values at bottom level, which favor species well adapted to oxygen deficiency and reduce competition for food. Because they are mostly deposit or suspension feeders, holothuroids abundance is linked to the fact that OMZ areas are known to be rich in organic deposits, which favor even more species adapted to hypoxy.

## Benthic carbon mineralization in hadal trenches: inter and intra-trench variations

Frank Wenzhoefer, Ronnie N Glud
HGF-MPG Group for Deep Sea Ecology and Technology Alfred-Wegener-Institute Helmholtz-Centrum for Polar and Marine Research & Max Planck Institute for Marine Microbiology

Hadal trenches are considered to act as depo-centers for organic material and host unique and elevated biomasses of living organisms as compared to adjacent abyssal plains. To explore the diagenetic activity in hadal trench environments we quantified in situ benthic O2 consumption rates and sediment characteristics in five Pacific trenches. The results from all trench systems indeed show highly elevated benthic oxygen consumption at the trench axis as compared to abyssal settings and confirm that trenches are biological hot spots and indicate that the mineralization at these great depths could be important for deep sea carbon (and O2) cycle. However, the measurements also show an unexpected high variation in biological activity within and between trenches. Large scale differences appear to be driven by ocean productivity while regional and local variations are driven by trench bathymetry and timing of mass vesting event delivering organic material to the trench axis at irregular intervals. The presentation will focus on data from two recent expeditions (December 2017 and March 2018) targeting the Kermadec and Atacama Trench respectively. The data will be discussed in the context of existing insight of deep sea mineralization and evaluate the importance of key drivers for hadal diagenesis. The project was supported by an ERC-advanced grant HADES-ERC (grant agreement No 669947).

## Uncovering morphological and molecular deep-sea biodiversity - NW Pacific amphipods case study

Anna Jażdżewska, Tomasz Mamos
Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Lodz, Poland

Recognizing species diversity belongs to basic tasks in deep-sea research. Although the number of abyssal and hadal areas studied is increasing our knowledge about their faunal richness is still far from satisfactory. One of the most abundant abyssal invertebrate groups are amphipods are but only 400 benthic species were hitherto identified below 2000 m worldwide of which 50 were recorded from the abyssal of NW Pacific. Deep-sea crustaceans are very fragile and can be easily destroyed already during sampling. Thus, obtaining proper morphological material is difficult. This makes DNA barcoding a precious tool for biodiversity assessment of deep-sea organisms. We studied the molecular diversity of deep-sea amphipods from Kuril-Kamchatka Trench (KKT) and adjacent abyssal plain. The material was collected using epibenthic sledge at 28 stations at the depth range 4830-9545 m. The identified amphipods belong to 22 families and were preliminary assigned to 65 morphospecies (almost half is potentially new to science). We have obtained over 500 DNA barcodes (COI sequences) that were automatically subjected to Barcode Index Numbers

(BINs) indicating putative species in Barcode of Life Data System (BOLD). BINs cluster barcode sequences algorithmically into molecular taxonomical units that show high concordance to species. The analysis divided barcodes into 138 BINs of which 134 are new to BOLD. At least one representative of each BIN was chosen for additional 16S rRNA gene analysis. The BINs were represented mainly by one to a few sequences/individuals, only two of them were shared by more than 20 individuals. Up to 7 BINs were recognized within a morphospecies, indicating existence of potential cryptic species. Eighty seven BINs were recorded at single stations, while among others seven different distribution patterns were observed. It appeared that the KKT restricts the distribution of some species whereas for another ones it does not constitute barrier for dispersal.

## Population density, size structure, and reproductive stage of *Elpidia heckeri* and *Kolga hyalina* (Holothuroidea, Elpidiidae) in the abyssal of Central Arctic Ocean

Antonina Kremenetskaia1, Elena Rybakova1, Anatoliy L. Drozdov2, Andrey Gebruk1, Antje Boetius3,4
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Two species of elpidiid holothurians, Elpidia heckeri and Kolga hyalina, are common in many deep-sea benthic communities of the Central Arctic, Greenland and Norwegian Seas. The elpidiids are considered as selective deposit-feeders, some species specialize on nutrition-rich fresh phytodetritus. Boetius et al. (2013) showed that E. heckeri and K. hyalina selectively utilize freshly sunken ice diatom Melosira arctica. In the present study we examined population density, size structure and reproductive stage of E. heckeri and K. hyalina aiming to understand their ecological preferences and possible competition. The material was obtained in the abyssal of the Nansen and Amundsen Basins during the Polarstern cruise IceArc in 2012 (02.08-29.09). The seafloor was photographed at nine stations using a towed camera platform OFOS. At seven of these stations Agassiz trawls were taken. The ice thickness at stations varied affecting the growth of ice algae. OFOS observations revealed algal patches covering from 0 to 10% of the seafloor suggesting notable difference in organic matter supply between stations. More stable populations of both species occurred closer to the ice margin east of 75°E. These populations were characterized by low to average density with normal distribution of the size curve and presence of age cohorts. Food supply in this area apparently is more regular.Further north, under the thicker ice, and also in the western part of the Nansen Basin, two types of populations was found. The first type was characterized by low population density and relatively small size of individuals. In the second type, density was high, especially of K. hyalina reaching 1.7 ind.*m-2, with right-skewed size distribution curve and absence of age cohorts. In this area with generally lower carbon flux massive algal falls apparently occur occasionally. Seasonal reproduction was found in both species. Smaller eggs in K. hyalina suggest its higher fecundity.This study was funded by RFBR projects No 17-05-00787 and No 18-05-60228. Boetius, A. et al. (2013) Export of algal biomass from the melting Arctic sea ice. Science 339 (6126), pp. 1430–2. doi: 10.1126/science.123134.

## Deep- sea nematode communities during Arctic spring bloom: a morphometric approach

Katarzyna Grzelak, Marta Gluchowska; Klaudia Gregorczyk; Nathalie Morata; Monika Kędra; Magdalena Błażewicz

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Body size is one of the most important trait of organisms that affects their behavioral life histories, physiologies, and energy requirements. For sediment dwelling organisms, as free-living nematodes, body size is a direct adaptation for living in the sediments of particle size but the other environmental factors, as water depth and food availability, directly or indirectly shape nematode morphology. Relative importance of environmental factors affecting body size of nematodes is often difficult to assess what leaves many questions that have still to be answered. To get insight into nematode community size structure during Arctic spring, we analyzed nematode biomass, body shape and morphometric attributes in three regions located north of Svalbard (Yermak Plateau, Nansen Basin, Northern Svalbard shelf) in relation to environmental variables. Sample locations covered a wide depth gradient from 300 up to 2200 m, different sea ice concentrations and subsequent bloom stage. Bloom development is crucial for the Arctic marine ecosystems functioning, yet data from this time of year, particularly for the deep-sea basins north of Svalbard are still scarce. Over 6800 individuals of the nematodes were measured and morphometric profiles through 5 cm were examined. Feeding types and life stages information was analyzed accordingly. We compared variations of morphometric attributes (length, width, L/W ratios) of nematode communities in different phases of spring bloom development and organic matter quantity and quality inputs to the seafloor. The results of the study build up our knowledge on nematode biomass and morphometry in the high Arctic during ecologically important spring to summer transition time. In this regard, ongoing changes in sea ice cover and primary production in the Arctic may significantly affect nematode functioning, by having marked impact on their morphological characteristics. The study was completed thanks to funding provided by the National Science Centre, Poland (grant no. 2016/20/S/NZ8/00432 and 2015/19/B/NZ8/03945). Presented material was collected during R/V Polarstern TRANSSIZ cruise (ARK XXIX/1; PS92), carried out under grant number AWI_PS92_00 and organized by Arctic in Rapid Transition (ART).

## Lessons learned since 2011 about cephalopods in the Gulf of Mexico

Heather Judkins, M. Vecchione, L. Timm, I. Romero, T. Richards, A. Cook, T. Sutton
University of South Florida St. Petersburg

Two recent studies that focused on the deep water column in the Gulf of Mexico (GOM) were the 2011-2016 Offshore Nekton Sampling and Analysis Program (ONSAP) and 2015-2017 Deep Pelagic Nekton Dynamics of the Gulf of Mexico (DEEPEND) program. These programs produced a combined dataset of over 12,500 midwater-cephalopod records for the northern GOM region and this talk summarizes multiple cephalopod-related projects that have been completed. These projects include: (1) a connectivity study of three species using Sanger and Nextgen sequencing between the GOM and the northern Atlantic Ocean; (2) a stable isotope analysis of selected species to evaluate the role of cephalopods in the midwater food web; (3) a temporal examination of polycyclic aromatic hydrocarbon concentrations relative to the Deepwater Horizon spill and their possible effect on cephalopods from 2011-2017; and (4) an update on cephalopod species richness of the GOM highlighting newly discovered cephalopods. The results of these collaborative studies demonstrate the importance of cephalopods in the midwater ecosystem of the GOM.

## Benthic habitat and megafaunal diversity on the Angolan Continental Slope (SE Atlantic)

Simone Pfeifer, Brian J. Bett, Daniel O.B. Jones
Ocean and Earth Science, University of Southampton

The increasing exploitation of marine resources from continental margins has reinvigorated interest in spatial patterns of bathyal habitat and species distributions, and the processes that control these patterns. Here we use an extensive set of photographic data from the Angolan Margin to better understand the ecology of benthic megafauna in the region. The area is geologically complex, and has largely been shaped by the subsurface movement of Aptian salt deposits, associated faulting, and by the migration and release of hydrocarbons. Consequently, it is not surprising that the region has an extensive deep-water oil and gas industry. The same geological complexity has created an heterogenous seabed environment of sedimentary habitats interspersed with a variety of distinct morphological features, including pockmarks, submarine channels, salt diapirs, and coral (carbonate) mounds. Our study locations extend over six degrees of latitude (6°S to 12°S) and water depths between 400 and 2400 m. We quantify bathymetric and geographic variation in biodiversity, standing stock, and distribution of megafaunal assemblages associated with the wider sedimentary environment. Preliminary analysis shows no general trends in diversity along the vertical and horizontal gradients. Assemblage composition changes continuously with depth. In addition, we also present observations of asphalt mounds, deep-water coral reefs, and reducing environments with authigenic carbonates, bacterial mats, and cold-seep bivalves. Direct evidence of the effects of demersal trawling was detected at one upper bathyal site (770-790 m), further substantiating the need for a better understanding of regional benthic ecology to inform integrated environmental assessment and management.

## Protected development in deep-sea invertebrates. The rule in the southwestern Atlantic?

Pamela Rivadeneira, Pastorino, Guido; Teso, Valeria; Martínez, Mariano; Lauretta, Daniel; Berecoechea, Juan José; Brogger, Martín; Flores, Jonathan; Pertossi, Renata; Sánchez, Noelia and Penchaszadeh, Pablo E.
Museo Argentino de Ciencias Naturales, CONICET

Biological deep-sea research off Argentina (beyond 1200 m) started since 2012 with focus in the Mar del Plata submarine canyon (up to 3500 m). Many of the more than 200 species found of benthic cnidarians, mollusk and echinoderms are being studied and new species are being described. Previous studies from different authors have pointed out the unusual proportion of species showing protective adaptations for its offspring in the Southern Sea, particularly in Antarctica. Many new cases were observed in the study area in different phyla showing some kind of protected development, with avoidance of a free swimming larval stage. Among Cnidaria, oocyte gigantism was found in the black coral Dendrobathypathes grandis with a diameter of up to 1.5 mm, when oocytes in Antipatharia are usually under 0.2 mm. Many deep-sea gastropods show encapsulated direct development, by the presence of supplementary food for the embryo as nurse eggs, adelphophagia (Buccinidae, Calyptraeidae), proteins in the intracapsular liquid (Naticidae, Volutidae), or by means of gigantic eggs of about 1.8 mm in diameter (Cochlespiridae). Peculiar egg mass morphologies are reported, i.e. in the moon snail Bulbus carcellesi where the egg capsules are the largest ever recorded for this family (8.8–14.1 mm in diameter vs 3 mm of the largest previously known). Brooding is found in the five classes of Echinodermata. The sea star Ctenodiscus australis protects its broods in the dorsal side between paxillae; the crinoid Isometra vivipara shows two phases, one with eggs brooded in a marsupium and a second phase in the cirrus. In some sea cucumbers (Cladodactyla crocea, Psolus patagonicus, and Psolus lawrencei) broods

could be found in pouches, sole or brooding chambers. The sea urchin Austrocidaris canaliculata, protect their young in the apical system. Brooding chambers have been also reported in ophiuroids as Astrotoma agassizi and Ophiochondrus stelliger. All this new evidence contributes to the understanding of the scenery for so many cases of parental care and the avoidance of planktonic larvae in the southwestern Atlantic.

## Pelagic-benthic coupling in a glaciomarine fjord, Andvord Bay (Antarctica)

Amanda Ziegler, Craig R. Smith, Mattias Cape
University of Hawaii at Manoa

The West Antarctic Peninsula (WAP) experiences extreme seasonal pulses in productivity and export flux to the seafloor (Ducklow et al. 2006; Smith et al. 2008; Mincks et al. 2008) heavily modulated by the timing and extent of sea-ice. Phytodetritus constitutes a major food input to the benthos on the deep Antarctic shelf, and megafaunal activity increases significantly in response to these intermittent pulses of food (Sumida et al. 2014). Though these trends have been well documented for fauna on the outer continental shelf of Antarctica, temporal studies of the fate and utilization of phytodetritus on the seafloor in coastal regions of the WAP are lacking. Our study aimed to develop automated color-recognition methods for quantifying seafloor phytodetritus cover over a 9-month period from a calibrated time-lapse camera. An intense pulse of phytodetritus was observed in early January 2017 which deposited at least 2 cm of phytodetritus on the seafloor in just 6 days. During this period, deposit feeder fecal cast production rate (a proxy for deposit-feeding rate) increased 4-fold indicating a tight coupling between plankton blooms and benthic detritivores in the fjord. Interestingly, the feeding rates decreases to background levels again after the high flux event, but megafauna remained active throughout the fall and into early winter (September). Most phytodetritus, however, was not consumed by megafauna but rather degraded by the microbial community or by macrofauna not visible with the camera system. This contrasts the open continental shelf where phytodetritus is consumed rapidly by holothurians and other mobile detritivores and highlights the substantial differences in pelagic-benthic coupling and carbon cycling in WAP fjords compared with the less productive open shelf.

## The Deep-sea Ecosystem: Assessment of the biodiversity and abundance of deep-water fauna in the Exuma Sound, Eleuthera, Bahamas, and the Northeastern Gulf of Mexico.

Mackellar Violich, Grubbs, R.D. 2; Brooks, E. 3
1 Department of Oceanography, Florida State University; 2 Florida State University Coastal and Marine Laboratory; 3 Cape Eleuthera Institute

The limited knowledge of the deep-sea is a paramount concern, affecting our ability to assess the overall health of the ocean's ecosystem. Technology has made deep-sea fishing more accessible, but management plans cannot be implemented on ecosystems lacking fundamental information of the biology and species within them. Comprehensive ecological studies are needed to identify factors that may influence distribution and abundance of the faunal groups that are becoming commercially relevant. This observational study was conducted over a 3-year period to provide an assessment of physical, environmental, and biological factors that drive benthic and benthopelagic community structure and function in Exuma Sound, the Bahamas. A series of 115 deep-sea traps were sampled from 360 to 1480 meters deep from spring 2014 to spring 2017. During this study two new species were discovered Booralana

maxeyorum and Booralana sp. nov. Crustaceans dominated the catch (98%) with Teleosts (1.2%) and Elasmobranchs (.1%) contributing the rest. We describe the community structure and assemblages of the deep-sea crustacean fauna, which will provide additional information to the benthic ecosystem of the deep-sea for future management in this area.

## Body-size spectra, ecological hypotheses, and metabolic theory in seafloor ecology

Noëlie Benoist
University of Southampton

Based on a simple equation for individual metabolic rate, the Metabolic Theory of Ecology (MTE) can be extended to higher levels of organisation to consider various hypotheses concerning ecosystem function. Various existing field data have shown that the numerical density of living organisms in logarithmic size classes may be related as a -3/4 power to body mass, suggesting energetic equivalence between those classes, and referred to as Damuth's rule. In shallow-water and deep-sea environments, it has been demonstrated that meio- to macrobenthic assemblages can be usefully modelled in that way. Here I examine whether these relationships might be extended to the megabenthos using mass photography from autonomous underwater vehicles (AUVs) in shelf-sea and abyssal environments. The resultant body-size spectra appear to show good agreement with this basic model, and indicate the joint influences of in situ temperature and local resource supply to the seafloor. Additional data are presented on the body-size spectra of physically sampled meio- and macrobenthos from the same locations, extending the spectra over c. 10 orders of magnitude in body mass. These joint spectra appear to suggest that a single relationships may hold across the full range of the metazoan benthos. If confirmed, such relationships offer the promise of a simple numerical framework that could readily be embedded in global-scale biogeochemical models, and be employed to generate and test ecological hypotheses; for example, relating energetics and biological diversity. For the present, I conclude that (a) AUV-based mass photography of the seafloor provides an effective means of collecting quantitative data on the size-based ecology of the megabenthos; and (b) that those data may be particularly valuable in the full assessment of seafloor biogeochemical cycles, where physically small-scale sampling and measurement may substantially underestimate benthic stocks and flows.

## Culturing deep-sea sponge associated microbes: systematic assessment of culturing methods

Poppy Best, Matthew Koch, Kerry Howell, Mathew Upton, Alistair Bishop, Nicola Foster and Phillip Warburton
Plymouth University

Deep sea organisms have been hailed as a new frontier for the discovery of new medical compounds produced by the phylogenetically diverse communities of microbes. Despite the culture-independent approach gaining momentum, there is an inconsistency in the methods used in order to culture and analyse sponge-associated microbes. From the seabed to the lab bench there is a need for a systematic review and testing of the published protocols to assess what generates the greatest diversity of recovered isolates.Following and altering published methods previously used for the study of deep-sea sponges and their microbial communities, we systematically tested their effectiveness in the culturing of microbes from Pheronema carpenteri sponges (n = 4) collected at around 1,200 meters from the North Atlantic. Treatments included a wash stage using a range of buffers (Ca and Mg free sea water, artificial sea water, filter sterilised seawater and distilled water), the inclusion of an enrichment

stage prior to plating, incubation at various temperature (5, 10, 15, 20 and 38°C), the addition of differing vitamin solutions, aerobic versus anaerobic conditions, salinity and pH.Sponge-associated bacterial culture optimisation revealed that low-nutrient media proved the most efficient in terms of abundance and diversity (A:D). The inclusion of natural sea water, aqueous sponge tissue, spicules and silica had a positive impact on the A:D of recovered bacteria. Additionally, a higher A:D was observed in correlation with lower temperature, reflective of the natural environment of the sponge sample. Optimising culturing methods through the mimicry of the sponge habitat to generate greater isolate diversity has implications in the discovery of novel compounds. Improving on existing methods may permit for the recovery of more isolates relevant for microbial conservation efforts and understanding the microbial process of the deep sea sponge microbiome.

## Filling in the Gaps: Forming Partnerships to Expand Genetic Libraries

Stephanie L. Bush, Michael J. V. O'Mahoney, Simon J. Pecnik, Marshall H. Boyd
Smithsonian Institution National Museum of Natural History

The US Bureau of Ocean Energy Management – Environmental Studies Program (BOEM-ESP) has been conducting intensive environmental studies on the Outer Continental Shelf (OCS) for more than 35 years in support of managing oil and gas development. The National Museum of Natural History, Department of Invertebrate Zoology (NMNH-IZ) has provided professional collection management services for the long-term curation of invertebrate specimens obtained during these surveys of the US East, West, Gulf, and Alaskan Coasts. The BOEM – NMNH partnership has recently expanded in response to analyses that reveal a substantial lack of accessible genetic information for invertebrates found in US marine habitats, with current coverage of OCS invertebrate genera below 5%. In an effort to reduce these gaps, NMNH-IZ is DNA barcoding existing BOEM collections, as well as forging partnerships with regional institutions to expand their holdings. These partnerships are providing new morphological vouchers paired with fresh tissue for DNA barcoding and deposition into the NMNH Biorepository for future genomic studies. Through these efforts, NMNH-IZ aims to improve the availability of high quality genetic information for the scientific community.

## Characterization of deep-sea sponge ecological function in the Azores comparison with other North Atlantic Banks

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Sponge grounds are structurally complex habitats and have been shown to provide numerous supporting, regulating, provisioning and even cultural goods and services to the ecosystems (including society). They are considered vulnerable marine ecosystems and have been impacted by fisheries, and being the issue of fiiheries closure at the NAFO and NEAFAc

areas. Numerous deep-sea sponges are known to provide microhabitats and food sources for a wide range of organisms. Yet, little is known about the ecological and trophic relations between deep-sea sponges and their associate small macrofauna in the Azores region. To investigate the functional ecology of deep-water sponges at the individual-level, by catch samples collected from fisheries observer campaigns and other scientific fisheries cruises in the Azores were analysed, together with samples from the Emerald Bank and Barent sea. Associate epifauna and infauna from sponges were collected on ice, examine, sorted and photographed Sponge morphometrics were measured and available POM was quantified. The tridimensional inner structure was also studied. The trophic links between fauna and sponge were characterized by stable isotope.The role of the sponge in the ecosystem is discussed in function of size, shape, innerspace, available food and location.Understand the function of the sponges in the área will give a contribution to the management of this vulnerable marine ecosystem.

## A genetic fingerprint of Amphipoda from Icelandic waters – the baseline for further biodiversity and biogeography studies

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The geological and oceanographic conditions of the Iceland region and its adjacent waters are very complex and result in the existence of three different marine environments: boreal, subarctic and Arctic zones. The international IceAGE project (Icelandic marine Animals: Genetics and Ecology) focuses on this climatic sensitive region. Amphipods constitute an abundant part of Icelandic deep-sea zoobenthos yet knowledge of the diversity of this fauna, particularly at the molecular level, is scarce. The aim of the present study is to use molecular methods to investigate the genetic variation of Icelandic amphipods and understand if changes in molecular diversity reflect the known characteristics of the regional benthic topography and hydrological conditions. The mitochondrial cytochrome oxidase subunit 1 (COI) of 167 individuals collected during two IceAGE expeditions was analysed. The amphipods were originally identified as 75 morphospecies and 21 families. The study resulted in 81 Barcode Identity Numbers (BINs) (of which >90% were published for the first time), while Automatic Barcode Gap Discovery revealed the existence of 78 to 83 Molecular Operational Taxonomic Units (MOTUs). Six nominal species (Rhachotropis helleri, Arrhis phyllonyx, Deflexilodes tenuirostratus, Paroediceros propinquus, Metopa boeckii, Astyra abyssi) appeared to have a molecular variation higher than the threshold usually used for amphipod species delineation. In some, but not all cases, the separation of the genetic lineages can be explained by depth and geographic partitioning. Conversely, two species of the Oedicerotidae regarded as separate morphospecies clustered together with divergences in the order of intraspecific variation. The incongruence between the BINs associated with presently identified species and the publicly available data of the same taxa was observed in the case of Paramphithoe hystrix and Amphilochus manudens. The results from this study are a baseline for further research

of species diversity and distribution in Icelandic and adjacent waters and other marine regions as well.

TUESDAY Evening • 17:45 • Serra Ballroom

## Diversity, abundance, and distribution of deep-sea Tanaidacea off Icealand – IceAGE project

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The North Atlantic, notably basins off the Icelandic coast, is one of the best studied area regarding to the deep-sea Tanaidacea fauna. The studies has continued for more than 100 years and till the moment over 50 deep sea tanaidaceans were described from this area. Here we present preliminary results on the tanaidacean fauna from 32 giant boxcorers (GKG) taken from 168 to 2748 m depth range during IceAGE project (Icelandic Animals Genetic and Ecology). In the samples taken a total of 498 specimens classified to 78 species were identified. The most speciose families were Akanthophoreidae, Colletteidae and Typhlotanaidae with 18, 10 and eight species, respectively; moreover nine species represented group 'family incertae sedis'. The overall tanaidacean density varied from 1 to 53 ind./0.25 m2, with mean value 15.6 ind/0.25 m2. The number of species per sample varied from 1 to 13 with mean 4.7 and the diversity values (Shannon Index) varied from 0 to 1.9 with mean 1.1. The highest abundances and numbers species were recorded at stations north off Iceland (Denmark Strait) while samples with single recorded tanaids were located west and southwest off Iceland (Irminger and Iceland Basins). Similarity analysis (based on Bray–Curtis similarity method) showed three groups, but with low level of similarity.The study was completed thanks to funding provided by the National Science Centre, Poland (grant no. 2016/21/B/NZ8/02495).

TUESDAY Evening • 17:45 • Serra Ballroom

## Megabenthic communities of Central Arctic based on photographic survey and trawl data

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A photographic survey was carried out during the expedition ARK-XXVII/3 of the research icebreaker Polarstern in summer 2012 (2 August-29 September) to the Eastern Central Arctic basins. The seafloor was photographed using a towed camera platform, the Ocean Floor Observation System (OFOS). Nine transects were performed: four in the Nansen Basin (3571-4066 m) and five in the Amundsen Basin (4041-4384 m). At seven of these stations benthic Agassiz trawls were taken for species identification and ground-truthing. Composition and structure of megabenthic communities were analysed and environmental control factors, including state of the sea ice were evaluated. Based on taxa dominating the benthic biomass, the following three types of megafauna communities were distinguished: 1) dominated by actiniarians Bathyphellia margaritacea, 2) by holothurians Elpidia heckeri and 3) by holothurians Kolga hyalina. Megafaunal abundance varied greatly between stations, but there was evidence of a pattern related to proximity of stations to the sea ice margin. One group of stations located closer to the ice margin under the first year ice was characterized by relatively high densities and biomass of B. margaritacea (mean 0.18-1.67 ind m-2; 0.16-1.50 g ww.m-2) and relatively high indicators of productivity in the sediment (including concentrations of pigments, carbon, prokaryotes abundance, nutrients and others). In the other group of stations located closer to the North Pole under the multi year ice, indicators of productivity were lower, at the same time relatively high density and biomass were found in holothurians E. heckeri (mean 0.92-1.53 ind m-2; 0.30-0.43 g ww.m-2) and K. hyalina (mean 0.004-1.68 ind m-2; 0.01-3.48 g ww.m-2). The relationship between the community structure and substantial food falls formed by freshly sunken ice diatom Melosira arctica was analysed. The present study is relevant in the context of currently observed rapid decline of sea-ice in central Arctic basins.The study was funded by RFBR research project № 17-05-00787 and supported by the AWI Helmholtz Centre and the ERC funds "Abyss" to AB.

TUESDAY Evening • 17:45 • Serra Ballroom

## Deep-sea Isopoda (Crustacea, Malacostraca) of the Northwest Pacific: new concept of biodiversity based on the results of expeditions SoJaBio, KuramBio, and SokhoBio

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The Northwest Pacific is one of the most highly productive and diverse regions of the World Ocean. Its deep-sea benthic communities were studied during the three Russian-German expeditions in 2010-2015. Isopoda were one of the dominant macrobenthic taxa, comprising ~ 300 species, 70 genera, 18 families, and 4 suborders. Suborder Asellota comprised 98% isopod specimens. Families Munnopsidae and Desmosomatidae prevailed constituting 54-99% isopods. About 80% species were new to science. The distribution of the deep-sea isopod fauna was influenced by the isolation degree of the studied abyssal basins and by hydrological barriers there. The diversity decreased with the increasing isolation of the basin. The Sea of Okhotsk (SO) is connected with the Pacific Ocean by the deep (~ 2000 m) Kuril Straits. Its abyssal isopod fauna was evidently linked with the Pacific abyssal fauna (46% species common). This community was limited in its distribution up to the bathyal zone by the warm oxygen-poor layer of the SO (~ 600–1350 m). The shelf asellote fauna of the SO appeared to be more similar to the low bathyal fauna of the adjacent Sea of Japan (SJ) (5 common species), than to the abyssal fauna of the SO (0 common species, 5 common genera). Nevertheless, we found that the representatives of the most successful and rich deep-sea families Munnopsidae and Desmosomatidae were the first colonists of the abyssal depths of the SJ. It indicates the ecological plasticity of species of some genera which allows them to spread through topographic barriers.

TUESDAY Evening • 17:45 • Serra Ballroom

## Sea anemones from deep sea in Brazil: What we already know and what is missing?

PAULA BRAGA GOMES, YAGO ARAUJO MELO, ALESSANDRA TARGINO
UNIVERSIDADE FEDERAL RURAL DE PERNAMBUCO

In Brazil there are about 44 species of anemones described, however, only five of them were recorded in the deep sea. In the last few decades, projects focused on the knowledge of the deep sea have made it possible to access unpublished material, especially prospecting and monitoring developed by Petrobras in areas near the oil basins. In this study, specimens from the Potiguar Basin, north-northeast coast of Brazil (04°21.3580'S, 036°44.2730'W) resulted in the identification of eight species collected at depths between 375 and 2123m. Of these, Monactis vestita, Amphianthus bathybium, Actinoscyphia saginata, Phelliactis robusta, Bathyphellia aff australis and Paraphelliactis sp. are new records

for the South Atlantic. In addition, two new species have been described: Actinauge sp. nov. and Amphianthus sp. nov. This study also extends the bathymetric and geographic distribution of families and genera, as well as demonstrating a certain homogeneity in the composition of the deep sea anemonofauna with species of wide geographic distribution. There are other collections currently under study (Campos Basin in Rio de Janeiro, material from the REVIZEE Program in the North and Northeast) and still numerous specimens collected in association with octocorals in the deep sea, which proves that the low representation of deep anemonofauna known in Brazil results exclusively from the lack of sampling and study of deep sea material. This scenario is beginning to change, from five to 13 deep-sea species in Brazil and, due to the enormity of the country's coast, will provide important data to understand biogeographic patterns in the deep sea.

## Oxygen minimum zones and vertical zonation of benthic fauna in the Revillagigedo Archipelago, Mexico

Karla Haiat Sasson, Brennan T. Phillips, Steven Carey, Christopher N. Roman, Claus Siebe, Esmerelda Morales Domínguez, Leigh Marsh, Karen F. Wishner
University of Rhode Island

Often referred to as "Mexico's Galapagos", and now the largest fully protected marine reserve in North America, the Revillagigedo Archipelago consists of four volcanic islands located 450km south of Baja California, Mexico. In November 2017, a team of scientists aboard the E/V Nautilus from the University of Rhode Island and the Universidad Nacional Autónoma de México, conducted several deep-water transects on the flanks of Socorro and San Benedicto Islands. An oxygen minimum zone (OMZ) from 200-800m, appeared to dictate strong vertical zonation of benthic fauna, including high abundances of corals, crinoids, and sponges at deep regions, a dense 'sponge garden' in a narrow depth zone and large regions of virtually depleted macrofauna higher up the slope in low oxygen water. At the lowest oxygen level, a filamentous bacterial mat completely covered all surfaces of the substrate. This was also the case at a newly discovered site of diffuse-flow hydrothermal venting presumably associated with a major eruption in 1993 about 4 km off the west shore of Socorro, located within the same hypoxic depth range. We present other discoveries from the OMZ, including comprehensive associated physical data and high-resolution video and stills of the deep-sea scyphozoan Deepstaria enigmatica in its natural state. This same species was also observed dead on the seafloor, acting as a 'jelly-fall' being actively consumed by several crustaceans.

## Spatial variability of benthic taxonomic diversity in the Atlantic and Pacific

Anita Hollingsworth, D.O.B. Jones, H.A. Ruhl, C.R. Young
University of Southampton

Abyssal microbes are crucial in biogeochemical cycles, regulate fluxes in energy and contribute to organic carbon production and remineralisation. Despite this, the biodiversity, function and connectivity of microbial communities within deep-ocean sediments remain poorly characterised. We investigated the effect of seafloor topographyon microbial populations in the upper centimetre of abyssal sediments at two sites: the oligotrophic Clarion-Clipperton Fracture zone (CCFZ) in the eastern equatorial Pacific; and more productive region in the northeast Atlantic, the Porcupine Abyssal Plain (PAP). The CCFZ has a high density of polymetallic nodules on the seafloor, making it the focus of potential seabed mining activities. The sampling sites in the CCFZ included an Area of Particular Environmental Interest (APEI-6), which is protected from mining by the International Seabed Authority (ISA), and UK-1, a mining exploration claim

area licensed to the UK. Here, amplicon surveys show that that the upper 0-1 cm layer of abyssal sediments at CCFZ and PAP harbour diverse and distinctive microbial assemblages. Results indicate that significant spatial diversity exists over large spatial scales (> 100 km2) rather than smaller scales (1 m2– 100 km2). The most abundant taxa within the sediments may have an important role in carbon fixation in abyssal sediments which has implication for benthic ecosystem functioning. Comparisons of benthic microbial communities between PAP and CCFZ will provide information on the microbial processes that may be impacted by anthropogenic disturbances. Abyssalhabitats have been observed to have slow recovery ratesafter disturbance events, such as deep-sea mining,so determining the distribution of benthic microbes is vital.

## Rapid changes and long-term cycles in an abyssal benthic megafaunal community observed over 29 years in the northeast Pacific

Linda A Kuhnz, Christine L. Huffard, Kenneth L. Smith, Jr.
MBARI

The seafloor community on the abyssal plain in the NE Pacific (Station M, ~4000 m depth) was studied between 2006 and 2017 using remotely operated vehicles (ROVs) as part of a continuing 29-year time-series study. New patterns continue to be revealed showing that the deep-sea is dynamic on short time scales, rather than static over long periods. Early in the study, megafaunal diversity was high, yet the community was depauperate in terms of density compared to later periods. In just over two years the community shifted from a sessile, suspension-feeding, sponge-dominated community to a mobile, detritus-feeding, sea cucumber-dominated assemblage. Changes in the megafaunal community as a whole continue, and we explore the dynamic abundance and diversity of individual groups of organisms over time. Large variations over decadal-scales indicate that remote abyssal communities are dynamic and are likely subject to impacts from anthropogenic changes like ocean warming, acidification, and pollution manifested in the upper ocean. The degree of dynamism indicates that one-time or short-term investigations are not sufficient for assessing biological community structure in conservation or exploitation studies in the deep sea.

## New Records of *Synallactes virgulasolida* Massin & Hendrickx, 2010 (Echinodermata: Holothuroidea) from the Eastern Pacific

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Postgrado en Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México. Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México

Up to 2013, 53 species of holothuroids had been registered from western Mexico (Alvarado & Solís-Marín 2013). Deep-water holothuroids have been poorly studied in this area and available records are based on studies realized prior to 1988 when a complete list of echinoderms occurring in the eastern central Pacific was compiled by Maluf (1988). A recent compilation of records indicated the presence of 31 species of deep-water holothuroids in western Mexico (Hendrickx 2012). Specimens of the sea cucumber Synallactes virgulasolida were obtained during sampling operations off western Mexico from oceanographic campaigns as part of TALUD project, on board the R/V El Puma, UNAM, at different times (August 1991, July-August 2012, May-June 2014). Based on a total of 185 specimens and on additional records available in the Scripps Institution of Oceanography collections, new geographical (southern California to Chile) and bathymetric (712-1300 m) distributions are provided. SEM photographs of

ossicles are provided for the first time for this species. New ecological data associated with the presence of this species are also provided: 4.17-5.81 °C, 0.15-0.48 ml O2/l, and in 34.40-34.48 ups. The species occurs in a wide variety of sediments with an organic carbon content of 17.93-52.02 mg/g (1.79-5.20 % of organic matter) and is occasionally very dense (up to 170.32 orgs/ha). All Mexican records correspond to a bathymetric fringe locates below the Oxygen Minimum Zone, thus indicating that S. virgulasolida is able to tolerate hypoxic conditions.

## The diversity and morphology of the echiurans in the deep-sea of the Kurile-Kamchatka Trench

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Echiura (spoon worms) is a group of marine worms that have a sausage-shaped body with an extensible scoop-like proboscis with approximately 200 valid species. They always live in protected places and are well adapted for living in burrows. Echiurans occur widely and their bathymetric range is extensive. As a part of the deep-sea biodiversity survey (KuramBio and KuramBio II) eight echiuran species were identified at various depths from 5200-9500 m. At the deepest stations in the Kurile-Kamchatka Trench (9500 m) echiurans attain large densities as great as 20 specimens per m2. All recorded species belong to the family Bonelliidae, that is a characteristic of the community of the abyssal and ultra-abyssal fauna and reach to the greatest depths of the ocean. The most abundant species collected at depths 6200-8100m are Alomasoma sp., Ikedella sp., Jakobia birsteini, Protobonellia zenkevitchi, whereas Vitjazema ultraabyssalis was collected only from 8700 m to 9500m. The small amount of information concerning the biology of deep-sea echiurans is mainly due to the hard to reach biotopes these worms inhabit. Investigations of morphology and anatomy of organ systems will help to understand the biology of this deep-sea worms. Study of anatomy and morphology of the collected species has been done using light microscopy and different technics of scanning electron microscopy. Morphological analysis will include comparison of proboscis fine morphology together with inside characters (gonoducts, anal sacs, intestine and circulatory vessels). Our findings suggest that morphology of the proboscis allowed to understand the position of worm in the sediment and mechanism of sorting of food particles as well as show which species are surface deposit feeders or superficial sediment feeders. Nevertheless, comparative studies of additional species are still required. Present finding increases the number of northwestern Pacific echiuran species and will contribute to an understanding diversity of Echiura.

## Element concentration and distribution in nematodes from 3 geographically distinct areas using synchrotron radiation X-ray fluorescence

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The concentration and distribution of various elements including metals may differ between organisms living under different environmental conditions as a result of adaptation. To increase our knowledge on the effect of high metal concentrations in marine sediments on deep-sea nematodes we collected nematodes from abyssal soft sediments in the Peru Basin, Antarctica and the Arctic Ocean (Fram Strait). The Peru Basin is characterized by the abundance of polymetallic nodules and high concentrations of copper and nickel inside the sediment (bulk metal content of the sediment) whereas these metals displayed rather low concentrations in the Antarctic and Arctic site. The selected nematodes were scanned with $\mu$-X-ray fluorescence to quantify element concentrations in the entire body tissue and, subsequently, detailed element maps were created of selected body parts (head and tail) of the same animals using synchrotron radiation. Obtained element distributions and concentrations will be presented and compared between sites.

## Physiological differences of abyssal holothurians to a varying OM input

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In the deep sea, megafauna play a key role in ecosystem functioning. Significant effects have been observed in the organic matter (OM) processing on the seabed when species changed in density, suggesting that faunal changes are mostly driven by environmental factors. However, it is still difficult to understand why seasonal OM fluxes play a crucial role in the structure of the benthic community via benthic-pelagic coupling. In this study we investigated whether the physiological differences in key abyssal holothurians vary according to different OM quality and quantity at the deep-sea floor, in two stations in the western Pacific Ocean (1N and 39N). At 39N, phytopigment concentrations in sediments were ~16 times higher than 1N. Total carbohydrates and protein concentrations were also higher at 39N than 1N, though the differences between the regions were not as large as the phytopigment concentrations. The lipid composition of most holothurian species analyzed was dominated by sterols, but differences between regions in terms of lipid classes' composition were not significant. However, differences between the regions with respect to concentrations of the main indices fatty acids (phytoplankton, zooplankton and bacterial biomarkers) were significant, implying a different food source in both areas. The dissimilarity between the regions with respect to diagnostic the lipid indices was explained by a higher contribution of phytoplankton to the diet in 39N. As for trophic web studies, our results suggest that holothurians feed on both fresh OM and bacteria. This study demonstrates that different OM supply may lead to differences in the abundance and physiological responses of deep-sea holothurians, giving a step forward on the understanding of the implications of OM cycling and ecosystem functioning in abyssal plains.

## Sea anemones on subantarctic sea pens: parasitism?

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Sea pens are a particular group of octocorals that could be found in all the world´s oceans, from tropical to polar regions and from intertidal to more than 6100 m. In deep seas, pennatulaceans could be patchily distributed in

moderately high energy environments, mostly sea mounts, slopes and along bases of ridges, and may be important members of coral gardens occurring in dense stands. In areas where the consolidated substrate is generally scarce, the structural three-dimensionality of the octocorals serves as a biogenic substrate. Compared to other cnidarians, there have been relatively few records of associated species with sea pens. In this study, we report for the first time the association between Anthoptilum grandiflorum and Halipteris africana with the sea anemone Hormathia pectinata in Argentine slope waters between 400-1000 m depth. Some small individuals of H. pectinata were observed settled on the rachis (soft tissue) of A. grandiflorum while adult specimens were strongly attached to the axis of the octocorals. In some of the observed specimens, the lack of soft tissue underneath adult sea anemones is consequence of its settlement. Then, can be hypothesized that the sea anemone larva colonize the dorsal part of the rachis (soft tissue) of the sea pens (free of polyps) and at the time it develops, it degrades the coenenchyme live tissue to finally attached to the central axis. In that sense the sea anemones benefit with hard surface to attach in a muddy seafloor. Loss of octocoral tissue and the instability of the colony caused by the presence of the sea anemones can characterize this association as parasitism. The association here reported represents the second report of the world (the first was Stephanauge nexilis on Halipteris finmarchica in Canadian waters) and the first one for the South Atlantic Ocean of a sea anemone with a pennatulacean.

POSTER 52 ⚡ Biodiversity and ecosystem functioning
TUESDAY Lightning Talks • 08:30 • Serra Room

## Computer Vision for Automated Identification and Enumeration of Deep-Sea Corals and Sponges

Andrea M. Quattrini 1, Yekaterina Kharitonova1, Anthony Romm1, Angela Zhao1, Amanda W.J. Demopoulos2
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Post-processing imagery data from a single deep-sea expedition can take 100s of hours of time as this analysis has often been done manually. Yet, in many cases, rapid analysis of benthic habitats is necessary to not only guide exploratory dives, but to also assess the health of habitats in the face of environmental perturbations. Thus, we are developing computer vision approaches coupled with machine-learning algorithms to produce an efficient image-processing pipeline of deep-sea imagery, allowing researchers to rapidly assess, review, and analyze both moving and still imagery data. We are using the open source computer vision algorithms available through the Open Computer Vision platform (www.opencv.org) and a state-of-art supervised deep-learning approach using Convolutional Neural Networks (CNNs). Our method allows extracted video frames to be processed for automatic detection and identification of deep-sea corals and sponges. Briefly, identical video frames are removed (e.g., when the ROV is stationary and the scene is not changing) and then distinct frames are analyzed for the presence of coral and sponges. Training data used to help identify the corals and sponges include images of species identified by taxonomic experts. From a test video clip, we analyzed 9,000 static frames and successfully classified the majority of corals and sponges. Thus, our preliminary results demonstrate the promise of our approach; however, our method would be improved upon by adding more training data to the pipeline. We plan on sharing our pipeline by providing all training data and code through a public server and an online code repository. Session choice: Biodiversity Observations in the Deep Ocean Format Poster

POSTER 53 - Biodiversity and ecosystem functioning
TUESDAY Evening • 17:45 • Serra Ballroom

## Evolving approaches for deep ocean observing and the collection of data for

## essential ocean variables in biology and ecosystems

Henry A Ruhl, The DOOS BioEco Task Team
CeNCOOS, MBARI, NOC

The past decade has seen major advances in the establishment and governance of deep ocean observing systems globally. Motivations for this work now come, in part, from the need to understand climate change and the United Nations Sustainable Development Goals which pose globally significant challenges to conserve and sustainably use the oceans, seas and marine resources. Nationally and internationally important efforts such as Argo, GO-SHIP, OceanSITES, the Ocean Observatory Initiative, the US Integrated Observing System, Ocean Networks Canada, and the European Multidisciplinary Seafloor and watercolumn Observatory – European Research Infrastructure Consortium contribute to the Global Ocean Observing System (GOOS). The Deep Ocean Observing Strategy (DOOS) project of GOOS is working to find common perspectives on key science questions and the means to address them. Likewise there has been a maturation of novel platforms and sensors for data and samples for biology and ecology observation. DOOS and other efforts are examining ways for observing systems to take advantage of tools that have reached an advanced technology readiness. Platforms such as deep Argo, fixed point observatories, and long range autonomous underwater vehicles provide a variety of fixed and mobile platforms in the water column and on the seafloor. For example, advanced digital camera technology including stereo, plenoptic, holographic and microscopic cameras, as well as computer vision tools, offer evolved ways to identify and quantify marine life. Tools using molecular approaches have also matured and are commercially available to address questions including those related to macro-ecology, genetic identity, relation and metagenomic function. Here we link platform and sensor capabilities with the DOOS science questions to help guide ocean observing development, including the ability to address sustainable development goals.

POSTER 54 - Biodiversity and ecosystem functioning
TUESDAY Evening • 17:45 • Serra Ballroom

## Intra- and inter-field variations in *Bathymodiolus azoricus* deep-sea faunal assemblages along the northern Mid Atlantic Ridge

Sarrazin, Jozee, Marie Portail, Cécile Cathalot, Agathe Laes, Bérengère Husson, Erwann Legrand, Pierre-Marie Sarradin
Ifremer EEP/LEP, Ifremer GM, Ifremer RDT

The dense faunal assemblages inhabiting hydrothermal vents have been the focus of numerous studies since their discovery in 1977. Community patterns and their links to environmental conditions at the scale of a single edifice have been explored. However, comparing biodiversity patterns at larger scales can bring additional insights on species habitat preferences and dispersal abilities. The symbiotic mussel Bathymodiolus azoricus is a dominant engineer species from northern Mid-Atlantic Ridge deep-sea vents. Mussel assemblages were sampled and their habitats characterised on Menez Gwen (MG), Lucky Strike (LS) and Rainbow (RB) vent fields. On LS, four edifices were sampled to assess intra-field variations in abiotic and biotic conditions. Community structure and biodiversity indicators were compared among 21 samples using multivariate analyses. Results show strong disparities in composition and abundance between the different LS edifices possibly due to the presence of distinct chemical signatures. Mussel assemblages also differ between the three vent fields. MG show a distinct community structure, with low species diversity and strong compositional dissimilarities. Knowledge on factors driving biodiversity patterns is becoming a prerequisite to develop effective strategies for the management of these ecosystems that are increasingly coveted for their mineral resources.

POSTER 55 ⚡ Biodiversity and ecosystem functioning

## A novel benthic ecosystem possibly associated to gas-emissions discovered in a high altitude Chilean lake by the NASA Planetary Lake Lander (PLL) Project

Virginie Tilot1,2, N. A. Cabrol3,4, V. A. Parro5, E. Moreno Ostos 8, Nieves Lopez-Gonzalez2, Fabian Figuero Rebolledo8, P. Sobron3, E.W. Smith3, C. Tambley6, V. Gallardo7 and the Planetary Lake Lander team.

1. UMS (AFB CNRS MNHN) Patrimoine Naturel, Muséum National d'Histoire Naturelle, Paris, France, 2. Instituto Español de Oceanografía, Malaga, Spain, 3. The SETI Institute Carl Sagan Center; 4. NASA Ames Space Science and Astrobiology Division; 5. INTA-CSIC, CAB, Madrid (Spain); 6. Campoalto Operaciones SpA, Santiago, Chile), 7. Universidad de Concepción (Chile), 8. Universidad de Malaga, Spain.

In the context of the NASA Planetary Lake Lander (PLL) project, mainly focusing on the development of technology for planetary lake and seas exploration of Titan, an innovative multi-parametric Rapid Environmental Assessment (REA) strategy, originally coupled to eco-hydrodynamics and used to explore unknown habitats in deep oceans, has been adapted to analyze the video data acquired in the extreme environment of a high altitude lake in the Chilean Andes. The REA coupled to water column and sediment sampling allowed to identify a series of habitats in the lake according to dominant parameters, environmental and community-associations, to propose taxa identification, and to estimate the state of the environment per habitat. The results show the vulnerability of this extreme environment, and the presence of peculiar biological features and a particular ecosystem on the deep lake floor, new to science. Data show that there is a rich benthic ecosystem with diverse fauna and that microbial metabolisms are driven by nitrification/denitrification processes. The hypothesis of tubeworm communities is reinforced by DNA analysis confirming the presence of marine ammonia oxidizing archaea (AOA) similar (97%) to Nitrosopumilus maritimus and nitrite oxidizing bacteria (NOB) from Nistrospira group, suggesting a coupling between ammonia and nitrite oxidation. The presence of these methanogens, usually found in association with marine sponges and polychaeta tubeworms, could be associated with past or present hydrothermal activity in the area and/or gas-emissions.

## Depth-related Skeletal Reduction in Snailfishes (Liparidae)

Abigail von Hagel, Tsoi, R; Kolmann, MA; Gerringer, ME; Orr, JW; Farina, SC
University of Washington

Skeletal reduction is a common feature among deep-sea fishes that have diversified from shallow-water relatives, such as snailfishes. These skeletal reductions may be an adaptation to environmental conditions of high pressures, low temperatures, declining luminosity and limited food availability. Snailfishes (family Liparidae) are found across a large bathymetric range (0 –>8,000 m), with intertidal ancestors giving rise to a large clade of deep-sea species. We used microcomputed tomography (micro-CT) to estimate average bone mineral density and examine jaw, pectoral girdle, and neurocranium morphology. Our results suggest at least three mechanisms of skeletal reduction: (1) reduction of bone size, (2) reduction of bone density, and (3) loss of skeletal elements. First, using phylogenetic generalized least squares (PGLS) analysis, we found that the change in cranial dimensions with depth was not uniform. While the size of the maxilla, dentary, and pectoral girdle decreased with greater depth, length of the upper premaxilla and the neurocranium did not vary with collection depth. Second, average density of the lower jaw decreased with increasing depth. Lastly, the ventral suction disc has been lost multiple times within the deep sea lineage. While all three methods are seen in

snailfishes, other groups may use some or all of these mechanisms to different extents. Some mechanisms of skeletal reduction may be more advantageous than others. The extent to which a structure is retained in deep-dwelling fishes may indicate its functional importance. Variable skeletal reduction in the family Liparidae provides insights into the physiological adaptations that allow fishes to survive in deep-water environments. We conclude that some skeletal elements are maintained at the expense of others as fishes balance the functional demands of life in the deep sea.

## Are fish associations with corals and sponges more than an affinity to structure: evidence across two widely divergent ecosystems

Rachel Wilborn, Chris Rooper-NOAA AFSC, Pam Goddard, Rachel Wilborn
NOAA-AFSC, Lynker Technologies

The role of deep-sea coral and sponge ecosystems as habitat for marine fishes has been widely deliberated. Almost all studies that have looked for associations between corals and sponges and fishes (especially rockfishes) have found significant relationships. However, rockfishes thrive in areas largely devoid of corals and sponges. The objective of this study was to compare the association of fish species with deep-sea corals and sponges and other available benthic structure across different spatial scales in the eastern Bering Sea (EBS) and Aleutian Islands (AI). The two ecosystems were found to have much different abundances of corals and sponges (with the AI densities roughly 3 orders of magnitude higher than the EBS). At broad scales, the results showed that rockfish species and Pacific cod were significantly correlated to more structured seafloors. At smaller scales (the scale of individual fish) only Pacific cod, northern rockfish and Pacific ocean perch had significant associations with structure. We used stereo imagery to measure the size and distance between fish and structure and found that the strength of associations (measured by distance to and overall affinity to structure) was weak for fish >40 cm. Over half of the individual fishes were associated with sponges, but this was because they were the most commonly available. When accounting for availability of the different types of structure, rockfish were not preferentially choosing sponges (or any other type of structure). These relationships were consistent across ecosystems, indicating that even though rockfish densities and coral and sponge abundance were very different between the EBS and AI, the ecological processes guiding habitat use by rockfish were consistent.

## A Novel and Kinetically Stable Cu/Zn-superoxide Dismutase from Hadal Sea Cucumber *Paelopatides* sp.

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Reactive oxygen species (ROS) are required for several cellular biological contents and for various physiologic functions. However, the accumulation of these reactive molecules in organisms will cause serious damage to DNA, proteins, and other bio-macromolecules and could result in cell death. Superoxide dismutases (SODs) play an important protective role during this process by preventing excessive ROS from damaging cells. In present study, cloning, expression, and characterization of a novel Cu,Zn superoxide dismutase (Ps-Cu,Zn-SOD) from a hadal sea cucumber (Paelopatides sp.) was reported. The open reading frame of Ps-Cu,Zn SOD was 459 bp encoding 152 amino acids without signal peptides.

Phylogenetic analysis showed that Ps-Cu,Zn-SOD clustered together with other echinoderm and belonged to a class of intracellular SOD. Its Km and Vmax were 0.0258 ± 0.0048 mM and 925.1816 ± 28.0430 units/mg, respectively. The low Km value of this enzyme represents a high substrate affinity and can adapt to the low metabolic rate of deep sea organisms. The enzyme functioned from 0 to 80°C with an optimal temperature of 40°C. Moreover, the enzyme activity was maintained up to 87.12% at 5°C. The enzyme was active at pH 4 to 12 with an optimal pH of 8.5. At tested conditions, Mn2+, Co2+ and Ni2+ had negative effect while Zn2+ had positive effect on enzyme activity. Furthermore, Ps-Cu,Zn-SOD is resistant to EDTA, DTT and SDS, and could retain activities in β-ME, Triton X-100, Chaps, and Tween 20. The SOD could also tolerate high concentration of urea and GuHCl, and resist the hydrolysis by proteases and maintain stability at high pressure. All these features demonstrated that the deep sea Ps-Cu,Zn-SOD is a kinetically stable enzyme and might have potential application in the biopharmaceutical field.

POSTER 59 ⚡ Biodiversity and ecosystem functioning
TUESDAY Lightning Talks • 08:30 • Serra Room

## Epifaunal communities at ridge, plateau and basin locations in the Chukchi Borderland, Arctic deep sea

Irina Zhulay, Katrin Iken, Paul Renaud, Bodil Bluhm
UiT, The Arctic University of Norway; University of Alaska Fairbanks; Akvaplan-niva and the University Centre in Svalbard; UiT, The Arctic University of Norway

Epifaunal communities were investigated in the poorly studied Chukchi Borderland, Pacific Arctic deep-sea, which is characterized by complex hydrography and bathymetry. The primary research question was if communities differed among three main habitat types: ridges, basins, and plateau with inactive pockmarks. Environmental factors affecting the communities were also examined, and biogeographic affinities of the epifauna were evaluated. Samples were collected from the US Coastguard icebreaker Healy in summer 2016 with a beam trawl (6 stations) and ROV (10 stations) from 486 to 2610 m depth. Seventy-eight and Eighty-six taxa were registered from the ROV and trawl samples, respectively. Echinodermata and Arthropoda dominated overall taxon richness. Epifaunal densities varied from 2,273 to 14,346 ind/1000m2 on the images and was much higher than those observed from trawl samples, where it varied from 342-2,029 ind/1000m2 . The epifaunal biomass based on trawl catches ranged from 173 to 906 g wet weight/1000m2. There was no significant difference between plateau and ridge communities in terms of community composition and taxon richness. Based on the images, ridge/plateau communities were dominated by annelids (Sabellidae and Ampharetidae) on the eastern side and by an unknown cnidarian (possibly, polyps of Atorella) on the western side of the study area. Trawl samples from these sites showed a clear dominance of Ophiopleura borealis and Pontaster tenuispinus echinoderms. Basin communities differed from plateau and ridge stations by significantly lower number of taxa and densities based on the images, this difference was not apparent from the trawl samples. Polynoid annelids (based on ROV samples only) and poriferans were characteristic taxa of the basin stations. Water depth and number of stones on the seafloor significantly influenced epifaunal community structure, with sediment pigments and grain size also being influential. Arcto-boreal-Atlantic species strongly dominated communities in the Chukchi Borderland.

POSTER 60 ⚡ Biodiversity and ecosystem functioning
TUESDAY Lightning Talks • 08:30 • Serra Room

## Exploring patterns of biodiversity in the deep-sea with National Geographic's Deep-ocean Dropcam

Jonatha Giddens1,2,3, Alan Friedlander2,4, Whitney Goodell1,4, Alan Turchik5

1. National Geographic Society Fellow 2. Fisheries Ecology Research Lab, University of Hawaii 3. NOAA NMFS 4. National Geographic Society Pristine Seas 5. National Geographic Society Exploration Technology Lab

Biodiversity in the deep ocean has remained largely un-described because exploration has historically been a challenge in this extreme and remote environment. Recently, National Geographic's Deep-ocean Dropcam, a high definition camera encased in glass pressure housing, has proven to be a robust and efficient platform for exploring the deep-sea. This tool enables observations of marine life in situ by capturing high quality imagery of the sea floor. To date, 20 sites from some of the most remote areas of the globe have been surveyed - from the Russian Arctic, to the Southern Ocean, spanning Pacific, Atlantic, and Indian Oceans. At these sites, between 10 and 30 deployments were conducted down to 2,450m depth, video recording one to three hours in duration. To date, we have examined species richness by depth (shallow vs. deep), and habitat (hard vs. soft bottom) for nine of these sites. Palmyra Atoll in the Central Pacific and the Galapagos Islands in the Eastern Pacific, were the most divers locations with an average of 8-10 species observed per drop on deep hard bottom habitat. Biodiversity can be used as an indicator of ecosystem health. We are expanding our sampling locations across a gradient of habitats and human impacts, with the goal of establishing a baseline index of deep ocean ecosystem health. This global synthesis will contribute to our understanding of how biodiversity varies across depths and locations in the deep-sea, and provide a framework for monitoring and stewardship of our deep ocean into the future.

POSTER 61 - Biodiversity and ecosystem functioning
TUESDAY Evening • 17:45 • Serra Ballroom

## Successful life strategies of isopods from the family Munnopsidae for colonizing deep-sea habitats

Marina Malyutina
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Munnopsidae Lilljeborg, 1864 is the largest among 19 families in the suborder Asellota, comprising primarily cosmopolitan, swimming deep-sea isopods. With 9 subfamilies, 42 genera, and <320 described species, it is one of the most diverse and abundant isopod families in deep-sea communities. Half of all Peracarida in the benthic samples belongs to Isopoda; around half of all isopods are from the Munnopsidae. This ratio is generally typical for all samples from worldwide abyssal. Peracarida have brood development. This is obviously a very successful strategy for deep-sea life, providing care for offspring, while the limited dispersal capabilities reduce the gene flow, which can be causes of active speciation. Asellota amazingly radiated in the deep-sea. Their adaptations to shallow-water mud habitats gave them advantage for the life in muddy abyssal plains. The key characters of Munnopsidae reflect their swimming ability, developing of which is the main trend in evolution of the family. Other trends are adaptations to life in muddy sediments: secondary transition to crawling and digging. Food specialization is the cause of great morphological diversity of Munnopsidae. Less specialized, most abundant munnopsids are seston-feeders and sorting detritus-feeders. Swimming and pelagization are associated with predation and size increase. Important adaptation to life at depths is neoteny and hypomorphism: the body size decrease is accompanied by various reductions. Neoteny is characteristic of the subfamily Lipomerinae, members of which resemble juveniles. This adaptation can be associated with more efficient energy consumption at depths, where food resources are limited. Shortening the ontogenetic stages leads to reduced body sizes, faster succession of generations, and, consequently, acceleration of evolution. The diversity and wide distribution of Munnopsidae in the deep-sea indicate their successful life strategy for deep-sea.

# Chemosynthetic ecosystems
## - TALKS

MONDAY Midday • 14:15 • Serra Room
### The KleptoShimp and the Yeti Crab: Cross-species symbiont transmission at methane seeps.

Andrew Thurber, Will Ridgeon, Gavin Thurston, and the British Broadcast Corporation
Oregon State University

Epibiotic bacteria are known from a variety of reducing habitat fauna, including arthropods such as alvinocarid shrimp and kiwa crabs. As our understanding of the distribution of these fauna expands, enigmatic patterns have emerged with taxonomy of the host and symbiont often at odds. While symbiont uptake from a common pool (i.e. horizontal transmission) may explain some of these patterns, an additional mechanism was observed at a methane seep off Costa Rica. Alvinocarid shrimp were observed approaching and grabbing epibiotic bacteria off of the setae of the yeti crab, Kiwa puravida. It is unclear whether the shrimp was simply grazing upon the bacteria or whether it is taking the bacteria to inoculate its own symbiont pool. When this observation is combined with genetic measures of symbiont identity found on Kiwa and alvinocarids, this proposed mechanism of symbiont transmission helps explain the anomalous similarity in symbionts between these two hosts even across ocean basins. This approach also likely provides key ecological advantages to the thieving shrimp. While symbiont and organelle theft is not unknown (such as chloroplasts and nematocysts by molluscs) our observation provides an alternative mechanism of symbiont transmission and insight into the biogeography of symbionts within and among deep-sea reducing habitats.

MONDAY Midday • 14:30 • Serra Room
### Faunal Microdistribution of the Pelagia hydrothermal vent field: A 3 D reconstruction approach

Klaas Gerdes, Pedro Martinez-Arbizu, Ulrich Schwarz-Schampera, Terue C. Kihara
Senckenberg am Meer - DZMB, Center for Natural History, Federal Institute for Geosciences and Natural Resources

Active hydrothermal vent fields are complex small scale habitats hosting endemic vent fauna. Within these vent fields the microdistribution of taxa changes at scales of centimeters and depends presumably on terrain variables. The distance to hydrothermal fluids is thereby considered a major structuring factor but lacks statistical approval. Imagery analysis based on two dimensional photo stitching revealed limited insights to the vent field zonation around fluid exits and a basic knowledge of faunal assemblages within hydrothermal vent fields. However, complex three dimensional structures could not be adequately replicated and the assemblage structure as well as their relation to abiotic terrain variables is often descriptive.We collected ROV video imagery from the Pelagia hydrothermal vent field on the southwestern Indian Ridge in the Indian Ocean. Structure from Motion (SfM) photogrammetry was used to build a high resolution 3 D reconstruction model of an active hydrothermal chimney complex. We successfully applied SfM to project quantified individual abundances to the 3 D model. Likewise, the reconstruction was used to derive terrain variables at scales of megabenthic individual sizes, which were related to the abundances of the faunal assemblages. The applied random forest model predicted the faunal assemblage distribution with an accuracy of 94.9 %. The most important structuring variables were the distances to diffuse- and black fluid exits, as well as the height of the chimney complex.This novel approach enabled us to classify the quantified individual abundances of megabenthic taxa to distinct faunal assemblages and relate terrain variables to their distribution. The successful prediction of the faunal assemblage occurrences, based solely on terrain variables demonstrates the importance of abiotic factors for the assemblage structure in hydrothermal systems.

MONDAY Midday • 14:45 • Serra Room
### Is it the Egg first or the Shrimp? – Diversity and evolution of the microbial communities colonizing broods of the vent shrimp *Rimicaris exoculata* throughout embryonic development

Pierre Methou, Ivan Hernández-Ávila, Valérie Cueff-Gauchard, Florence Pradillon, Marie-Anne Cambon-Bonavita
Ifremer EEP/LEP, Ifremer EEP/LM2E

Rimicaris exoculata is one of the most well-known and emblematic species from the vent endemic fauna. As with many others species from those ecosystems, Rimicaris shrimps house important communities of chemosynthetic bacteria living in symbiosis with their host inside the branchial cavity and the gut. For many of the symbiotic partners, transmission mode has still to be elucidated and the beginning of the symbiotic relationship is not clearly defined yet within the lifecycle of the animal. In this study, sampling of a large number of Rimicaris exoculata broods during the shrimp's reproductive period, has allowed us to explore the microbial diversity throughout embryonic development. Combining sequencing and microscopy techniques, the presence, relative abundance and diversity of microbial communities colonizing broods have been described in two hydrothermal vent sites for different egg stages. Our results highlight, among others, important variations in microbial communities' abundance between broods occurring throughout embryonic development but also between eggs from within a single brood, being all at the same developmental stage. Comparisons were also made between the diversity of egg communities and those found on the pleopod of the same brooding female, a non-symbiotic tissue subject to similar environmental conditions. This provides a basis to discuss both the acquisition of symbionts during this life stage and the potential roles of these bacterial communities within their host.

MONDAY Midday • 15:00 • Serra Room
### Environmental conditions, substratum nature and biotic interactions on hydrothermal fauna colonization patterns at Lucky Strike

Joan Alfaro-Lucas, Martin Foviaux, Loïc Michel, Gauthier Schaal, Daniela Zeppilli, Florence Pradillon, Jozée Sarrazin
Ifremer EEP/LEP, IUEM

Isolated and fragmented nascent hydrothermal vent sites are rapidly colonized by a regional pool of species. However, colonization processes are complex and depend on several interacting biotic and abiotic factors playing at different scales. Furthermore, reducing habitats, such as sunken woods or whale carcasses, may be used by some hydrothermal vent fauna as dispersal stepping stones. Here, we studied macrofaunal communities colonizing wood and slate substrata deployed during two years (2013-2015) at 5 sites of varying hydrothermal activity (from high to non-active) on the Lucky Strike vent field (Mid-Atlantic Ridge). Our objective was to shed light on how environmental characteristics, substratum type and biotic factors influence vent colonization processes. We hypothesized that environmental filtering largely drives community composition and structure at sites characterized by the presence of hydrothermal vent activity, whereas other factors take over at external sites. A redundancy

analyses (RDA) model supported our hypothesis and showed that vent fluid inputs strongly drove assemblage structure at active sites regardless of substratum type, whereas this parameter played a stronger role at inactive sites. The assemblages of active site substrata were mainly characterized by regular vent inhabitants, while wood at inactive sites created a typical "wood-fall" assemblage. Slate assemblages at inactive sites where a subset of their counterparts at active sites. Hydrothermal vent species, such as Amphisamytha lutzi and Bathymodiolus azoricus, did not colonize external site substrata, supporting their strong reliance on hydrothermal vent conditions. Finally, we coupled traditional taxonomic approaches with trophic structure and functional trait analyses to further clarify the role of biotic interactions on colonization processes. Characterizing such ecological aspects of vent ecosystem is critical to be able to elaborate management strategies to mitigate the future impacts of anthropogenic activities such as deep-sea mining.

## Discovery of an extensive deep-sea fossil serpulid reef associated with an active cold seep, Santa Monica Basin, CA
Magdalena N. Georgieva [1,2], Charles K. Paull3, Crispin T.S. Little, Mary McGann, Diana Sahy, Daniel Condon, Lonny Lundsten3, Jack Pewsey, David W. Caress3 and Robert C. Vrijenhoek3
1 Natural History Museum UK, 2 University of Leeds UK, 3 Monterey Bay Aquarium Research Institute, 4 United States Geological Survey, 5 British Geological Survey
Multi-beam mapping of the Santa Monica Basin, southern California, has revealed the existence of a number of elevated bathymetric features, or mounds, harbouring cold seep communities. During 2013-2014, mounds at ~600 m water depth were observed for the first time and sampled by Monterey Bay Aquarium Research Institute's ROV Doc Ricketts. Active cold seeps were found, but enigmatically one of these mounds was characterised by massive deposits composed of fossil calcareous serpulid worm tubes (Annelida: Serpulidae) exhibiting various states of mineralisation by authigenic carbonate. No living serpulids with tubes resembling those of the fossils were found at the site; hence the mound was termed 'Fossil Hill'. Vast serpulid aggregations or reefs are commonly associated with shallow waters, usually occurring within enclosed embayments or lagoons. However, there are also reports of high serpulid abundances at deep sea sites of organic enrichment, such as at cold seeps of Costa Rica and the Barbados Accretionary Prism. During the present study, the identity of the fossil serpulids and associated fossil community, the ages of fossils and carbonates, and the geological structure of the mound are explored. Results of radiocarbon dating of the serpulid tubes indicate that they date to the Late Pleistocene, specifically to the Last Glacial Maximum ~20,000 years ago. Additional U-Th analyses corroborate the radiocarbon dates, and also suggest that seepage was occurring at this time. The extent, structure, and fossil community of Fossil Hill will be discussed to shed insights into the relationship between chemically-reduced fluid availability and fossil abundance at this site as well as to the timing of formation of this anomalous structure.

## Comparative host anatomy and bacterial associations in chemosymbiotic *Alviniconcha* gastropods
Sven R. Laming, Katia Leglise, Marie-Anne Cambon-Bonavita, Florence Pradillon
Ifremer, Centre de Bretagne, REM/EEP/LEP, UMR LM2E
The chemosymbiotic gastropod genus Alviniconcha (Provannidae) is one of the most prolific hydrothermal-vent taxa from the Central Indian Ridge and sites located in the Mariana volcanic arc and the Mariana, Manus, Fiji and Lau back-arc basins in the SW Pacific, where they inhabit the walls and bases of active chimneys characterised by commercially lucrative mineral deposits. These species are known to harbour species-specific, gill-associated bacterial symbioses. Three species – recently described based on robust phylogenetics – are known from the SW Pacific (A. kojimai, A. strummeri and A. boucheti), where they occur in unusually close proximity at active sites from the small-scale back-arc system around the Wallis and Futuna islands (French EEZ) forming a sympatric species complex. While data already exists regarding gill-associated bacterial assemblages from other sites in the SW Pacific, little is known concerning host developmental biology, both in terms of functional anatomy and symbiotic state. To advance our understanding of the onset of these gill symbioses during the host lifecycle, the developmental anatomy and symbiotic nature of these species following settlement is assessed for the first time, based on a synergy of anatomical imaging, histological and in-situ hybridisation analyses and molecular biology performed on post-larval, juvenile and adult specimens. Formerly considered to be 'cryptic' species, anatomical studies reveal distinguishing morphoanatomical characters. Gill symbioses identified appear to be synonymous with, but not identical to, those of specimens from other sites in the SW Pacific. Analyses of non-gill tissues suggest that bacterial associations may extend beyond the gill, alluding to hitherto unknown symbiotic associations. Data provide an illuminating insight into the Alviniconcha lifecycle from a holobiont perspective, and identify knowledge gaps that warrant further investigation.

## Heterogeneity of Methane Seep Biomes Across a Margin Ecosystem
Sarah Seabrook, Fabio C. De Leo, Andrew R. Thurber
College of Earth, Ocean, and Atmospheric Sciences
The Cascadia Margin has been found to host a high density of cold seeps, with over 2,500 individual seep sites identified with multibeam technology to date. The myriad of environmental conditions found across the margin, and the distinct biogeochemistry of seep systems, leads to questions of how these numerous seep sites vary both locally and regionally, and how they interact with the surrounding margin environment. We investigated these questions with 8 recently discovered seeps, and 2 known seeps, that span 800 km of the Cascadia Margin and vary across 2000m water depth. To investigate the microbial community in the sediment at the various seep sites, we used 16S rRNA gene sequencing and multidimensional statistical modeling. We identified surprising latitudinal trends in microbial species diversity and richness, and high variability in the spatial distribution and community structure of microbial communities at the various sites. This includes multiple groups of anaerobic methane oxidizing Archaea (ANME; 1, 2ab, 2c, and 3) often co-occurring within one site, and atypical patterns in the vertical distribution of certain microbes. Further, we found novel megafaunal communities in the geographic region in unexpected environmental conditions, namely an abundance of vestimentiferan Sibglonids at a site in the lower extent of the persistent oxygen minimum zone. In June of this year, we are furthering our explorations of seep habitats on the margin, revisiting sites sampled in 2016 and exploring many new sites. Integrating preliminary results from this upcoming expedition with what we have learned thus far, we will highlight the variability within and among seep communities across the margin, and discuss the power of cross-margin studies to increase our understanding of both seep dynamics, and the interactions of seep habitats with the surrounding environment.

## First record of frenulate siboglinids on cold seep carbonates and their influence

## on the biology and geochemistry at a seep site in the north Atlantic

Arunima Sen, Tobias Himmler, Wei Li Hong, Raymond W. Lee, Jochen Knies, Aivo Lepland
Centre for Arctic Gas Hydrates, Environment and Climate (CAGE)

Frenulates are hair-like siboglinid worms that usually inhabit reduced sediment. In 2017, Oligobrachia haakonmosbiensis frenulates were recovered in association with carbonate crusts at a methane seep site in a canyon off the coast of Lofoten (Norway). This is the first and only documented record of frenulates among hard substrates. However, we hypothesize that individuals do not settle on carbonate rocks. Instead, we suggest that O. haakonmosbiensis, similar to seep vestimentiferan tubeworms, releases sulfate as a waste product into the surrounding sediment, which enhances methane oxidation and carbonate precipitation in shallow sediment layers and over time, carbonate deposits around them. Overgrowth of carbonates on the tubes of the worms can block the transport of chemicals, but similar to seep vestimentiferans, we hypothesize that the excretion of protons by the worms prevents the direct growth of carbonate on their tubes. This carves tunnels into the blocks around the worms, which allows for gas exchange, and gives the appearance of the worms being attached to or within the carbonates. We tested our hypothesis by comparing the mineralogy and oxygen isotope composition of carbonates with and without frenulates. Carbon isotope ratios ($\delta$13C) of the frenulates and their respective carbonates were compared to confirm their association to the same dissolved inorganic carbon (DIC) pool. Thin sections and 3D models of carbonates were also examined. The relationship between frenulates and carbonates at this site creates a truly unique situation because hard-bottom animals colonize carbonates and therefore co-occur with soft-sediment frenulates. Moreover, frenulates likely promote such colonization. Frenulate-free carbonates were strikingly devoid of fauna and extensive bacterial mats and filamentous bacteria on the worms suggest toxic sulfide levels in the bottom water. Frenulates likely reduce toxicity through their uptake of sulfide. Therefore, both biotic and abiotic features of the site appear to be directly influenced by frenulates.

## Characterization of western Atlantic margin seeps and their contribution to the deep-sea red-crab fishery.

Phillip J Turner, Bernard Ball, Ian Grace, Doreen McVeigh, Craig Young, Cindy L Van Dover
Duke University Marine Lab, University College Dublin, North Carolina State University, Oregon Institute of Marine Biology

In 2014, the discovery of 570 gas plumes on the western Atlantic margin (WAM) extended the northern boundary of the US Atlantic gas hydrate province and revealed chemosynthetic communities north of the Blake Ridge and Cape Fear diapirs. These WAM seep sites are hotspots for chemoautotrophic productivity and biomass, provide nutrition to benthic heterotrophs, and may support deep-sea fisheries. During a July 2015 R/V Atlantis expedition, scientists used the submersible Alvin to explore 10 seep sites at depths of 300 to 1500 m, from Cape Hatteras to Cape Cod. The chemosynthetic mussel Bathymodiolus childressi was observed at seven of the seep sites, with only small populations at Shallop Canyon West and New England Seep 2. Bathymodiolus heckerae, the dominant mussel at Blake Ridge seeps (2150 m), was only observed at the Norfolk Canyon West seep (1600 m). Using video transects and photo-mosaics, this study compares the megafauna associated with WAM seeps and tests the hypothesis that shallow seeps (300-500m) support more diverse assemblages than deep seeps (1000-1500m). In addition, due to the presence of the commercially fished deep-sea red crab (Chaceon quinquedens) at many of the sites, this study uses a range of approaches to explore the contribution of WAM seeps to the red crab fishery. Stable isotope analysis characterizes crab diet, plankton sampling documents

crab larvae above the seep site, and the spatial overlap of the red crab fishery and WAM seeps is investigated using Automatic Identification Systems (AIS) data on crab fishing along the WAM. Overall, the data supports the hypothesis of at least a limited contribution of WAM seeps production and habitat to the red-crab fishery, with relatively dense aggregations of crabs (up to 2 per 10m2) associated with seeps.

## Adaptation to the deep-sea hydrothermal vents and cold seeps: insights from the transcriptome and lysine acetylome of *Alvinocaris longirostris* in both environments

Min Hui, Jiao Cheng, Zhongli Sha
Institute of Oceanology, Chinese Academy of Sciences

Deep-sea hydrothermal vents and cold seeps are unique chemoautotrophic ecosystems with harsh conditions. Alvinocaris longirostris (Kikuchi and Ohta, 1995) is one of the few species co-distributed in both environments. We performed the transcriptome analysis for A. longirostris and identified differentially expressed genes (DEGs) between samples from the Iheya North hydrothermal vent (HV) and a methane seep in the South China Sea (MS). Multi-copies of enzyme family members for eliminating toxic xenobiotics were isolated and seven putatively duplicated gene clusters of cytochrome P450s were discovered. Eight single amino acid substitutions of a Rhodopsin gene with low expression in two alvinocaridid species were positively selected when compared with shallow water shrimps. 408 DEGs were identified with 53 and 355 up-regulated in HV and MS. Various genes associated with sulfur metabolism, detoxification and mitochondria were included, revealing different mechanisms of adaptation to the two types of extreme environments. Lysine acetylation has been known to play critical roles in the regulation of many cellular processes. We comprehensively investigate lysine acetylome in A. longirostris for the first time. 501 unique acetylation sites from 206 proteins were identified. Arg, His and Lys occurred most frequently at the +1 position downstream of the acetylation sites, which were all alkaline amino acids and positively charged. Acetylated proteins were found enriched in mitochondrion and peroxisome, and many stress response related proteins were also discovered to be acetylated, like arginine kinases, heat shock protein 70, and hemocyanins. In the two hemocyanins, nine acetylation sites were identified, among which one acetylation site was unique in A. longirostris compared with other shallow water shrimps. Further studies are warranted to verify its function. All results supply abundant genetic resources and bring new insights in exploring the molecular basis for adaptation to the deep-sea chemoautotrophic ecosystems in A. longirostris and other shrimps.

## Across-axis transition of hydrothermal vent fauna in southern Mariana Trough

Hiromi Kayama Watanabe, Stace E Beaulieu, Florence Pradillon, Kana Komaki, Susan Mills, MiHye Seo, Tomomi Ogura, Hiroka Hidaka, Sayaka Mino, Takenori Sasaki, Katsunori Fujikura, Jun-ichiro Ishibashi, Shigeaki Kojima
Japan Agency for Marine-Earth Science and Technology

Dispersal is an important event to sustain metapopulations in ephemeral and patchily distributed environments such as deep-sea hydrothermal vent fields. Most hydrothermal vents are distributed along spreading axes, and across-axis dispersal of vent fauna is little known. In the present study, phase transition of hydrothermal benthic communities was observed and dispersal was inferred among three hydrothermal vent fields, the on-axis Snail site, the off-axis Pika-Urashima site and the Archaean site, which are distributed across axis in the Southern Mariana Trough. Size frequencies

of Austinograea williamsi, Chorocaris vandoverae and Alviniconcha hessleri showed that populations in the Snail site were the largest among three sites. However, genetic diversities of Al. hessleri, C. vandoverae and Neoverruca brachylepadoformis were the highest in the Pika and Urashima sites, although no significant genetic subdivision was detected among the populations of all the examined species. Tidal analysis of a current meter deployed near the Snail site supported the possibility of dispersal from on- to off-axis. These results suggested the possibility that across-axis dispersal promotes on-axis to off-axis transition of hydrothermal fauna.

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## Vertical migration of gastropod larvae from hydrothermal vents: oxygen isotope and trace element analyses

Takuya Yahagi, Kentaro Tanaka 1, Tomihiko Higuchi 1, Kotaro Shirai 1, Yasunori Kano 1
(1) Atmosphere and Ocean Research Institute, The University of Tokyo. (2) Japan Agency for Marine-Earth Science and Technology.

The stable isotope and trace element measurements of biogenic carbonates are invaluable for the reconstruction of past oceanographic and climatic changes as well as autoecology including ontogenetic migration of individual animals. However, such measurements have not been made to characterize the early life history of vent endemics. The present study first describes the oxygen isotope and trace element compositions of molluscan shells before and after metamorphosis for the inference of larval migration from deep-sea vents.We analyzed the red-blood limpets of the genus _Shinkeilepas_ (_S. myojinensis_ and _S. kaikatensis_), which develop as long-lived planktotrophic larvae and show wide geographic distributions. The adult individuals along with juveniles immediately after settlement were collected from a vent site on the Kaikata Seamount with a habitat temperature of 11°C. The oxygen isotope analyses of protoconchs and teleoconchs demonstrate that (1) the larvae of these limpets invariably experience warmer temperatures (17–23°C) that approximate conditions in the surface water above the vent site. This strongly suggests the vertical migration and surface dispersal to be compulsory parts of the life cycle of the study taxa. The relative concentrations of trace elements in larval and adult shells provide another clue for ontogenetic migration. (2) The concentrations of Mn and Ba were much higher in the teleoconch than in the protoconch of _Shinlailepas_. Such elements are present at very different concentrations in surface waters and hydrothermal fluids. These results show perfect concordance with (3) the larval behavior and (4) temperature optimum observed in culture experiments and (5) population genetic structure of _S. myojinensis_; the migration provides them the advantages of high food supplies and strong currents (Yahagi et al. 2017). Other planktotrophic species among vent endemic molluscs await similar integrated studies of analytical chemistry and behavioral observations to establish the presence or absence of comparable vertical migration.Takuya Yahagi 1,2, Kentaro Tanaka 1, Tomihiko Higuchi 1, Kotaro Shirai 1, Yasunori Kano 11 Atmosphere and Ocean Research Institute, The University of Tokyo, Kashiwa, Japan.2 Japan Agency for Marine-Earth Science and Technology, Yokosuka, Japan.

# Chemosynthetic ecosystems - POSTERS

POSTER 62 - Chemosynthetic ecosystems
TUESDAY Evening • 17:45 • Serra Ballroom

## 'Do not stop listening. Message forthcoming'

Ana Hilário, Eva Ramirez-Llodra; Fredrik Soreide
CESAM & Department of Biology, University of Aveiro, Portugal

Whale falls provide a resource for diverse faunal assemblages that vary in species diversity and community structure according to the stage of decomposition. The sulphide and lipid-rich nature of decomposing bones is thought to create an habitat intermediate to that of hydrothermal vents and hydrocarbon seeps, and a faunal overlap across whale falls, vents and seeps as led to the suggestion that whale-falls may act as evolutionary and dispersal stepping stones for vent and seep taxa. However, data on whale-fall communities is still limited, constraining biogeographic analyses and knowledge on evolutionary links between these environments. Despite huge advances have been made by studying experimentally implanted whale remains, discovering natural whale falls allow to study carcasses that have been decomposing on the seafloor for longer periods and provide a unique view into the natural processes of the taphonomy of large cetaceans on the seafloor. In 2009, three whale-falls were discovered and imaged with an ROV in the Barents Sea during a search mission for the wreck of the flying-boat Latham 47, which disappeared in 1928 with the Norwegian polar explorer Roald Amundsen on board. The three carcasses, between 125 and 180 m depth, are located on a radius of approximately 3Km and presented different stages of decomposition and ecological succession: mobile-scavenger; enrichment-opportunist/sulphophilic and reef stages. The site will be re-visited in August 2018 and if possible samples will be collected. Videography (and samples) will be used to investigate succession and community structure. These are, to the best of our knowledge, the only record of whale falls in the Atlantic sector of the Arctic and may provide new insights on the biogeography and connectivity of deep-sea reducing habitats in this unexplored region of the seafloor. Quoting the last radio communication from the missing Latham 47: 'Do not stop listening. Message forthcoming'.

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TUESDAY Lightning Talks • 08:30 • Serra Room

## Symbiont-host decoupling in eastern Pacific vesicomyid clams

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Deep-sea clams of the family Vesicomyidae harbor sulfide-oxidizing endosymbiotic bacteria that are inherited from mother to offspring each generation. Such a vertical transmission mode usually results in co-evolution of host and symbiont lineages as mitochondrial and symbiont genomes become genetically linked. Although this pattern is seen in the clam-bacteria symbiosis, various instances of incongruent host-symbiont phylogenies have been found, which implies that vesicomyid clams acquire their symbionts occasionally from an environmental source. Even so, the potential pathways of horizontal transmission in clam symbionts remain largely unknown. In the present study we report a new case of untypical symbiont compositions in the two cold-seep species Archivesica gigas and Phreagena soyoae by showing that several A. gigas individuals harbor the P. soyoae specific 16S rRNA symbiont phylotype. Using restriction-site associated DNA sequencing we address the hypothesis that contemporary hybridization between the two host species caused a symbiont switch in A. gigas. In addition, we carry out phylogenetic analyses to examine whether incomplete lineage sorting or asymmetric historical introgression led to the retention of the P. soyoae symbiont phylotype. The results from this study will shed new light onto the evolution of symbionts with vertical transmission in deep-sea chemosynthetic environments.

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## Metagenomics of symbiont communities in *Bathymodiolus* mussels from the US mid-Atlantic reveals complex elemental cycling

D. Katherine Coykendall, Lakyn Sanders1, Robert S. Cornman2, Nancy G. Prouty3, Christina Kellogg4, Sandra Brooke5, Amanda W. J. Demopoulos6, and Cheryl L. Morrison1

1U.S. Geological Survey, Leetown Science Center; 2U.S. Geological Survey; 3U.S. Geological Survey, Pacific Coastal and Marine Science Center; 4U.S. Geological Survey, St Petersburg Coastal and Marine Science Center; 5Florida State University, Coastal

Mussels of the genus Bathymodiolus are among the most widespread colonizers of hydrothermal vent and cold seep environments and are sustained by endosymbiosis with chemosynthetic bacteria. In recent years, unknown species of Bathymodiolus were discovered at cold seeps on the US Mid-Atlantic continental slope. We used mitochondrial and nuclear sequences to classify species found at three seep sites (Baltimore Canyon seep (BCS; ~400m); Norfolk Canyon seep (NCS; ~1520m); and Chincoteague Island seep (CTS; ~1000m)). Molecular data suggests that Bathymodiolus childressi predominates at these sites, although single B. mauritanicus and B. heckerae individuals were detected. Isotopic results from mussels at the same sites suggested they have dynamic roles in methane, sulfur, and nitrogen nutrient cycling. To further explore the role of symbionts in nutrient cycling, we characterized the gill microbial community of a subset of mussels from NCS and BCS using metabarcoding techniques and four primer sets spanning the 16S gene. The metabarcoding results revealed three main taxa: a Gammaproteobacterial methanotrophic haplotype from the Marine Methylotrophic Group 1 family in all samples from both sites, and two distinct sulfur-oxidizing, Epsilonproteobacteria in gills from NCS only. We constructed consensus sequences for the common methanotroph and two Epsilonproteobacteria haplotypes and designed target-specific primers. Using qPCR techniques, we screened gill tissue from all the mid-Atlantic mussel samples for the presence of these three taxa, to determine how these dominant taxa vary in abundance within and between seep sites. We also used conventional cloning techniques to isolate the prokaryotic nifH gene, known to be part of the nitrogen fixing cycle, and identified potential microbial participants in nitrogen fixation. Further classification is underway. Continued characterization of endosymbionts from cold seeps will provide a greater understanding of the ecology of these unique environments as well and their geochemical footprint in elemental cycling and energy flux.

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TUESDAY Lightning Talks • 08:30 • Serra Room

## Deep-sea hydrothermal vents as natural egg-case incubators at the Galapagos Rift

Brennan Phillips, Pelayo Salinas-de-Leon, David Ebert, Mahmood Shivji, Forencia Ceritti-Pereyra, Cassandra Ruck, Charles R. Fisher, Leigh Marsh

University of Rhode Island

In 2015, scientists and crew aboard the E/V Nautilus exploring the deep regions of the Galapagos Islands made a surprising discovery: aggregations of skate eggs surrounding 'black smoker' hydrothermal vents at ~1600m. By correlating visual transect data, physical samples of the eggs, and temperature data recorded by the ROV, we conclude that deep-sea skates appear to be actively using the elevated temperature of a hydrothermal vent environment to naturally "incubate" developing egg-cases. Morphological and genetic analysis of sampled egg-cases indicate with 100% certainty that the species is the deep-sea skate Bathyraja spinosissima. We hypothesize that this behavior accelerates embryo development time given that deep-sea skates have some of the longest egg incubation times reported for the animal kingdom. Similar egg incubating behavior, where eggs are incubated in volcanically heated nesting grounds, have been recorded in Cretaceous sauropod dinosaurs and the rare avian megapode. To our knowledge, this is the first time incubating behavior using a volcanic source is recorded for the marine environment. In addition, these findings highlight the need to explore and

conserve hydrothermal vent environments currently under pressure from deep-sea mining interests.

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TUESDAY Lightning Talks • 08:30 • Serra Room

## Nematode-prokaryote interactions in deep-sea hydrothermal vents

Daniela Zeppilli, Laure Bellec, Valérie Cueff-Gauchard, Lucile Durand, Marie Portail, Loïc Michel, Jozée Sarrazin, Ann Vanreusel, Marie-Anne Cambon Bonavita

Ifremer EEP/LEP, Ifremer EEP/M2E, Ghent University

Nematodes are among the most abundant and diversified organisms on Earth. Some nematodes are able to cope with extreme environmental conditions, where most of other animals cannot survive. The association between prokaryotes and eukaryotes (through symbiosis) is a winning strategy allowing the survival of extreme fauna. Little is known about nematode-prokaryote interactions in marine environments, and even less in deep-sea extreme ecosystems. The present study aims to unveil nematode-prokaryote interactions in deep-sea hydrothermal vents. We selected one of the most abundant thought still overlooked nematode species of Oncholaimidae at the Lucky Strike vent field (Mid-Atlantic Ridge). We analyzed the abundance, biomass, diet and diversity of this nematode. Associated prokaryotes were analyzed by microscopic observations (FISH and SEM) and metabarcoding of 16S rRNA. We revealed that this species is very abundant in the most active vent sites and is detritus feeder and/or bacterial grazer which could rely on consumption of multiple groups of free-living chemoautotroph microorganisms. This species harbored a microbial community highly represented by sulfur-oxidizing bacteria related to Epsilonproteobacteria and Gammaproteobacteria lineages. This study opens the way to the discovery of unexplored prokaryote–eukaryote interactions in deep-sea hydrothermal vents.

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## Stable isotopic insights into chemosynthetic food webs at two methane seeps in the US Atlantic margin

Amanda W.J. Demopoulos, McClain-Counts, J., Bourque, J., Brooke, S., Ross, S.W., Prouty, N

USGS, FSU, UNCW

Along the U.S. Atlantic margin, hundreds of seeps have been documented, and detailed investigations at a few seeps revealed distinct environments containing mussels, microbial mats, authigenic carbonates, and soft sediments. The dominant mussels Bathymodiolus childressi contain methanotrophic endosymbionts, but are also capable of filter feeding. Stable isotope analysis (SIA) of mussel-shell periostracum suggest these mussels are mixotrophic, assimilating multiple food resources. However, it is unknown whether mixotrophy is widespread or varies spatially and temporally. We used SIA ($\delta^{13}C$, $\delta^{15}N$, and $\delta^{34}S$) to characterize food webs at two seep locations along the U.S. mid-Atlantic margin. Low mussel $\delta^{13}C$ values suggested a dependence on methane-derived carbon. However, isotopic mixing models revealed mixotrophy for mussels at both sites, including reliance on a mixture of methane, phytoplankton-derived and local particulate organic carbon. Mussel isotopes also differed by tissue type, with gill having the lowest $\delta^{15}N$ values relative to muscle and mantle tissues. Variations in isotopic routing among the tissues and tissue-specific turnover time may contribute to these differences. Isotopic differences were also spatially discrete, possibly reflecting variations in the underlying seep geochemistry at the two sites. The proportion of live mussels and mixture of habitat type (i.e., sediment, hard substrate, and shells) significantly influenced mussel isotopic variance. Other taxa collected at the seeps exhibited $\delta^{13}C$ values consistent with reliance on chemosynthetic production, including the fishes, Dysommina rugosa and

Symphurus nebulosus, and echinoderms, Odontaster robustus, Echinus wallisi, and Gracilechinus affinis. In contrast, several mobile and sedentary fauna were enriched in 13C relative to chemosynthetic food sources, and likely rely on phytoplankton-derived organic matter. The presence of these seeps, and the variety of food resources available within, increase the overall trophic and community diversity of the U.S. mid-Atlantic continental slope.

## Meiofaunal diversity at the hydrothermal vent site ABE in the Eastern Lau Spreading Center

Coral Diaz-Recio Lorenzo, Daisy ter Brugge, Sabine Gollner
NIOZ

It is estimated that meiofauna species contribute about 50% to species richness at deep-sea hydrothermal vents, but meiofauna is still understudied in most regions. Vent meiofauna species have distinct traits compared to mega- and macrofauna, and respond differently to disturbance events. The hydrothermal vents off the east coast of the Kingdom of Tonga (Lau Spreading Center, South Pacific) fall geographically within the areas licensed to exploratory mining of massive sulphides. To date, we lack knowledge on meiofauna diversity in the entire region. We explore abundance and diversity of meiofauna associated with foundation species at the active vent site ABE on the Eastern Lau Spreading Center. The site ABE is dominated by three foundation species: (1) the snail Alvinoconcha spp. being exposed to average vent fluid temperatures of ~20°C, (2) the snail Ifremeria nautilei at ~11°C, and (3) the mussel Bathymodiolus septemdierum in average temperatures of ~5°C. In each habitat, three samples were taken using a quantitative collection device (mussel-pot). Meiofauna abundance ranged from 1-160 ind. per 10 cm^2. In the two snail habitats, copepods prevailed, with one species, Stygiopontius lauensis, dominating the meiofauna communities and representing 90% of the individuals. Interestingly, S. lauensis females were highly abundant among Alvinoconcha, whilst males were dominant among Ifremeria, suggesting gender- specific niche specialization within this copepod species. Meiofauna species richness was similarly low in the two snail habitats. In contrast, meiofauna richness was higher in the mussel habitat, with nematodes being the dominant higher taxon. Only three of the meiofauna species collected were known to science, the large majority (>20; study ongoing) are new to science.

## Distribution and ecological succession of hydrothermal vent communities on a sulfide edifice characterized from 3D photogrammetric reconstructions

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With advances in undersea technology, image analysis has become an invaluable tool to study and monitor deep-sea ecosystems. In the Lucky Strike vent field (Mid-Atlantic Ridge), the analysis of high resolution images of different sides of the Eiffel Tower (ET) sulfide edifice has allowed the characterization of the distribution of faunal assemblages and community succession on the edifice. However, these studies were based on 2-dimentional representations (images) of a 3-dimentional structure and, thus, did not capture the effect of the structural complexity of the edifice on

fauna distribution. Here we used 3D photogrammetry from ROV-based video to create 3D georeferenced models of the entire ET edifice in 2015 and 2016. We combined the analysis of the 3D reconstructions with in situ environmental measurements in order to (1) characterize the distribution of mega fauna and how it is affected by abiotic factors such as hydrothermal activity, temperature, water chemistry, currents and micro topography, (2) Assess fine-scale changes in fauna distribution between 2015 and 2016, and (3) compare measurement accuracies between 3D and 2D. Although data analysis is still ongoing, we expect that this study will allow us to refine the definition of microhabitats on ET by including additional abiotic factors (e.g. micro topography, currents), and to better grasp the influence of natural changes in the environment on community dynamics. With the imminent start of deep-sea mining activities, collecting baseline ecological data on hydrothermal vents is paramount to assess the resilience of these chemosynthetic ecosystems to potential impacts and appropriately inform conservation decisions.

## First insights into the biodiversity of the Colombian Caribbean deep sea

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Although approximately 44% of the Colombian territory is ocean, knowledge of the deep-sea beyond a depth of 150 m is limited. Deep-water biodiversity in the southern Caribbean region is currently poorly known, as no systematic exploration has been conducted. The major limitation for this exploration and characterization is the lack of technological assets capable of reaching depths below 1000 m. Anadarko Colombia Company (ACC) is an international company that performs off-shore exploration of oil and gas resources in the Colombian Caribbean. During the resource exploration phase (2015-2017), ACC carried out several cruises with ROVs, towed camera systems, and piston core samplers that allowed the first observations of benthopelagic, soft bottom and cold-seep ecosystems to a depth of 2700 m in the area known as Gran Fuerte. Approximately 5,500 photographs and 9 hours of video revealed a diversity of invertebrate and fish species; including new records for the region. Extensive cold seeps habitats were located through analyses of multibeam data (bathymetry, backscatter and gas plumes). Chemosynthetic communities at these sites resemble communities found off Trinidad and Tobago and the Gulf of Mexico. Dominant species include tubeworms (Lamellabranchia sp.), mussels (Bathymodiolus sp.), shrimp (Alvinocaris sp.), and squat lobsters (Munidopsis sp.). These results represent foundational knowledge of Colombian deep-sea ecosystems. They also represent the starting point for the understanding of the patterns and processes that have shaped biodiversity in the deep waters of the Southern Caribbean.

## Distribution patterns of chemosymbiotic bivalves of the subfamily Pliocardiinae (Bivalvia: Vesicomyidae) from the North-West Pacific

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Bivalves of the subfamily Pliocardiinae Woodring, 1925 (Vesicomyidae) are highly specialized symbiotrophic molluscs often dominating chemosynthetic communities all over the World Ocean. The North-West Pacific is one of the regions where pliocardiines exhibit great species diversity. We studied distribution patterns of 21 pliocardiine species living

along the Asian continental margin at depths from 300 m to 6809 m. The study area was limited by the latitude 61°N in the north and 30°N in the south. The analysis included new records from the Sea of Okhotsk and the Bering Sea; these are the northernmost known records of live populations of pliocardiins. Species identifications from new localities were confirmed by molecular data. The species of Pliocardiinae in the study area demonstrate three main distribution patterns: amphi-Pacific (8 species), Indo-West-Pacific (3) and endemic for the North-West Pacific (10). Our study confirmed earlier suggestions about strong faunistic affinities of the North-West and East Pacific. Amphi-pacific species are characterized by low genetic variation, suggesting either recent migration or even the contemporary gene exchange between western and eastern populations. Besides, two endemics of the North-West Pacific have closely related counterparts in the East Pacific. The share of amphi-pacific species increases from south to north along the Asian continental margin. All species from the Bering Sea and the Sea of Okhotsk also occur in the eastern Pacific. Abyssal endemics (species occurring deeper 3000 m) are characterized by more restricted geographical distribution than bathyal species: distribution of all seven abyssal endemic pliocardiines from the study area is limited to the North-West Pacific. Six species of eight with broad amphi-Pacific distribution are bathyal. Molecular estimations of the diversification time of pliocardiine taxa and paleontological data that could be relevant to modern distribution of pliocardiins are discussed. This study was in part funded by RFBR project No 18-05-60228.

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## Community structure and spatial distribution of vent fauna in the hydrothermal fields of North Fiji Basin based on ROV visual survey

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1Ulleungdo Dokdo Ocean Science Station, KIOST 2Biological Oceanography & Marine Biology Division, KIOST 3Deep-sea and Seabed Resources Research Center, KIOST

This study was conducted to investigate the community structure and distributional pattern of hydrothermal and adjacent deep-sea fauna at two hydrothermal vent fields (KF2 and KF3) on the central spreading axis in North Fiji Basin, from November to December 2016. Parts of these areas have been explored previously locating vent community sites named 'White Lady' and 'Mussel Valley'. This study further investigates KF2 and KF3 areas thoroughly, which extends the regions from previously found vent sites by visual inspections. During the ROV surveys by ROPOS, we obtained a total of ~160 hrs of video clips and ~14,000 still images along with specimen samples. In these areas, more than 30 species from active and inactive vent sites were identified and most taxa showed. In Active hydrothermal vent area, 2 kinds of mussel Bathymodiolus sp. and limpet Lepetodrilus sp., 2 kinds of snail Ifremeria sp., Alviniconcha sp. were observed. In Annelida tax, scaly worm Branchinotogluma sp. and Provinella sp. were dominant on the surface of hydrothermal chimney. In Arthropoda taxa, Munidopsis sp. and Paralomis hiretella, Austinograea sp. and Nautilocaris sp. were major fauna near hydrothermal vent area. In inactive vent area of common deep-sea area, 4 kinds of cnidarian Actiniaria, Chrysogorgia sp. Primnoidae sp. were observed. In mollusca taxa, smail Turridae sp. and 2 kinds of octopus Octopodidae sp. were also observed. Swimming holothuroid Paelopatides sp., and Enypniastes sp. were most dominant at sediment area. In comparison with the similarities of this community to other hydrothermal communities on the hydrothermal vent fields of spreading axis and arc of the Lau Basin located the southern part of Tonga islands, faunal composition were similar in active vents while there are difference in dead chimney community.

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## Patterns of microbial community assemblages and chemical fractionation of the Rainbow hydrothermal vent plume

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Microbial assemblages play an important role in the composition of hydrothermal vent plumes, ultimately influencing the wider ocean geochemistry. However, knowledge about the spatial ecology and community composition of microorganisms in relation to the biogeochemistry of the plume is sparse. The Rainbow vent field produces a vast plume, which extends for more than 50km. Using Next Generation Sequencing methods, the microbial communities of the neutrally buoyant plume-, above plume-, below plume-, near bottom water and sediment were assessed, most of which were classified as different biotopes on the basis of the microbiome. The composition and chemistry of suspended particulate matter from the water column was determined using scanning electron microscopy and HR-ICP mass spectrometry. Sampling stations followed the plume downstream to 25km. Each biotope displayed distinct microbial signatures with the exception of plume and below plume water, which had relatively similar communities presumably due to the vertical migration of the plume and plume deposition (including microbial aggregates). Biodiversity appeared reduced within the plume, likely due to the extreme chemical environment, where only specialised bacteria species can thrive. The plume was dominated by Epsilonproteobacteria groups (17-64% of the community), notably the sulphur oxidising bacteria genus, Sulfurimonas. Net removal of manganese, oxidative dissolution or preferential settling of chalcophile elements with sulphides, co-precipitation of phosphorus and vanadium with iron, and absorption of Rare Earth Elements occurred within the plume with distance from source. In tandem, bacterial community assemblages changed as the plume aged and travelled, reflecting chemical and physical gradients. Epsilonproteobacteria were more dominant at stations further away from the vent in contrast with previous research, suggesting that this group is well adapted to the diluted plume, driving a decrease in biodiversity with distance. Community succession patterns within the plume occurred on a time scale of days, indicative of a dynamic environment.

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## Biomarker fingerprint of anaerobic oxidation of methane in authigenic carbonate precipitation from cold seeps along the Mid-Atlantic, USA

Nancy Grumet Prouty, Pamela Campbell-Swarzenski
USGS

Anaerobic oxidation of methane (AOM), mediated by Archaea and sulfate-reducing bacteria, is common in continental margin sediment. AOM can result in authigenic carbonate precipitation, with the carbonate minerals incorporating biomarkers reflecting their origins. A lipid biomarker study was undertaken to determine biomarker composition and variability in authigenic carbonates and associated soft bottom cold seep habitats along the US mid-Atlantic margin. Seep and background sediment, in addition to authigenic carbonates, were collected and analyzed for a suite of biomarkers, including sterols, alcohols, alkanes and fatty acids, as well as carbon stable isotope ($\delta13C$) values of select biomarkers to elucidate pathways of organic matter cycling. The authigenic carbonates contained isoprenoid hydrocarbons with light $\delta13C$ values (up to -120.6‰ for pentamethyl eicosane-IV (PMI-IV)) whereas the seep sediment was characterized by high molecular weight (HMW) n-alkanes in the range of C17 through C33 and heavier $\delta13C$ values. The three principle Archaea lipid biomarkers (crocetane, 2,6,10,15,19-pentamethylicosane (PMI) and

sn-2-archaeol) can be used as diagnostic biomarkers of methantrophic archaea in the carbonates given enriched concentrations relative to the sediment. These methanotrophic archaea are responsible for AOM and suggest carbonate authigenesis most likely under high methane flux conditions. The values found for the Archaea lipid biomarkers were depleted (e.g., PMI δ13C= -114.8‰), especially compared to marine lipids (-30‰), suggesting incorporation of methane-derived carbon in archaeal biomass. Variation in archael lipid δ13C suggest archaeal community consists of multiple organisms. The terminally branched fatty acids were present in all the samples. In particular iso-C15:0 and anteiso-C15:0 are indicative of sulfate-reducing bacteria, highlighting the coupling of SRB with Archaea in AOM. These data provide further evidence of the involvement of Archea methanogens in the sequestration of methane-derived carbon through anaerobic oxidation of methane and robust fingerprint of both hydrocarbon seep activity and the conditions under which carbonates formed.

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## A new yeti crab phylogeny. East Pacific regional extinctions?

Christopher Roterman, Won-Kyung Lee, Xinming Liu Rongcheng Lin, Xinzheng Li Yong-Jin Won
University of Oxford

The recent discovery of two new species of kiwaid squat lobsters on hydrothermal vents in the Pacific Ocean and in the Pacific sector of the Southern Ocean has prompted a re-analysis of kiwaid biogeographical history. Using a larger alignment with more fossil calibrated nodes than previously, we consider the precise relationship between Kiwaidae, Chirostylidae and Eumunididae within Chirostyloidea (Decapoda: Anomura) to be still unresolved at present. Additionally, the placement of both new species within a new "Bristly" clade along with the seep-associated Kiwa puravida is most parsimoniously interpreted as supporting a vent origin for the family, rather than a seep-to-vent progression as previously proposed. Based on the present-day location of known species, it is likely that the common ancestor inhabited hydrothermal vents in the SE Pacific. Fossil-calibrated divergence analysis indicates an origin for the clade around the Eocene-Oligocene boundary in the eastern Pacific ~33-38 Ma, coincident with a lowering of bottom temperatures and increased ventilation in the Pacific deep sea. Likewise, the mid-Miocene (~10-16 Ma) rapid radiation of the new Bristly clade also coincides with a similar cooling event in the tropical East Pacific. The distribution, diversity, tree topology and divergence timing of Kiwaidae in the East Pacific is most consistent with a pattern of extinctions, recolonisations and radiations along fast-spreading ridges in this region and may have been punctuated by large-scale fluctuations in deep-water ventilation and temperature during the Cenozoic; further affecting the viability of Kiwaidae populations along portions of mid-ocean ridge. The known locations of kiwaids in the tropical East Pacific for example, strongly suggests that kiwaids once inhabited portions of the East Pacific Rise and the Galapagos Ridge, but have subsequently gone extinct, although the causes for this are unclear. This represents the strongest circumstantial evidence yet for the regional extinction of vent-associated megafauna in the past.

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## What does *Calyptogena* sp move looking for? Behavior observation of *Calyptogena* sp in rearing tank

Makoto Sugimura, Yuka Koyano, Yoshiriro Suzuki, Miku Ota, Takami Nobuhara, Yukiko Ngai, Takashi Toyouku
Enoshima Aqurium, JAMSTEC

Deep-sea creatures found in chemosynthetic ecosystems are known to have unique trophic acquisition strategy with symbiotic bacteria. Many of these animals receive organic matter produced by intracellular symbiotic bacteria as their main energy source. At Enoshima Aquarium, we developed a chemosynthetic ecosystem tank system (Miyake et al, 2012) that simulating the seep environment in order to study and display deep-sea creatures of chemosynthetic ecosystem. In this study, Calyptogena sp. were collected using the ROV Hyper-Dolphin, operated by the R/V Shinseimaru of University of Tokyo/ JAMSTEC. Sampling site was off Hatsushima Island seep site in Sagami Bay at depths of 855m（35°00.9507 'N, 139°13.327'E）on 6th of May, 2016. Calyptogena sp. individuals were then housed in the chemosynthetic ecosystem tank at Enoshima Aquarium. To monitor the daily migration of individuals, we took time lapsed video every 3 minutes from the top of the tank in total of 484 hours 14 minutes. As the result of the observation, we found that Calyptogena sp. individuals moves intermittently, average moving distance of one move was about 3.22 cm / 15 min, and the average moving speed was about 0.38 cm / min. On the surface of sediment in the tank, heterogeneously mat-like biofilm cover area considered to be caused by bacteria activity were formed in mosaic pattern and we observed Calyptogena sp. individuals tend to moves along with the outline of the discoloration region. In this biofilm cover area, 50 to 300 μmol of hydrogen sulfide was detected from sediment. From these facts, we inferred that Calyptogena sp. individuals are moving to adopt environmental change, exploring optimal living environments such as suitable level of hydrogen sulfide and condition of bacterial mats. In the future, we would like to investigate further relationship between behavior of clams and environmental condition in order to clarify the ecology of chemosynthetic Calyptogena sp.

POSTER 77 - Chemosynthetic ecosystems
TUESDAY Evening • 17:45 • Serra Ballroom

## Meiobenthic communities from cold seeps of the Olimpi mud volcano field in the eastern Mediterranean

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The community structure of bathyal benthic communities found at six different mud volcanoes (Napoli, Milano, Leipzig, Moskow, Gelendzhik and Nice) of the Olimpi Mud Volcano field located south of Greece and along the Hellenic Arc were compared with a view to understand their patterns, interconnection and drivers of biological diversity. The mud volcanoes were explored during the LEVECO (LEVantine ECOsystem) cruise (2016) with the R/V AEGAEO of the Hellenic Centre for Marine Research. Meiofaunal densities were higher compared to deep-sea basin stations, ranging from 28 to 631 ind/10 cm2 at the Nice and Gelendzhik mud volcanoes respectively. Nematodes predominated at all stations with an average percentage contribution between 85–99%. Meiobenthic standing stocks showed strong spatial variability within stations, with densities occasionally differing between replicates by one order of magnitude. Richness of meiofauna major taxa was generally very low, ranging between 3 and 9 with the highest numbers occurring at Milano mud volcano. nMDS ordination based on ÖÖ transformed data, clearly separated meiofaunal communities at the Nice mud volcano from the rest, except for one sample from Gelendzhik site. PCO indicated that benthic communities were separated based on sediment type, while SIMPER analysis attributed the differences between habitats to differences in nematode abundances. DISTLM analysis indicated CPE, chla/CPE, % of clay and depth as the variables explaining nearly 96% of the benthic variation. The higher meiofaunal parameters at the Olimpi mud volcano field suggest that seep conditions favour meiobenthos, while the high variability may reflect different seepage activity that cause environmental variability and heterogeneity. Sediment type, food availability and depth appear as the major drivers of meiofaunal spatial distribution. Meiofaunal structure differences were attributed to nematode densities suggesting that certain species may proliferate on chemosynthetic conditions.

## Environmental Controls of Nitrogen Sources to Chemosynthetic Mussels using Amino Acid Nitrogen Isotopes

Natasha Vokhshoori, Matthew D. McCarthy1, Hilary G. Close2, Nancy Prouty3

1. Ocean Sciences Department, University of California, Santa Cruz, Santa Cruz, California 2.Rosenstiel School of Marine and Atmospheric Sciences, University of Miami, Miami, Florida 3.United States Geological Survey, Santa Cruz, California

The distribution and abundance of deep sea epifaunal communities found in methane seep environments are positively correlated with fluid flow of geochemical compounds. In areas of active fluid flow, high productivity of free-living bacteria causes accumulation of organic matter in sediments, resulting in high concentrations of ammonium and nitrate. The chemosymbiotic mussel Bathymodiolus childressi primarily uses methane as a source of energy and nutrition by housing methanotrophic endosymbionts in its gills, while still retaining its ability to filter-feed. It is less well understood how the mussel holobiont reaches its nitrogen demands. Commonly, light bulk nitrogen isotopes ($\delta^{15}N < 2$‰) measured in mussel tissues (e.g. mantle, gill, adductor) have been attributed to nitrogen fixing microbes, even though concentrations of ammonium and nitrate in the sediment porefluids may be relatively high (>20 mM). Furthermore, in areas where seep activity is low and mussel bed density is sparse, it is not known if mussels switch from a symbiont-mediated feeding mode to filter-feeding. Here we employ a more precise isotopic method to better understand nitrogen sources and assimilation for B. childressi and address if mixotrophy allows this species to adapt to variable fluid flow conditions. We measure the $\delta^{15}N$ value of specific amino acids (AA) in sinking organic matter, sediment, and mussel tissues from three sites of varying mussel bed density at methane seeps along the U.S. Atlantic Margin. We compare the $\delta^{15}N$-AA results to AA isotope fingerprinting of known metabolic endmembers (e.g. heterotrophic bacteria, phytoplankton). Allochthonous (planktonic) signatures are evident in particles and sediments, but some novel, autochthonous seep metabolisms are apparent in mussel tissues. Using a mixing model, we quantify the degree to which mussels depend on allochthonous resources along a spatial gradient of seep activity. These results can reveal the degree of adaptability of these invertebrates to environmental change.

## Genomic comparison of symbionts in deep-sea tubeworms reveals their functional similarities and differences in symbiotic relationships with the host

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1. Department of Ocean science and Division of Life Science, Hong Kong University of Science and Technology, Hong Kong 2. Department of Biology, Hong Kong Baptist University, Hong Kong

Without mouth and gut, deep-sea siboglinid annelids depend on their chemoautotrophic endosymbionts housed in a special organ called trophosome for nutrition. Here, we sequenced the genome of the Paraescarpia echinospica symbiont and compared it with the symbiont genomes of the siboglinid annelids Ridgeia piscesae, Riftia pachyptila and Tevnia jerichonana to understand 1) how P. echinospica symbionts infect their host then provide energy and nutrients, and 2) functional differences among the four siboglinid genomes. The results showed that 1) the quality of the assembled P. echinospica symbiont genome is the best among the four published siboglinid symbionts; 2) the P. echinospica symbiont genome has nearly a full set of flagella system and a complex chemosensory system, indicating that it has a free-living stage; and the

presence of genes related to pili, fimbriae and some adhesion-like proteins indicates its capability of horizontal infection, and genes for DNA replication and cellular division suggest its capacity to proliferate in the host; 3) the symbiotic bacteria generate energy from oxidizing sulfide and use the energy to fix carbon through both the CBB and rTCA cycles, then produce nutrients for the host as shown by expression of genes involved in metabolism and biosynthesis of carbohydrates, amino acids and vitamins; 4) the P. echinospica symbionts have a complete Sox system for converting thiosulfate to sulfate, whereas this system is incomplete in the other three siboglinid symbionts; whereas the other three symbionts have the potential to produce cyanophycin as storage compounds, the P. echinospica symbionts lack this ability. Our study reveals the genomic basis of symbiosis in P. echinospica symbionts, and contributes to a better understanding of how sibognilids have adapted to deep-sea chemosynthetic environments.

## Cold-seep ostracods from the western Svalbard margin: direct palaeo-indicator for methane seepage?

Moriaki Yasuhara, Kamila Sztybor, Tine L. Rasmussen, Hisayo Okahashi, Runa Sato, Hayato Tanaka

School of Biological Sciences and Swire Institute of Marine Science, The University of Hong Kong, Pok Fu Lam Road, Hong Kong SAR, China

Despite their high abundance and diversity, microfossil taxa adapted to a particular chemosyntheticenvironment have rarely been studied and are therefore poorly known. Here we report on an ostracod species, Rosaliella svalbardensis gen. et sp. nov., from a cold methane seep site at the western Svalbard margin, FramStrait. The new species shows a distinct morphology, different from other eucytherurine ostracod genera. It hasa marked similarity to Xylocythere, an ostracod genus known from chemosynthetic environments of wood fallsand hydrothermal vents. Rosaliella svalbardensis is probably an endemic species or genus linked to methaneseeps. We speculate that the surface ornamentation of pore clusters, secondary reticulation, and pit clusters maybe related to ectosymbiosis with chemoautotrophic bacteria. This new discovery of specialized microfossil taxais important because they can be used as an indicator species for past and present seep environments.

# Connectivity and biogeography - TALKS

## Barriers in the deep sea: is cosmopolitism possible?

Simon Bober, Saskia Brix, Torben Riehl, Martin Schwentner, Angelika Brandt

University of Hamburg (CeNak), German Centre for Marine Biodiversity Research (DZMB), Senckenberg Research Institute and Natural History Museum, University of Hamburg (CeNak), Senckenberg Research Institute and Natural History Museum

For a long time abyssal species were considered cosmopolitan due to the assumed lack of barriers within the abyssal habitat. However, the deep sea is structured by substantial physical barriers in form of landmasses, seamounts, mid-ocean ridges and hadal trenches. We assessed in the course of three projects the impact of different structures - the Mid-Atlantic Ridge, the Kuril-Kamchatka Trench and landmasses- on the distribution and genetic differentiation of deep-sea isopod species. Isopoda is an abundant, highly diverse and relatively well-studied deep-sea taxon without a free-swimming larval stage. A barrier effect was tested on species with differing adaptations to their habitat and we hypothesized a stronger barrier

effect for less mobile species (inbenthic and epibenthic). We were able to show that three out of four families had representatives that were able to cross barriers. But in total only six out of 95 analyzed species were found across such barriers. Mid-ocean ridges and hadal trenches had a measureable effect on inbenthic and epibenthic families. Within the inbenthic family Macrostylidae and epibenthic family Desmosomatidae a reduced gene flow was found across the Mid-Atlantic Ridge and evidence for regular unrestricted gene flow is still lacking. The epibenthic Nannoniscidae were most restricted and hardly sampled at more than one station. Only the supposedly cosmopolitan suprabenthic isopod Acanthocope galatheae WOLFF, 1962 was seemingly unaffected and furthermore proved to be a cosmopolitan species.We conclude that the occurrence of true benthic cosmopolitans in the abyssal deep sea shows that there are no definitive barriers in the deep sea. However dispersability and ecological fitness varies among species and distributions across barriers are still rather exceptional than common.

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THURSDAY Morning • 10:00 • San Carlos Room

## The evolutionary origins of abyssal biodiversity — new ideas from biogeography and habitat mapping

Torben Riehl, Nico Augustin, Simon Bober, Saskia Brix, Colin Devey, Nele Heitland, Lidia Lins, Anne-Cathrin Woelfl, Angelika Brandt
Senckenberg Research Institute

The abyss is a homogeneous and barrier-free sediment habitat. At least that is what the text books say. Yet, at the same time we know that abyssal communities are locally highly diverse. It appears contradictory that a seafloor habitat free of barriers and poor in heterogeneity can host a rich biodiversity. Likewise the evolutionary origins of this diversity remain in the dark, although it has been proposed that the organisms we encounter at abyssal depth originated from the much more heterogeneous bathyal zone. During the interdisciplinary Vema-TRANSIT project, biological, bathymetrical, and geological data were collected in the North Atlantic. Following the Vema Fracture Zone and crossing the Mid-Atlantic Ridge, abyssal habitats and communities were studied. Using high-resolution bathymetric scans in conjunction with rock sampling and video surveys, we encountered a surprisingly high habitat heterogeneity. From the spreading axis to a crustal age of over 90 Ma, the seafloor represented a patchwork of sediment (dominating) and bare rock formations. Furthermore, taxonomic, phylogenetic and population genetic data for isopod crustaceans, one of the most abundant macrofaunal elements in abyssal soft sediments, suggests that bathymetric features, such as the Mid-Atlantic Ridge, contribute to genetic differentiation in some benthic species. Interspecific differences seemed to be connected in dispersal capacity. We present these new insights and discuss their implications for our understanding of the origins of abyssal biodiversity.We conclude: the abyssal seafloor is much more heterogeneous than commonly assumed and seafloor topography is a limiting factor for dispersal thus contributing to diversity.

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THURSDAY Morning • 10:15 • San Carlos Room

## Biogeography of the upper bathyal of the Pacific Ocean

Natalie Summers, Les Watling
University of Hawaii

The deep sea is being impacted by a multitude of anthropogenic threats from fishing to mining, making a biogeographical scheme for the deep sea a crucial conservation priority. Schemes such as the Marine Ecoregions of the World (MEOW) have been developed for coastal and shelf areas where each unit or region is homogeneous and distinct from adjacent regions. Because of the lack of data on organism distribution in the deep sea, biogeographical units based on temperature, salinity, dissolved oxygen and particulate organic matter flux as oceanographic proxies were used for the lower bathyal (800 to 3500). The addition of nitrate, phosphate and silicate data were imported into ArcGIS to create 37 3D global Ecological Units (EMUs). The aim of this study is to test three proposed biogeographical schemes for the upper bathyal (200-800m) in the Pacific Ocean using octocoral data and hierarchical cluster analysis. The analysis was conducted on data from the Ocean Biogeographic Information System (OBIS) database supplemented with identifications from the Program Tropical Deep-Sea Benthos (ex MUSORSTOM, run by the French National Museum of Natural History) and the Siboga expedition reports. MEOW ecoregions generally need to be grouped together to be considered as distinct units. This is clearly seen in the North Pacific where the upper bathyal of the west coast of North America appears to be one biogeographic unit related to North America and the Aleutians. The EMU scheme adds an important depth dimension suggestion that the upper bathyal cannot be seen as a single depth layer. Testing these units for the Pacific is an important step in determining the usefulness of oceanographic variables in predicting the location of biogeographic provinces of the deep sea.

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THURSDAY Morning • 10:30 • San Carlos Room

## Hiding in plain sight: cryptic new species of *Bolinopsis*.

Shannon Johnson, Lynne Christianson, Jacob R. Winnikoff, Steven Haddock
MBARI

Bolinopsis infundibulum (Ctenophora: Lobata) are common, relatively large, and abundant comb jellies thought to occur in both Pacific and Atlantic oceans. Sequence data from the 18S locus show no differentiation amongst populations worldwide. In contrast, sequence data from the mitochondrial locus COI revealed divergence between Atlantic and Pacific populations that might be consistent with species-level differentiation. Sequence data from the 28S and ITS rRNA, and H3 nuclear data, confirmed species-level differentiation between Pacific and Atlantic populations. COI sequences also revealed two distinct Bolinopsis mitotypes that are sympatric in the Monterey Bay. The sympatric lineages were often collected together and they do not segregate by depth or geography. Further nuclear genomic sequencing and morphological investigations are underway to determine if mitochondrial differentiation reflects speciation and to examine if the lineages are able to hybridize.

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THURSDAY Morning • 10:45 • San Carlos Room

## Describing benthic assemblages of conservation interest (VMEs) in South Atlantic UK Overseas Territories

Amelia Bridges, David Barnes, James Bell, Rebecca Ross, Kerry Howell
Plymouth University, British Antarctic Survey

Although Regional Fisheries Management Organisations & United Nations member states have been tasked with adopting the precautionary approach to protect Vulnerable Marine Ecosystems (VMEs), little is known about their distribution in the South Atlantic Ocean. This preliminary analysis uses a clustering approach to map the distribution of vulnerable marine ecosystems across the Exclusive Economic Zones of two UK Overseas Territories: Ascension Island & Tristan da Cunha. Similarity Profile Analysis (SIMPROF) revealed >20 distinct biological assemblages across 61 transects (170 – 1000m), 11 of which were considered to fulfil the FAO criteria required to be designated as VMEs. A Similarity Percentage Routine (SIMPER) was used to compare the dominant taxa responsible for the similarity within clusters with the ICES WGDEC VME Indicator Taxa List. VME presence was recorded across sites within the national waters of both Tristan da Cunha & Ascension Island, with ecologically relevant splits occurring at a VME Habitat Subtype level (cold-

water coral reef type). A new VME Habitat Type of 'hard-bottom cup coral fields' is suggested based on the findings. The results of this study will act as a preliminary analysis on which habitat suitability modelling will be used to model the distribution fo VMEs within other UKOT EEZs & ABNJ in the South Atlantic.

## Modelling of key species dispersal and population connectivity at different habitats of the MAR"

Ana Colaço, Maria Rakka, Pedro Ribeiro, Marina Carreiro e Silva; Manuela Juliano
IMAR//MARE- University of Azores

In recent decades, deep-sea ecosystems have been suffering under different anthropogenic pressures such as fishing, oil and gas extraction, climate change and, more recently, the prospect of deep seabed mining. Species can cope with impacts and changes if they are able to maintain their genetic diversity, reproduce, disperse to suitable new habitats, settle and grow to reproduce again. This process, termed connectivity, has recently been the focus of numerous population genetics studies. There is, however, the need to better understand how physical (ocean currents, habitat suitability) and biological parameters (reproduction mode, larval traits and behaviour) influence population connectivity. The Azores region hosts several hydrothermal vent fields and seamounts that might host mineral sulphide deposits and cobalt crusts, some of which are of interest to mining companies. These prospective mining sites may potentially be source or sink populations of bathyal fauna and will be either potentially mined or impacted by mining plumes. Identifying larvae sources and sinks for this specialised fauna is essential for spatial planning and strategic regional conservation plans.Here we present results from a biophysical model of larval dispersal run for two benthic invertebrate species, the vent mussel Bathymodiolus azoricus (Cosel & Comtet, 1999) and the cold-water coral Lophelia pertusa (Linnaeus, 1758). The results presented here estimate how larvae originating from hydrothermal vents in the Azores might disperse, and quantify the pattern and scale of population connectivity among vents. Several scenarios were implemented, and we discuss the implication of the different scenarios to environmental management. Characterization of deep-sea sponge ecological function in the Azores comparison with other North Atlantic Banks

## High Genetic Diversity and Connectivity in Common CCZ Taxa

Thomas G Dahlgren, Helena Wiklund, Adrian Glover, Craig Smith, Dan Jones, Annika Janssen, Pedro Martinez Arbizu, Lenka Neal, Paulo Bonifacio, Sergio Taboada, Lenaick Menot, Bart de Smet, Ann Vanreusel, Ellen Pape, Ascensao Ravara, Marina Cunha.
Uni Research, Norway, University of Gothenburg, Sweden

It's important to understand the levels of genetic diversity and connectivity between populations in several aspects of science and management of natural resources, from evolutionary processes and speciation to resilience to disturbance and re-colonisation abilities after local extinction events. Population connectivity in nature has been studied using molecular data for over half a century but little is known about deep-sea taxa, in particular species inhabiting the relatively featureless abyssal areas away from vents, seeps, seamounts and continental slopes. These areas make up most of the planets surface. We have studied the genetic diversity and connectivity in ten common benthic invertebrate taxa inhabiting the eastern part of the Clarion Clipperton Zone in the Central Pacific Ocean. We observed high genetic diversity in the sediment dwelling species but a low diversity in species associated to polymetallic nodules. There was no

evidence of population genetic structure in any of the studied species. Analysis the haplotype mismatch distribution suggests demographic change or selective sweeps across a broad range of phyla with a diversity of life history and functional traits. In this paper we also discuss the implications of this new data for evolutionary hypothesis of deep-sea taxa and management plans for natural resources in the light of polymetallic nodule extraction for mineral exploitation.

## Genetic connectivity from the Arctic to the Antarctic: *Sclerolinum contortum* and *Nicomache lokii* (Annelida) are both widespread in reducing environments

M.H. Ellertsen, Georgieva, MN, Kongsrud, JA, Linse, K, Wiklund, H, Glover, AG, Rapp, HT
Department of Biological Sciences and K. G. Jebsen Centre for Deep-Sea Research, University of Bergen

The paradigm of large geographic ranges in the deep sea has been challenged by genetic studies, which often reveal putatively widespread species to be several taxa with more restricted ranges. Recently, a phylogeographic study revealed that the tubeworm Sclerolinum contortum (Siboglinidae) inhabits vents and seeps from the Arctic to the Antarctic. Here, we further test the conspecificity of the same populations of S. contortum with additional mitochondrial and nuclear markers. We also investigate the genetic connectivity of another species with putatively the same wide geographic range - Nicomache lokii (Maldanidae). Our results support the present range of S. contortum, and the range of N. lokii is extended from vents and seeps in the Nordic Seas to mud volcanoes in the Barbados Trench and Antarctic vents. Sclerolinum contortum shows more pronounced geographic structure than N. lokii, but whether this is due to different dispersal capacities or reflects the geographic isolation of the sampled localities is unclear. Two distinct mitochondrial lineages of N. lokii are present in the Antarctic, which may result from two independent colonization events. The environmental conditions inhabited by the two species and implications for their distinct habitat preference is discussed. The environmental conditions inhabited by the two species and implications for their distinct habitat preference is discussed.

## Latitude and depth gradients explain distribution patterns of hydroids (Cnidaria) in the deep Atlantic Ocean

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The geographical distribution of every species is shaped by complex evolutionary and ecological processes. Thus, biogeographical patterns, which emerge from the simple reflection of overlapping species ranges, reflect highly complicated biological history. Gradual or rapid shifts in species composition may, therefore, reflect physical or environmental barriers to species dispersal and survival as well as biotic factors. This study reports distribution patterns of hydroids in the deep Atlantic Ocean and adjacent polar seas along depth and latitude. Hydroids from 50 to 5,330 m deep were studied primarily based on museum collections. Identifications were checked or made by the authors, improving uniformity within the data set by avoiding variations in taxonomic interpretation. Data totaled 3,699 records belonging to 432 species, at 1,444 unique sites. Records were assigned to three depth strata (50–200 m, 201–1,000 m, and 1,001–5,330 m) and 8 latitudinal bands of 20˚ each (61˚–80˚N, 41˚–60˚N, 21˚–40˚N, 0˚–20˚N, 0˚–20˚S, 21˚–40˚S, 41˚–60˚S, and 61˚–80˚S), totaling 24 sample areas. Species compositions and abundances per area were used for multivariate analyses. Assemblages are primarily differentiated between those to the north and south of 40˚S, regardless of

depth, with an internal separation between Patagonian and Antarctic assemblages. Northwards of 40˚S, assemblages gradually differentiate along both depth strata and latitude, although a faunal turnover occurs at 1,000 m deep. Finally, assemblages at the 1,001–5,330 m stratum tend to be more similar to each other than those at shallower strata, suggesting deep-sea connectivity along great distances. We also raise the problem of largely unequal hydroid sampling in the Atlantic Ocean across depths and latitudes, especially in the southern hemisphere and below 1,000 m deep. To a great extent, biogeographic distributions of hydroids in the deep Atlantic Ocean can be explained by latitude and depth gradients.

THURSDAY Midday • 13:30 • San Carlos Room

## Phylogeography and phylogeny of Spionidae and Polynoidae (Annelida) from the Vema-Transit expedition and the Puerto Rico Trench

Theresa Guggolz, Martin Schwentner, Karin Meißner, Angelika Brandt
CeNak, University of Hamburg; Senckenberg research Institutes
The Vema Fracture Zone is one of the largest fracture zones of the Mid-Atlantic Ridge and it is characterized by a large left-lateral offset. During the Vema Transit expedition (SO237), benthic communities of the transect and the abyssal basins on both sides were investigated to examine whether the Mid-Atlantic Ridge serves as a physical barrier for these organisms, or if there is a potential connection from east to west via the Vema Fracture Zone. Samples comprised 4149 polychaetes, belonging to 42 families. Exemplary, molecular (16S, COI, 18S) and morphological studies of the spionids Laonice, Aurospio and Prionospio, as well as the polynoid Bathypolaria were conducted. Molecular species delimitation showed a higher diversity compared to morphological studies, but all investigations revealed species occurring at both sides of the Mid-Atlantic Ridge. Haplotype networks indicated that the Mid-Atlantic Ridge is no barrier for the distribution of most of the analysed species as several haplotypes are shared between both sides of the Ridge and even with the abyssal of the Puerto Rico Trench, spanning a total over 3000 km. Phylogenetic analyses show a monophyly for most of the species compared to available data for spionids and polynoids from other deep-sea areas, even if their distribution was shown to be widespread. As the knowledge of deep-sea polychaetes is sparse, this study provides relevant new data, helping to understand the distribution and diversity in this habitat.

THURSDAY Midday • 13:45 • San Carlos Room

## Do modelled larvae disperse well over the depth gradient?

Howell, K.L., Foster, N.L., Nimmo-Smith, A., Rogers, A.D., Ross, R.E., Stashchuk, N., Vlasenko, V.
Plymouth University
Knowledge of how populations are connected is central to our understanding of population persistence, isolation, divergence, speciation and radiation. The bathyal region has been identified as the primary site of adaptive radiation in the deep sea from molecular and morphological studies. Evidence suggests that gene-flow is low over the depth gradient. While there are many possible explanations for this observation, limited larval exchange in the vertical may be a contributing factor. Here, we investigate the potential role of the physical environment as a population structuring mechanism in the context of the depth differentiation hypothesis, using the cold-water coral Lophelia pertusa as a model system. Our specific question is what percentage of theoretical L. pertusa larvae moves between depth bands within and between sites in the North East Atlantic? We used two different passive models to investigate movement of larvae between depth bands. A fine-scale model of the Anton

Dohrn Seamount (ADS), based on bespoke Massachusetts Institute of Technology general circulation model; and a broad-scale model of the UK and Irish deep sea based on HYCOM coupled with the connectivity modelling system (CMS). For both models passive larvae were tracked for 57 days and models were restricted to 1100m depth. Source / sink dynamics were recorded for both models with a particular focus on movement between established depth bands. For both fine-scale and broad-scale models the vast majority of released larvae remain in the same depth band where they were initially released. 5% or less end up in depth bands >200m from where they started and this is observed both within and between sites. Interestingly the fine-scale model also suggests that only 10% of theoretical larvae are able to escape ADS with the opportunity to then be advected to an alternative site, but these escapees come from all modelled depths.

THURSDAY Midday • 14:00 • San Carlos Room

## Can small brooders be widely distributed? – diversity and distribution of Tanaidacea (Crustacea) in CCZ

Magdalena Błażewicz, Piotr Jóźwiak1, Anna Stepień1, Aleksandra Jakiel1, Lenaick Menot2
1 University of Łódź, Faculty of Biology and Environmental Protection, Łódź, Poland 2 REM-EEP-LEP, Ifremer, Plouzane, France
Tanaidacea crustaceans are a diverse and abundant component of benthic deep-sea ecosystems. As they are brooders and have no planktonic larvae, their mobility is low, and thus their dispersal ability is considered to be limited. Tanaidacea of the suborder Apseudomorpha, which dwell actively in the sediments, are potentially more motile organisms than tube-building Tanaidomorpha. During Biological Aspect of the deep-sea mining the initiative organized under the umbrella of JPIO Ocean, a collection of about 1100 specimens of Tanaidacea has been collected with epibenthic sledge (18 samples; >500 ind.) and boxcore (34 samples; 600 ind.) in five locations of the Clarion-Clipperton Fracture Zone (GBR, IOM, IFREMER, GSR, APEI3). In the boxcore samples over 140 morphospecies were identified. The morphological identification of the material was compared against molecular results. Species delimitation was achieved by applying distance-based (ABGD) and three-based (GMYC and PTP) methods. Most species (>97%) were rare and apparently new for science. The accumulation curve showed no sign of reaching an asymptote with increasing area sampled. For the most numerous species, haplotype network was investigated. All of the studied taxa presented low genetic diversity of the analyzed population. The study was completed thanks to funding provided by the National Science Centre, Poland (grant no. 2016/21/B/NZ8/02495).

THURSDAY Midday • 14:15 • San Carlos Room

## Does the Mid-Atlantic Ridge hinder dispersal in the deep sea?

Lidia Lins, Sofie Derycke, Tania Nara Bezerra, Ann Vanreusel
Senckenberg Research Institute and Natural History Museum
Most of the deep-sea (< 200 m) habitats are contained within abyssal plains, covering depths between 3500 and 6000 m. Moreover, the presence of topographic features, such as mid-ocean ridges, can divide the abyss into basins, which can be interconnected through gaps and potentially affect species distribution and dispersal. Exhibiting both endemic and widespread species, nematodes represent ideal model organisms to study dispersal, species-range sizes, distribution, and turnover in the deep sea. The knowledge of how deep-sea communities are distributed and how they are affected by anthropogenic impacts and environmental changes will help to mitigate potential impacts to this environment in the future. Samples for this study were collected on board of the RV Sonne to the Vema Fracture Zone (VFZ), and we aimed to investigate the following topics: 1) The VFZ represent a barrier to gene

flow; 2) Genetic differentiation increases with increasing geographic distance; 3) Species-range size for nematodes (< 100 km vs. > 1000 km)? Based on community analyses and integrative taxonomy (molecular and morphology-based methods), our results indicate no geographical trend, suggesting a weak correlation between genetic divergence and geographical distance. Nonetheless, most species were restricted to one area (62.5 – 76 %), while 24 – 37.5 % of the species were shared between areas. These results suggest that the VFZ may not completely limit dispersal, reacting like a sharp boundary, but it might act as a transition zone, restricting dispersal.

## Diversity and biogeography of deep-sea nematodes in the Clarion-Clipperton Fracture Zone: a molecular approach

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The Clarion-Clipperton Fracture Zone (CCFZ) in the equatorial East Pacific is the largest known reserve of polymetallic nodules, a potentially highly lucrative source of precious metals required for todays hi-tech devices. Abyssal sediment samples were collected from four potential mining areas and the Area of Particular Environmental Interest #3 (APEI3) during the RV Sonne239 cruise with the objectives of identifying nematode assemblages as well as patterns of connectivity via gene flow. Lacking a planktonic larval stage, nematodes are inherently limited in their dispersal capability and as such can provide insights into population structuring in such a vast area. Morphological identification of deep-sea nematodes is arduous because the existing taxonomical knowledge is insufficient for species-level identification as the majority have yet to be comprehensively described. In addition, a high degree of phenotypic plasticity and cryptic speciation further complicate species delineation when using morphological characteristics exclusively. Currently, High-Throughput Sequencing (HTS) has the potential to efficiently describe biological communities yet comprehensive assessment of diversity with species-level resolution remains one of the most challenging aspects of metabarcoding studies. As a first step, we investigated the utility of curated nematode reference sequence databases for determining species-level Operational Taxonomic Unit (OTU) clustering thresholds in HTS data. The databases which consisted of 438 small ribosomal subunit (18S) and 290 mitochondrial Cytochrome Oxidase 1 (CO1) sequences identified 99% and 94% OTU similarity for each marker respectively. These thresholds as well as several bio-informatic pipelines were validated against a mock nematode community and an environmental sediment sample (Macheriotou et al. 2018, submitted). Finally, the best-performing pipeline was applied to the CCFZ samples to provide the first attempt at describing deep-sea nematode diversity and connectivity using HTS.

## The shelf as pathway for peracarid crustaceans

Saskia Brix, Jörundur Svavarsson, Sarah Schnurr, Robert M. Jennings, Anna Jażdżewska, Anne-Nina Lörz
Senckenberg am Meer: DZMB

Results of the IceAGE project (Icelandic marine Animals: Genetics and Ecology) detect the shelf as pathway from Norway to Iceland and further on to Greenland and at the same time showing specific patterns in local scale distribution for isopod and amphipod crustaceans. Our results show the slope area North-East of Iceland around the Faroes and the Norwegian Channel with the highest number of species, especially stations in the thermocline between 400 and 800 m depth where we observed the

turnover from shallow to deep-water faunal elements. Integrative taxonomy approaches set the baseline for feeding the ecological analysis with data including the detection of cryptic species enhancing the understanding of the ecosystem in Icelandic and adjacent waters.

## Climate Change Effects on Dispersal from the Western Pacific Hydrothermal Vents

Satoshi Mitarai, Kirk B. Sato, Sasha Shchepetkin, James C. McWilliams, Lauren S. Mullineaux, and Lisa A. Levin
Okinawa Institute of Science and Technology

Climate change that affects ocean circulation has the potential to influence dispersal of vent species. On one hand, enhanced western boundary currents may extend dispersal distance. On the other, metabolic rates of vent larvae will increase with water temperature, which may substantially reduce larval durations, thereby limiting dispersal distances. Furthermore, stronger offshore winds may create more mesoscale eddies, increasing deep-water transport and stochasticity of annual connectivity. By developing a biophysical model under IPCC future climate change scenarios (e.g., RCP 8.5), we quantify potential larval dispersal of vent species via ocean circulation in the western Pacific Ocean. The model domain covers all active western Pacific vent fields between 32°N and 36°S registered in the InterRidge vents database with a 5-km mesh resolution. The 3D hydrodynamic Regional Ocean Modeling System (UCLA ROMS version 2013) was used to integrate rotating primitive equations with a realistic equation of state, nested within CMIP5 (Coupled Model Inter-comparison Project Phase 5) global climate models (GFDL-ESM2M, MRI-CGCM, HadGEM2-CC, etc.). We examined climate change effects on connectivity of vent fields within back-arc basins, in terms of directionality and frequency of basin-to-basin dispersal, by comparing potential dispersal patterns within two time periods of 2006–2015 and 2091–2100. Outcomes of this study should help marine ecologists design optimal marine conservation plans to protect one of the most unusual ecosystems on Earth in the era of climate change.

## Larval dispersal contributes to genetic diversity and connectivity of limpet (*Lepetodrilus nux*) populations in the Okinawa Trough

Yuichi Nakajima, Masako Nakamura, Hiromi Kayama Watanabe, Satoshi Mitarai
Okinawa Institute of Science and Technology Graduate University

Various invertebrate species maintain chemosynthetic ecosystems around deep-sea hydrothermal vents. For vent-endemic benthos, larval recruitment is presumably critical for population maintenance and colonization via dispersal among hydrothermal vent sites. The lepetodrilid limpet, Lepetodrilus nux, is a hydrothermal vent-endemic species and one of the most abundant gastropods at hydrothermal vents in the Okinawa Trough, in the northwestern Pacific Ocean. However, detailed assessment of genetic diversity and connectivity based on individual genetic profiles has not been possible previously. We examined these parameters in L. nux at five hydrothermal vent sites (maximum geographic distance: ~550 km, depth range: ~700 m to ~1,650 m) using population genetic analysis of 14 polymorphic microsatellite loci. Genetic diversity based on allelic richness and expected heterozygosity has been maintained at hydrothermal vent sites investigated. Meanwhile, low genetic differentiation among populations was detected and pairwise FST values ranged from –0.003 to 0.023. Genetic clustering reflected the relative geographic distances between sites. There was a positive relationship between genetic differentiation and geographic distance known as isolation-by-distance (P = 0.010), but there was no significant relationship with depth (P = 0.350).

Relative migration rates also showed a tendency toward isolation-by-distance, but migration direction was not necessary unidirectional. Larvae of L. nux apparently ascend via the thermal plume to wander in the water column, utilizing currents closer to the surface for stochastic long-distance dispersal. This behavior suggests that stochastic stepping-stone dispersal contributes significantly to population connectivity and maintenance of this species in the Okinawa Trough.

### Reproduction and connectivity of the vent/seep ophiuroid *Ophioctenella acies*

Craig M. Young, Caitlin Plowman, Cliff Cunningham, Bernard Ball, Christina Ellison, Zoe Wellschlager, Cindy Lee Van Dover
University of Oregon, Duke University

Ophictenella acies, a small ophiuroid first discovered at the Lucky Strike and Broken Spur vent sites on the mid-Atlantic ridge, has subsequently been found at a number of other vent and seep sites throughout the Atlantic, Caribbean and Gulf of Mexico. CO1 sequencing of both seep and vent populations suggests occasional transport between the Blake Ridge and the Gulf of Mexico, unidirectional transport from the Blake Ridge to the Mid-Cayman Ridge, and occasional transport from the Blake Ridge/West Florida Escarpment to Snake Pit on the Mid-Atlantic Ridge. The species is divided into two ancient (>1 Ma) clades, with the MAR population closest to the Blake Ridge/Gulf of Mexico clade. We used histological and SEM analysis of specimens from 3000m depth at the Logachev vent field to infer aspects of the reproductive biology. Sexes are separate; no hermaphroditic individuals were found. Gonads are concentrated near the base of each arm in larger individuals, and each female gonad contains fewer than 20 vitellogenic oocytes. Arm lengths suggestive of asexual (fissiparous) reproduction were found in a small percentage of individuals. Maximum oocyte size observed was 100 $\mu$m. Although some ophiuroids (e.g., Amphipholus squamata) with similar egg sizes are known to brood, the complete absence of embryos or juveniles in the bursae of O. acies suggests that this species spawns gametes freely and that larvae develop in the water column as planktotrophs. At Logachev, ophiuroids occurred at densities greater than 4000 per m2. We hypothesize that these high densities are maintained asexually and that planktotrophic larvae are responsible for the wide biogeographic range and for occasional connectivity among distant metapopulations.

# Connectivity and biogeography - POSTERS

### Deep Sea Biodiversity Patterns of Tanaidacea (Crustacea: Peracarida) in the Gulf of Mexico

Adelaide Rhodes, Melissa Rohal, Elani Morgan, Paul Montagna, Jill Bourque, Amanda Demopoulos
University of Vermont Department of Microbiology and Molecular Genetics, Texas A&M Corpus Christi Ecosystems and Modeling Group Harte Research Institute for Gulf of Mexico Studies, USGS Wetland and Aquatic Research Center Gainesville Florida

Tanaidacean crustaceans are an important ecological indicator of benthic community resilience in the deep sea Gulf of Mexico, an area under pressure from oil exploration and extraction. Tanaids are the most numerous crustacean found below 1000 meters in the Northern Gulf of Mexico, and patterns in their biodiversity strongly influence benthic community structure. This study provides an update on the species and locations of Gulf of Mexico deep sea tanaids with two approaches; a

comprehensive search of historical records from the region and a compilation of observations from research cruises led by Texas A&M University–Corpus Christi, Harte Research Institute (TAMUCC–HRI) and the US Geological Survey between 2010 and 2017. This new database contains about 9346 total biogeographic observations and 109 of the approximately 1200 known species. About 5541 observations are from samples taken below 200 meters. These depths have been historically undersampled for tanaidacean diversity. During the recent research cruises, 23 of the 30 families and genera incertae sedis were sampled. Eleven genera and one family were new records for this region. Between 10 and 15 new species are currently being described. Estimates based on these new observations indicate that tanaidacean diversity is significantly higher than previously reported (e.g. a 72% increase in species richness between 1000 m and 1500 m and a 216% increase in species richness between 1500 m and 2000 as compared to historical records). This database can be an important tool for establishing a baseline description of the dominant crustacean taxa and associated species in a highly exploited region of the deep sea.

### Elemental fingerprints of cold-seep mussel larvae: insights to deep-sea connectivity

Luciana Genio, Brandon Puckett, David B. Eggleston, Fredrick J. Fodrie, Marina R. Cunha, Craig M. Young
Universidade de Aveiro

Population connectivity - the exchange of individuals (genetic material) among geographically separated subpopulations, plays a vital role in local and metapopulation dynamics, biogeography, and resilience of marine communities to human and natural disturbances. The growing concerns of the effects of climate change as well as the increasing exploitation of deep-sea resources and their sustainable management demand improved knowledge on the patterns of population connectivity to advance our understanding of source-sink dynamics in deep pelagic and benthic ecosystems. In recent years, integrated multidisciplinary approaches, incorporating high-resolution biophysical modelling and genetic markers have been increasingly applied to assess spatiotemporal scales of dispersal and connectivity in the deep sea. However, these two approaches suffer from fundamental limitations in the knowledge of biological and oceanographic processes, preventing realistic estimates of connectivity. Determination of geochemical signatures in larval and juvenile shells provides independent empirical data to complement inferences on potential larval sources and discriminate local vs immigrant recruitment. In this study, we explored spatial variability in geochemical fingerprints of postlarvae and juvenile bathymodiolin shells (shell length: 505-957 $\mu$m) from 11 cold seep sites in the Gulf of Mexico and West Atlantic Margin, at depths ranging from ~600 m to 3600 m. We found significant differences in geochemical signatures of bathymodiolin mussels collected from seeps located below 2000 m depth and individuals from shallower sites. This depth pattern was shown by independent analysis of geochemical signatures at both larval (prodissoconch I and prodissoconch II) and juvenile shells, providing evidence that larvae colonizing deeper sites come from a different larval pool than those colonizing shallower sites.

### Combining connectivity and biogeography: How *Pheronema carpenteri* aggregations may be particularly vulnerable marine ecosystems

Rebecca E. Ross, Edward J.G. Wort, Kerry L. Howell

School of Biology & Marine Science, University of Plymouth

Habitat suitability models are being used worldwide to help locate and manage areas of conservation importance. We created one such model targeting Pheronema carpenteri (WyvilleThomson, 1869) deep sea sponge aggregations, in UK and Irish waters, now with some support from preliminary targeted groundtruthing. However, the picture is incomplete without knowing how connected these predicted habitat patches could be. This study explores the potential connectivity patterns at play and re-evaluates how hydrodynamically fragmented predicted habitat patches might be. As little is known of P. carpenteri's reproductive methods, two different dispersal models were used (MGET & CMS, both driven by HYCOM), with different implicit assumptions, and six simulations were run in each assuming planktonic larval durations from 1-50 days. The results suggest that 3%-36% of the predicted habitat may be reachable in one generation. Yet, even after an optimistic 50 days of dispersal, the known populations in the North (Hatton-Rockall Basin, partially protected) and the South (Porcupine Sea Bight) stay unconnected. These aggregations exist in prime fishing grounds, and with only 3% of the predicted habitat in the North currently protected, P. carpenteri aggregations may be a particularly vulnerable ecosystem.

POSTER 84 + Connectivity and biogeography
TUESDAY Evening • 17:45 • Serra Ballroom

## Mitochondrial phylogenomics resolves the origin and evolution of deep-sea hydrothermal vent alvinocaridid shrimps (Decapoda, Caridea)

Shao'e Sun, Zhongli Sha
Deep Sea Research Center, Institute of Oceanology, Chinese Academy of Science

The deep-sea hydrothermal vent is one of typical extreme environments on Earth that assembles with the early life circumstance. It is important for elucidating the life origins by exploring the origin and develop mechanisms of representative species in hydrothermal vents. This study focus on the deep-sea hydrothermal vent alvinocaridid shrimps, the vent-endemic species. The phylogenetic analysis based on the complete mitogenomes suggested that the vent-endemic species migrated from non-hydrothermal environments. Fossil-calibrated divergence analysis indicated that the alvinocaridid shrimps invaded hydrothermal vents at 64.89 Mya, around the late Mesozoic and early Cenozoic. This result support the extinction/repopulation hypothesis which postulates recent diversification times for most hydrothermal vent species due to their mass extinction by global deep-water anoxic/dysoxic events during the Late Cretaceous and Early Tertiary. In addition, the alvinocaridid shrimps are not only the vent-endemic species, but also have a high proportions of endemic species in different hydrothermal vent. We determined the dispersal evens and alternative pathways of alvinocaridid shrimps, coincided with major ocean geographic evens. The results showed that the alvinocaridid shrimps originated in Southwestern Pacific, and subsequently underwent two dispersal events to Northwestern Pacific at 42.36 Mya and 7.79 Mya, respectively. At about 4.15 Mya, the genus Rimicaris split into two lineages, with one invaded into Indian Oceans and another invaded into Atlantic. As the Central American seaway closed at 14-4.2 Mya, species were unable to spread from the Pacific to Atlantic through the Central American seaway. Instead, they may spread into Atlantic through Indian Oceans. This result supported that the Western Pacific was the origin center of hydrothermal vent species, and the Indian Oceans was the transition point between the Pacific and Atlantic. Our findings provided theoretical and practical evidence for revealing the origin and the evolution of the chemosynthetic-fauna in deep-sea hydrothermal vents.

POSTER 85 • Connectivity and biogeography
TUESDAY Evening • 17:45 • Serra Ballroom

## Species Distribution Modeling: Utility and Applications for Midwater Fishes

Shannon C. DeVaney
Pierce College

Species distribution modeling (SDM) methods can predict species occurrence in unsampled areas and detect environmental variables that correlate with species presence. The ocean's midwaters — vast, sparsely sampled, and difficult to access — seem to constitute a habitat ideal for SDM applications. However, the very sparseness and biased nature of existing species occurrence data, and the fact that most globally available environmental datasets are from either the sea surface or bottom, present challenges to reliable SDM analyses for midwater species. These challenges are addressed here in a series of distribution models for midwater fishes performed with the maximum entropy modeling program MAXENT. Sampling bias is accounted for via a Target Group Sampling approach, in which only grid cells that contain midwater species data are included in the background. Midwater species, even those that do not themselves undergo vertical diurnal migrations, are influenced by conditions at the sea surface and bottom; environmental data representing those zones can be useful in modeling midwater fish distribution. Distribution models from widespread and relatively abundant midwater species including Eurypharynx pelecanoides, Anoplogaster cornuta, and Opisthoproctus soleatus demonstrate the viability of SDM for midwater species using MAXENT and existing environmental datasets, while providing insight into the ecological parameters driving each species' distribution.

POSTER 86 - Connectivity and biogeography
TUESDAY Evening • 17:45 • Serra Ballroom

## Population structure and reproduction of the alvinocaridid shrimp *Rimicaris exoculata* on theMid-Atlantic Ridge: variations between habitats and vent fields

Ivan Hernandez-Avila 1,3, Marie-Anne Cambon-Bonavita2, Jozée Sarrazin1 and Florence Pradrillon1
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Rimicaris exoculata is one of the dominant species at most vents on the Mid-Atlantic Ridge (MAR), and lives especially close to vent emissions at depths bellow 2000 m. Although it is an iconic vent species that has been relatively well studied, many gaps persist in our understanding of its life cycle, reproduction and larval biology. Here, we present the population structure and reproduction of R. exoculata at two vent fields, TAG and Snake Pit, located around 3500 m depth on the MAR. Shrimps were sampled in January-February 2014, both close to the vent emissions (active emission habitats, AEH) and away from the focused fluid emission (diffuse emission habitat, DEH and inactive emission habitat, IEH). Major differences in population structure were observed between the habitats. Females widely dominate the large swarms in the AEH meanwhile DEH are colonized mainly by small juveniles of R. exoculata and R. chacei, and IEH are inhabited by large males. Size structure of the population in AEH is polymodal at both vent fields, suggesting a non-continuous recruitment. Body size of males is larger than females, but no differences are detected between vent fields for each sex. Similarly, male body size did not vary between habitats. Brooding females were collected from AEH exclusively, bearing embryos at all developmental stages. This contrasts drastically with previous collections on the MAR, of which a very limited number of brooding females had been reported, and thus may indicate seasonal spawning. More brooding females were found with aborted eggs at TAG than at Snake Pit, and they also exhibited significantly lower reproductive output, with both smaller brood size and smaller egg size, perhaps reflecting differences in local environmental conditions. A hypothetical reconstruction of the benthic phase of R. exoculata life cycle is proposed.

TUESDAY Evening • 17:45 • Serra Ballroom

## Genetic diversity and connectivity of the endosymbionts of *Riftia pachyptila* tubeworms

Sook-Jin Jang, Yong-Jin Won
EWHA Womans University

The siboglinid tubeworm, Riftia pachyptila, flourishes at the eastern Pacific hydrothermal vents and relies its nutrition on obligate autotrophic endosymbiotic bacteria that are horizontally acquired via infection from environments when the host larvae settle. This horizontal transmission mode allows the tubeworms to obtain 'locally optimal' symbiotic bacterial strains. The goal of this study is to examine the genetic diversity and connectivity of the endosymbionts of R. pachyptila along the Guaymas basin and East Pacific Rise (EPR). We conducted community analysis of the endosymbionts using pyrosequencing data of 16S rRNA and populations genetic analyses based on PCR-sequencing data of two protein-coding genes, cbbM (RubisCO) and filC (Filagellin). Unexpectedly, the community analysis revealed different bacterial species between samples from the Guaymas basin and the EPR. The most bacteria (> 90%) within a host from the Guaymas were identified as the endosymbionts of cold seep tubeworms, Escarpia and Lamellibrachia species. In contrast, Endoriftia Persephone bacteria were the most endosymbionts of the EPR tubeworms as reported in previous studies. In consistent with this community analysis, we observed a distinctive haplotype of cbbM only from the Guaymas bacterial population that is 100% identical with symbiont sequences from E. spicata and L. barhami tubeworms in the Gulf of California, but differs from other haplotypes by 23%. The present study suggests that the different geochemical processes between the sediment-based system in the Guaymas basin and the basalt-based system in the EPR may sustain different composition or even different species of free-living symbiotic bacteria. If then, the tubeworms may take advantage of hosting 'locally optimal' symbiotic partners. To verify this hypothesis, additional investigations based on more samples and more sequence data are needed.

TUESDAY Evening • 17:45 • Serra Ballroom

## Predictive distribution of vulnerable marine ecosystems in arctic and subarctic waters.

Steinunn H Olafsdottir, J.M. Burgos, L. Buhl-Mortensen, P. Buhl-Mortensen, P. Steingrund and S.Á. Ragnarsson
Marine and Freshwater Research, Iceland; Institute of Marine Research, Norway; Faroe Marine Research Institute, Faroes Island

The Nordic project on vulnerable marine ecosystems and anthropogenic activities in arctic and subarctic waters (NovasArc) is mapping the distribution of vulnerable marine ecosystems (VME´s) in the Greenland and Norwegian Seas, and between 62°N and the Svalbard archipelago. NovasArc is carried out by the Marine Research Institutes in Norway (IMR), Iceland (MFRI) and Faroe Islands (FMRI) and is funded by the Nordic Council of Ministers. Cold-water coral reefs, coral gardens, and deep-sea sponge aggregations are found in the area. NovasArc contributes to the need for increasing knowledge of the factors influencing the distribution and connectivity of these VME´s. This is essential to predict the effects of changes in the environment and of anthropogenic pressures. NovasArc has compiled >40 thousand records of VME indicator species. Records were obtained from national habitat mapping surveys, bycatch data from bottom fish surveys, reports and peer reviewed publications. A Maximum Entropy Approach (MaxEnt) model was used to produce the maps using as predictors terrain analysis parameters, bottom temperature and salinity estimates obtained from the NISE (Norwegian Iceland Seas Experiment) project and estimates of particulate organic carbon. We present maps showing the predictive distribution of VMEs at relatively coarse scales (500m) within the whole study area. More detailed

distribution map of corals and sea pens off Iceland is also presented. Iceland is positioned in the center of the Greenland-Iceland-Scotland Ridge, a well-known biographic barrier between the arctic and the North Atlantic waters. Varied sea floor geoforms including ridges, troughs, landslides and glacial landforms influence the distribution of the corals and sea pens. The fauna is also strongly influenced by the cold arctic waters and the warm North Atlantic waters. The output of the NovasArc project is important contribution to management planning, sustainable management of fisheries and conservation of vulnerable habitats in the arctic and subarctic waters.

TUESDAY Lightning Talks • 08:30 • Serra Room

## HACON: assessing the role of the Gakkel Ridge as a connectivity pathway between ocean basins

Eva Ramirez-Llodra, Stefan Buenz, Hans Tore Rapp, Tina Kutti, Ana Hilario, Chris German, Autun Purser, Eoghan Reeves, Benedicte Ferre, Giuliana Panieri & Odd Aksel Bergstad
NIVA

The remote Arctic Gakkel Ridge remains largely unexplored and ecosystems in this under-ice region are largely unknown. First evidence of active venting in the Gakkel Ridge has been available since 2001, but visual confirmation was not obtained until 2014 on the Aurora seamount. The newly-funded project HACON will return to the Aurora seamount in 2019, using the most modern infrastructure for oceanographic and Arctic research, including the new Norwegian icebreaker Kronprins Haakon, Norwegian ROV Ægir and hybrid AUV Nereus Under Ice (WHOI, USA). HACON will conduct the first full-scale multidisciplinary study of deep (4000 m) hydrothermal vents under permanent ice cover in the Arctic (82°N). HACON will answer 3 questions: 1) What are the geologic controls on the vent-site's setting and how do chemical signatures evolve in the water column? 2) What microbial and faunal communities are supported by such geochemical settings and how do they function? 3) What are the pathways and barriers to population connectivity between the deep Pacific, Arctic and Atlantic oceans? HACON will unravel the processes that shape the Aurora communities and test the hypothesis that the Gakkel Ridge provides a connecting pathway for gene flow between the Pacific and Atlantic oceans. The project will provide empirical robust data of a pristine system prior to expected climate-change variations and increased human activities in the Arctic region.

TUESDAY Evening • 17:45 • Serra Ballroom

## Population structure and connectivity of deep-sea amphipods in geographically isolated trenches

Heather Ritchie, Alan J. Jamieson2, and Stuart B. Piertney1
1School of Biological Sciences, University of Aberdeen; 2School of Natural and Environmental Sciences, Ridley Building, Newcastle University

The ecological drivers of patterns of connectivity and speciation within and among species assemblages in the deep sea remain poorly understood. This is especially the case abyssal (4000-6000m) and hadal (>6000m) depths which represent the most poorly explored and least understood ecosystems on Earth. The hadal zone primarily consists of trenches formed along subduction zones around the Pacific Rim. Trenches disrupt the abyssal plains by forming spatially-distinct habitats which are isolated by large geographical distances. Due to this isolation it was conventionally believed that trenches lacked connectivity through dispersal and gene flow, which would promote speciation and localised endemism. This assertion is difficult to reconcile with the presence of some species with cosmopolitan distributions across the abyssal and hadal zones. Here we use the geographic distribution of genetic variation to infer connectivity between

abyssal-hadal trench populations of two Paralicella sp. amphipods which constitute a significant and ubiquitous component of the abyssal-hadal fauna. Microsatellite DNA markers were developed to examine the genetic similarity, patterns of species distribution and population connectivity between 109 individuals from five trenches around the Pacific Rim. Our results highlight distinctive patterns of species distribution and connectivity between the two Paralicella species, which we found to be closely associated with deep ocean currents, sea floor topography and the geological history of trench formation.

POSTER 91 - Connectivity and biogeography
TUESDAY Evening • 17:45 • Serra Ballroom
### Connectivity between shallow and deep reef communities around Bermuda
Paris Stefanoudis, Lucy Woodall, Alex Rogers
Nekton Foundation, UK, University of Oxford, UK
Benthic megafauna significantly differ depending on depth. From data collected in Bermudian waters using submersibles and technical divers, we explore these relationships for the first time across depths of 15 m to 300 m. Here we present the faunal communities and show that there are distinct assemblages at each depth with substantial species turnover. Typically, faunal changes occur across wider depth zones, but we reveal this is not the case and the differential is much greater, even in areas that are exposed to a high degree of human activities. The assemblages we describe include species that are abundant but new to science and others that are endemic to Bermuda, thus revealing these assemblages are novel. This benthic megafauna heterogeneity includes habitat-forming organisms, has potential implications for the 'deep reef refugia' hypothesis and is an important consideration for spatial planning and ocean management.

POSTER 92 - Connectivity and biogeography
TUESDAY Evening • 17:45 • Serra Ballroom
### Connecting ocean physical and biogeochemical properties with the spatial distribution of mesopelagic fish abundance/biomass
Jeanna Hudson, Donglai Gong
Virginia Institute of Marine Sciences
Estimates of the global distribution of mesopelagic fish biomass/ abundance are based on a very limited number of studies (i.e. Gjøsaeter and Kawaguchi (1980), Proud et al. (2017), Sutton et al. (2017)). Spatial distribution estimates are coarse and are not linked with specific mesopelagic physical and biogeochemical properties. Current constructions of mesopelagic biogeographic domains are mainly based on cluster analyses that do not provide dynamic linkages to underlying variables (i.e. temperature, dissolved oxygen, surface productivity). We are building and testing a set of models using supervised machine learning that utilize ocean physical and biogeochemical parameters that are consistent with prior global scale mesopelagic biomass/abundance estimates to model the distributions on the grid scale (~1 deg resolution). The models would include temperature, salinity, and dissolved oxygen data from World Ocean Atlas, GEBCO ocean bathymetry, surface chlorophyll from the NASA MODIS satellites, oceanographic current data from the Simple Ocean Data Assimilation (SODA3) reanalysis, global estimate of ocean turbulent mixing based on Argo floats data, and biomass/abundance data from Gjøsaeter and Kawaguchi (1980) and Ocean Biogeographic Information System. We hypothesize that areas of high mesopelagic fish biomass correlate with high surface primary production as well as particular physical conditions (i.e. specific bathymetric feature, temperature range, dissolved oxygen levels, ocean fronts, and turbulent conditions that maximize food availability and organismal interactions). The goal of this study is to identify what those physical conditions are and how they influence mesopelagic fish distribution and density. The study will test a

variety of models ranging from simple linear models to more complex neural networks.

# **Corals** - TALKS

Corals - ABSTRACT 286
THURSDAY Afternoon • 16:15 • San Carlos Room
## Multi-Species Comparative Connectivity Patterns of Deep-Sea Coral Populations
Santiago Herrera1, Matthew Galaska1, Andrea Quattrini2, Annalisa Bracco3, Guangpeng Liu3, Peter Etnoyer4
1Lehigh University, 2Harvey Mudd College, 3Georgia Institute of Technology, 4NOAA NCCOS
Due to the pervasive threats of global ocean change and other anthropogenic impacts, such as pollution and destructive extraction of resources, there is an urgent need to make decisions that will lead to the effective management and conservation of vulnerable marine ecosystems. The establishment of marine protected areas (MPAs) is not only essential to protect and conserve deep-sea benthic ecosystems, but has been identified as one of the key restoration strategies for benthic communities impacted by catastrophes like the Deepwater Horizon (DWH) oil spill in the Gulf of Mexico. Understanding the factors that promote or impede the connectivity among populations of key foundation species over horizontal and vertical spatial dimensions is essential to manage deep-sea MPAs. Populations of species found at deeper depth ranges are hypothesized to have greater horizontal connectivity than species at shallower depth ranges, thus potentially requiring different management strategies. We test this hypothesis by focusing on four foundation deep-sea coral species, including species directly impacted by the DWH oil spill, living across the northern Gulf of Mexico. Target coral species occur at three depth ranges: mesophotic (70-150 m), upper continental slope (400-1100 m), and lower continental slope (1300-2400 m). We quantified population connectivity in these species through the integration of field sampling, state-of-the-art population genomic analyses and physical oceanographic modeling approaches. We will present comparative results defining spatial scales of coral population genetic structure and differentiation at different depths, indicating directionality and relative rate of genetic exchange among coral populations. Outcomes from predictive models of larval dispersal integrated with genetic data to estimate dispersal distances and connectivity networks will also be presented. These results, produced in collaboration with resource managers, will directly inform the design and management of MPAs in the Gulf of Mexico.

Corals - ABSTRACT 220
THURSDAY Afternoon • 16:30 • San Carlos Room
## Methodologies and tools for restoration of degraded deep-sea coral gardens in the Azores
Marina Carreiro-Silva, M Carreiro-Silva, Bilan M, Godinho A, Martins I, Rakka M, Morato T
1MARE – Marine and Environmental Sciences Centre and IMAR – Institute of Marine Research, Rua Frederico Machado 4, 9901-862 Horta, Portugal
Cold-water coral (CWC) ecosystems have been increasingly degraded by human activities. Thus, restoration actions are urgently needed to assist the recovery of these ecosystems as part of their sustainable management. Within the MERCES project, we are developing methodologies and tools for restoration of degraded deep-sea coral gardens. The main pilot action consists in testing the use of CWC transplantation techniques as an assisted regeneration tool to aid the recovery of coral gardens potentially impacted by human activities (e.g. seafloor mining, fishing). Fragments of the octocoral Dentomuricea meteor, a common species in coral gardens in the Azores, were collected, maintained in the lab, and transplanted to the summit of Condor seamount using fauna landers in 2016. Landers were deployed in three areas of

differing CWC densities (low, medium, high) with the objective of determining the effect of proximity to natural populations on the transplanted CWC survival, growth, physiological condition, and ability to attract associated fauna, thus restoring natural ecosystem functioning. Additionally, the potential of natural regeneration of CWC communities impacted by deep-sea mining, fishing and both is being assessed by deploying landers with D. meteor intoxicated with cooper (the main trace metal present in SMS sediment plumes), injured with superficial scratches (to mimic fisheries impact), and with both impacts. The survival rates and physiological condition of coral fragments were assessed with ROV video and photography 1 week, 8 months and 1 year after coral deployment. Results of these studies are currently being processed and will be presented. We will also present the progress made towards the transplantation of a larger and more representative number of CWC species. This work resulted from a close collaboration with local fisherman and fisheries observers who brought different species of CWC accidentally caught as bycatch during their hook-and-line fisheries operations. The proposed restoration actions will be discussed in terms of their challenges, benefits and weaknesses for the recovery of deep-sea coral gardens, and in terms of defining achievable metrics to measure restoration success.

Corals - ABSTRACT 348
THURSDAY Afternoon • 16:45 • San Carlos Room

## Population genomics reveals complex connectivity patterns among southeast Alaskan red tree coral (*Primnoa pacifica*) populations

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U.S. Geological Survey, Leetown Science Center, Kearneysville, WV, USA

Red tree corals, Primnoa pacifica, are the dominant structure-forming coral species in the Gulf of Alaska (GOA). Red tree corals serve as important habitat to fishes and invertebrates, yet this long-lived species is highly susceptible to disturbance from fisheries, and as such, some protection has been afforded to several offshore populations in the GOA. Red tree corals are often a dominant component of emergent fjord communities in southeastern Alaska, occurring as shallow as six meters. The variable combination of tides, storms, freshwater discharge, plus complex passageways to the sea may restrict larval exchange between offshore and fjord P. pacifica populations, or conversely, fjord populations could become important larval sources should offshore populations become depleted. We assessed putative population structuring among P. pacifica populations from three offshore GOA populations (Dixon Entrance, Shutter Ridge, the Fairweather Grounds) and three fjords (Tracy Arm, Endicott Arm and White Thunder Ridge in Glacier Bay National Park) using both traditional microsatellites and high-throughput restriction-site associated DNA (RAD-tag) sequencing. Over 300 discreet, geo-referenced samples of P. pacifica were collected via remotely operated vehicles or SCUBA divers on NOAA-sponsored research cruises in 2013-2016. Both datasets revealed high levels of genetic diversity and a complex pattern of connectivity, with offshore populations being more highly connected than fjord populations. We will assess the consistency of estimates of genetic diversity, population structuring, and levels of admixture obtained through analysis of the different datasets. Estimated population structuring will also be compared to the reproductive ecology of the sampled offshore and fjord populations. This study provides important insights regarding the most appropriate tools available to resource managers to protect sensitive coral habitats and the ecosystem services they provide.

Corals - ABSTRACT 302
THURSDAY Afternoon • 17:00 • San Carlos Room

## Cold-water coral communities on rocky walls: Distribution from global to colony scales

Katleen Robert, Daniel O.B. Jones, Aggeliki Georgiopoulou and Veerle A.I Huvenne
Fisheries and Marine Institute of Memorial University, St. John's, Canada

Similar to their shallow water counter parts, vertical and overhanging walls in the deep sea provide a different set of environmental conditions than the surrounding terrain. Because of their geometry, these habitats can also harbour highly diverse communities and provide protection to vulnerable cold-water coral ecosystems from trawling activities. As such, it is important to assess their global importance and understand their ecology. In this study, we assess coral wall systems at three scales: (1) review globally available datasets (bathymetry, presence records, habitat suitability models and geomorphic catalogues), (2) analyse community patterns of megafaunal species inhabiting six walls in the Northeast Atlantic and (3) reconstruct in three dimensions and at very high resolution (<1 cm) a section of a wall using photogrammetry techniques. Globally we found over 6,000 features likely to harbour rocky walls and cold-water corals, demonstrating their importance. The investigated walls showed significant differences in diversity and community composition, while within individual walls, differences in ecological niche could be demonstrated between closely-related taxa. Rocky walls represent an important cold-water coral habitat with significant differences in species composition across walls within a region, illustrating their role in driving diversity patterns. These results highlight the role of terrain heterogeneity in driving cold-water coral spatial patterns over a range of scales and highlight the need to consider deep-sea vertical habitats in current conservation efforts. This work is part of the ERC CODEMAP project (Starting Grant no 258482) and data were collected during the CODEMAP2015 cruise and the SORBEH expedition (Marine Institute, Ireland).

Corals - ABSTRACT 60
THURSDAY Afternoon • 17:15 • San Carlos Room

## Thermal acclimation range of two Mediterranean cold-water coral species

Stéphanie Reynaud, Orejas Covadonga, Campagno Andrea, Gori Andrea, JimenezCarlos, Ferreier-Pages Christine
CSM

Cold-water corals (CWCs) are among the main engineer species in the deep-sea ecosystems of the world. Among a few factors, their distribution is linked to seawater temperature, which controls all physiological processes. The thermal range of CWC is generally 6°C-12°C in most seas and oceans, except in some cases, such as in the eastern Mediterranean Sea, where Dendrophyllia ramea thrives at higher temperatures (16°C-17°C). In order to assess the thermal acclimation range of Mediterranean CWCs, and their response to the predicted increase in seawater temperature, Dendrophyllia cornigera and D. ramea, (found naturally in the Mediterranean at 12°C and 16°C, respectively), were cultured under temperatures of 12°C, 16°C, 20°C and 24°C. Rates of calcification, respiration and total organic carbon (TOC) release were measured after 6 weeks and 16 months of acclimation. Our results show that D. cornigera, adapted to 12°C, died within few weeks at 20°C, but survived at least 2 years at 16°C, with a similar calcification rate than at 12°C. On the contrary, D. ramea showed a very large thermal tolerance (from 12 to 24°C) for more than 2 years, with a significant increase in growth rates at 24°C. Although temperature had a significant effect on CWC's calcification rates, it didn't induce any changes in respiration rates for either species or TOC release rates of D. cornigera. However, on the long-term, it decreased TOC release rates of D. ramea. Overall, our results indicate that, in the Mediterranean Sea, not all CWC species are living at their upper thermal tolerance boundary.

Corals - ABSTRACT 319
THURSDAY Afternoon • 17:30 • San Carlos Room

## Genotype Specific Response of *Lophelia pertusa* to Low pH

A. Glazier, Weinnig A, Gomez C, Kurman M, Herrera S, Cordes E
Temple University

The deep sea is the world's largest ecosystem and supports a unique, diverse fauna. Lophelia pertusa reefs are among the ecosystem's most diverse habitats, supporting a biotic diversity that rivals shallow-water reefs. Ecosystems throughout the world are already influenced by ocean acidification, but these deep-sea reefs are among the first to be impacted by these threats. The aragonite saturation horizon (ASH), the boundary between waters where calcification or dissolution is favored, is shoaling due to the decline in pH in the ocean and exposing more reef communities to waters low in aragonite. Physiological and transcriptomic responses of corals to ocean acidification have been related to underlying genotypic makeup and native environmental conditions. To investigate this in L. pertusa, coral fragments were sampled from sites with different environmental conditions in the Gulf of Mexico and preserved in situ. Corals were also transported to the lab where they were kept alive for experimentation and subsequent transcriptomic analyses. Three genotypes were maintained at pH 7.9 and 7.6 and fragments were sampled after 2 weeks, 4 weeks, and 6 weeks for RNA sequencing. Genotype had the greatest impact on variation in these expression patterns, with the unique patterns among genotypes suggesting each was responding to low pH conditions differently. Some of the variance in these responses could be related to their unique native environmental conditions and expression patterns of the in situ preserved samples. A greater ability to cope with ocean acidification suggests certain genotypes are more likely to survive contemporary and future conditions under ocean change. This might lead to strong selection for these genotypes, which would have consequences for genetic diversity but could provide a mechanism for these corals to persist in future conditions of low pH.

Corals - ABSTRACT 133
FRIDAY Morning • 09:45 • Serra Room

## Deep-Sea Coral and Sponge Ecosystems of the US: A Decade of Discovery and Stewardship

Thomas F. Hourigan, Peter J. Etnoyer; Stephen D. Cairns
NOAA Fisheries Service; NOAA Ocean Service; Smithsonian Institution, National Museum of Natural History

In 2017, the National Oceanic and Atmospheric Administration (NOAA) published the State of Deep-Sea Coral and Sponge Ecosystems of the United States. The peer-reviewed report brought together over 40 authors to review advances in deep-sea coral and sponge research, and shows how this new information is shaping ocean conservation. Report highlights include: (*)The first comprehensive inventory of deep-sea coral diversity in U.S. waters, revealing 662 species of deep-water corals, including 62 new species discovered from 2007-2016. (*)New deep-sea coral "gardens" discovered in every U.S. region, especially Alaska, where new evidence points to their role as habitat for fisheries of national and international importance. (*)New exploration and research of previously unexplored U.S. Pacific Island slopes, oceanic ridges, and seamounts. (*)A summary of deep-sea coral damage assessments and management responses after the Deepwater Horizon oil spill. (*)Development and use of habitat models to aid protection of 38,000 square miles of the Northeast deep sea, which has helped make the U.S. a leader in deep-sea conservation. (*)Enhanced protection in the Southeast U.S. across areas containing one of the most substantial concentrations of deep-sea coral reefs in the world. (*)Deepwater expansion of National Marine Sanctuaries along the West Coast. (*)A conservation status and threat analysis for U.S. deep-sea coral and sponge ecosystems reveals progress in conservation over the last decade and potential implications of emerging industries such as deep-sea mining. Our presentation will reflect on progress achieved, and look forward to key challenges for further advancing research in support of conservation in the coming decade.

Corals - ABSTRACT 234

FRIDAY Morning • 10:00 • Serra Room

## Oxygen and nutrient dynamics of a cold-water coral reef in the North-East Atlantic Ocean.

Evert de Froe, Sandra Maier, Furu Mienis, Gerard Duineveld, Marc Lavaleye, Dick van Oevelen
Department of Ocean Systems, Royal Netherlands Institute for Sea Research and Utrecht University, the Netherlands

Cold-water coral reefs play an important role in the biogeochemical cycling of the seafloor. These reefs are distributed globally across the deep seafloor but grow mostly on the edges of continental margins. Recently, research on the biogeochemistry of cold-water coral reefs has intensified, aiming for a better understanding and quantification of organic and inorganic cycling on these reefs. Previous work on the biogeochemistry of cold-water coral reefs has mainly focused on benthic community oxygen uptake or oxygen uptake and nutrient dynamics of individual components of a cold-water coral reef (e.g. coral fragments, sponges). However, to our knowledge, there are no studies on the nutrient dynamics of a cold-water coral reef community. In this research, we measured oxygen and nutrient fluxes of a cold-water coral reef and a nearby soft-sediment station using whole box core incubations of sediment or reef framework from Rockall Bank (NE Atlantic). A total of six large box cores (50 cm diameter) was taken from two coral carbonate mounts and subsequently incubated for ±24h for oxygen consumption and nutrient release. Oxygen consumption of the coral box cores ($16.2 \pm 11.3$ mmol O2 m-2 d-1, mean ± SD) was significantly higher than the soft-sediment cores ($2.12 \pm 1.42$ mmol O2 m-2 d-1, mean ± SD). Also, the ammonium (NH4+) efflux was significantly higher in the coral mound box cores than in the sediment cores. Other coral framework nutrient fluxes (PO4, NO2-, NO3- and, SiO2) had higher mean fluxes as compared to the sediments, but the difference was not statistically significant. These results provide further evidence of the increased metabolic activity of a cold-water coral reef compared to its surrounding sediment and highlight the importance of these reefs in marine biogeochemical cycling.

Corals - ABSTRACT 148
FRIDAY Morning • 10:15 • Serra Room

## Energy and nutrient recycling on cold-water coral reefs: The use of bacterial and DOM-derived carbon by key reef filter feeders

Sandra R. Maier, Kutti, Tina; Bannister, Raymond; van Breugel, Peter; van Rijswijk, Pieter; Tramper, Anton; van Oevelen, Dick
Royal Netherlands Institute for Sea Research (NIOZ)

Cold-water coral (CWC) reefs play a major role in carbon and nitrogen cycling in the deep-sea, but their high productivity and diversity stands in sharp contrast to typically low available resources. An important part of the C and N cycling on CWC reefs is mediated by the diverse fauna associated with the living and dead reef framework. The limited resource availability in the water column may foster efficient recycling pathways involving the reuse of dissolved organic matter (DOM) or the uptake of bacteria growing on DOM. We studied these recycling pathways for the bivalve _Acesta excavata_ and the sponges _Geodia barretti_ and _Mycale lingua_, which are considered important contributors to C and N cycling on Norwegian CWC reefs. In a stable isotope tracer experiment, all species were provided with either a bacterial or a DOM substrate, which was artificially enriched in the heavy stable isotopes 13C and 15N. Incorporation of 13C and 15N in tissue and specific tissue compounds, including fatty acids and amino acids, and subsequent respiration of 13C, provided direct evidence for the ability of all studied filter feeders to utilise these resources. Overall, bacteria were incorporated at higher rates, and sponges benefitted more of this resource than the bivalve _A. excavata_. Subsequent production of particulate organic matter in the form of bivalve

(pseudo)faeces or sponge detritus may feed reef detritivores such as ophiuroids. We discuss the potential of those recycling pathways to supply the CWC reef community, and comment whether a CWC reef should be considered a cycling or a recycling system.

## *Antipathella subpinnata* as model species: life history and autoecology

Martina Coppari, Mestice Fulvia, van de Water Jeroen, Ferrier-Pagès Christine, Betti Federico, Costantini Federica, Bertuccio Valentina, Bavestrello Giorgio, Bo Marzia
Dipartimento per lo Studio del Territorio, dell'Ambiente e della Vita, Università degli Studi di Genova

The black coral fauna of the Mediterranean Sea includes seven species belonging to five different families distributed throughout the basin from 60 to 2000 m depth. For long time considered extremely rare species, in the last 10 years, remotely operated vehicle (ROV) explorations completely overturned this paradigm such that, now, at least 4 of these species are considered common or dominant components of the deep circalittoral and bathyal cold-water corals (CWC) assemblages. A large effort has been dedicated to map the distribution of populations, however very little information exists on the life history and ecological role of these paramount species. In particular, Antipathella subpinnata, a large arborescent species, is known to thrive from 60 to 600 m depth on exposed hardgrounds commonly forming dense aggregations. Over 70 populations have been currently mapped in the Mediterranean basin; therefore, this species may well represent a model for the entire order. A 360° approach (coupled to literature search) has been carried out to investigate, in the field and in controlled systems, numerous traits of the life history of this species and to elucidate its ecology. In particular: i) phylogenetic position, ii) morphological characteristics, iii) phenotypic plasticity, iv) geographic and bathymetric distribution, v) size frequency distribution, vi) habitat preferences, vii) associated fauna, viii) associated microbiome, ix), sexual reproductive cycle, x) asexual reproduction through fragmentation, xi) genetic structuring and connectivity among populations, xii) growth rates, xiii) isotopic diet, xiv) skeletal degradation, xv) 3D modelling and biomass, xvi) response to anthropic impact. Although various aspects have not been investigated yet (e.g. age, skeletal architecture, larval ecology), such extensive dataset is crucial when identifying the vulnerability traits of a species and of the ecosystem it sustains.

## Using 3D photogrammetry to investigate how cold-water coral reef structural complexity influences biodiversity and community assemblages.

David Price, Veerle Huvenne, Katleen Robert, Claudio Lo Iacono, Alex Callaway, Rob Hall, Laura Grange
National Oceanography Centre, UK. University of Southampton, UK. Memorial University of Newfoundland, Canada. Centre for Environment, Fisheries and Aquaculture Science, UK. University of East Anglia, UK

Fine-scale structural complexity induced by reef building coral in shallow-water environments is influential on biodiversity, community assemblages and species' functional traits. Also, cold-water coral reefs are hotspots for biodiversity, often attributed to the hard surface and structural complexity provided by the coral. However, rugosity has seldom been quantified in cold-water coral reefs on a centimetre scale, unlike their shallow-water counterparts, and has therefore never been linked to the reef inhabitant community. Structure from Motion techniques which create high-resolution 3D models of habitats from sequences of photographs are being increasingly utilised, in tandem with 3D spatial analysis to create useful 3D metrics, such as rugosity. Here, we demonstrate the use of ROV video transect data to survey cold-water coral reefs for 3D reconstructions at depths of nearly 1000m in the Explorer Canyon, a tributary of the Whittard Canyon, NE Atlantic. The resulting imagery was used to construct forty 3D models of 25m length transects in Agisoft Photoscan software, resulting in sub-centimetre reconstructions. Digital elevation models were utilised to derive rugosity metrics and photomosaics used for habitat classification. We provide some of the first fine-scale measurements of rugosity derived from cold-water coral reefs, and found values comparable to shallow-water tropical coral reef rugosity. Reef and nearby non-reef communities differed in assemblage composition, which was driven by depth and rugosity. Biodiversity and fish abundance increased with structural complexity, being attributed to an increase in niches, food, shelter and alteration of physical water movement. Depth, rugosity and presence of dead coral framework influenced the community assemblages within coral reef habitats, with dead coral framework likely providing further settling potential for sessile organisms. Cold-water coral structural complexity appeared to be integral to local-scale ecological patterns and is threatened by ocean acidification and destructive fishing practices, which may result in loss of local terrain complexity.

## Large-scale survey of deep-sea coral microbiomes in the Gulf of Mexico reveals potential symbioses

Sam Vohsen, Iliana Baums, Chuck Fisher
The Pennsylvania State University

The bacterial communities associated with shallow-water corals plays important roles for the host ranging from disease resistance to nitrogen fixation. The microbiomes of deep-sea corals, however, are poorly studied without known roles. Deep-sea coral communities occur throughout the Northern Gulf of Mexico and can overlap with cold seep environments characterized by potential exposure to hydrogen sulfide and hydrocarbons. This chemical environment may shape the coral microbiome and provide new abilities to the coral holobiont as it does in shallow-water corals. To characterize the deep-sea coral-associated microbial community, we collected samples from over 30 coral species, water, and sediment from across the Northern Gulf of Mexico for 16S tag sequencing. The coral associated microbial communities were species-specific and distinct from the sediment communities. Single groups of bacteria often dominated the microbiomes of particular coral species, including a relative of Apicomplexans in Leiopathes glaberrima and a novel Mollicute in Callogorgia delta. The genome of this Mollicute is very reduced suggesting a symbiotic lifestyle. FISH microscopy revealed aggregates of bacteria within the mesoglea of C. delta that surround anomalous DAPI staining structures. Specific primers have been developed to identify the bacteria present in these aggregates. Further, the microbiomes of Acanthogorgia sp., Muriceides sp., and Paramuricea sp. B3 in areas with active seepage were dominated by a close relative of the sulfide-oxidizing endosymbionts of Bathymodiolus spp. In P. sp. B3, the percentage SUP05 in the microbiome was correlated with depleted carbon-13 and nitrogen-15 in coral tissue and therefore incorporation of chemoautotrophic primary production into the coral holobiont. Thus, the microbial communities associated with corals including those in the deep-sea may play important roles and may serve as a mechanism for corals to interact with their environment around seeps.

## Deep-sea corals document changing stable isotope chemistry in the Southern California Bight.

Branwen Williams, Sarah Barnes, Mark Knaak, Chris Caldow, Matt McCarthy, and Peter Etnoyer
Claremont Colleges

Upwelling in the Southern California Bight promotes diverse and abundant benthic communities. Yet, recent changes in the source of the upwelled water and the resulting biogeochemical changes may affect the organisms that live here, such as deep-water gorgonian octocorals. Eugorgia rubens and Acanthogorgia sp. are among the most common deep-water gorgonian taxa in the region. Here, we measured the skeletal radiocarbon and stable carbon and nitrogen isotopic composition in five colonies of these two species from the Southern California Bight. Identification of "bomb" radiocarbon in the coral skeletons indicates ages of less than a century. We find significantly higher carbon isotope values and lower nitrogen isotope values in the two shallower Eugorgia colonies collected from 65 m compared to the three deeper Acanthogorgia colonies collected from 205 m. The stable isotope values are stable over the lifespan of the Eugorgia colonies while the stable isotope values change over the lifespan of the deeper Acanthogorgia colonies: carbon values decrease and nitrogen values increase through time. Measurements of the amino acid molar percentages and compound-specific isotope values in coral skeletons will allow us to examine different feeding strategies by these two species of gorgonian corals, or different nutrient chemistry between depths and geography within the Southern California Bight, drive the different isotopic skeletal signatures. With this information, we will interpret the changes in the coral colonies skeletal geochemistry in the context of hydrographic and environmental reanalysis data. This work will advance our understanding of historical variability in nutrients available to deep-sea marine life in the Southern California Bight related to changing oceanic regimes.

## A window opens from the mesopelagic: A proteinaceous deep-sea coral's view of biogeochemistry and ecosystem change above.

Thomas P. Guilderson, Robert Dunbar, Matthew McCarthy, Kelton McMahon, E. Brendan Roark, Yuan Shen, Owen Sherwood, and Branwen Williams
University of Californica-Santa Cruz, Stanford University, University of California - Santa Cruz, University of Rhode Island, Texas A&M University, University of California - Santa Cruz, Dalhousie University, Claremont-McKenna

Oceanic biological-ecosystem variability is most often linked to changes in sea surface temperature (SST) but SST is a reflection of dynamic processes, which influence: the stability of the water column, nutrient input, entrainment, and advection. Coherent and significant North Pacific spatio-temporal SST and sea level pressure (SLP) patterns at seasonal to inter-decadal timescales imply a close coupling of atmospheric and ocean dynamics, so it is not surprising that there are biological-ecosystem responses. We have been coupling high resolution paleorecords derived from deep-sea proteinaceous coral together with new compound-specific amino acid isotope (CSI-AA) measurements to create reconstructions of both biogeochemical change (e.g., source of nitrogen) and basic plankton ecosystem shifts crossing the North Pacific. We will highlight recent work exploring the response of the North Pacific Subtropical Gyre to large-scale climate forcing and delve into some of the outstanding questions associated with utilizing these deep-sea 'living sediment traps.'

# Corals - POSTERS

## Relationships among ages, growth rates, banding periodicities, and gross morphology in deep-sea Primnoidae corals.

Emma Choy, Branwen Williams, Kelly Watanabe, Mary Knaak, Bob Stone, Thomas Lorenson, and Peter Etnoyer
Claremont McKenna College

Massive deep-sea gorgonian Primnoid corals live for up to hundreds of years, forming a solid, layered axis with alternating bands of calcite and gorgonin skeletal material. They are abundant on the outer continental shelf and upper slope on the USA west and Alaskan coast, providing significant habitat for fish and invertebrates. Yet, despite the ecological importance of these corals, logistical difficulties in collecting deep-sea colonies limits our knowledge of their growth characteristics, particularly in younger specimens. As a result, understanding recovery of coral ecosystems after disturbance is difficult. Here, we evaluated relationships between growth rates and gross morphological characteristics in three Primnoid colonies collected from depths of 100-350 m off the Alaskan coast. We determined 1) colony ages using complimentary 210Pb and 14C measurements, 2) the number of skeletal bands by counting the bands physically and in digital images, and 3) gross morphology biometrics. From these measurements, we calculated changes in growth rates of the colonies through time, banding periodicities, and relationships between ages and growth rates, and coral biometrics. The colonies dated to less than 75 years old. Radial and linear growth rates decrease logarithmically with age indicating that the growth and size of the colonies plateau overtime. Band counts varied systemically between the two counting methods such that physically peeling off sequential layers generated higher band counts than were evident in photographs of a colony cross section. Depending on the counting method used, the average banding periodicity ranged from 8-22 bands per year. Results suggest that in situ age estimates based on gross morphology can yield minimum but not maximum colony age. Relative consistency among band counts provides a non-destructive method for determining ages of physically collected and cross-sectioned specimens. This work refines techniques for age determination of deep-sea corals with the goal to improve our estimates of the vulnerability of Primnoid ecosystems.

## Ecology, distribution and time-series analyses of mesophotic and deep-water coral assemblages on a tropical island slope, Isla Roatán, Honduras

Peter Etnoyer, Charles Messing, Karl Stanley, Tomasz Baumiller, Thomas Shirley
NOAA National Centers for Coastal Ocean Science, Nova Southeastern University, Roatan Institute for Deepsea Exploration, University of Michigan, Texas A&M University- Corpus Christi/Harte Research Institute

The Meso-American Reef in the western Caribbean Sea extends from Bay Islands of Honduras to Yucatan Channel of Mexico, from depths of 20 m to over 3500 m. The tropical island slope is incised by submarine channels and canyons with exposed hard substrate. Shore-based submersible operations since 2008 have allowed examination of megabenthic assemblages associated with these features, working in a small area along the island margin of Isla Roatán from depths of <100 to 750 m, including repeated observations of the same organisms. The sessile habitat-forming taxa were predominantly deep-sea corals and sponges. Crinoidea were also abundant and diverse. At least 15 morphological species of corals were observed, including large (> 1 m) octocorals in families Plexauridae, Primnoidae, Coralliidae, Isididae, and Ellisellidae. There were fewer colonies and taxa among the Antipatharia, Zoanthidea, and Scleractinia (Lophelia prolifera, Dendrophyllia alternata, Madracis myriaster, and solitaries). Epifaunal assemblages associated with corals include 24 macroinvertebrate species (e.g., Asteroschema laeve (Ophiuroidea) and Chirostylus sp. (Decapoda: Brachyura). The highest highest diversity of epifauna was observed on Plumapathes sp. octocorals and D. alternata stony corals. Coral taxa exhibit vertical zonation as expected (e.g., Nicella in 100-200 m; Paramuricea in 300-700 m), but many were observed only in restricted microhabitats within their depth ranges, associated with specific

topographic features and presumably different near-bottom hydrodynamic conditions. Repeated observations of octocoral colonies showed predation, regeneration, and epibiont host fidelity, as well as a multi-year decline of a Paramuricea octocoral and loss of its resident ophiuroids. The shore-based submersible provides a relatively inexpensive platform from which to carry out time-series observations of otherwise rarely visited mesophotic and deep coral assemblages.

## Ecological Role of Patchy Cold-Water Coral Habitats in Submarine Canyons of the Bay of Biscay

Lenaick Menot 1, Inge MJ van den Beld1, Sophie Arnaud-Haond1,2, Jean-François Bourillet3, Jaime S. Davies1,4, Brigitte Guillaumont1, Karine Olu1
1 Ifremer, Centre de Bretagne, REM/EEP/LEP, France, 2 Ifremer, Station de Sète, UMR MARBEC, France, 3 Ifremer, Centre de Bretagne, REM/GM, France, 4 University of Plymouth, United Kingdom

In the Bay of Biscay, Cold Water Coral (CWC) habitats have been mapped in 24 out of a hundred known submarine canyons. The footprint of ROV or towed-camera transects is small compared to the size of these canyons but still, known CWC habitats totalize a linear of 46 km. The distribution of these habitats, dominated by reef-building scleractinians, antipatharians, alcyonaceans and pennatulids, is however patchy and their median size is small, ranging from 6 to 65 m. While the preservation of these Vulnerable Marine Ecosystems has become essential, all CWC habitats will not be benefit from conservation strategies due to their widespread and patchy distribution. Priorities must thus be defined. Among the criteria for such prioritization, we explore here the ecological role of CWCs as ecosystem engineers.The abundance, the diversity and the taxonomic composition of megafaunal assemblages associated with each CWC habitat are compared. Scleractinian reefs, antipatharians and alcyonaceans on hard substrates as well as pennatulids on soft substrates host different megafaunal assemblages and each should be considered as separate management units. Within each of these three units, we further test the influence of coral cover or coral density, as well as the influence of patch size, on the abundance and the diversity of the associated fauna. In the different habitats, the megafauna shows different patterns according to coral cover, coral density and habitat size, suggesting that aggregations of CWCs do not all have the same ecological role within submarine canyons. The consequences for conservation prioritization are discussed.

## Black Coral Garden on the Summit of Middle Bank (Hawaii)

Tina Molodtsova, Christopher Kelley, Meagan Putts
Shirshov Institute of Oceanology RAS

The Hawaiian Archipelago is one of the best surveyed areas for black corals (Antipatharia) in the world. Until now, 8 species of black corals have been reported from depths shallower than 150 m and at least 12 species have been sampled or have been recognized from underwater imagery below this depth. During the 2015-2017 CAPSTONE project conducted by the NOAA ship Okeanos Explorer, the Papahānaumokuākea Marine National Monument and adjacent areas were intensively explored, resulting in a significant amount of new information on the distribution and depth range of black corals in Hawaii. An enigmatic pinnacle located on the summit of Middle Bank was selected as a target in 2015 to explore fish and invertebrate boundary communities and habitat suitability for true corals. However, the dive on this site had to be postponed until September 2018 (dive 20 of EX1708) due to the weather and logistic problems. Surprisingly, the ROV transect from 475 m to 355 m found that the most important group of suspension feeders was Antipatharia with very few other corals presented. Three of four black coral species had not been reported in the

Hawaiian Archipelago before. One of them, Antipathella sp. (Myriopathidae), formed a dense monospecific coral garden near the top of the pinnacle, where a significantdiversity of fish species was also documented.. Similar communities formed by a single species of the genus Antipathella in SCUBA depth ranges has been reported from the Fijorland (New Zealand), Callabrian coast (the Medditerranean Sea), Azorez, Ouessant Island (the Bay of Biscay) and also in slightly deeper waters (100-150 m) off Saint Paul and Amsterdam Islands (Southern Indian Ocean). We discuss monospecific coral gardens formed by other species and also patterns of distributions and depth ranges of black corals of Hawaii and adjacent areas.

## Reproductive traits of the cold-water coral *Dendrophyllia cornigera* (NE Atlantic)

Albert León, Alfredo Veiga, Amalia Grau, Patricia Puerta, Covadonga Orejas
Instituto Español de Oceanografía.

Dendrophyllia cornigera, Lamarck (1916) is a scleractinian coral with Mediterranean and Atlantic distribution. This species inhabits mostly hard bottoms and the bathymetric distribution known for this species ranges from 70 to 500 meters depth. Despite its importance as ecosystem engineer nothing is known about its reproductive traits and gametogenic cycle.We studied the reproductive biology of Dendrophyllia cornigera analysing histologically specimens sampled in Costa da Morte (off Galicia, NE Atlantic, Spain). Samples have been collected in spring, summer and autumn of 2017. The collection of samples in the winter season was not possible due to the rough weather conditions in the sampling area. However, reproductive studies on cold-water corals rarely present results from all year seasons consequently having specimens from three seasons allows a good insight in the reproductive dynamics of the species.Here we present the results of the study on Dendrophyllia cornigera reproductive traits and the gametogenic cycle of this cold-water coral species. This is the first time that the reproduction of this species is being studied. The results are discussed in the light of the reproductive characteristics of other cold water coral species.

## Evaluation of the fertility of deep-water corals in southeastern Brazil

Nathalia Bastos (1,3), Halesio Barros (2), Ricardo Coutinho (3)
(1) PhD student of Postgraduation Program in Ocean and Earth Dynamics UFF/DOT (2) Research and Development Center CENPES/PETROBRAS (3) Department of Marine Biotechnology IEAPM/Brazil Navy

Habitat formers with high spatial complexity, deep-water corals create environments with high ecological importance. Anthropogenic activities, such as bottom trawling, oil and gas production and ocean acidification have been the major drivers of degradation of these ecosystems. In Brazil, due to logistical restrictions and high costs involved in studies of these organisms, the knowledge of aspects of these corals biology is still limited. Recently, a study on the complete gametogenesis cycle of the four main species of habitat formers corals in Brazilian waters (Madrepora oculata, Solenosmilia variabilis, Lophelia pertusa and Enallopsammia rostrata), has generated important information about reproductive activity. That previously work provided us the basis for new studies on the fecundity of the same species as a clue to further understanding of the reproductive biology of these species. Studies of coral fecundity are of high relevance for better understanding the negative impacts that these ecosystems may be exposed to. We aim to estimate the reproductive effort of the corals on different depth ranges in three sedimentary basins of the Brazilian coast, based on data from the production of female gametes, obtained through

sequential cuts of the polyps. The number of mesenteries, volume, area and height of the polyps with the rate of production of gametes (fecundity) will also be compared. Preliminary results will be presented and will contribute to expand the knowledge of these environments providing greater information on the life strategies of these corals and helping to set better management actions regarding conservation goals. Brazilian state-owned energy company (PETROBRAS), is the funding granter of this study, wich is a technical cooperation agreement between it's Research and Development Center (CENPES) and the Brazilian Navy's Sea Studies Center (IEAPM).

## Polyp to Population: A Tale of Two Corals

C. Tyler Fountain, Rhian G. Waller, Peter J. Auster
University of Maine

Deep-sea corals are of conservation concern in the North Atlantic due to prolonged disturbances associated with the exploitation of natural resources and the inevitability of a changing environment. Subsequently, understanding the resilience and recovery of deep-sea coral communities are of heightened interest and importance. Reproduction is a central component for adaptation and response to change, and recovery rates are suggested to be on the order of decades to millennia, based on the slow growth and longevity of deep-sea corals. In 2014 and 2017, two research cruises in the Gulf of Maine collected samples of two locally dominant species, Primnoa resedaeformis and Paramuricea placomus. These specimen collections were coupled with video surveys, conducted by remotely operated vehicles (ROVs), and used in conjunction with paraffin histologic technique. This study establishes an understanding of local scale gametogenic variability between coral subpopulations within the Gulf of Maine. By investigating relationships between morphology and reproduction, this study also provides the data necessary for producing size relative reproductive models, used to quantify whole colony reproductive potentials and estimate population scale reproductive potentials. This will allow for future survey work to use colony heights as a proxy measurement for estimating the reproductive output of these coral habitats. In addition, previously published data on growth rates provided a means of calculating the size of first reproduction in these species. As a result, these combined data strengthen our fundamental understanding of the reproductive ecology of deep-sea corals, and will help to further identify key source populations to protect and mitigate future damage and thus facilitate recovery.

## Identification of the black coral family Antipathidae (Cnidaria: Antipatharia) using a multi-faceted taxonomic method

Poppy Keogh, Raissa Hogan, Louise Allcock
National University of Ireland, Galway

Black corals are a well-known component of the Whittard Canyon deep-sea fauna and in some areas the family Antipathidae is the most abundant taxon, representing more than 75% of all the species. A multi-approach taxonomic method is implemented to identify members of family Antipathidae, which are a key group in the black corals. This particular group is notorious for its high levels of variance within the species themselves. This research uses in situ photographs from ROV images, scanning electron micrographs as well as morphometric measurements of the corallum and spines to identify a collection of 24 Antipatharia specimens. Two specimens were identified as Antipathes dichotoma due to their branch angles of 90°, the single series of polyps on small branches and the multiple series on larger branches. Eight specimens were identified as Stichopathes gravieri by the unbranched corallum and the single row of polyps on the axis, as well as by the number of spines rows visible from one side. A group of five specimens were identified as Stichopathes aff.

gravieri due to their shared traits with S. gravieri. These specimens are branched and so could not be identified as S. gravieri. The use of morphometrics is key in the revision of taxonomy for families such as Antipathidae. Due to the difficulties with genetic analysis of the class Anthozoa the use of morphological characterisation plays a valuable role in identification. There was a significant correlation between the collection depth and the diameter of the corallum, revealing that corals with smaller coralums tend to be found at greater depths. This could be due to environmental factors, such as current speed. If this correlation is found to be consistent, it could potentially be used as a way of classifying deep-sea black corals.

## Habitat Suitability Mapping for Southern California Bight Deep Sea Corals and Sponges

NIssa Kreidler, Andre Buchheister, Mark Henderson
Humboldt State University, NOAA

Deep-sea coral and sponge species (DSCS) are some of the longest-lived marine species and their complex, three-dimensional structure provides habitat for demersal fish and invertebrates. Until recently, the relationship between DSCS and fish species in the Southern California Bight was not fully understood; however, recent work on benthic assemblages in Southern California revealed relationships between several DSCS and demersal fishes. Habitat suitability maps, which predict where these DSCS species may occur, are needed to understand what areas of suitable habitat are currently protected and what areas are still exposed to potential destruction. In this study, we used Generalized Additive Models (GAMs) to identify environmental factors that are the best proxies for predicting DSCS occurrence. We explored seven main categories of environmental variables which have been hypothesized or demonstrated to affect the distribution of DSCS species of interest. These variables include (1) bottom currents using Regional Oceanographic Modeling System, (2) temperature, (4) depth, (5) seafloor slope, (6) surface primary productivity, and (7) dissolved oxygen. All variables were chosen due to their influence on DSCS physical and/or metabolic needs. We then used these models to develop habitat suitability maps for several species of DSCS that were associated with increased occupancy of 26 species of demersal fishes. These maps expand the current knowledge of DSCS distributions in southern California and provide a tool to inform management decisions, such as where to draw boundaries for new areas of conservation and protection.

## First assessments of a poorly known deep-sea coral fauna: the Northern Brazilian Slope

Carlos Daniel Perez 3, Ralf T.. Cordeiro
Centro Academico de Vitoria, Universidade Federal de Pernambuco

Deep-sea coral communities are poorly known in the Southwestern Atlantic (SWA), particularly within the Northern Brazilian Slope (NBS). Such gap has lead to the notion that the latter hosts low species richness when compared with southern regions. Surveys carried out at the Potiguar Basin (BPot), Rio Grande do Norte State, in 2011, from 25 trawl stations, yielded at least 51 coral species, of which 28 are octocorals, 16 scleractinians, and seven antipatharians. As results, five new records are reported for the SWA (Stephanocyathus coronatus, S. laevifundus, Nicella gracilis, N. spicula and Riisea paniculata) and seven are documented for the first time in NBS (Desmophyllum dianthus, Caryophyllia barbadensis and Caryophyllia berteriana). The upper slope communities showed the highest richness, with 27 species, in dense scleractinian-octocoral-antipatharian agregations. Lower slope is less diverse, with six species recorded, all soft-

bottom associated. In comparison with southern Brazil, from which 25 species were recently sampled from 28 stations, our results recorded 51 species in 25, indicating a higher richness in the NBS. A preliminary zoogeographic analysis shows a continuous faunal composition from ~3°S to ~19°S (NBS and Eastern Brazil), with more than 60% of species shared with the Caribbean region. The southern Brazilian region has a more Antarctic and cosmopolitan fauna. Topographic heterogeneity and proximity to the Caribbean fauna may influence the species richness found in NBS, which is still underestimated. Based on our results, we suggest that the NBS is potentially hosts the most diverse deep-sea coral fauna in Brazil. Oil and gas exploration and small-scale fisheries are the main economic activities in the NBS. In face of new and old threats to these vulnerable ecosystems, the persistent paucity of knowledge reinforces the need of urgent research efforts for better mapping and describing the diversity of the Brazilian fauna.

POSTER 103 - Corals
TUESDAY Evening • 17:45 • Serra Ballroom

## Stylasterid corals in the deep sea of New Caledonia region

Daniela Pica 1, Stefania Puce 1, Sarah Samadi 2 and Magalie Castelin 2
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Stylasterid corals are calcified hydroids living mainly in the deep sea where they represent an important component of the coral community. To date 321 species belonging to 29 genera have been described but information about their ecology and biology are still scant. Stylasterid species are worldwide distributed and the area of higher abundance is the south west Pacific. In fact, one third of the known species have been described in New Caledonia and New Zealand waters. Moreover, 12 species belonging to 6 genera have been exclusively recorded from this area. Recently, new Stylasterid specimens have been collected in New Caledonia by the Tropical Deep Sea Benthos program through KANACONO and KANADEEP deep-sea cruises (100-1500 m). The first cruise provided samples from the northern Norfolk Ridge seamounts and the southern slopes of New Caledonia, whereas the second cruise provided samples from the Lord Howe Ridge and the adjacent Lansdowne-Fairway Banks. Preliminary analysis of the material has led to the identification of 18 genera and 106 species, including several potential new species. Although the two cruises held similar numbers of stations (138 vs. 139), KANACONO turned out to be particularly rich with 15 genera and 78 species, while a total of 12 genera and only 49 species was found in KANADEEP. Overall, only 9 genera and 21 species co-occurred on the two studied areas suggesting a high level of endemism. Moreover, many species have been observed in symbiosis with other metazoans, such as polychaetes, Pedicularia snails, crustaceans, and in some cases, the association is responsible of huge changes in the coral morphology. Molecular analyses are underway to investigate: (i) the taxonomic diversity and phylogenetic relationships of the stylasterid species of New Caledonia; (ii) their respective dispersive capacities across the seamount ridges; and (iii) the role of the symbiosis in the coral plasticity.

POSTER 104 • Corals
TUESDAY Evening • 17:45 • Serra Ballroom

## Black corals of the Whittard Canyon, Ireland

Raissa Hogan (1), Giulia La Bianca(2), Marina Wirth(3), Martin White(1), Louise Allcock(1)
(1) Ryan Institute, National University of Ireland, Galway, Ireland; (2) University of Plymouth, UK; (3)University of Kiel, Germany

In parts of the Whittard Canyon, a submarine canyon on the Irish Atlantic margin, black corals (order Antipatharia) are remarkably common. Antipatharians are widely distributed in all oceans and occur in water depths from just a few meters down to >8000 m. During cruise CE14009 of RV Celtic Explorer to Whittard Canyon in June 2014, we collected HD image data and black coral samples for taxonomic and genetic work (not yet complete), using ROV Holland I. We have analysed 65 hours of HD videos from seven ROV dive events in depths ranging from 580 to 2820 m, and recorded more than 2000 black coral specimens. Two ROV dives, each 8 – 10 hours long, climbing from depths of approximately 1400 m to 900 m, and 1100 m to 900 m, and a third 15-hour dive, climbing from 1400 m to 600 m, each recorded more than 500 black coral specimens. Preliminary estimates of density and data on black coral distribution based on these three dives and four other dives that revealed fewer specimens suggest that Stichopathes is by far the most abundant genus, representing 1,550 of all records. However, there were also more than 100 records of each of *Bathypathes*, *Parantipathes* and *Antipathes*. Working to identify black coral specimens that we collected, we present in situ photographs, light microscopy and SEM images of what appears to be 15 morphotypes of black corals, represented by one species of each of the genera *Antipathes*, *Dendrobathypathes*, *Telopathes* and *Trissopathes*, two species of *Leiopathes*, *Parantipathes*, *Stichopathes*, and *Stauropathes*, three species of *Bathypathes*. Molecular sequence data produced to date, based on mitochondrial intergenic regions, lack sufficient variation to effectively delimit species. Understanding what drives their spatial distribution is paramount to ensuring future protection of these vulnerable taxa.

POSTER 105 ⚡ Corals
TUESDAY Lightning Talks • 08:30 • Serra Room

## Overlooked diversity of mesophotic (coral) ecosystems

Erin E. Easton1,2, David Hicks1, Javier Sellanes2, Ariadna Mecho2
1University of Texas Rio Grande Valley; 2Ecology and Sustainable Management of Oceanic Islands

Mesophotic coral ecosystems (MCEs) are defined as reef communities characterized by the presence of light-dependent (zooxanthellate) corals and associated fauna at depths below 30 m. These communities can extend to over 150 m in tropical and subtropical regions, and have been understudied worldwide compared to their shallow- and deep-water counterparts. Despite an increase in research focused on obtaining basic information on MCE distribution, biodiversity, and ecology, substantial data are lacking on variation in communities with depth, within and among regions, and connectivity both among MCEs and between MCEs and their shallow- and deep-water counterparts. In addition, many studies limit their consideration of MCEs to those < 150 m depth and those with zooxanthellate corals. This narrow definition results in substantial diversity being overlooked at other mesophotic communities, which harbor substantial biodiversity that remains comparatively understudied. Here, we present preliminary data on the biodiversity of mesophotic coral ecosystems of the South Texas Banks and the southeast Pacific, including those of Easter Island, Desventuradas, and Juan Fernandez Archipelago and the shallow seamounts surrounding these islands. These data reveal unprecedented depth records for coralline algae and numerous new species reports, including potential new species.

# Deep-ocean stewardship - TALKS

Deep-ocean stewardship - ABSTRACT 8
FRIDAY Morning • 09:45 • San Carlos Room

## Linking climate change to societal issues in the deep ocean

Lisa A. Levin, Maria Baker, Marina Careirro Silva, William Cheung, Ana Colaco, Daniel Dunn, Ron Etter, Nadine LeBris,

Telmo Morato, Craig Smith, Tony Thompson, Cindy Van Dover, Chih Lin Wei, Joana Xavier
Scripps Institution of Oceanography

Despite relatively limited observation of both climate change (warming, acidification, deoxygenation, POC flux) and faunal biodiversity in the deep ocean, there is a growing societal need to understand how future environmental change will modify deep-sea habitats, ecosystems and the functions and services they provide. This talk provides 3 examples, where earth system model climate change projections and basic scientific research are employed to address specific questions in the service of climate policy and deep seafloor environmental management. (1) The Intergovernmental Panel on Climate Change (IPCC) special report on Oceans and Cryosphere addresses the nature of climate change, the responses of ecosystems, and consequences for ecosystem services in all marine ecosystems including the deep ocean. (2) The strategic environmental management plan in the Atlantic Basin (SEMPIA) for deep seabed mining of massive sulfides incorporates projected climate change as part of a representivity assessment for different protected area scenarios (APEIs). (3) In the realm of high-seas deep-water fishing, the FAO has teamed with DOSI to examine the effects of climate change on deep-sea habitats, fish and fisheries. All of these studies identify major gaps in our ability to interpret the consequences of changing environment on deep-sea ecosystems. There will be additional needs by the Biodiversity Beyond National Jurisdiction (BBNJ) treaty negotiators for deep climate information to guide the development of MPAs and EIAs for the high seas. New deep-ocean observing efforts are needed that addresses the nature of physical and biogeochemical change, biotic responses at the population, community and ecosystem levels, and the resulting decreases or increases in ecosystem functions. By working with the UNFCCC/IPCC, ISA, FAO, and the IOC deep-ocean scientists can make important contributions to global, sustainable policy development.

Deep-ocean stewardship - ABSTRACT 70
FRIDAY Morning • 10:00 • San Carlos Room

## A habitat classification to support spatial planning associated with deep-sea mining

Kirsty McQuaid, Martin Attrill, Adrian Glover, Daniel Jones, Erik Simon-Lledo, Kerry Howell
Plymouth University

The reality of deep-sea mineral exploitation is edging ever closer, and with this comes a global responsibility to ensure adequate protection of marine life for future generations. In order to conserve biodiversity, spatial planners need insight into the distribution of the species, assemblages or features they are trying to protect. However, areas targeted for deep-sea mining are often large and remote, particularly in the case of polymetallic nodule mining. Although there has been much exploration in recent years to identify organisms living on the abyssal plains of the Clarion-Clipperton Fracture Zone (CCZ), there are still vast areas in this region that remain undiscovered, and this makes spatial planning difficult. In areas like this, where there is poor biological data, environmental surrogates can be used to represent biological diversity and predict where different habitats will be found. We present a top-down, broad-scale habitat classification of the CCZ based on a hierarchical clustering of oceanographic and topographic variables, Particulate Organic Carbon flux to the seafloor and nodule density. The classification identifies 46 habitats within the region, and can be used to assess representativity of the current protected area network, acting as a useful tool to support spatial management of nodule mining. A major assumption of these methods is that the habitats produced through this classification are representative of underlying biological diversity, and this will be tested through the analysis of historical image data collected across the region.

Deep-ocean stewardship - ABSTRACT 26
FRIDAY Morning • 10:15 • San Carlos Room

## The effect of research effort on global biodiversity and anthropogenic risk at deep-sea hydrothermal vents

Andrew Thaler
Blackbeard Biologic

Seafloor mining is emerging as one of the leading anthropogenic threats to deep-sea hydrothermal vent ecosystems, yet international regulation of seabed mining is in its infancy. Deep-sea hydrothermal vents represent a collection of ecosystems that vary extensively in species composition, abundance, and biodiversity. This presents a challenge in anticipating the potential short- and long-term impacts of deep-sea mining on vent ecosystems.The impact of that biodiversity loss to regional and global vent systems depends on the resilience of surrounding vent communities, the degree of connectivity between vent systems, and the biodiversity of these ecosystems. Global assessment of biodiversity at deep-sea hydrothermal vents is confounded by uneven sampling effort. Some vent systems have been visited hundreds of times by research vessels from multiple nations, while others have been visited by fewer than ten research expeditions. This broad disparity in sampling effort makes it difficult to directly compare biodiversity between different vent systems, and, in some cases, entire biogeographic provinces. Consequently, a biodiversity-based model for prioritizing deep-sea mining sites will favor well-studied vent systems.How is the known biodiversity and species richness of hydrothermal impacted by sampling effort? What inferences can be made about the relative resilience of hydrothermal vent ecosystems based on biodiversity and species richness? Can biodiversity be used to inform the potential impact of deep-sea mining at relatively understudied vent systems?An accurate assessment of global deep-sea hydrothermal vent biodiversity normalized against research effort is critical in informing long term, multi-stakeholder approaches to managing the nascent deep-sea mining industry.

Deep-ocean stewardship - ABSTRACT 359
FRIDAY Morning • 10:30 • San Carlos Room

## Scoping the value of additional deep-sea Marine Protected Areas in the seas around Scotland, UK

Alice Cornthwaite
Joint Nature Conservation Committee

The government's programme for Scotland 2017-18 includes a commitment to 'evaluate options to create a deep-sea national marine reserve'. The designation of a deep-sea reserve would complement the existing marine protected area (MPA) network in Scottish waters and provide legal framework for the protection of additional vulnerable deep-sea marine habitats and species against emerging threats. A study area of 174,000km2 has been identified in offshore Scottish waters, following the 800 metres depth contour on the continental shelf break and within the Exclusive Economic Zone. Deep-sea habitats, species and large-scale features of biological and conservation importance, such as deep-sea sponge aggregations, seamounts, and deep-sea species of shark, are known to exist within Scottish waters. Deep-sea features of interest, which are thought to be suitable for designation, have been identified using OSPAR Threatened and/or Declining Species and Habitats, ICES Vulnerable Marine Ecosystems and the Scottish Priority Marine Feature lists. Work is underway to collate, synthesise and present information on the presence, distribution and range of these features within the study area. Using data from survey and literature reviews, information on species life history characteristics and the biotic and abiotic drivers of feature distribution within the study area is being explored. Preliminary results suggest many deep-sea features identified would be suitable for assessment against MPA selection criteria, due to their function significance, degree of natural biological diversity and/or status of being under threat from human activity. The challenges faced centre on difficulties in collating evidence in the deep-sea and the paucity of available information for many species. Questions including how to monitor change within a deep-sea MPA need to be addressed.

FRIDAY Morning • 10:45 • San Carlos Room

## Exploring the Seafloor to Achieve Deep-Sea Habitat Conservation Victories off the US West Coast

Geoffrey Shester, Ben Enticknap, Erin Kincaid, Ashley Blacow, Mariel Combs, Jon Warrenchuk, and Susan Murray
Oceana

In 2006, the U.S. National Marine Fisheries Service adopted sweeping protections in federal ocean waters off the U.S. West Coast to protect Essential Fish Habitat. Based on proposals from the conservation group Oceana, the approach freezes the bottom trawl footprint on a precautionary basis and designates a network of conservation areas to protect priority habitats sensitive to bottom trawling. Between 2010-2016, the conservation organization conducted seafloor expeditions using remotely operated vehicles at six sites along the U.S. West Coast from Southern California to the Salish Sea, in support of a proposal to designate new and expanded Essential Fish Habitat Conservation Areas that offer long-term protection from trawling in federal waters. We analyzed video footage to characterize physical substrate, biogenic habitats such as corals and sponges, and managed fish and invertebrate species. The proposal also includes new discretionary measures to protect the deep-sea ecosystem at depths greater than 3500 m within the US West Coast Exclusive Economic Zone from all bottom contact fishing. In April 2018, the Pacific Fishery Management Council is scheduled to take final action, and we will present the outcome of their decision. Seafloor expeditions not only advance the science of seafloor ecology and habitat distribution, but also provided compelling information in support of policy changes that advance the conservation of seafloor biodiversity while maintaining the productivity of groundfish fisheries. We provide recommendations for expedition design, advocacy, and communications strategies to more effectively link scientific exploration to policy change.

FRIDAY Morning • 11:00 • San Carlos Room

## A deep-sea mining decision-making process using the Guided Interactive Statistical Decision Tools

Aharon Fleury, Tom Stockton, Paul Black
Neptune and Co, Inc

The International Seabed Authority regulations on exploitation for mineral resources states 'risk assessments are fundamental to the effective implementation of the Environmental Regulations/ EIA process,' which inherently necessitates decision making by stakeholders in the future. For deep-sea mining, stakeholders may include scientists, governments, the international seabed authority, deep-sea mining companies, and the public. Neptune and Co, Inc. has created the Guided Interactive Statistical Decision Tool (GiSdT) to implement a value-focused approach to structured decision making with an emphasis on stakeholder involvement to advise future risk assessments. GiSdT combines value-focused thinking with Bayesian decision analysis to provide a quantitative framework whereby all aspects of a decision problem can be addressed quantitatively, and hence, defensibly, transparently and traceably. The goal of GiSdT is to provide access to useful or usable methods and approaches for solving complex decision problems (e.g. the deep-sea mining) that may be applicable with multiple stakeholders. GiSdT provides an effective and user-friendly interface to decision methods and approaches that empower decision-makers to explicitly and routinely incorporate all aspects of problem solving into their decision-making. GiSdT is an open source web application that provides the tools needed to address the relevant components of a deep-sea mining-based decision problem, including describing the decision landscape, translating that landscape into goals and objectives, valuing the measureable attributes that describe each

objective, identifying decision options and addressing the uncertainty in the impact of options (e.g., biodiversity) on attributes (e.g., environmental risk) through appropriate probabilistic models using Bayesian Networks. In addition to addressing these quantitative technical components, the GiSdT program is aimed at facilitating stakeholder involvement so that the perspectives, values, and objectives of all relevant stakeholders are addressed explicitly in the decision making process. Here we present an example focusing on deep-sea mining utilizing GiSdT in the decision-making process.

FRIDAY Morning • 11:15 • San Carlos Room

## Selective commercial line fishing and biodiversity conservation co-exist on seamounts in a deep-sea marine reserve

Alan Williams, Judy Upston, Mark Green, Ken Graham
CSIRO

Enhanced socio-economic and conservation outcomes for both an existing fishery and a new deep-water marine reserve network off eastern Australia were achieved by identifying additional options for conservation managers. Commercial power hand-line fishing was able to continue on productive seamount fishing grounds within the reserve because new information enabled boundaries and zoning proposed in the reserve's draft Management Plan to be revised and consistent fisheries regulations to be formulated. The draft plan would have removed access to fishing grounds that provide approximately 25% of the annual regional Australian total allowable catch of the premium fishery species, Blue-eye Trevalla (Hyperoglyphe antarctica). Day-time power handline fishing in 280-550 m depths avoided Harrisson's Dogfish (Centrophorus harrissoni) – the primary species of conservation concern – because the shark is a diel vertical migrator, residing deeper than Blue-eye during the day before ascending to shallower depths at night to feed on micronekton. These results, together with expectation of low mortality of any incidental dogfish bycatch and low impacts on benthic habitats, supported changes to management arrangements which preserve the seamount Blue-eye fishery worth approximately A $1M annually whilst protecting more seamounts and greater areas of benthic habitat in the restricted 200-700 m depth range. Research uptake was facilitated by clarifying policy options at a critical stage in the planning process. This required having clearly articulated management objectives that aligned conservation and fishery imperatives, involving knowledgeable fishers in making robust field observations to address specific knowledge gaps and management needs, and identifying the requirements for ongoing fishery monitoring that addresses remaining management uncertainties. This potential to identify win-win outcomes in marine planning processes provides some general signposts for future policy decisions as marine reserve networks are implemented and reviewed, and for scientists wanting to effectively engage in decision-making processes.

FRIDAY Morning • 11:30 • San Carlos Room

## Merging dance and science: An offbeat combination

Kyra Schlining, Fran Spector Atkins
Monterey Bay Aquarium Research Institute (Kyra); SpectorDance (Fran)

The Monterey Bay Aquarium Research Institute (MBARI) has been collaborating with the nonprofit SpectorDance on a project exploring ways to use dance as a novel mode of science communication. Featuring original choreography by local artist Fran Spector Atkins, the project, Ocean Trilogy, highlights the challenges confronting the world ocean and hopeful possibilities arising from cutting-edge science research. The program includes a live performance piece (customizable for a variety of audiences), associated presentations by an MBARI scientist, and student workshops investigating the process of expressing scientific content through movement and music. The performance weaves dance together

with underwater images, contemporary classical and rap music, and audio sound bites from interviews with MBARI scientists and other ocean experts. This blending of elements aims to reach audiences on sensory, intellectual, and emotional levels. Through a strategic partnership with Monterey County Free Libraries, the Ocean Trilogy project offers an innovative way to bring urgent ocean issues to underserved communities who might not otherwise have access to this type of exposure.

# Deep-ocean stewardship - POSTERS

POSTER 106 ⚡ Deep-ocean stewardship
TUESDAY Lightning Talks • 08:30 • Serra Room

## The Deep Ocean Stewardship Initiative - Advancing Science in Policy

Dr Maria Baker, Prof Lisa Levin, Kristina Gjerde, Harriet Harden-Davies, Elva Escobar
University of Southampton

The Deep Ocean Stewardship Initiative (DOSI) supports vital science-policy engagement efforts to safeguard the deep ocean as activity ramps up in national and international deep-ocean governance. Members of the DOSI community provide expert scientific input to ocean policy development processes such as those linked to a new UN treaty for biodiversity conservation in areas beyond national jurisdiction (BBNJ), the International Seabed Authority environmental regulations, regulation of deep-ocean fisheries and the habitats they affect and the international climate deliberations that are crafting rules that will define humankind's relationship with the deep sea for future decades. As an interdisciplinary network of >550 experts from 45 countries dedicated to maintaining the integrity and functions of deep-ocean ecosystems, DOSI provides a unique, independent platform for deep-sea science-policy engagement. Deep-sea ecologists and other stakeholders from across the globe need to be mobilized to be part of the process to ensure essential mechanisms are established, based on science, to manage and protect ocean resources.

POSTER 107 • Deep-ocean stewardship
TUESDAY Evening • 17:45 • Serra Ballroom

## Effects of sampling effort on species richness results at hydrothermal vents, and implications for building baselines.

Cobley, A (1,2), Glover, A.G.,(2) Copley, J.T.,(1) Baker, M.(1)
(1) University of Southampton, Waterfront Campus, Southampton, UK & (2) Natural History Museum, London, UK

Three mineral resource types are being explored on the seabed of national and international waters: polymetallic nodules, seafloor massive sulphides (SMS) and cobalt-rich ferromanganese crusts. The International Seabed Authority (ISA) is responsible for regulating Activities with regard to non-living resources on the seabed, ocean floor and subsoil thereof, beyond the limits of national jurisdiction ( "The Area"). The ISA has approved 29 exploration contracts to date, seven of which are SMS deposits around hydrothermal vents. Attractive for their high concentrations of Copper, Zinc, Cobalt, Gold and Silver, SMS deposits could be mined by 2019 in national waters.Hydrothermal vents host unique ecosystems that create hotspots of biomass in an otherwise food-limited environment. Since their discovery in 1977, a vast amount of research has dramatically advanced knowledge of vent ecosystem composition and function. However, there are still significant gaps in our understanding and many discoveries left to make.This project quantifies how sampling effort at individual vent fields affects species richness results. This is acheived by plotting and analysing species accumulation curves at individual vent fields. Datasets from recent UK expeditions with a large number of species records (e.g. East Scotia Ridge, Cayman Trough, South West Indian Ocean) are the initial focus. We

are also collaborating with others to include additional vents where datasets are comprehensive enough to allow similar analysis.This research is of particular importance to inform the current development of the ISA's recommendations and guidelines to deep-seabed mining contractors in the Area. If we determine the effect sampling effort has on the completeness of species richness estimations, recommendations for best-practice approaches to quantify baseline diversity at vent sites targeted for exploration and exploitation can be made.

POSTER 108 - Deep-ocean stewardship
TUESDAY Evening • 17:45 • Serra Ballroom

## Status of the environmental regulatory landscape of deep-seabed mining, and how to engage as experts

Cobley, A (1,2), Glover,A.G.,(2) Copley,J.T., (1) Baker,M.(1)
(1) University of Southampton, Waterfront Campus, Southampton, UK & (2) Natural History Museum, London, UK

Deep-seabed mining of hard mineral resources is close on the horizon. Three resource types are being prospected and explored in both national and international waters for their commercial metal values.: polymetallic nodules, seafloor massive sulfides (SMS deposits) and cobalt rich ferromanganese crusts. The International Seabed Authority (ISA) bears the mandate to organise and control deep-seabed mining in areas beyond national jurisdiction, and has currently entered into 29 contracts for exploration across all three resource types. The ISA is currently developing Draft Regulations on Exploitation of Mineral Resources in the Area as a part of their larger Mining Code, with more stakeholder consultations planned before final Council adoption and Assembly approval in July 2020. Major efforts are being made to bring expertise together on an international level to develop these regulations, as part of a toolkit to enable sustainable management of deep-sea ecosystems. This project synthesises the current international regulatory framework with regards to deep-seabed mining. Furthermore, it highlights avenues for the scientific community to engage with the development of ISA regulations and other environmental issues to ensure they are underpinned by best scientific evidence and practice.

POSTER 109 - Deep-ocean stewardship
TUESDAY Evening • 17:45 • Serra Ballroom

## Designating Marine Protected Areas in the deep-sea, the UK's experience to date

Alice Cornthwaite
Joint Nature Conservation Committee

The UK government is committed to establishing an ecologically coherent network of Marine Protected Areas (MPAs). To date, over 10 MPAs have been designated in UK water's which occur off the continental shelf break from depths of 200m to greater than 2200m. These cover a range of habitats and species listed for national and international importance, from seamount communities to deep-sea sponge aggregation and vibrant cold water coral reefs. This poster would examine the difficulties that have been faced by JNCC in collating the evidence required to support feature presence for designation and the ongoing challenges relating to management and monitoring feature condition in these deep-sea MPAs.

POSTER 110 • Deep-ocean stewardship
TUESDAY Evening • 17:45 • Serra Ballroom

## The deep sea and me: Development and evaluation of an exhibit to gauge public perception of Oregon's deep sea

Katherine D. Darr, Sarah Seabrook, Steven J. Dundas, Andrew R. Thurber
Oregon State University

The deep sea is the Earth's largest ecosystem and provides diverse benefits, termed ecosystem services, to mankind. A barrier to effective

management of marine resources, especially those in the deep sea, is a lack of understanding by society of the benefits received from the oceans. Although exploration and exploitation of the deep sea are increasing, the general public remains largely unaware of the diversity of deep-sea habitats and the services they provide. Here we ask how we can best communicate the importance of the deep sea to visitors at a public science center. We are using mobile Cyberlab tools to passively collect video and audio data of visitor interactions with an interactive video exhibit at the Hatfield Marine Science Visitor Center in Newport, Oregon. The facial detection and recognition capabilities of the Cyberlab enable us to calculate the duration of visitor interaction, a factor correlated with recall and retention. Additionally, custom filters allow for data collection so granular that we can count every time a visitor breaks a certain plane to determine how often they interact with a specific element of the exhibit. The exhibit, informed by numerous focus groups, is evaluated for efficacy through these passive, as well as active (pre- and post-visit surveys), approaches. These mechanisms allow us to understand visitors' learning behaviors, what parts of the deep sea they find interesting, and what specifically they are learning about the deep sea. Our ultimate aim is to find the most effective way to convey the services deep-sea habitats provide, while reinforcing ocean literacy principles. This project provides insight into how to effectively communicate information about the deep sea to an audience that likely has little to no prior knowledge of the ecosystem, yet who will be increasingly responsible for making use decisions of this habitat in coming years.

POSTER 111 ⚡ Deep-ocean stewardship
TUESDAY Lightning Talks • 08:30 • Serra Room
### Protecting the Deep-Sea: Geospatial Analysis of Pacific Essential Fish Habitat and Rockfish Conservation Area Changes
Ben Enticknap, B. Mecum, G. Shester, A. Blacow, E. Kincaid, M. Combs, S. Murray
Oceana
In April 2018, the federal Pacific Fishery Management Council took final action on a range of alternatives to protect over 140,000 square miles of marine habitats off the U.S. West Coast from bottom trawling and other bottom contact fishing gears. The fishery council's unanimous decision followed an intensive review of existing essential fish habitat (EFH) conservation areas closed to bottom trawling, bottom trawl fishing effort, and new science on the location and extent of priority habitat features like deep-sea corals, sponges, submarine canyons and rocky substrates. The decision reflects public proposals for new and modified conservation areas, including a comprehensive coastwide conservation proposal developed by the international marine conservation organization, Oceana, and its partners. Central to the success of this effort were comparative geospatial analyses prepared by Oceana examining the net change in habitat features protected under a combination of alternative scenarios designating new conservation areas, while simultaneously opening 'trawl rockfish conservation areas' that were closed while overfished species recovered. Using publicly available spatial data developed for the fishery council's EFH review and final action, we analyzed the extent of biogenic habitats, physical substrates and habitat for overfished groundfish protected at coastwide and regional biogeographic scales. Here we present the results of our Geographic Information Systems analysis of the fishery council's final combined deep-sea conservation area, EFH and rockfish conservation area recommendations, compared with current, status quo management. Once implemented by the National Marine Fisheries Service, the new U.S. Pacific West Coast deep-sea conservation area (123,172 mi2) and new essential fish habitat conservation areas (17,533 mi2), combined with opening the trawl RCA off California and Oregon (3,051 mi2), will result in 90% of the U.S. West Coast exclusive economic zone closed to bottom trawling, while maintaining and restoring significant bottom trawl opportunity.

TUESDAY Evening • 17:45 • Serra Ballroom
### Engaging Undergraduate Students in Live Deep-Sea Expeditions with the Okeanos Explorer
Tara Harmer Luke
Stockton University
Undergraduate students benefit from participating in hands-on research and access to new scientific discoveries. Telepresence enabled research cruises, such as those conducted by NOAA's Okeanos Explorer provide an excellent platform to engage undergraduate students in the discovery process of science. During the fall of 2017, I began a crowd-sourcing expedition annotation project with my undergraduate students in a course called Deep Sea Biology. This course is open to upper level undergraduate Biology and Marine Science students, and provides a comprehensive study of the diverse and unusual biological communities found in the deep sea. Over the course of 23 days in September, 29 students observed and recorded their observations of a series of live dives along the Musicians Seamounts, north of Hawaii during Okeanos Explorer expedition EX1708 Deep Sea Symphony: Exploring the Musicians Seamounts. Each student spent an average of 30 hours each watching the live ROV video feed with audio commentary by the on-board and shore-based science team from this expedition, and have developed a group document, including both text and screen-shots of dive images in the form of a wiki, describing all of the dives that occurred during this expedition. This annotation may be beneficial to future expeditions to the Musicians Seamounts, and can contribute to our body of knowledge about these ecosystems. While not as complete an annotation as that conducted by the science team involved in the expedition, students in an undergraduate setting can contribute to overall scientific knowledge in a meaningful way. In addition, this gives undergraduate students the opportunity to both to actively engage with course material in a way that increases interest and excitement in ongoing scientific exploration, and also the ability to disseminate scientific information to the general public.

POSTER 113 - Deep-ocean stewardship
TUESDAY Evening • 17:45 • Serra Ballroom
### What is the 'worth' of the deep sea to the public?
Sarah Seabrook, Katie Darr, Steve Dundas, Andrew Thurber
College of Earth, Ocean, and Atmospheric Sciences
The deep sea is likely to experience new and expanding uses and threats in the coming years, many of which can be impacted by public opinions influence on legislation. However, the role of the deep sea to society remains unknown to its stakeholders. This creates an opportunity to make significant advances in informing the public about an ecosystem that is integral to their lives while concurrently learning: 1) the value that individuals and communities place on this habitat and 2) what impacts the publics decisions about resource use and allocations at these depths? When answered, these questions can provide non-use and non-market values that can be used to inform policy and decision making by managers. We have addressed these questions through a series of focus groups and expert opinion inputs that we have conducted to develop a choice experiment survey ('instrument') focusing on the deep sea off of Oregon, USA. In this instrument we contrast the potential impacts of deep sea mining, altered fishing regulation, or oil and gas exploration after building a foundation of knowledge that allows informed decisions. In many cases the greatest challenges are presenting non-biased (or perceived non-biased) information at an 8th grade reading level in a format that will keep readers engaged. Here, we present the lessons learned through this process as they transcend this project and can help inform communication and engagement strategies. While our overall goal is an economic valuation of one state's deep sea habitats, we hope that this can be used to build a framework that can be used elsewhere to create a more holistic understanding of the values that the public places on the deep sea, its

functions and resources – aiding in the development of sustainable management strategies.

TUESDAY Evening • 17:45 • Serra Ballroom

## Developing effective outreach tools to communicate fishing impacts in Greenland

Chris Yesson, Kirsty Kemp, Mona Fuhrmann, Stephen Long, Nanette Hammeken, Martin Blicher
Zoological Society of London, Greenland Institute of Natural Resources

Fishing is the cornerstone of Greenland's economy. The Coldwater Prawn fishery alone accounts for almost half of the nations exports. However, some of the largest fisheries, are deep demersal trawl fisheries (Coldwater prawn depths 200-500m, Greenland Halibut depths 700-1400m). These have the potential to create significant negative impacts on benthic habitats. Conservation measures that involve restricting fishing access or adaptation of gear, requires support from the industry and the public at large, if these are to gain traction. Arctic deep seabed habitats are poorly known, even within fishing communities. Finding ways to communicate scientific findings and the ecological value of these habitats is vital for garnering support for conservation. We report on our efforts to share our findings from over 10 years of research on benthic biodiversity/habitats and deliver conservation messages to the Greenlandic public, through public engagement events, collaboration with a teacher training program, production of videos and notably the development of an online computer game. The game teaches sustainable fishing practise with regards to environmental impacts and involves the user fishing with scoring for catch and penalties for over exploitation and damaging vulnerable habitats. We describe the difficulties of delivering a complex and potentially controversial message with a simple, gamer-friendly approach.

TUESDAY Lightning Talks • 08:30 • Serra Room

## Going deeper: Fragments of hope in the deep sea.

Charles A. Boch, Andrew DeVogelaere, Erica Burton, Chad King, and James P. Barry.
MBARI and Monterey Bay National Marine Sanctuary

Ongoing human impacts on the deep biosphere have raised new questions about the sustainability of deep sea organisms. Deep sea coral communities function as critical habitats for a diversity of deep sea organisms and thus the loss of deep sea coral communities can have profound impacts throughout the deep sea food web. Unfortunately, documentation of trawling, deep sea mining, and oil spills are becoming more common as demands on the deep sea resources continue to rise. This raises an age-old question: can we restore what was lost or has become more vulnerable to continued negative impacts? Like any other ecosystem, possible restoration of deep sea corals through active rehabilitation remains a challenge due to costs, scale of work involved, and poorly understood factors involved in post-transplant survivorship. This latter part remains a technological limitation in all restoration practices to date and understanding how this can be done for deep sea organisms demands considerable attention even as a proof of concept. Here, we report lessons learned from ~3 years of deep sea coral transplant studies and discuss some of the steps needed to overcome current limitations.

TUESDAY Evening • 17:45 • Serra Ballroom

## Assessing the microbial ecosystem service impacts of deep sea mining

Beth N. Orcutt
Bigelow Laboratory for Ocean Sciences

Mineral deposits on the seafloor – such as hydrothermal vent chimneys, ferromanganese and cobalt crusts – support unique microbial and macrofaunal communities at the seafloor. Commercial ventures to exploit deep-sea mineral resources have accelerated substantially, despite international oversight and understanding of the impacts of this exploitation lagging behind. Although a community of scientists interested in seafloor macrofauna ecology have been engaged in this topic, the involvement of disciplines related to microbial ecology and biogeochemistry is somewhat deficient. In April 2018, with support from the Center for Dark Energy Biosphere Investigations and the Deep Carbon Observatory, a community of scientists met to define the microbial ecosystem services that should be considered when assessing potential impacts of deep sea mining, and to provide recommendations for how to evaluate these services. This presentation will present the outcomes and recommendations of this workshop.

# Deep-sea omics - TALKS

MONDAY Morning • 09:45 • Serra Room

## Genomics of habitat choice and adaptation to ocean depth

Michelle R. Gaither, Georgios A. Gkafas, Menno de Jong, Fatih Sarigol, Francis Neat, Thomas Regnier, Daniel Moore, Darren R. Gröcke, Neil Hall, Xuan Liu, John Kenny, Anita Lucaci, Margaret Hughes, Sam Haldenby, A. Rus Hoelzel
University of Central Florida

Marine species live in a complex three-dimensional environment. Substantial changes in species assemblages occur with depth but less is known about the impact of depth on intraspecific divergences. Here we generate an annotated genome assembly for the deep sea fish Coryphaenoides rupestris and combine this with re-sequencing and genome sampling data to show that fixed non-synonymous differences in functional loci distinguish individuals living at different depths, independent of horizontal distance. Our data indicate disruptive selection at these loci across only 800 m of depth, but no clear evidence for assortative mating as would be expected if there was incipient ecological speciation. We propose that individuals with distinct genotypes at relevant loci, maintained by strong selection, segregate by depth as they mature, and that these adaptive genotypes are likely associated with distinct phenotypic requirements at different depths. An important implication is that an evolutionary radiation could proceed rapidly by building on established intraspecific polymorphisms linked to resource partitioning in distinct habitats.

MONDAY Morning • 10:00 • Serra Room

## The (meta)genome of a single worm: Unexpected evolutionary and ecological insights from nematode -Omics

Holly M. Bik, Taruna Schuelke, Tiago José Pereira, Sarah M. Hardy
University of California, Riverside

Nematodes comprise 85-96% of all benthic meiofauna in deep-sea sediments, and in marine habitats this phylum is both abundant and speciose. Due to their ubiquity and high biodiversity, nematodes are likely to play key ecological roles in marine sediments, particularly in regard to nutrient cycling and food web dynamics. However, traditional (morphological) studies of nematodes and other meiofauna are time consuming and labor-intensive due to the small body size of these animals. Furthermore, most marine nematode species cannot be cultured, limiting the utility of lab-based experimental studies. Advances in high-throughput sequencing technologies (e.g. Illumina HiSeq/Miseq) and molecular

reagents (DNA extraction protocols and library preparation kits designed for low quantities of DNA) are rapidly facilitating the study of microscopic metazoa such as nematodes. Here, I will present recent work focused on reconstructing the (meta)genomes of individual nematodes isolated from global deep-sea sediments. Single specimens were extracted and morphologically identified via microscopy, followed by extraction of total DNA. Metagenomic sequencing as well as metabarcoding of the 16S and 18S ribosomal RNA genes was subsequently carried out on each individual specimen. The resulting datasets provide an unprecedented view of ecological interactions and evolutionary relationships amongst nematode morphospecies. Nematode 18S rRNA OTUs can be immediately linked to morphological voucher images and unveil cryptic species complexes. The combination of 16S and 18S rRNA provides information on the bacterial microbiome of nematodes as well as putative ecological interactions including prey items and parasitic associations. Finally, metagenomic data from each specimen provides an expanded suite of single-copy orthologous genes which can be used in conjunction with 18S rRNA to infer deep evolutionary relationships amongst deep-sea nematodes. This workflow enables a strong link between -Omics approaches and traditional (morphological) taxonomy, facilitating a rigorous and systematic exploration of nematode contributions to biological and ecological processes in the deep-sea.

Deep-sea omics - ABSTRACT 185
MONDAY Morning • 10:15 • Serra Room

## The sexually dimorphic visual system of lanternfishes (Myctophidae)

Fabio Cortesi, Fanny de Busserolles; Justin Marshall
The University of Queensland

Many deep-sea fishes are bioluminescent and the light they emit is used to either camouflage themselves (counterillumination) or to interact with prey (attraction or illumination), predators (distraction), and/or congeners (communication). In several of these species, the light emitting luminous organs are sexually dimorphic in that they are located on different parts of the body, differ in size and shape, and/or in the number of organs present. However, whether the light emitted by these luminous organs also differs in spectral composition and whether this could be used to distinguish between sexes is unknown. Here we present recent findings showing that not only the luminous organs but also the visual system is sexually dimorphic in some lanternfish species (Myctophidae). Specifically, we found a remarkable difference in the retinal morphology of females and males which is only found in species that are also sexually dimorphic with respect to their luminous organs. The investigation of the first fully sequenced lanternfish genome, further revealed the duplication and spectral differentiation of multiple rod opsin (Rh1) genes potentially conferring color vision to these fishes. Supporting a theory of color signal and color vision co-evolution in dimorphic lanternfish species, retinal transcriptomes revealed that sexually dimorphic fishes, which show differences in both luminous organs and retinal morphology, also express multiple rod opsin pigments that are distinct between sexes. Monomorphic species which do not differ in luminous organs or retinal morphology between species, on the other hand, were found to only express a single, identical rod opsin between sexes. These results therefore further support the long-standing hypothesis that some deep-sea fishes use their luminous organs for sexual communication and even highlight a possible private communication channel between potential mates.

Deep-sea omics - ABSTRACT 157
MONDAY Morning • 10:30 • Serra Room

## The evolution of bioluminescent light organs in deep-sea shrimp

Heather Bracken-Grissom, Danielle De Leo, Charles GoLightly
Florida International University

Deep-sea shrimp belonging to the family Sergestidae provide a unique system for studying the evolution of bioluminescence. Most species within the family possess several types of autogenic bioluminescent light organs thought to function in counterillumination (a form of camouflage) and congener recognition, while other species lack light organs completely. The driving force behind such a diverse range of luminescent adaptations remains unclear. The species that emit bioluminescence have one of three distinct forms of light organs including lensed photophores, lens-less photophores or internal Organs of Pesta. The Organs of Pesta are modified digestive glands that are morphologically diverse and often species-specific. However, the full functionality of these specialized gastric modifications and the magnitude of interspecific structural differences is poorly characterized. In addition to their ability to produce light, the family Sergestidae is remarkably diverse and abundant, constituting a significant proportion of animal biomass in epipelagic and mesopelagic waters. The wide range of morphological diversity across Sergestidae has resulted in major taxonomic revisions, dividing the two major genera (Sergia and Sergestes) into 15, based on morphology. Here, we capitalize on genomic data to construct an updated genus-level phylogeny of sergestid shrimp. DNA was successfully extracted from approximately 130 individuals belonging to 13 of the 15 newly proposed genera. We implemented a "genome skimming" approach which allowed us to capture full mitochondrial genomes and a suite of nuclear genes across 23 species. Additional individuals have been incorporated into the phylogeny through Sanger sequencing of both nuclear (H3, NAK, PEPK) and mitochondrial (16S and COI) genes. The resulting phylogeny was used to test the recent taxonomic revisions and trace the evolution of bioluminescent light organs across an important family of deep-sea shrimp. Findings from this study will provide valuable insight into complex systems vital to communication, defense, camouflage, and congener recognition.

Deep-sea omics - ABSTRACT 76
MONDAY Morning • 10:45 • Serra Room

## Deep-sea fishes use multiple rod opsins for vision

Zuzana Musilova, Fabio Cortesi, Michael Matschiner, Wayne IL Davies, Sara M Stieb, Fanny de Busserolles, Martin Malmstrøm, Ole K Tørresen, Jessica K Mountford, Reinhold Hanel, Kjetill S Jakobsen, Karen L Carleton, Sissel Jentoft, Justin Marshall, Walter Salzburger
Dpt of Zoology, Charles University in Prague

Vision in vertebrates is based on different visual proteins (opsins) in the cone and rod cells in the retina. Under dim-light conditions, mostly rod receptors are thought to mediate rather color-blind vision by expression of a single rod opsin gene (RH1), while the cones enable colour vision in substantial light intensity. By inspecting 101 fish genomes, we found that three teleost lineages from the dim-light environment of the deep sea have independently expanded their RH1 gene repertoire via gene duplication and subsequent functional diversification. An extreme case of the silver spinyfin (Diretmus argenteus) stands out with a total of 40 opsin genes in its genome (2 cone + 38 rod opsins), and has the highest number of visual opsins known for animals so far. We found that 14 RH1 genes are simultaneously expressed in the morphologically unique retina of D. argenteus. The in-vitro synthesis and functional prediction revealed that these genes encode for photopigments with different spectral sensitivities (λmax spanning 65 nm), covering efficiently the range of the residual daylight in the deep sea, as well as bioluminescence emitted from deep-sea organisms. By additional modeling, we tested for the putative function of such unique set-up: does such system serve to colour vision, or rather to boost sensitivity within the entire light spectrum in the depth? In any case, we present the first molecular evidence for exclusive multiple (>3) rod-opsin-based vision among vertebrates, and not surprisingly such system has been discovered in the fascinating deep-sea fishes constantly challenged by their extreme environment.

Deep-sea omics - ABSTRACT 129

## Evidence for extraocular photoreception among deep-sea bioluminescent crustaceans

Danielle De Leo, Heather Bracken-Grissom
Florida International University

Photoreceptor cells inside the complex eyes of animals are responsible for light detection and subsequent signaling cascades linked to vision. Though light detection in animals is typically associated with ocular photoreceptors, the ability to detect and respond to light can also occur in extraocular tissues and structures. Extraocular photoreception has been documented across a range of structures and taxa, including the dermal chromatophores of cephalopods, tube feet of echinoderms and the central nervous systems of arthropods. Despite the occurrence across diverse metazoans, knowledge regarding the functionality of extraocular photoreceptors remains limited. Deep-sea shrimp provide a unique system for examining extraocular photoreception as some genera possess autogenic bioluminescent light organs- either as dermal photophores or internal organs of pesta (modifications of the digestive tract). These light emitting organs are thought to function in counterillumination and congener attraction. Preliminary evidence for the family Oplophoridae suggests photophores contain photopigment proteins (opsins) and other phototransduction genes that would allow for light detection. In this study, RNA was extracted from several species of oplophorid (n=3) and sergestid (n=2) shrimp and sequenced on an Illumina HiSeq4000. Transcriptomes were assembled discretely from eye (n=22), photophore (n=15) and organs of pesta (n=6) tissues and analyzed to characterize opsin diversity and visual pathway genes within a phylogenetic context. To further elucidate potential differences in visual sensitivities, gene expression analyses were also conducted to quantify species-specific differences in opsin expression between eye and light organ tissues. This study sheds light on the visual systems of deep-sea bioluminescent shrimp and provides the first sequenced transcriptomes for the organs of pesta. Our findings suggest the bioluminescent light organs are light sensitive and may be used to fine-tune bioluminescent emissions during counterillumination. Furthermore, we illustrate the strength of employing next-generation sequencing and phylogenetic approaches towards the study of deep-sea sensory systems.

## Genomics of gelatinous zooplankton: challenges and progress

Darrin T. Schultz, N.K. Schaefer, W.R. Francis, L.M. Christianson, S.H.D. Haddock, R.E. Green
MBARI/UC Santa Cruz

The genomes of gelatinous zooplankton are often difficult to assemble using contemporary genome assemblers and sequencing technology. While genome assemblers are often able to resolve the infrequent polymorphisms in mammalian genomes, they struggle to reconstruct genomes with a high number of polymorphic sites and structural variants such as highly heterozygous genomes that are commonly found in the gelatinous zooplankton. Here, we describe a novel technique for genome assembly that uses polymorphism information to independently and simultaneously assemble both haplotypes of each chromosome. We call this method JARED. In addition to testing JARED on existing datasets, we assembled the genome of the highly heterozygous ctenophores _Beroe forskalii_ and a deep-sea platyctenid ctenophore.

## Environmental drivers of bacterioplankton community structure in the northern Gulf of Mexico

Joe Lopez, Cole Easson
Nova Southeastern University

The Gulf of Mexico (GoM) is a dynamic ecosystem influenced by multiple natural and anthropogenic processes and inputs, such as the intrusion of warm oligotrophic water via the Loop Current (LC), freshwater from the Mississippi River (MSR), hydrocarbons via natural seeps and industrial spills, and surprising depths. Bacterioplankton communities start pelagic food webs in the GoM, but understanding their precise roles as ecosystem drivers can be challenging in such a large and heterogeneous system. As part of the DEEPEND consortium, we applied high throughput 16S rRNA sequencing to investigate the spatial and temporal dynamics of pelagic bacterioplankton related to several environmental conditions during GOM offshore cruises. Our results show dramatic community shifts across depths, especially between photic and aphotic zones. Temporal shifts in bacterioplankton communities were restricted to the seasonally influenced epipelagic zone (0-200m), and mainly driven by changes in temperature. Environmental selection in bacterioplankton communities was depth-specific, with variables such as turbidity, salinity, and abundance of photosynthetic taxa strongly correlating with community structure in the epipelagic zone, while variables such as oxygen and specific nutrient concentrations were correlated with community structure at deeper depths. The current study advances our understanding of bacterioplankton dynamics with a specific focus on the GOM pelagic environment. We show that over the GOM spatial scale, environmental selection is likely a strong driver of community composition, which may have cascading effects into higher trophic levels. Recent GoM research has highlighted dramatic responses of bacterioplankton communities to inputs of hydrocarbons or anoxia. Through the DEEPENDconsortium.org, we have also attempted to link bacterioplankton community composition and structure to mesoscale oceanic models in the Gulf of Mexico (GoM). Co-occurrence analyses of dominant GOM taxa are ongoing. The significance of our study also stems from developing the effort as a useful tool in future GoM oceanographic research.

## From Genomes to Populations to Communities: Using Genomic Techniques to Study Deep-sea Coral Diversity

Meredith V. Everett, Linda K. Park
NOAA-NWFSC

Understanding the biodiversity and connectivity of deep-sea coral communities is key to understanding both their role in the deep-sea ecosystem and how to effectively manage and protect them. High throughput genomic techniques (genome sequencing, RAD sequencing, and eDNA (amplicon) sequencing) can help overcome the challenges of the limited samples associated with work on deep-sea species. We are applying these techniques, particularly RAD sequencing and eDNA sequencing, to study the diversity, taxonomy and population connectivity of deep-sea coral communities along the United States west coast. First, we have carried out RAD-sequencing in groups including Pennatalucea in the genus Halipteris and two genera of plexaurid gorgonians, Chromoplexaura and Swiftia. DNA barcode analysis for these groups carried out in our lab has demonstrated discrepancies with traditional taxonomic methods. To clarify the taxonomy in these genera and develop additional markers that can be used to separate groups where appropriate, we have carried out traditional RAD sequencing, on individuals collected coast wide. Within each species group, these markers will be used to assess population connectivity. Second, in partnership with the Ocean Exploration Trust, we have collected eDNA samples from deep-sea coral communities along the United States west coast. A previous study by our lab established the utility of eDNA sequencing for profiling deep-sea coral communities. In the current study we use eDNA to examine differences in fish communities between areas of high and low coral density.

MONDAY Midday • 13:30 • Serra Room

## Under pressure: adaptation of deep-sea amphipods revealed using a multi-'omics approach

Heather Ritchie, Alan J Jamieson, Stuart B. Piertney
School of Biological Sciences, University of Aberdeen; School of Natural and Environmental Sciences, Ridley Building, Newcastle University

Understanding how extreme environmental conditions in the deep sea, mediated by high hydrostatic pressure, low temperatures, low food availability and geographic isolation, shape the patterns of adaptation, levels of genetic diversity and distribution of species is a fundamental question in ecology and evolution. Due to its remote nature and the technical difficulties associated with sampling, there have been a paucity of studies that have explicitly examined the genetic basis of adaptation in the deep sea. Using several 'omics approaches we investigate the evolutionary history and molecular signatures of adaptation to the environmental gradient of hydrostatic pressure using multiple shallow and deep-sea amphipod species collected from several locations. Amphipods are an excellent model system for addressing such issues as they form a significant and ubiquitous component of marine fauna, and occur throughout the entire water depth range from the shallow intertidal zone down to the hadal trenches (>6000 metres). Here we combine RNA-seq derived transcriptome characterisation and third-generation MinION mitogenomic DNA sequencing from more than 15 species of Lysianassoidea deep-sea amphipods to: 1) examine the signatures of selection in gene orthologues from patterns of synonymous and non-synonymous DNA sequence substitution, comparison of GC content and codon bias relative to shallow water species; 2) resolve patterns of convergent and parallel evolution in structural polymorphisms in response to high hydrostatic pressure; 3) characterise gene synteny across taxa within a phylogenetically-informed framework. We discuss potential future avenues and research priorities to enable generic understanding of genome-wide adaptation to life in the deep sea.

MONDAY Midday • 13:45 • Serra Room

## A Phylogenomic Perspective on the Relationships of Gadiform Fishes (Paracanthopterygii: Gadiformes)

Adela Roa-Varon, Chenhong Li, Carole Baldwin, Rebecca Dikow, Guillermo Orti, Eric J. Hilton
Virginia Institute of Marine Science, Smithsonian Institution (NMNH), Shanghai Ocean University (SHOU), George Washington University (GWU)

The phylogeny of gadiform fishes (e.g. cods, hakes, rattails) is the subject of broad controversy based on morphological and molecular evidence. Currently, different authors recognize between 11 and 14 families, approximately 84 genera, and over 600 species. The monophyly of the order has been supported by both morphological and molecular data, yet the relationships among families and subfamilies remain poorly understood. To study the higher-level relationships of Gadiformes, a gene-capture approach was used in which coding DNA sequences from single-copy protein-coding genes were targeted. We generated matrices of 8,478 and 14,208 loci (~2.8 M bp) from a total of 57 species representing all recognized Gadiformes families and subfamilies. Maximum likelihood analyses of the species tree and concatenation frameworks recovered a highly congruent and well-supported phylogeny at both shallow and deep levels that contributes towards stabilizing higher-level Gadiformes classification. At least six lineages were recovered with strong support, an overall consensus on a number of fundamental points resolve historical discrepancies related to the relationships among gadiform lineages. Specifically, the family Macrouridae including only macrourids; the other three subfamilies traditionally included within the family (Bathygadinae, Macrouroidinae and Trachyrincinae) were placed in two independent

families (Bathygadidae and Trachyrincidae). This study also sheds light into the phylogenetic position and composition of several enigmatic families such as Ranicipitidae, Euclichthyidae, Gadidae, Lyconidae (not previously sampled in phylogenetic studies). The placement of Bregmacerotidae as the sister group of all other gadiforms remains provisional until more evidence is considered. The large amount of congruence across the analyses and sequence-bias testing increases confidence in the results, and validates the use of gene-capture approaches for analyzing phylogenetic relationships at a range of evolutionary depths.

MONDAY Midday • 14:00 • Serra Room

## Investigating sponge microbiome and metabolome along a depth gradient

Karin Steffen, Anak Agung Gede Indraningrat, Ida Erngren, Jakob Haglöf, Lisa Becking, Hauke Smid, Ellen Kenchington, Curt Pettersson, Paco Cárdenas & Detmer Sipkema
Pharmacognosy, Department of Medicinal Chemistry, Uppsala University, Husargatan 3, Uppsala 751 23, Sweden.

Sponges are often described as holobionts, since they are hosting a particularly rich associated microbiome. However, the presence of this extensive microbiome makes it difficult to assess the contributions by the host and bacteria to the sponge's overall chemical repertoire.We used 16S amplicon sequencing and UPLC-MS to study microbial and chemical diversity in three sponge species (Geodia barretti, Stryphnus fortis, Weberella bursa) sampled along a depth gradient in the Labrador Sea (400 m to 1400 m).Our aim was to investigate variations in microbiome and metabolome with depth and to test whether these data set allow for a combined analysis and interpretation of the bacterial contribution to the metabolome.We find that microbiome and metabolome change with depth. In Geodia barretti where this trend is the strongest, we find significant underlying trends between OTUs and mass spectrometry features produced by HILIC chromatography.

## Deep-sea omics - POSTERS

TUESDAY Evening • 17:45 • Serra Ballroom

## Revising abyssal biodiversity through eDNA based biodiversity inventories

Sophie Arnaud-Haond, Brandt Miriam, Zeppilli Daniela, Liautard-Haag Cathy, Leblais Erwan, Poulain Julie, Patrick Winckler, Orejas Covadonga, Florence Pradillon
IFREMER

Biodiversity in the marine environment still mostly remains to be discovered. However, the difficulty to access it, particularly the deep sea, and the time needed to deliver rigorous morphological descriptions of the many new species discovered during each oceanographic expedition render this task unrealistic at the scale of human life time. Environmental DNA offers, adopting a phylogenetic species concept, a parallel avenue to provide rapid and standardized biodiversity inventories, provided molecular and bioinformatics pipelines are adapted and improved to address eukaryotic diversity. In 2016 the project "Pourquoi Pas les Abysses" was launched with the objective to provide new assessments of marine biodiversity based on eDNA extracted from ocean seafloor sediments and water. A first step was the development of adapted molecular protocols and bioinformatics pipelines to better understand their strength and pitfalls, and ultimately apply them to a worldwide collection of samples of sediment and water of the deep oceans. In a first step comparing molecular and morphological inventories, we tackled the molecular challenges of sample strategy, preservation for DNA and/or RNA applications, presence of extracellular DNA and extraction methods, and choice of barcode regions maximizing the coverage of the Tree of Life. Our bioinformatics pipeline

was simultaneously selected and improved on the basis of mock communities composed of deep sea species. Here we will present the molecular methods and bioinformatics suites selected to deliver the best standardized and conservative biodiversity inventories. We will demonstrate their ecological application on a subset of samples from the North Atlantic and the Mediterranean, both to deliver a molecular appraisal of the extent of biodiversity present in the environments sampled and to illustrate the use of those data in a biogeographic framework.Acknowledgements: This project was launched by Ifremer, and benefits is supported by France Génomique National infrastructure.

TUESDAY Evening • 17:45 • Serra Ballroom

## Phylogeography of *Paramuricea*: The role of water mass and depth in the evolution of deep-sea corals

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Paramuricea is one of the most common genera of octocorals inhabiting the deep North Atlantic, enhancing habitat complexity in hardground, submarine canyon, and seamount environments. We used a Restriction-Site Associated Sequencing (RADSeq) approach to first delimit species and then examine how depth and water mass influence the evolution of this genus in the N. Atlantic. RADSeq was completed for 47 specimens from the Whittard Canyon and Mediterranean Sea in the NE Atlantic and from the Labrador Sea, Gulf of Maine, and Gulf of Mexico in the NW Atlantic. With a dataset of 7,983 loci (700,393 bp, 7,953 bi-allelic SNPs), we used coalescent and allele-sharing methods to delineate species. Results indicate widespread distribution of species across the N. Atlantic, with further population structure between regions. Notably, species boundaries suggested by these methods are highly incongruent with the conventionally-used mtMutS octocoral barcode, indicating that the mtMutS gene performs poorly in species delimitation of Paramuricea. We further used ancestral reconstruction methods to explore historical biogeography relative to different water masses, regions, and depths. Preliminary analyses suggest that Paramuricea rapidly diversified from mesophotic to deeper depths in the N. Atlantic, with two major deepwater clades found primarily in water masses characterized by median temperatures of either <8 or >8 °C. Furthermore, diversification of extant clades into distinct water masses occurred infrequently, with clades each diversifying only once into, for example, Antarctic Intermediate Water and North Atlantic Deep Water. Deep water masses may have facilitated the spread of Paramuricea spp. across the Atlantic, while also preventing dispersal and/or recruitment across different water masses. Water masses with their associated abiotic characteristics, particularly temperature, may play a more important role than depth per se in the biogeography and species diversification of this enigmatic genus of deep-sea coral.

TUESDAY Evening • 17:45 • Serra Ballroom

## The enigmatic genome of an obligate ancient *Spiroplasma* symbiont in a hadal holothurian

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Protective symbiosis has been reported in many organisms, but the molecular mechanisms of the mutualistic interactions between the symbionts and their host were unclear. Here, we sequenced the 424-Kbp genome of "Candidatus Spiroplasma holothuricola" isolated from the hindgut of a sea cucumber, a major scavenger captured in the Mariana trench. Phylogenetic relationships indicated that the overwhelmingly

dominant bacterium in the hindgut was derived from a basal group of Spiroplasma sp. In this organism, the genes responsible for biosynthesis of amino acids, glycolysis and sugar transporters were lost, strongly suggesting endosymbiosis. The highly decayed genome harbors genes coded for proteolysis, microbial toxin, restriction-methylation systems and clustered regularly interspaced short palindromic repeats (CRISPRs), composed of three cas genes and 76 CRISPR spacers. We propose that the holothurian host is protected against invading viruses by the CRISPRs/Cas and restriction systems of the endosymbiotic spiroplasma. The protective endosymbiosis highlights the important ecological role of the ancient Spiroplasma symbiont in maintenance of hadal ecosystems with respect to their contribution to fitness of the dominant scavenger animals.

TUESDAY Evening • 17:45 • Serra Ballroom

## The use of high-throughput sequencing to elucidate deep-sea ecosystem services

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The development of high-throughput sequencing has transformed the fields of molecular biology and ecology, providing new information, tools, and applications. In the deep sea, these fields have been largely focused on characterizing biodiversity, but it is still unclear how this biodiversity translates into ecological functions and ecosystem services. Ecosystem services are benefits derived by humans from ecosystems. As human impact on the deep sea increases (e.g. fishing, oil and gas drilling, climate change, and potentially mining), ecosystem services can provide a framework to facilitate the balance between commercial extraction and conservation. Here, we explore the use of high-throughput sequencing to elucidate deep-sea ecosystem services in the context of impact assessment. We discuss several molecular methodologies, the advantages and disadvantages relative to morphology-based taxonomy, and present one case study. Metabarcoding has been used to detect bioindicators of environmental health and may also help to identify drivers of ecosystem services. Metagenomics and metatranscriptomics provide additional molecular tools to assess ecological functions and ecosystem services. Currently, they are most readily applied to microbe-mediated processes and regulating services, identifying novel genes in ecosystems and their potential role in element and nutrient cycling. With a focus on mining of polymetallic nodules, sediment samples were collected from the Clarion-Clipperton Fracture Zone. Their environmental DNA content was sequenced for metagenomics analysis. Data will be interpreted through an ecosystem services lens. Providing tools to identify and characterize deep-sea ecosystem services is an essential step for their consideration during the current development of deep-sea environmental policy and management.

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## Biomineralization toolkits of the deep-sea mussel *Bathymodiolus platifrons* and its shallow-water relative *Modiolus philippinarum*

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As calcium carbonate is more soluble at lower temperature and higher pressure, understanding how deep-sea mollusks form their shells through bio-mineralization can reveal the potential adaptation to deep-sea environment. Mollusca shell matrix proteins (SMPs) are known to play

multiple roles in shell formation such as prompting the calcium carbonate crystal formation. To address the potential different biomineralization process between deep-sea and shallow-water mussels, the shell proteomes of the deep-sea mussel Bathymodiolus platifrons and its shallow-water relative Modiolus philippinarum were conducted with the aim to bridge such knowledge gaps. A total of 75 and 55 SMPs were identified from the shell matrices of B. platifrons and M. philippinarum, respectively, with 31 of them being shared by two species. The shell proteome of B. platifrons had much more arginine-rich SMPs, which might be an adaptive strategy to cope with the high pressure and low temperature in the deep sea. The biomineralization toolkits of these two mytilids can be categorized into six broad groups: calcium binding, polysaccharide interaction, enzyme, extracellular matrix-related proteins, immunity-related proteins, and those with no predicted functions. Many of these proteins, such as tyrosinases, carbonic anhydrases (CAs), shell matrix proteins, collagens, chitin-related proteins, peroxidases, proteinase, and proteinase inhibitor domain-containing proteins, have been commonly found in the calcified shells of molluscs. In contrast, some others, such as cystatins, were found for the first time in molluscan shell matrices, whereas ferric-chelate reductase-like proteins, heme-binding proteins, and peptidoglycan recognition proteins (PGRPs), were for the first time to be detected in metazoan calcified tissues. Our study not only revealed the SMP compositions of these two mytilids, but also generated valuable resources for various follow-up studies to better understand the functions of these SMPs, especially in relation to environmental adaptation.

## Genomic signals of convergent evolution in Lake Baikal sculpin and deep sea fishes

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Lake Baikal (Russia) is the deepest body of freshwater on the plant and home to numerous endemic adaptive radiations. Of interest to our group is the adaptive diversification of freshwater sculpins (family Cottidae) to the novel environments of Lake Baikal. The radiation of Lake Baikal sculpin is unique from many aspects, it is the only lake adaptive radiation of fishes in the northern hemisphere and contains the evolution of benthic forms adapted to abyssal habitats and pelagic forms. Our phylogenetic analysis indicates that independent invasions of deep and pelagic environments have occurred in the Lake Baikal sculpin. Our current work is focused on adaptive genomic evolution in pelagic and abyssal species. We are using exome sequence data and a comparative genomic approach to identify convergent evolution between Lake Baikal pelagic and marine species with similar physiological and morphological adaptations.

## Response of Deep-sea hydrothermal vent Epsilonproteobacteria *Sulfurovum* sp. NBC37-1 and *Nitratiruptor* sp. SB155-2 to heavy metals

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Deep-sea hydrothermal vents are one of the most extreme physico-chemical environments on our planet. In the Okinawa Trough, in areas proximal to deep-sea vents, metal and metalloid-rich fluids and mineral deposits abound, making these habitats ideal for isolation of potential metal-resistant microorganisms, such as the Epsilonproteobacterias, Sulfurovum sp. NBC37-1 and Nitratiruptor sp. SB155-2. Previous studies estimated that fluid concentrations in Iheya-North field (Okinawa Trough) ranged between 0.5 to 10 ppm for Cu, Fe, Pb, Zn. The organisms inhabiting these environments are expected to exhibit efficient genetic and physiological mechanisms to cope with elevated levels of metals and metalloids. However, unlike terrestrial metal-resistant microbes, studies of hydrothermal vent microbes are still very scarce, and mechanisms underlying metal tolerance in these prokaryotes are essentially unknown. The aim of this study is to comprehensively characterize primary mechanisms of metal tolerance in deep-sea Epsilonproteobacteria using cutting-edge microscopic techniques and high-throughput RNA sequencing. We present our preliminary data on (1) tolerance assessment of these strains, exposed to different concentrations of heavy metals (i.e. Cd, Cu, Fe, Mn, and Zn), (2) bioaccumulation levels determined by Inductively Coupled Plasma Mass Spectrometry (ICP-MS), and (3) ion localization within cells of strain SB155-2 by Energy Dispersive X -ray Spectroscopy (EDS) coupled with Transmission Electron Microscopy (TEM). In addition, by performing whole-cell transcriptomic analyses, we will identify responses of differentially expressed genes (DEGs) and will determine whether similar expression profiles are elicited by different metal treatments.Elucidation of mechanisms utilized by extremophiles will offer insights into development of novel biotechnological applications such as efficient and low-cost remediation of heavy metals.

## Partnering with the Ocean Genome Legacy to Advance our Understanding of Black Corals (Order Antipatharia)

Naomi Chery 1, Katherine Parra 1, Annie Evankow 2, David Stein 2, Daniel Distel 2, Hannah Appiah-Madson 2, Rachael Ross 1, Emmanuelle Sanon 1, Nadia Alomari 1, Raven Johnson 1, Angela Vasovic 3, Annie Horowitz 4, Horia (Lee) Popa 5, Benjamin Short 6, Daniel Kourehjan 7, Danny M. Vasquez 8, Estefania Rodriguez 9, Dennis M. Opresko 10, Mercer R. Brugler 1,8,9,10
1 NYC College of Technology (CUNY), 2 Ocean Genome Legacy, 3 Frank McCourt High School, 4 Irvington High School, 5 Stony Brook University (SUNY), 6 Fairfield College Preparatory High School, 7 Rutgers University, 8 NYU-SPS DAUS, 9 American Museum of Natural History, 10 National Museum of Natural History, Smithsonian Institution

Black corals (Phylum Cnidaria: Class Anthozoa: Subclass Hexacorallia: Order Antipatharia) are a largely deep-water group with 75% of the 247 currently recognized species occurring at depths >50 meters (deepest: 8,600m). The Smithsonian Institution's National Museum of Natural History (NMNH) in Washington D.C. houses one of the most extensive collections of black corals in the world. Many specimens in the collection are representatives of species for which a DNA signature remains elusive. Obtaining DNA sequence data is imperative as we currently have at least two examples of species classified in the wrong family based on misleading morphological characters. In an effort to obtain genetic signatures from as many black corals in the NMNH collection as possible, we have partnered with the Ocean Genome Legacy (OGL), which is a non-profit, marine research center and genome bank dedicated to exploring and preserving threatened biological diversity of the sea (black corals are listed in Appendix II of the Convention on the International Trade of Endangered Species [CITES]). OGL is currently sequencing two mitochondrial gene regions per individual: cox3-IGR-cox1 and nad5-IGR-nad1 (IGR: intergenic region). Several undergraduates from NYC College of Technology (CUNY) are cleaning the raw ABI-3730xL sequence traces. City Tech is the largest 4-year public college of technology in the northeast and ranks #1 in ethnic diversity among northern regional colleges. As of March 30, 2018, students have edited chromatograms from 35 black corals

and just received raw sequence traces from an additional 25 specimens. All newly sequenced taxa will be added to the phylogenetic tree presented in Brugler, Opresko & France (2013) to verify or revise the original morphology-based identifications.

## Molecular adaptation of a deep-sea fish inferred from transcriptome sequencing

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Deep sea is a harsh environment characterized by high hydrostatic pressure and low temperatures. For instance, high hydrostatic pressure can disrupt actin organization and microtubules assembly, which contribute to maintain intracellular movements and cell motility. Nucleic acids structures can be influenced by not only high hydrostatic pressure but also cold temperature. These adverse effects caused by the high hydrostatic pressure and cold are challenging for the deep-sea animals. To study the potential mechanisms of biological adaptation to deep-sea environment, one individual of *Aldrovandia affinis* fish that is a typical habitant in the deep sea was captured from 1550 m deep in the Okinawa Trough, and its transcriptome was sequenced. A total of 27,633 protein coding sequences were predicted and then compared with sequences of other shallow-water fish. Analysis of 4918 single copy orthologous genes identified 138 positively selected genes in *A. affinis*, including genes related to microtubules regulation. Particularly, functional domains response to cold shock and DNA repair were under positive selection in *A. affinis*. Herein, a set of positively selected genes related to cytoskeleton structures, DNA repair and genetic information processes were identified in the present study, depicting potential mechanism of deep-sea adaptation.

## Microbiomes and Bacterial Symbionts of Deep Sea Anglerfish in the Gulf of Mexico

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As part of the DEEPEND consortium (www.deependconsortium.org), our laboratory has focused on the intersection of microbiology and deep-sea anglerfishes. Most female deep-sea anglerfishes possess a "lure" (esca) containing extracellular bioluminescent bacterial symbionts. We examined whether symbiotic microbes were specific to anglerfish hosts in the Gulf of Mexico, and thus distinct from surrounding seawater. Thirty-six anglerfish specimens were collected on DEEPEND cruises DP01 through DP04. These specimens consist of adult and larval individuals belonging to six of the families with the suborder Ceratioidei: Ceratiidae, Centrophrynidae, Melanocetidae, Oneirodidae, Gigantactinidae, Linophrynidae. Esca, skin, caruncle, fin, gill, and gut tissues, as well as seawater microbial communities ("microbiomes") were compared. High-throughput sequencing of the 16S rRNA hypervariable V4 region was carried out and revealed that escal microbiomes of each anglerfish species were primarily dominated by only a few operational taxonomic units (species delineation in microbes is equivocal) relative to the surrounding seawater. Three potential-symbiont taxa had the greatest relative abundance (25.2% - 98.7%) within 12 of 21 adult specimens. These taxa belong to the family Vibrionaceae and were found in high abundance in the escal samples of adult anglerfishes belonging the families Ceratiidae and Melanocetidae, but were not found in high abundance in larval individuals of the same families. By contrast, non-escal organs did not reveal dominant microbes or any strong specific patterns similar to esca. When compared to other anatomical locations and seawater, the potential-symbiont taxa are of greatest abundance within the

esca, supporting their identification as potential symbionts. Preliminary results still under analyses show possible horizontal connections between anglerfishes and the surrounding water column. Additionally, the unique symbiont taxa have led to whole-symbiont genome characterizations by our collaborators. We show that unlike most luminous symbionts, which are facultatively host-associated, anglerfish symbionts have been undergoing genome reduction on evolutionary timescales. The genomes appear reduced in size by about 50% compared to free-living relatives and possess limited metabolic capabilities.

## Circadian Clocks in Mesopelagic Fish

Inga Angelica Frøland Steindal, David Whitmore, Kjetill Jakobsen, Sissel Jentoft
UCL

As a result of evolving under a 24-hour day, many organisms, from bacteria and plants to humans, possess a cell autonomous, circadian clock and show rhythmic, daily behaviour. The circadian clock is set by sunlight at dawn and dusk which regulates the daily timing of approximately 1/3 of all of cellular processes. The clock is so important to our biology, that disruption of the clock is strongly associated with many common pathologies, such as diabetes and increased cancer risk. Animals that live on land, in lakes and in shallow waters all use sunlight to set their clocks, but how do animals that live in perpetual darkness or extremely dim light set their clock? Do they even have a clock? To unravel whether deep-sea animals have a clock or not and if sunlight is a zeitgeber, I am comparing two fish species in the Sternoptychinae family (caught in the Indian Ocean), Argyropelecus hemigymnus which is a vertical migrator, and the non-vertical migrator Sternoptyx diaphna. By using RNAseq, I am examining whole transcriptome changes in response to light, focusing on known light inducible genes and clock genes in particular. Do the vertical migrators have a clock while the deeper living, non-migrators do not? Do we observe any differences in light responsive genes and signalling pathways? Our studies on molecular clocks in deep sea fish are the first to examine this phenomenon in such an extreme environment and will provide novel insights into circadian clock function.

## Episodic Diversifying Selection, Recombination, and Symbiont Capture Characterize the Evolutionary History of Maternally-transmitted Clam Symbionts

Deborah Yarrow, C R Young
National Oceanography Centre

The shift from a free-living bacterial lifestyle to a vertically transmitted intracellular lifestyle is hypothesized to result in major genome-scale changes including a shift to AT-rich genomes, reduced recombination, and a reduction in genome size. In this study, host-symbiont coevolution, genome structure, recombination and diversifying selection were examined by applying comparative methods to symbiont and mitochondrial genomes from 11 vesicomyid deep-sea clam taxa. A pervasive pattern of natural selection affects many loci with functions such as DNA metabolism, transcription and translation as well as loci that are central to the chemosynthetic role of these symbionts reflecting the diverse selective pressures of an intracellular symbiont lifestyle. These signatures of selection are not limited to one or a few lineages, but are distributed throughout the history of the group. Recombination occurs frequently, but it is not randomly distributed among taxa. The non-random distribution of recombination among symbiont lineages might reflect constraints imposed by host distribution and physiology. One recent instance of a symbiont genome replacement was observed between two different host genera. These results suggest that both recombination and natural selection have

been important features of adaptation to a vertically transmitted, intracellular lifestyle in this group of symbionts.

# James J. Childress - TALKS

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## Darnit Jim, I'm a biologist not an engineer: Or…how I learned to stop worrying and love deep sea biology

Peter Girguis, Roxanne Beinart
Harvard University

The discovery of animal-microbial symbioses was a watershed in our understanding of life in sulfide-rich habitats. These associations fueled three decades of research into their ecology, physiology, and evolution. To date, we have learned much about how these partners each contribute to supporting net chemoautotrophy. However, due to the technical challenges associated with studying live vent symbioses (whether in situ or ex situ), there remains a paucity of data on the metabolic rates of many species, and what factor(s) govern their productivity. Many of these symbioses are considered foundation species, yet we remain woefully unaware of how their metabolic activity might further influence the ecology (and evolution) of associated microflora and fauna.Using many technologies inspired by Dr. Jim Childress, our labs focus on addressing such questions by conducting "omics-informed" high-pressure experiments to measure metabolic activity (including carbon, sulfur and nitrogen metabolism) among a variety of associations. We have developed tools to study patterns of host and symbiont gene expression in different microhabitats, as well as tools to make in situ geo-referenced geochemical measurements around these associations. We are also extending the application of these technologies to study new aspects of symbioses and free-living bacteria, including development, reproduction, and evolution. We have found that many of these technologies, developed for use in the deep sea, also have great value when applied to other marine organisms that don't need higher pressures or temperatures. Altogether, the resulting data has re-shaped our thinking about these associations, the nature and extent of their biogeochemical transformations, and, ultimately, their role in shaping vent ecosystems. Here we present our recent and ongoing research, and our latest ideas about how these symbioses govern matter/energy flux throughout the vent ecosystem.

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## Critical oxygen levels of marine zooplankton and the consequences of ocean deoxygenation

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Oxygen supply to the sites of cellular respiration requires a partial pressure (PO2) gradient from the environment to the mitochondria to drive diffusion. In surface waters, the PO2 drops from 21 kPa in ambient water to an estimated 0.5 kPa at the mitochondria. In pronounced oxygen minimum zones (OMZ), the PO2 in the ambient water is already less than 0.5 kPa. Thus, the gradient driving diffusion across the gills into the blood and from the blood into cells and mitochondria is far below that required for aerobic metabolism in most marine environments. While animal diversity and abundance are reduced in the OMZ core, aerobic life does thrive there. Here I show that zooplankton in OMZs have the greatest tolerance of low oxygen (lowest critical oxygen partial pressures, Pcrit) of any animals measured to date. I review the influence of regional adaptation, metabolic rate, temperature, PCO2, size and taxon on hypoxia tolerance. I demonstrate that changes in oxygen of only a few micromolar, which occur over very short vertical and horizontal distances, are important in

structuring zooplankton communities in OMZs. Ocean deoxygenation will reduce environmental oxygen supply while global warming will increase metabolic demand, reducing the metabolically available habitat and dramatically restructure mesopelagic communities.

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## Vision and Bioluminescence in Deep-sea Crustaceans

Tamara Frank
Nova Southeastern University

Adaptations of the visual systems of deep-sea crustaceans to dim light environments are driven not only by environmental light, but also biologically produced light, or bioluminescence. Decades of study on the visual systems of deep-sea crustaceans have demonstrated that almost all of them possess a single, blue-sensitive, visual pigment. However, work completed in the 1980s demonstrated that three genera of deep-sea pelagic crustaceans (family Oplophoridae) have an unexpected dual visual pigment system that includes a near-UV sensitive visual pigment in addition to the standard blue sensitive visual pigment, which appears to be correlated with their bioluminescence. In the pelagic zone, almost all bioluminescent crustaceans possess one of two forms of bioluminescence – a bioluminescent spew, used for defense, and photophores, used for counterillumination. The three genera with the unusual dual visual pigment system are amongst the very rare crustacean genera that possess both forms of bioluminescence. New research presented here will describe the presence of a dual visual pigment system in another deep-sea pelagic family – the Pandalidae. The genera with two visual pigments have also been reported to possess the rare combination of both photophores and a bioluminescent spew. This work provides further support for the hypothesis that the unusual dual visual pigment system in deep-sea crustaceans evolved in these species to help them discriminate between the different forms of bioluminescence (secretion vs. photophore).

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## A biomechanical description of tomopterid polychaetes using high-speed video analysis

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Tomopteridae is a globally distributed family of highly motile, holopelagic, gelatinous, predatory polychaete wormss with approximately 60 described species. Despite the lack of chaetae and internal septation, which are both critical parts of the explanation of how "typical" polychaetes swim, tomopterids swim with a high degree of maneuverability and speed. This project provides a basic kinematic description of forward swimming in Tomopteris. We recorded high-speed video of 10 individual Tomopteris in the lab, used MATLAB to digitize the 2-D positions of 52 body points on the animals, and analyzed the kinematics of the body wave and movements of the parapodia (swimming appendages). Similar to other polychaetes with large parapodia, tomopterids swim using a combination of metachronal paddling of their parapodia and the propagation of an anteriorly travelling body wave. However, we find that unlike what is modeled for polychaetes and other rough-bodied animals, parapodial paddling alone generates forward movement. We discuss the purpose of the body wave in relation to generating sufficient difference between parapodial power and recovery strokes. We examine our results in light of models of sinusoidal and sequential rowing and find that tomopterids use a combination of these models to maximize the difference between power and recovery strokes. Our results provide valuable insights

into the kinematics of tomopterid polychaetes and have potential applications for biomimetics and soft robotics.

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## Swimming activity of a vertically migrating deepwater shark in relation to temperature

Mark Royer, Danny Coffey
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The bluntnose sixgill shark (Hexanchus griseus) is a large bodied shark that inhabits cold waters around the world, staying at deep depths in tropical regions. They exhibit diel vertical migration, swimming at depths deeper than 500m with temperatures below 6°C during the day and at night swimming between 200-300m with temperatures around 15°C. A recent study has shown that deep-water sharks such as H. griseus have positive buoyancy in deep habitats and exert greater effort to maintain a given swimming speed during descents, whereas they are able to glide up the water column during ascents. We hypothesize that this positive buoyancy may allow deep-water sharks to conduct upward migrations when their body temperatures are coolest, and swimming activity is reduced, after spending the day in deep cold water. To determine how H. griseus body temperature and swimming performance change between different thermal environments on a diel cycle, we equipped adult individuals with instrument packages capable of directly measuring depth, ambient water temperature, activity rates and swimming muscle temperature. Our specific objectives were to determine whether: (1) H. griseus rely on simple thermal inertia for regulating their core body temperature and (2) whether there will be a difference in swimming activity with relation to body temperature. We obtained 20 total days of data from 5 free-swimming adult H. griseus with individual deployment durations lasting 5 days. Our data suggests swimming activity increases as body temperature warms due to thermal inertia during their shallower nighttime distribution, but temperatures over 13 degrees would cause a decrease in swimming activity. Core muscle temperature warmed and cooled at a rate to match the ambient temperature when it was time to vertically migrate. This study further characterizes how deep-water sharks utilize positive buoyancy for diel vertical migration.

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## Black holes in the deep: II. optics of the skin of deep-sea fish

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Although color is increasingly studied in both animals and plants, black is often overlooked, even though it can serve important functions. In the case of deep-sea fishes, black surfaces strongly absorb (and thus do not reflect) the bioluminescent searchlights of predators, therefore providing a form of camouflage. So, it is perhaps not surprising that many deep-sea fishes appear to be exceptionally black. We investigated this in several species of mesopelagic fishes in three ways: (1) reflectance spectroscopy (2) scanning and transmission electron microscopy, and (3) optical modeling. The spectroscopy showed that many species reflected very little light, in some cases less than 0.5%, which is one tenth of that seen in most black surfaces found in normal human experience. Interestingly, even though the reflectances were already quite low, they were generally lower in the blue-green portion of the spectrum that comprises bioluminescence, suggesting further optimization. The microscopy studies showed that the outer layers of skin of the black fishes were quite complex and the pigment granules found here were approximately 0.2 to 1.0 microns in diameter. Using methods developed for understanding the reflective properties of lunar soil, which is similarly composed of close-packed strongly absorbing spheroidal particles with high refractive index, we found that the melanin granules

found in the black fishes were the optimal size for achieving the greatest absorption of incident light with the least amount of material. Together, this study highlights the importance of blackness to deep-sea fishes and the strong evolutionary pressures for camouflage in even this dark environment.

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## Pressing Concerns: New Approaches to Studying Protein Adaptation to High Pressure in Ctenophores

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Hydrostatic pressure can have a strong influence on the physiology of deep-sea animals, since many proteins do not function constantly over a pressure range of hundreds of atm. Ctenophores, or "comb jellies," comprise a group of gelatinous animals that has repeatedly colonized most of the oceanic water column, from sea level to ~7 km deep, where ambient pressure is about 700 atm. Consequently, phylum Ctenophora is a useful system for studying physiological adaptation to pressure in an evolutionary context, namely asking the question: "is protein adaptation to life in the deep sea predominantly parallel (occurring in a consistent set of genes), or convergent?" We have begun to assess the functional diversity of ctenophore metabolism by cloning the glycolytic enzyme pyruvate kinase (PK) [EC 2.7.1.40] from several species living across a depth gradient. We then expressed these PK orthologs in _E. coli_ and assayed their activity under pressure. Major advantages of cloning such an enzyme are (1) the option of site-directed mutagenesis, which can be used to reveal sequence features that confer pressure resistance, and (2) the ability to produce unlimited amounts of protein from a single small individual. PK was chosen based on its apparently adaptive pressure resistance in deep-sea fishes. The pressure/activity data reported here are novel among invertebrates and offer a ready comparison to fish datasets. In addition, we briefly discuss novel tools used to carry out the above work and to place its results in evolutionary context. These tools include: (1) systems for low-temperature expression of cloned deep-sea proteins, and (2) algorithms that use comparative transcriptomics to predict which amino acid sites in a protein most affect a phenotype such as pressure resistance.

James J. Childress - ABSTRACT 242
WEDNESDAY Morning • 11:30 • San Carlos Room

## The brains and sensory specializations in the midwater hyperiid amphipods

Chan Lin, Karen J. Osborn
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Studying the nervous systems of animals with highly specialized sensory systems often provides insight into how a brain has evolved in response to the animal's natural surroundings. However, correlations between the modifications of certain brain regions and an animal's ecology are mostly suggestive, due to a lack of intermediate forms among closely related species. Here we present a group of crustaceans that provides an excellent opportunity to study how brains adapt when light limitations have driven the evolution of a diverse morphology of eyes. Hyperiidea is a suborder of amphipod crustaceans that are abundant members of zooplankton at mesopelagic depths (200-1000 m), where sunlight is reduced to increasingly dim and down-welling blue light. At least 10 different eye types are found, ranging from no eyes, tiny simple eyes, to several forms of compound eyes. Using a combination of techniques in neuroanatomy, we show that neural arrangements in the visual brain area generally follow the malacostracan-insect ground pattern, but with various modifications. Photoreceptor axons project to the first optic neuropil (lamina), whose axons, in turn, project to the second optic neuropil (medulla). One exceptional taxon, Paraphronima spp., possesses a true third optic neuropil (lobula) and three additional ones after the lobula, an

arrangement that has never been described in any crustacean. While the neural organization of each hyperiid reflects the result of sensory adaptation in its own surroundings, mapping all the neural and habitat characteristics onto the hyperiid phylogeny enables us to reconstruct the evolutionary history of sensory adaptations in this closely related but highly diverse group.

## James J. Childress - POSTERS

### Not all ctenophores have evolved equally: Ecophysiological interpretation of metabolic enzyme activities of deep-sea ctenophores

Telissa M. Wilson, Steven H.D. Haddock§, Erik V. Thuesen*
*The Evergreen State College, Olympia, WA USA; Monterey Bay Aquarium Research Institute. Moss Landing, CA USA

Ctenophores are marine predators that are well known for the beautiful display of light diffracting off their many cilia. They are the largest organisms to utilize cilia to power locomotion. Ctenophores belonging to a range of habitat depths (surface – ~3700 m) and six distinct orders were collected in order to examine their enzymatic activities to better understand their ecophysiological characteristics. Morphometric parameters such as mass, number of comb plates and ctene row surface area, and ecological parameters such as feeding type and minimum depth of occurrence were used in these analyses. The number of comb plates did not vary with body mass, although the specific surface area of ctene rows increased with increasing body mass, and specific density of comb plates decreased as body mass increased. Creatine kinase (CK) activity increased as comb plate density increased. There was no significant correlation of metabolic enzyme activity to body mass when analyzing all the individuals from all the taxonomic groups. However, metabolic enzymes of specific taxonomic and functional groups did display metabolic scaling with body mass. In the order Lobata, citrate synthase (CS) declined with increasing body mass. Similar scaling pattern of CK were found for Beroida and Lobata. When viewed by feeding strategy, CK significantly scaled with body mass. In contrast, CS activity did not significantly scale with mass when grouped by feeding strategy, but did display unique scaling patterns. There was no significant difference in enzyme activities between epi-, meso-, and bathypelagic species supporting the visual interactions hypothesis that suggests visually-orienting predators and prey should have lower metabolic activities in the deep sea as selection for more powerful metabolic machinery is relaxed in permanently dark habitats. This research demonstrates the diversity of biochemical adaptations found throughout Ctenophora, and subsequent studies may benefit by treating each group within the phylum individually.

### Effects of Hydrostatic Pressure on the Metabolic Enzymes of Ctenophores from Different Habitat Depths

Tiffany S. Bachtel*, Telissa M. Wilson*, Jacob.R. Winnikoff ‡§, Erik V. Thuesen*, Steven H.D. Haddock§
*The Evergreen State College, Olympia, WA USA; ‡University of California, Santa Cruz, CA USA; §Monterey Bay Aquarium Research Institute. Moss Landing, CA USA

Deep-sea animals have evolved various biochemical strategies to live at great depths. Our knowledge of evolutionary changes in enzymes is limited to very few enzymes and species, mostly fishes. Functionality of enzymatic machinery may decrease with increasing depth due to increasing pressure. Hydrostatic pressure not only affects physiological performance, but also influences evolutionary and phylogenetic patterns of deep-sea organisms. To better understand biochemical adaptations to high hydrostatic pressure in deep-sea animals, the phylum Ctenophora was chosen since both closely related and phylogenetically distant species inhabit the deep sea. Enzymatic activities (Vmax) were recorded during each pressure treatment and recovery to investigate the effects of pressure. Both native enzymes and cloned enzymes were examined at 1, 3000, 6000, and 9000 atmospheres. The glycolytic enzyme pyruvate kinase (PK) has shown adaptive pressure resistance in deep-sea fishes, and was targeted first for comparison. Shallow and deep-sea ctenophore species were examined to explore flexibility/rigidity of depth ranges. Initial results indicate that species inhabiting similar vertical ranges can display unique pressure tolerance characteristics. The PK of both shallow and deep-water Beroe species exhibited a high-pressure threshold. PK from the shallow species Lampea sp. displayed a low capacity to function under high pressures. Phylogenetically, results indicate that adaptations to moderate depth (100 m) is not necessarily convergent at the scale of a single enzyme. Further assessing functional diversity of Ctenophore metabolism will indicate parallel or convergent protein adaptation in the deep sea. The effects of pressure reported herein are novel for invertebrates, and they offer a good comparison to fish biochemical adaptations.

### Are reproductive functional traits in polychaetes and bivalves from deep-sea reducing habitats phylogenetically or environmentally constrained?

Gaudron SM, Lefebvre S and Duperron S
1 Univ. Lille, CNRS, Univ. Littoral Côte d'Opale, UMR 8187, LOG, Laboratoire d'Océanologie et de Géosciences, F 62930 Wimereux, France 2 Sorbonne Université, UFR 918, 4 place Jussieu, 75005 Paris, France 3 Muséum national d'Histoire Naturelle et Ins

Understanding life history of deep-sea organisms is mandatory if we want to understand their persistence and adaptation in a changing environment. Global warming may change the distribution of some species, and the planned deep-sea mining activities may impact biodiversity. This paper aims to test if different life history traits in Molluscs and Annelids are linked to the characteristics of deep-sea reducing habitats (pressure, sulfure compounds, etc.), with an emphasis on reproduction, as hypothesized by Le Pennec et Beninger (2000), or whether these are linked to their phylogeny (Eckelbarger and Watling 1995). Molluscs and Annelids are among the most significant benthic deep-sea taxa, and both belong to the Lophotrochozoa. To reach this goal, meta-analyses were carried out to fill up three matrices: 1) a matrix of 13 reproductive traits documented in 35 bivalves species (Mollusca) and in 35 polychaetes species (Annelida) from shallow to deep-sea habitats and 2) a matrix of environmental data (temperature, latitude, depth, type of reducing habitats) and 3) a matrix containing pairwise phylogenetic distances based on the 18S rRNA-encoding gene. In this paper we will specifically test whether these adaptations are best explained by characteristics of the habitats (environment-linked) or by the phylogenetic history of organisms. Results are being processes using constrained multivariate analysis (e.g. distance based RDA) further completed by variance partitioning. Expected results are the highlight of specific adaptations in reproductive traits of deep-sea reducing habitats compared to shallow water species within each phylum or for all Lophotrochozoa. References: Eckelbarger, K.J., Watling, L., 1995. Role of phylogenetic constraints in determining reproductive patterns in deep-sea Invertebrates. Invertebrate Biology 114 (3), 256-269.; Le Pennec, M., Beninger, P.G., 2000. Reproductive characteristics and strategies of reducing-system bivalves. Comparative Biochemistry and Physiology Part A: Molecular & Integrative Physiology 126, 1–16.

## The kinematics of *Tomopteris* swimming: differences between power and recovery strokes

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Smithsonian National Museum of Natural History, Cornell University, Monterey Bay Aquarium Research Institute, George Washington University, University of California, Berkeley,

Tomopterids are ubiquitous, midwater, polychaetes worms with an unusual body form – gelatinous body with no internal separation of segments, large paddle-like lateral appendages (parapodia), and lacking bristles (chaetae) except to a single internal, extremely elongate pair on the anterior end. These morphological differences to all other polychaetes, and prior modeling of polychaetes swimming suggest that they should be slow swimmers and generally incapable of sustained fast swimming. However, we see the opposite when observing them in situ. They are active predators who are highly maneuverable and quite capable of sustained fast swimming. Using high high-speed video of animals in the lab, and the Video Analysis Toolkit and DLT in MatLab, we were able to analyze the kinematics of tomopterid swimming. Swimming is accomplished in tomopterids almost entirely by parapodial paddling, indicating that the difference between drag generated during power and recovery strokes of the parapodia is critical to the efficacy of their movement. Here we examine the magnitude of parapodial displacement created by the body wave. We also examine the change in parapodial extension and spread between power and recovery strokes. All three of these results show us that tomopterids are able to generate a substantial difference in drag between power and recovery strokes of individual parapodia and this accounts for the majority of their forward motion.

## Black holes in the deep: I. ultrastructure of the skin of deep-sea fish

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Smithsonian National Museum of Natural History, Duke University, Monterey Bay Aquarium Research Institute

Many midwater fishes are exceptionally black – this is most obvious when trying to photograph them and ending up with a lovely series of silhouettes. For years it has been assumed that black fish were simply highly pigmented, but we asked if there is more to it than this. We sampled representative black and non-black mesopelagic fish from across the fish tree of life to learn how "black" these fishes are (reflectance spectroscopy) and how blackness is achieved structurally. We used histological techniques with light, scanning and transmission electron microscopy to document the skin and pigmentation of these fishes. Microscopy showed spherical to short rod-shaped pigment granules ranging in diameter from 0.2 to 1.0 microns arranged in compact, extracellular layers organized by collagen fibers. This extracellular arrangement and organization into thin layers is not known from any other animals. The particulars of these layered arrangements vary slightly between taxa in the thickness and organization of the layers, arrangement of collagen fibers, and number of layers. Despite these small differences, this extracellular concentration of highly structured pigment granules remain surprisingly consistent across black, deep-sea fishes and loosely resemble melanoma in other fishes. We hypothesize that the thin layer arrangements coupled with the size of the particles (see part II) work together to optimize blackness of deep-sea fishes. This study highlights unique, convergent adaptations of deep-sea fishes and expands our knowledge of the structure of fish skin.

## Bioactive Compounds from a Marine Yeast *Cystobasidium benthicum* Isolated from Deep-Sea Sediment

Hwa-Sun LEE, Hyi-Seung LEE, Jong Seok LEE, Yeon-Ju LEE, Jihoon LEE, and Hee Jae SHIN*
Korea Institute of Ocean Science & Technology

Natural products and their derivatives have been recognized as a attractive source of drug discovery.1 In particular, microorganisms from the marine environment, a rich source of structurally unique bioactive metabolites, have produced a number of drug candidates.2 Among them, marine microbes from the deep-sea are relatively untapped reservoir of unique structural and biological diversity waiting to be discovered because of lack of technology and difficult to collect.3 In our continuing search for bioactive substances from deep-sea microorganisms, we encountered a marine-derived yeast Cystobasidium benthicum. This strain was isolated from a deep-sea sediment sample collected by a multicorer in the Indian Ocean in August, 2017. We report here the isolation of bioactive compounds from the ethyl acetate extract of culture broth of C. benthicum by chromatographic methods along with their structure determination by analysis of spectoscopic data.1. Butler, M. S.; Robertson, A. A. B.; Cooper, M. A., Natural product and natural product derived drugs in clinical trials. Nat. Pro. Rep., 2014, 31 (11), 1612-1661.2. Skropeta, D.; Wei, L., Recent advances in deep-sea natural products. Nat. Prod. Rep., 2014, 31, 999-1025.3. Skropeta, D., Deep-sea natural products. Nat. Prod. Rep., 2008, 25, 1131-66.

## Trimethylamine oxide and betaine as potential piezolytes (pressure counteractants) in deep-sea pelagic cnidaria, fishes and ctenophores

Paul H. Yancey, Erin Hennessey, Elizabeth Wong, Chloe Weinstock
Whitman College

Hydrostatic pressure perturbs protein structures and functions. Many proteins in deep-sea animals have evolved partial pressure resistance, but many appear to require piezolytes: small organic molecules, first discovered as osmolytes, which block pressure's perturbing effects on water structure around proteins. The best known piezolyte, trimethylamine N-oxide (TMAO), has been found to increase precisely with depth (and thus pressure) in benthic fishes, anemones and crustaceans. However few studies have examined pelagic animals which often have more rapid vertical migrations than benthic ones, and perhaps might not be able to regulate piezolytes with depth as readily. Here we present piezolyte analyses of selected pelagic animals from epi-, meso- and bathypelagic zones (Salish Sea, Monterey Bay, and Hawai'i). In 15 teleost fishes from 450-1400 m (e.g., bristlemouth, barreleye, anglerfish), TMAO increased with depth (p = 0.013) though less precisely than in benthic fish. In 16 scyphozoan Cnidaria from 0-3000 m (e.g., Atolla parva, Periphylla periphylla), TMAO also increased with depth (p < 0.0001), but again with more scatter than in benthic Cnidaria (anemones). In two siphonophore (hydrozoan) Cnidaria from 895 m (Bargmannia elongata) and 2800 m (Erenna sp.), TMAO also correlated with depth. However in 5 medusa-type hydrozoans (e.g., Halitrephes maasi, Colobonema sericeum), TMAO was present but with no depth trends (albeit caught only over a narrow 710-1376 m). Ctenophores (0-2131 m; 7 species) had low to no TMAO, but all but two species were too gelatinous for accurate analysis; however those two (a vermillion lobate and Bathytena chuni) had higher levels of betaine (N-trimethylglycine) than shallow species. Betaine is a known piezolyte, although not as effective as TMAO (at least with vertebrate proteins). These results suggest that Ctenophora and Cnidaria differ in pressure adaptations in some ways. We thank Steve Haddock and Erik Thuesen for specimens collected under NSF grant DEB#1542679.

# Mining impacts - TALKS

## Very high macrofaunal diversity in an area targeted for nodule mining in the eastern CCZ

Craig R. Smith1, Iris Altamira1, Diva Amon1,2, Amanda Ziegler1, Clifton Nunnally1,3, and Cassandra Turner1
1University of Hawaii at Manoa, USA; 2Natural History Museum, UK; 3Louisiana University Marine Consortium, USA

The Clarion-Clipperton Zone (CCZ), a vast abyssal area of >4 million square km, now contains at least 16 nodule-mining exploration contracts stretching across 42 degrees of longitude. Despite intense international interest in nodule mining, baseline studies of sediment macrofaunal biodiversity and community structure are very sparsely distributed across this enormous region, including in the easternmost CCZ. Here we describe macrofaunal morphospecies diversity and community structure from the UK1 contract area in the easternmost CCZ based on 24 quantitative box-core samples randomly distributed within two 30 x 30 km strata separated by ~130 km. Macrofaunal abundance in the UK1 contract area is relatively high, exceeding that in all but one other locality sampled within the CCZ. Rarefaction diversity for the total macrofaunal (measured in only 12 box cores due to a lapse in funding) and polychaete rarefaction diversity exceed those measured in any other CCZ location. Species richness is also very high, with 227 macrofaunal species and 154 polychaete species (within 42 families) collected. The 10 most abundant families of polychaetes include a surprisingly broad range of putative feeding types, including surface deposit feeders, carnivores, subsurface deposit feeders, suspension feeders, and omnivores. Species richness estimators (Chao 1 and 2) indicate that the two UK1 strata are still undersampled by >33%, and are likely to contain ~340 macrofaunal, and ~250 polychaete, species. The high macrofaunal community abundance and very high species diversity suggest that the UK1 contract area may be distinct from other areas thus far sampled in the CCZ and falls within a regional biodiversity hotspot. Protection of high biodiversity within this area must be considered in the CCZ the regional environmental management plan.

## Cetacean and shark fossils are abundant in the eastern Clarion Clipperton Zone

Diva Amon, Erik Simon-Lledo, Robert Boessenecker, Daniel Jones, Chee Kong Chim, Helen Pei San Wong, Koh Siang Tan, Amanda Ziegler, Adrian Glover, Craig Smith
Natural History Museum, London

There is mounting interest in mining polymetallic nodules in the abyssal Clarion-Clipperton Zone (CCZ) in the Pacific Ocean despite limited knowledge of the biological and geological characteristics of this region. The CCZ is thought to host unique, abundant and novel biodiversity in all size classes, so it is widely acknowledged that caution should be exercised with regards to deep-sea mining. As additional evidence of the potential sensitivity of this area to mining disturbances, we report a high abundance of fossils on the abyssal seafloor. This is based on observations during the ABYSSLINE and MIDAS expeditions in 2013 and 2015. Observed fossils were mostly cetacean skulls and ear bones, as well as shark teeth encrusted in polymetallic ore. While organic falls are known from this area, there has been little published on fossil falls, although there are records stretching back to the Challenger Expedition. During this presentation, the types of fossils and potential ages will be discussed, although given the known encrustation rate of the polymetallic ore, they are likely millions of years old. Additionally, many of these fossils host fauna either attached to the fossil itself or sheltering underneath (poriferans, cnidarians, polychaetes, ophiuroids, asteroids, etc.), showing that these fossils act as an additional source of hard substratum and may impact the benthic community. The high abundance of easily accessible fossils, the uniqueness of this paleontological site, as well as the potential damage resulting from mineral exploitation, has led us to conclude that special attention and perhaps additional conservation and management measures should be considered in the Regional Environmental Management Plan for the CCZ, including protecting areas from mining to preserve this remarkable fossil record.

## Seamounts as refuge areas for fauna from mined nodule fields?

Daphne Cuvelier, Pedro Ribeiro, Sofia Ramalho, Daniel Kersken, Pedro Martinez-Arbizu, Ana Colaço
MARE – Marine and Environmental Sciences Centre, IMAR - Instuto do Mar

When nodule fields will be mined, hard substrata will be removed from the otherwise soft sediment abyssal plains. Set-aside areas are often proposed as a mitigation technique to safeguard undisturbed areas within the nodule fields and to guarantee faunal survival. Alternative refuge areas can be considered, featuring adjacent ecosystems with hard substrata that could host a (partial) recolonisation potential, able to aid the ecosystem in its recovery.Within the Clarion Clipperton Fracture zone (CCZ), seamounts are such nearby features offering hard substrata. In 2015, 4 seamounts in 2 different license areas (GSR, BSR) and 1 area of Particular environmental interest (APEI3) were visited with a ROV, performing imagery transects towards the summit. An additional six ROV dives from the same cruise visited the nodule fields within the same license areas where the seamounts were located and were analysed for comparison purposes. All images were annotated to family level when possible, also assessing the number of morphotypes within a single family. Besides a first description of the seamount fauna of the CCZ, an in-depth comparison between nodule field community composition and nearest seamount fauna will be presented. Taxon-overlap will be discussed at various levels. The recolonisation potential hosted by the seamounts is quantified for a first time and implications for their use as a potential hard substratum refuge area for disturbed nodule fields are discussed.

## Evaluating the nature of midwater mining plumes and their potential effects on midwater ecosystems: a workshop report

Jeffrey C. Drazen, Craig R. Smith, Kristina Gjerde and the workshop participants
University of Hawaii, IUCN, and DOSI

The International Seabed Authority (ISA) is mandated, through contractors, to generate environmental baselines and assess the potential environmental consequences of deep seafloor mining. Mineral resources are found as precipitated deposits near hydrothermal vents, on the abyssal seafloor as manganese nodules, and on seamounts as manganese and cobalt crusts. Nearly all environmental research has focused on the seafloor where the most direct effects will occur. However, sediment plumes and other impacts (e.g., noise) from seafloor mining are likely to be extensive in the water column where both mining effects and communities are unlikely to be restricted to single claim areas. Midwater ecosystems are important in vertical carbon flux and as forage for commercially important species and also require baseline characterization and evaluations of sensitivity and resiliency to deep-sea mining. We will report on the workshop outcomes that brought together a small group of experts to evaluate mining scenarios, their creation of sediment plumes and other impacts, and their likely effects on the midwater environment and communities. We will report on the major knowledge requirements to

establish environmental baselines of the water column in mining regions and strategies for monitoring midwater ecosystems to evaluate short and long term mining impacts. It is our hope that these results will stimulate future research and inform policy makers and ISA managers enabling them to most effectively protect the marine environment.

## The biodiversity of animals living on polymetallic nodules in the eastern Clarion-Clipperton Zone

Adrian Glover [1], Dahlgren TG [2], Wiklund H [1], Smith CR [3]
[1] Natural History Museum, UK; [2] University of Gothenburg, Sweden; [3] School of Ocean and Earth Science and Technology, University of Hawaii, USA
How many types of animals live on polymetallic nodules, and how abundant are they? Given that research into nodule habitats started in the late 1960's, it might be expected that this simple question would be answered by now. However, if we exclude studies of the animals that live in the sediments around nodules, exclude studies that are concerned with foraminifera (not animals) living on nodules and exclude studies that use photography from ROV or AUV survey (which cannot record small animals on nodules) then, remarkably, there are only two published studies in the whole history of nodule research. We present new data from the largest study to date of nodule animal biodiversity and abundance, based on 40 box core samples taken across the eastern Clarion-Clipperton Zone (CCZ). For each box core, every nodule was examined, the animals photographed and identified to species level using morphology and multiple genetic markers. We have already shown in a previous publication that the most abundant animal living on nodules in the eastern CCZ is an entirely new genus of sponges, Plenaster craigi Lim & Wiklund, 2017, that is impossible to observe in AUV survey but is easy to recognize in box core samples. In this paper, we present the abundance and biodiversity of all of the nodule-dwelling animals we found, compare the data to other hard-substrate habitats and discuss the implications for conservation of this region in the light of deep-sea mineral exploration.

## Sample size and biological estimation in abyssal megafauna

Daniel Jones, Erik Simon-Lledo, Noelie M. Benoist, Brian J. Bett, Jeff Ardron, Veerle A. I. Huvenne
National Oceanography Centre
Reliable estimation of ecological parameters relies on adequate sampling of the populations under investigation. Precise description of patterns is key to most aspects of ecology, as information on relative abundance of organisms can be often the sole basis for conservation management decisions. The determination of reliable minimum sample sizes is particularly important in oligotrophic abyssal environments, where extremely low densities but high diversity can lead to under-sampling and imprecise parameter estimates. Exploration of power of the sampling strategy is commonplace in terrestrial and shallow marine ecology. However, except for richness estimators, it is rarely reported for deep-sea studies, which adds uncertainty to the conclusions of most studies and constrains the comparability between them. Here, we investigated the effect of sampling unit size on the precision of different biological estimators commonly applied in ecological assessments of deep-sea megafauna (>10 mm). We used a large imagery dataset covering 18,000 m2 of seafloor (>7000 metazoans) to investigate the relation between sampling effort and precision in the estimation of density, biovolume, diversity of different Hill's numbers (q= 0 to 2), and community dissimilarity. Our analysis shows that precision of ecological estimates was strongly dependent on sample size. While metrics like density and higher order (q>0) diversity measures were less sensitive to sample size, metrics like

richness, biomass or community dissimilarity showed higher dependency on sample size. In the presentation we will discuss how power of a given sampling size can be extremely variable depending on the biological metric calculated. Studies that demonstrate sufficient sampling power to support their conclusions can be key, particularly those implemented for conservation and monitoring purposes, where efficiency must be balanced with the requirement to generate reliable information.

## Experimental assessment of the effect of sediment disturbance and substrate burial on deep-sea meiobenthic communities

Lisa Mevenkamp, Katja Guilini, Alastair Brown, Antje Boetius, Johan De Grave, Brecht Laforce, Dimitri Vandenberghe, Laszlo Vincze, Ann Vanreusel
Ghent University, Belgium; National Oceanography Centre, UK; Max Planck Institute for Marine Microbiology, Germany
Abyssal sediment communities live in a very stable environment where currents and tidal wave action are generally low and sediment disturbances happen at a low frequency. With the mining of deep-sea mineral resources, this condition may change for large areas of the abyssal seafloor. Direct sediment disturbances will be inevitable at mined sites but the activity will likely also produce sediment plumes that resettle in more distant areas. To gain insights in the responses of deep-sea meiobenthos to sediment removal and blanketing of undisturbed seafloor, two short-term, in-situ experiments were conducted in an abyssal polymetallic nodule area in the Peru Basin, SE Pacific. In these experiments, the sediment community from an undisturbed site was buried with crushed nodule particles and artificial sediment. The results of these experiments were compared with those from a similar laboratory experiment on a bathyal fjord community. In all experiments, a consistent migratory response of all major meiobenthic groups into the added substrate was observed. Additionally, this migratory response was accompanied by increased nematode mortality (only assessed in the laboratory experiment). Due to their relatively high importance in deep-sea sediments, the observed responses of the meiobenthos to substrate burial may have wider consequences for the structure and functioning of abyssal communities.

## Do nodules matter for meio- and macrofauna in the Clarion Clipperton Fracture Zone?

Ellen Pape, Nene Lefaible, Tania Nara Bezerra, Hendrik Gheerardyn, Bart De Smet, Ann Vanreusel
Marine Biology Research Group, Ghent University, Belgium
To adequately assess potential environmental impacts of deep-sea polymetallic nodule mining, the establishment of a proper environmental baseline, which incorporates spatial variability, is essential. In the Global Sea Mineral Resources (GSR) license area in the east of the Clarion Clipperton Fracture Zone (CCFZ), distant (60-270 km apart) nodule-bearing sediments harbour similar meio- and macrofaunal communities concerning abundance, composition and diversity. Here, we evaluated the importance of nodule presence for these two benthic size groups in this license area. To this end, a nodule-bearing and nodule-free site were sampled for meio- and macrofaunal abundance, composition and diversity in concert with potentially relevant sedimentary environmental variables. Additionally, nodules were examined for meio- and nematofauna to compare with the sediments. The nodule-bearing and nodule-free site displayed overall comparable environmental characteristics. Nevertheless, chlorophyll a was not detected in any of the nodule-rich sediment samples unlike the nodule-free sediment samples. The two sites were similar

concerning macrofauna abundance, macro- and meiofauna higher taxon composition, nematode genus composition as well as copepod species composition and diversity. However, meiofaunal abundances and total nematode genus richness (pooling all samples per site) were higher in nodule-free than in nodule-rich sediments, which may be related to the presence of fresh organic matter in the former. In contrast, nodule-rich sediments displayed higher total meio- and macrofaunal taxon richness relative to the nodule-free sediments. The higher sediment heterogeneity in the nodule-rich site may have (partly) driven this pattern. Nodules and sediments were both dominated by nematodes and the same nematode genus prevailed in both nodules and sediments. Nonetheless, nematode genus composition and diversity significantly differed between these two habitats. These results imply that nodule-bearing sediments offer a habitat distinct from nodule-free sediments, showing the importance of habitat mapping for the spatial management of mining areas.

Mining impacts - ABSTRACT 173
TUESDAY Afternoon • cancelled • Serra Room
## Broad and fine scale variations affect local megafauna at the CCZ

Erik Simon-Lledo, Jennifer M. Durden, Noelie M. Benoist, Timm Schoening, Rachel M. Jeffreys, Brian J. Bett, Veerle A. I. Huvenne, Daniel O.B. Jones
National Oceanography Centre

The potential for imminent polymetallic nodule exploitation within the Clarion Clipperton Fracture Zone (CCZ) has attracted considerable scientific awareness. Mining disturbances are presumed to extend over extremely large seafloor areas and lead to major changes in benthic fauna. Baseline knowledge of the environmental drivers of biodiversity in the region are hence in high demand. However, the precise roles of key environmental factors regulating the local ecology of these environments are still very poorly understood, and the effect of most individual drivers is yet not appropriately quantified. Here, we explored the response of the megafauna community of the APEI6 (CCZ) to variations in two key environmental drivers operating at different spatial scales. We investigated the effect of geomorphological variations, mapped at a broad scale (few kilometres), and polymetallic nodule coverage levels, mapped at a fine scale (tens of meters). In the presentation we will discuss how these regulate megafauna density, diversity and community compositions across the APEI6 landscape. Carrying capacity was regulated by both factors, geomorphology was a bigger control on the functional composition of the community, and nodule cover was more important for diversity. Combined, these factors added to the ecosystem heterogeneity, generating changes in assemblage composition. Our results go some way to explaining the fundamental drivers of ecosystem structure in polymetallic nodule fields. We believe that appreciation of this complexity in regulations implemented within the CCZ will be key for future conservation strategies to succeed.

Mining impacts - ABSTRACT 105
TUESDAY Afternoon • 16:00 • Serra Room
## Alpha and beta diversity of polychaete assemblages across Clarion-Clipperton Zone

Paulo Bonifacio, Lénaick MENOT
Ifremer EEP/LEP

In the abyssal Equatorial Pacific Ocean, polymetallic nodules from the Clarion-Clipperton Fracture Zone (CCFZ) arouse strong industrial interest, which may threaten the biodiversity of benthic communities. Studies in the CCFZ started many decades ago but the benthic communities remain poorly known. The JPI Ocean cruise SO239 contributed to fill this lack of knowledge by sampling four different contract areas in the CCFZ (4000-5000 m depth): BGR, IOM, GSR and Ifremer. The Area of particular environmental interest number 3 (APEI#3) was sampled as well. Between 5 and 10 box cores (0.25m2; 0-10 cm) were sampled in each area resulting in a large collection of polychaetes which were morphologically

and molecularly (COI, 16S and 18S genes) analyzed. The aim of this study are: (a) to evaluate the diversity and connectivity patterns of polychaetes and (b) to describe their community composition within the CCFZ. A total of 1279 polychaetes were sampled with spionids, cirratulids, paraonids and lumbrinerids accounting for more than 50% of the abundance. The polychaete abundance presented significant positive correlation with the presence of nodules (rho=0.40, p=0.018) and POC flux (rho=0.43, p=0.009). The species-level identification of 85% of polychaete specimens based on morphological and molecular criteria suggested that among the areas: (a) the patterns of diversity are very close at family, genus or even species-level level; (b) the community composition changes along a longitudinal gradient that may be linked to the presence of nodules and POC flux; and (c) among the 319 morphotypes that have been identified, a majority is restricted to only one contract area while only 3 have a widespread distribution over all 5 areas. Evaluating the biodiversity of benthic communities as well as the scales of species turnover and connectivity is essential to predict and mitigate the impacts of nodule exploitation.

Mining impacts - ABSTRACT 188
TUESDAY Afternoon • 16:15 • Serra Room
## Biodiversity of megabenthos in the western Clarion Clipperton Zone

Jennifer M. Durden, Craig R. Smith, Astrid Leitner, Jeff Drazen, Diva Amon and the DeepCCZ Project Scientists
University of Hawaii at Manoa

The Clarion Clipperton Zone (CCZ) in the equatorial Pacific, a vast (1000 x 4000 km) region of abyssal plain punctuated by topography such as seamounts and ridges, is targeted for seabed mining for polymetallic nodules. Topographic heterogeneity is known to influence the diversity and structure of deep-sea megabenthic communities. However, the ecosystem consequences of topographic habitat heterogeneity are not well known at regional scales in the CCZ. Such knowledge is important to understanding regional-scale variation in abyssal benthic communities and their function, and necessary to manage and conserve biodiversity and ecosystem function in the face of nodule mining. Nine 400x400 km areas within the CCZ have been provisionally protected by the International Seabed Authority from mining to conserve biodiversity across the region; their designation was based on environmental correlates of biodiversity and ecosystem function, but whether they represent the wider region, especially in the western CCZ, remains to be tested. In addition, much of the work to characterize the megabenthos within the CCZ has focused on the eastern portion. This study examines the diversity and community structure of megabenthos in three areas protected from mining in the western CCZ, assessing habitats from abyssal plains to seamounts. In particular, we test the hypothesis that seamounts provide refugia and/or larval sources for abyssal populations potentially impacted by mining. Preliminary findings on biodiversity and community structure will be presented from photographic surveys conducted with an ROV in the western CCZ. In the future, our results from the western CCZ will be synthesized with studies from the eastern/central CCZ to characterize biodiversity, biogeography, and connectivity across the region.

# Mining impacts - POSTERS

POSTER 136 + Mining impacts
TUESDAY Evening • 17:45 • Serra Ballroom
## Meiofaunal communities in the Clarion-Clipperton Zone: geographic distribution and link with environmental conditions

Freija Hauquier , Macheriotou L, Bezerra TN, Egho G, Martínez Arbizu P, Janssen F, Vanreusel A
Marine Biology Research Group, Ghent University (UGent), Gent, Belgium

Polymetallic nodule mining in the abyss is a nascent industry hoping to meet the growing worldwide demand for metallic minerals. Given that prospective mining is likely to have a profound impact on deep seafloor communities, knowledge on their wider geographic distribution is pivotal in order to provide sound guidelines for environmentally sustainable mining practices. We therefore studied benthic meiofaunal communities spread along four prospective mining areas and one non-mining Area of Particular Environmental Interest in the Clarion-Clipperton Zone (CCZ) of the east Pacific Ocean. Meiobenthic abundance in the upper sediment layer followed an eastward increase in particulate organic matter input, indicating their dependence upon water-column processes. Additionally, standing stock was clearly correlated with the degree of nodule coverage at the different prospective mining areas, with high nodule coverage leading to less sediment volume and thus lower numbers. Future nodule removal through mining activities might therefore lead to an increase in numbers for smaller-sized benthic taxa.In terms of community composition, nematodes were the most abundant meiobenthic taxon, yet showed no pronounced variation in diversity or genus composition between the different mining and non-mining areas. Assemblages were typically dominated by a few genera accounting for the majority of community totals, as well as a large number of rare genera contributing only little to overall abundances. Dominant genera were widely spread within the CCZ and shared among all sampled areas, whereas rare genera were usually limited to one area. The same trend was present when looking at the level of morphospecies, implying that it might be mainly those taxa with a more limited spatial distribution that will be affected by changes in their habitat and/or reduced connectivity between different areas.

## Experimental polymetallic nodule mining affects deep-sea microbial communities and functions

Felix Janssen, Tobias Vonnahme, Massimiliano Molari, Frank Wenzhöfer, Matthias Haeckel, Antje Boetius
Deep Sea Ecology and Technology group, Max Planck Institute for Marine Microbiology and Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research, 27515 Bremerhaven, Germany

Potential effects on deep-sea benthic microbial communities and biogeochemical functions in response to seafloor disturbance by polymetallic ('manganese') nodule mining were investigated in the DISCOL Experimental Area (DEA). In 1989 the >10 km2 large DEA in the Peru Basin was disturbed by repeated ploughing, representing the largest benthic impact experiment ever carried out to date to investigate ecosystem impacts of deep-sea mining. Historical 'plough tracks' and a 5 weeks old track from Epibenthic Sledge sampling ('EBS-track') were studied in Sep. 2015 as part of the JPI Oceans project 'MiningImpact'. Microbial communities and functions were assessed based on sediment analyses, shipboard incubations, and in situ flux studies with autonomous benthic chamber and micro-profiler systems. Investigations were carried out by ROV at specific microhabitats in plough- and EBS-tracks and compared to conditions off track and in reference areas outside the DEA. In the tracks where the disturbance removed parts of the reactive surface layer or even exposed organically poorer and more consolidated subsurface sediments, microbial and biogeochemical characteristics were affected and resembled conditions in deeper sediment layers, even after 26 years. Microbial biomass, organic matter degradation activity, respiration rates, and microbial secondary production were generally reduced. Microbial community structure in the EBS-track differed significantly from undisturbed surface sediments while in the historical plough marks recovery of communities over the past decades cannot be ruled out due to their large spatial heterogeneity. Extending the scope of earlier post-impact studies to microbiology, the results suggest long-term effects of nodule mining right at the basis of the benthic food web. Further studies are required to assess consequences for higher trophic levels and the time needed for ecosystem recovery, and to address the suitability of

microbial communities and functions as impact indicators for routine monitoring in the context of nodule mining in the deep sea.

## Polynoids from Clarion-Clipperton Fracture Zone: new species and phylogenetic insights

Paulo Bonifácio, Lénaick MENOT
Ifremer EEP/LEP

The family Polynoidae contains approximately 900 species within 18 subfamilies, some of them restricted to the deep sea. The subfamily Macellicephalinae is the most diverse among these deep-sea subfamilies. In the abyssal Equatorial Pacific Ocean, the biodiversity of benthic communities is at stake in the Clarion-Clipperton Fracture Zone due to increased industrial interest for polymetallic nodules. To date, the records of polychaetes in this region are scarce. Data gathered during the JPI Ocean cruise SO239 significantly contributed to fill this gap with five different localities sampled in the CCFZ between 4000-5000 m depth. The samples were collected using an epibenthic sledge or a remotely operated vehicle, that resulted in a large collection of polynoid worms. The aims of this study are: (a) to describe news species of deep-sea polynoids using morphology and molecular data (COI, 16S and 18S genes) and (b) evaluate the monophyly of Macellicephalinae. Based on molecular and morphological phylogenetic analyses ten subfamilies are synonymized with Macellicephalinae in order to create a monophyletic and homogeneous clade. Further, 17 new species and four new genera are described highlighting the high diversity hidden in the deep sea.

## Contrasting distributional patterns in closely related isopod species from the Pacific nodule province (CCZ) inferred from mtDNA and morphological data

Stefanie Kaisera,2, Saskia Brix2, Terue Cristin1 Kihara3, Inga Mohrbeck3, Annika Janssen3, Rob Jennings4
1Centre of Natural History, CeNak, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany; 2German Centre for Marine Biodiversity Research (DZMB), Senckenberg am Meer, c/o CeNak, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany; 3DZMB, Senckenberg am Meer, Südstrand 44, 26382 Wilhelmshaven, Germany; 4Temple University, Biology Department, 1900 North 12th Street, Philadelphia, PA 19122, USA

For long, the abyssal seafloor has been among the most pristine and stable environment on Earth. However, human pressures are currently increasing to exploit its prevailing mineral resources (such as polymetallic nodules), which would cause unprecedented impacts for the resident fauna. Assessing species` realized biogeographic range and its potential drivers is important to forecast recovery and recolonization potential following mineral mining activities; that is, wide-ranging species with high genetic connectivity are potentially more robust and have a greater recovery potential following disturbance events than species with a narrow geographic range, low dispersal ability (such as brooders) and/or limited gene flow among sub-populations. We examined geographic patterns of genetic variation for closely related species in the isopod genus Nannoniscus that occur broadly across the central Pacific nodule province (Clarion Clipperton Fracture Zone, CCZ). Sampling conducted in different license areas across the CCZ (e.g. German, French, GSR, OMS) as well as two APEIs enabled assessment of phylogeographic patterns at multiple spatial scales (tens to several hundred kilometers). Molecular analyses using two mtDNA markers (COI, 16S) were coupled with morphological examinations to aid and increase confidence in species identification and unravel the nature and the primary mechanisms of biological variability. Due to their prevailing reproduction mode (brooding) coupled with putatively poor swimming abilities of species within Nannoniscus we

expected to find strong population divergence or even presence of cryptic lineages in relation to distance. Nevertheless, out of the six species identified we found two lineages to be distributed over large geographic distances (up to 1300 kms), while the remaining were locally restricted. Furthermore, we found several sibling species to co-occur in the same geographic area. Insights obtained from these analyses may help to understand the mechanisms and drivers affecting faunal connectivity and thus population differentiation or maintenance in abyssal waters.

## Effects of sedimentation from deep-sea mining: a benthic disturbance experiment

Malcolm Clark, Craig Stevens, Scott Nodder, Ashley Rowden, Vonda Cummings
NIWA, New Zealand

There is a lot of interest, but also concern, about the potential environmental effects of deep-sea mining in New Zealand. There are a number of likely impacts from mining operations, but a key issue is uncertainty about the effects of sediment plumes created by disturbance to the seafloor and discharge of processed waters. This research project, scheduled from 2016 to 2021, aims to improve our understanding of such impacts (relevant to both mining and trawl fisheries), by examining the extent and persistence of sediment plumes, the immediate impact and subsequent recovery of seafloor exposed to these plumes, and the effect on functioning of ecologically significant speciesWe will use a combination of field survey experimentation with in situ observations, and controlled laboratory-based experiments. •The field work begins in May 2018 when an area (of up to 1km2) at depths of 400-500 m will be subjected to disturbance by the NOAA Benthic Disturber. The suspended sediment load created by the disturbance will be tracked and monitored, with the effects on seafloor animals examined by pre-and post-disturbance sampling. Monitoring surveys will be repeated in 2019 and 2020 to determine the longer-term resilience and recovery of disturbed communities. •The laboratory-based side of the programme, also starting in 2018, involves holding live deep-sea corals and sponges in tanks at NIWA, and exposing them to various levels and duration of particle loads in the water in order to reveal lethal thresholds as well as sub-lethal effects of settled and suspended sediment. This poster will outline project aims and describe work to date.

## Biogeography of Bait-Attending Fauna Across the CCZ

Astrid Leitner*, Sage Morningstar*, Jens Greinert**, Jennifer M. Durden*, Craig R. Smith*, and Jeffrey C. Drazen**University of Hawaii Manoa** GEOMAR
*University of Hawaii Manoa; **GEOMAR

The Clarion-Clipperton Zone (CCZ) is a vast region of the Pacific that has been targeted for large-scale deep-sea manganese nodule mining. The biogeography of the animals found in this and neighboring abyssal regions is still poorly understood despite the imminent threat of biodiversity loss as a consequence of mining activities. Though there has been a recent flurry of work in the CCZ, research looking at the top-predators and scavengers of the region is still limited. Sampling the top of the food web is crucial since predators can exert significant top-down pressures on prey populations. Baited cameras provide the opportunity to quantitatively assess highly mobile predators, since most are also opportunistic scavengers in the deep-sea. Moreover, these animals are generally undersampled by other techniques due to avoidance. Here we present baited camera data from two mining claim areas and 4 proposed mining reserve areas known as Areas-of-Particular-Environmental-Interest (APEI) spanning the entire CCZ and including abyssal plains, abyssal hills, and seamounts. We place our findings into biogeographic context through

comparison with recent abyssal deployments near Hawaii and recent analysis of baited camera deployments from the DISCOL site in the neighboring South Pacific, as well as through comparisons with published work from the abyssal Kermadec, California slope, and the Main and Northwest Hawaiian Islands. Understanding the biogeography of top predators of the CCZ will be crucial to mitigating biodiversity loss due to manganese nodule mining.

## Meiobenthos at a former deep-sea experimental disturbance test site twenty years post-disturbance

Teresa Radziejewska, Joanna Rokicka-Praxmajer, Brygida Wawrzyniak-Wydrowska
Faculty of Geosciences, University of Szczecin

In July 1995, an experiment (IOM BIE) aimed at producing disturbance on the seafloor imitating that generated during nodule mining was conducted in the Pacific's Clarion-Clipperton Fracture Zone by the Interoceanmetal (IOM), a 6-nation consortium aiming to prepare future nodule development. A 1.5 x 2 km area of the seafloor, at ca. 4300 m depth, was impacted by a series of tows of a device called the Benthic Disturber. The magnitude and intensity of the disturbance was assessed by examining changes in metrics pertaining to the meiobenthic assemblage structure as the major proxie, both qualitative (genus-level taxonomic composition of nematodes and harpacticoids) and quantitative (abundance of the total meiobenthos and dominant taxa as well as the relative abundances of the latter). An attempt was also made, by resampling the test site during follow-up cruises undertaken at various time intervals (22 months and 5 years) post-disturbance, to determine the degree of recovery in the disturbed area and its recolonization. The meiobenthos did respond to habitat disturbance, the major response being seen in the reduction of abundance immediately after the disturbance. Effects observed during the follow-up studies involved some degree of recovery, accompanied by alteration in the taxonomic composition of nematode and harpacticoid taxocoenes. To answer questions of how persistent those effects are and whether recovery can be observed in the long-term, the site was resampled in April 2015, 20 years after the disturbance, during Cruise SO239 of RV Sonne undertaken within the Joint Programming Initiative (JPI) Oceans Pilot Action project "Ecological Aspects of Deep-Sea Mining". The resultant data on the meiobenthic assemblage structure are compared with the community status before and after the experimental disturbance.Support from the JPI Oceans Pilot Action "Ecological Effects of Deep-Sea Mining" and from the Polish National Science Centre grant No. 2014/13/B/ST10/02996 is acknowledged.

## Approach to the Management of Benthic Megafaunal Assemblages of the CCZ (Eastern Pacific) in the Face of Anthropogenic Impacts

Virginie Tilot1,2, R. Ormond3,4, J. Moreno Navas5, T.S.Catala6,7, J. Mallefet 8
1 UMS (AFB CNRS MNHN) Patrimoine Naturel, Muséum National d'Histoire Naturel, Paris, France, 2 Instituto Español de Oceanografía, Malaga, Spain, 3 Centre for Marine Biodiversity and Biotechnology, Heriot-Watt University, Edinburgh,U.K. 4Marine Conservation International, Edinburgh, United Kingdom, 5 Physical Oceanography Research Group, Universidad de Málaga, Málaga, Spain, 6 Institute for Chemistry and Biology of the Marine Environment (ICBM), 7University of Oldenburg, Oldenburg, Germany, 8Earth and Life Institute, Université Catholique de Louvain, Belgium

Megafaunal assemblages serve as a good indicator of the status of a habitat in the face of natural and anthropogenic impacts. On basis of a comprehensive baseline study of photos and videos taken at 5 different

areas of the polymetallic nodule ecosystem of the CCZ of the eastern Pacific Ocean, the structure of the epifaunal populations associated with the benthic biotopes has been investigated with the support of IFREMER and UNESCO/IOC. An appropriate set of management tools including species diversity and vulnerability indexes, GIS systems, zoning, eco-hydrodynamic modeling, 3D rapid environmental assessment (REA) and predictive modeling with alert systems have been developed on a pilot site to monitor impacts of future deep sea mining and propose management strategies. The general characteristics of nodule ecosystem and assemblages and their sensitivity to deep-sea mining is discussed in relation to water masses, surface to seabed water circulation, the nepheloid layer and processes taking place at the sediment interface. As a team (DSMMWG), the authors propose a Multilayer Assessment Programme (MAP) connecting data analysis, modelling and decision making within a spatial context adapted to a marine spatial planning and management perspective. The MAP is composed of a) A Preferred suite of Biological Indices of ecosystem value and health highlighting the importance of key functional groups b) A Protocol for Rapid Environmental Assessment (REA) with a suite of indicator species and parameters for sensitivity and effectiveness including bioluminescence c) a permanent Tri-Dimensional Monitoring System in the entire water column, in particular in the 2 identified vulnerable water masses d) An Environmental Sensitivity Index (ESI) for the different nodule habitats coupled to GIS maps, e) A Management Alert System (MAS), with threshold values for harmful effects that will signal to managers the need for caution or immediate ameliorative actions, f) A Predictive Ecohydrodynamic Model to assist management in building scenarios to react to impacts of mining.

POSTER 144 ⚡ Mining impacts
TUESDAY Lightning Talks • 08:30 • Serra Room

## Environmental Risk Assessment of Deep-Sea Mining at Manganese Nodule Beds and Hydrothermal Vents

Travis Washburn, Phil Turner, Cindy Van Dover
Duke University

A number of desk studies have generated long lists of potential environmental risks of deep-sea mining, but it can be challenging to understand which risk sources are of greatest concern. In this study, we use expert opinion obtained from a 2016 survey of deep-sea scientists to rank the level of concern regarding risk sources (scale: 0 to 4) that might result from mining activities in manganese nodule beds (19 respondents) and at active hydrothermal vents (7 respondents). Risk sources associated with habitat removal and alteration were of greatest concern in both systems. In addition to risks associated with removal of nodules and sulfides, sediment compaction, changes in habitat heterogeneity, changes in porewater and hydrothermal fluid geochemistry, excavation, and organic enrichment of the sediment due to mortality and decomposition of organisms were of concern (3.2 > x nodules; 2.2 > x vents). Risk sources associated with vehicle-generated plumes and tailings (i.e., tailings from the surface ship) were more variable in terms of risk. Greatest risks in the 'plume' category were perceived to come from burial of organisms, impacts to deposit feeders, and changes in particle size distributions in sediments from vehicle-generated plumes and by alteration of ambient temperature, pH, POC, and/or O2 from return plumes near the seabed. Toxicity of plumes was of lower concern (X = 2.7 nodules; 1.8 vents). Mining-tool-generated risk sources (i.e., light, sound, electromagnetic radiation, introduced species) at the seabed were perceived to have lowest risk for nodule beds, while changes to the water column from the plume had the lowest risk for vents compared to other risk-source categories considered. This risk assessment suggests that mitigation efforts should focus on minimizing the footprint of mining tools and the plume and that monitoring efforts (including baseline assessments) should include metrics that assess these risks.

POSTER 145 - Mining impacts

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## Characterization of deep-sea macrobenthos in the Korea exploration claim area in the Clarion-Clipperton Fracture Zone

Ok Hwan Yu, Hyung-Gon Lee, Dongsung Kim, Kyeong Hong Kim, Chan-Min Yoo
Korea Institute of Ocean Science & Technology

Macrobenthos in the Clarion-Clipperton Fracture Zone remains poorly understood, due both to gross undersampling and to the fact that most species collected from the area are new to science. Evaluation of the diversity and species distribution of the benthic fauna in this area is critical to predicting and managing the impacts of manganese nodule mining. In this study, we investigated the distribution of macrobenthos to understand the natural variability in the macrobenthic community and, by extension, to establish a baseline for environmental risk assessment. Samples were collected from KR5 block of the Korea Contract Area, within the abyssal area of the Clarion-Clipperton Fracture Zone in the northeastern Pacific Ocean, by the RV Onnuri from 2012-2014. A total of 36 core samples were examined in the survey, from which we identified 183 macrobenthic species in 25 faunal groups with a mean density of 257 ind/m2. Not taking into acount meiofaunal groups such as nematodes and harpacticoid copepods, the highest percentage of individuals was represented by Arthropoda. The dominant species (>1% of total density) were the tanaids Typhlotanais sp.1, and Akanthophoreus spp. and Stenotanais sp., the isopod Macrostylis sp.1, and the polychaetes, Cirratulidae spp. and Levinsenia uncinata. The abundances of two dominant species, the tanaid Typhlotanais sp1. and isopod Macrostylis sp.1., were positively correlated with total organic carbon (TOC). There were no differences in macrofaunal density and community structure between preserved areas (PRA), the potential benthic impacted site (BIS), and other areas near the BIS. In general, higher diversity was associated with homogeneous environmental conditions, with high nodule coverage (> 50%) and TOC.

# Natural and anthropogenic disturbance - TALKS

## Benthic habitats in West Greenland

Chris Yesson, Kirsty Kemp, Mona Fuhrmann, Stephen Long, Nanette Hammeken, Martin Blicher
Zoological Society of London, Greenland Institute of Natural Resources

Benthic habitats in West Greenland. West Greenland is home to commercially important Coldwater Prawn and Greenland Halibut fisheries. These demersal trawl fisheries operate at depths of 200-1400m in Davis Strait and Baffin Bay. The entry of these Arctic and sub-Arctic fisheries into the Marine Stewardship Council sustainability scheme has highlighted the lack of information about benthic habitats in the region. Epibenthic organisms are a critical component of the marine ecosystem, understanding their composition and distribution is an important step in ensuring sustainable management of fisheries. This talk will review the findings of 8 years of benthic imaging surveys along the West Coast of Greenland, spanning 2000km of coastline from 60-75 N. The surveys, using low-cost camera equipment, have braved iceberg encounters to document a great variety of benthic fauna, including VME species in the region. We demonstrate the impact of trawling on benthic habitats in the region. Impacts differ by habitat, with muddy habitats more resilient, potentially recovering in under 5 years, while impacts on rockier areas may last 20 years. This study represents the first quantitative characterization of epibenthic megafaunal assemblages on the west Greenland continental shelf. These data constitute a critical baseline, albeit impacted by trawling, to enable long term monitoring and observations of change. Positive

engagement with the local fishery organisation has led to notable conservation outcomes, including gear changes to reduce the impact on vulnerable species, and protection of 1900km2 of Arctic seabed habitat within Melville Bay.

## Understanding UK deep-sea biodiversity sensitivity from sediments to seamounts

Laura Robson, Ellen Last, Harvey Tyler-Walters, Heidi Tillin
JNCC

As an island nation, the UK is surrounded by water, spanning from the coast and intertidal, to the circalittoral and deep-sea. Understanding the changing condition and resilience of marine biodiversity within these vastly different water masses is of key importance to understanding both the impacts of, and how to best manage, human activities whilst enabling continued sustainable development. The Joint Nature Conservation Committee (JNCC) has recently part-funded the Marine Life Information Network (MarLIN) project undertaken by the UK's Marine Biological Association. This has developed a method to assess the sensitivity of marine habitats and species to a range of pressures caused by human activities. The Marine Evidence Based Sensitivity Assessment (MarESA) method uses best available evidence within literature to review the tolerance (resistance) and recovery rates (resilience) of key and characterising species, and their associated physical habitat, of UK biotopes (Connor et al, 2004), against a list of pressures such as physical damage, siltation and chemical contamination. A final sensitivity score is provided for each biotope per pressure. Whilst evidence for these sensitivity assessments is becoming more widely available for offshore waters, there is a large evidence gap on deep-sea biodiversity sensitivity, and understanding how to manage this little-studied environment. With ongoing pressures from fishing and oil and gas activity, and future threats from deep-sea mining, this is a key area of research which is urgently needed to help develop effective and sustainable management measures. As such, JNCC are currently reviewing the literature available on the sensitivity of UK deep-sea biotopes (Parry, 2015) to a set of key pressures associated with deep-sea activities. This talk will showcase results achieved to date on assessing deep-sea resistance and resilience of these biotopes, and identify some of the key gaps and challenges that have been identified during the process.

## Exploring partial effects of environment and trawling on biodiversity and ecosystem functioning

Jesse van der Grient, Alex Rogers
University of Oxford

Structural equation modelling is a technique developed to test multivariate theories. Here, we developed such a model to investigate the influence of environmental factors on diversity measures and the effect of bottom trawling in the system. 300 polychaete box cores were taken from around the Flemish Cap and Grand Banks area in the north-western Atlantic, a soft-bottom area. By incorporating both environmental and anthropogenic factors, we explore their effects on changes in the biodiversity-ecosystem functioning (BEF) relationship. We show the first positive and saturating BEF relationship for macrofauna, and how trawling impacts this relationship. Community composition changes, with high capitellids numbers comparable to carbon-enriched areas such as under fish farms While much work has been done on trawling impacts on seamounts, these results suggest that soft-bottom macrofaunal communities also show high signatures of impacts.

## Impacts of deep-sea Greenland halibut trawling on benthic ecosystems

Stephen Long, Dr Chris Yesson, Dr Mona Fuhrmann, Dr Martin Blicher
Institute of Zoology (Zoological Society of London), Department of Geography (University College London)

Over-exploitation of fish stocks in recent decades has driven fishing effort deeper and further offshore. In polar waters climate change is causing increasing temperatures and reductions in sea ice extents, altering the distribution of stocks and associated fisheries. Greenland's fisheries sector makes up 90% of the country's exports, with the Greenland halibut (Reinhardtius hippoglossoides) fishery accounting for 14% of national catch. The west Greenland offshore Greenland halibut fishery operates in Arctic and sub-Arctic waters, deploying demersal trawl gear at depths of 800 – 1400m. Entrance of this fishery into the Marine Stewardship Council (MSC) certification process has highlighted the paucity of existing knowledge of deep-sea habitats in the Arctic, including the distribution of vulnerable marine ecosystems (VMEs). This ongoing research aims to quantify the impact of trawling on benthic habitats within this fishery by deploying a purpose built benthic video sled across a spectrum of fishing effort. Fishing effort data has been obtained from Greenlandic regulators and Global Fishing Watch (GFW). The sled employs a low-cost commercially available action camera (GoPro), paired with lights and scaling lasers. New deep-sea imagery from the Davis Strait is showcased, with VME indicator species' abundance estimates used to provisionally assess trawling impacts. Numerous VME indicator species were identified in the study area, with the density of the stony cup coral Flabellum (Ulocyathus) alabastrum found to be as high as 4.6 individuals m-2. The abundance of some VME sponge and coral species, including Asconema foliatum and Acanella arbuscula, was found to be higher in untrawled areas. Trawl scars and other regular linear features were observed at multiple stations within the fishery footprint. Improved knowledge of these ecosystems and their response to demersal trawling pressure will be vital to inform management and critically assess the sustainability of deep-sea fisheries in the Arctic.

## Microplastics are a serious threat for deep-water coral reefs

Leila Chapron, Peru E., Engler A., Godéré I., Ghiglione J.F., Lebris N., Meistertzheim A.L., Pruski A. M., Purser A., Vétion G., Galand P. E., Lartaud F.
Laboratoire d'Ecogéochimie des Environnements Benthiques

Cold water corals are key ecosystem engineers in the deep sea and reefs act as hotspot of biodiversity. In submarine canyons, hydrological events such as downwellings are essential for food supply and influence the growth of deep corals. However, these currents also export a considerable amount of plastics to these deep ecosystems. The increase in plastic litter in marine environments is now recognized as one of the most serious environmental issue. Among the variety of debris accumulated in the oceans, both macro and micro plastics are by far the most abundant, in surface and in deep waters. However little is known about their impact especially on the emblematic reef-building cold-water corals. The aim of this project was to investigate the physiological effects of macro- and microplastic exposure, under different time scales (from week to months), on the main deep engineer species, Lophelia pertusa. The study was based on an integrated approach at different levels of biological organization. It included the joint analysis of the growth processes, the measure of stress level and energy status of the host, and the characterization of the associated microbiome. Our results showed that both micro- and macroplastics had a significant negative impact on the skeletal growth rate. Macroplastics acted as a physical barrier for food supply limiting energy acquisition and allocation. The mechanisms behind the impact of microplastics were less clear since basic physiological

functions (e.g., prey capture, polyp activity) were not impacted after several weeks of exposure. Possible toxicological effects or increased energy costs induced by plastic ingestion/egestion might be responsible for lower skeletal growth. Considering the local accumulation of macroplastics and the widespread distribution of microplastics in the ocean, our results suggest that plastics may constitute a major threat for the resilience of deep-water coral reefs and their associated biodiversity.

## Is the northern expansion of Atlantic cod (*Gadus morhua*) impacting scavenging communities in high Arctic fjords?

Katherine Dunlop, Paul Renaud, Jørgen Berge, Andrew Sweetman
Akvaplan-niva

Recent warming events in the Arctic have coincided with a northward expansion of Atlantic cod (Gadus morhua) into western Svalbard fjords. Atlantic cod is a highly adaptive demersal feeder and its expansion is likely to cause significant changes in structure and function of deep fjord benthic communities in the Arctic. Scavengers play a key role in the cycling of organic material in the marine environment, but knowledge of Arctic scavenging communities is sparse and little is known about how this group may be affected by the direct and indirect impacts of rapid climatic changes. This study compares scavenging dynamics among Svalbard fjords where Atlantic cod are present (Kongsfjorden, Raudfjorden, and Isfjorden) and fjords where Atlantic cod are absent (Rijpfjorden and Billefjorden). The "Anonyx`" deep-sea camera lander captured time-lapse imagery of scavenger communities consuming herring bait over 10 hours between water depths of 189 and 360 m. Scavenger community composition was significant different between cod-influenced and cod-free fjords. In Atlantic cod fjords, scavenger numbers were lower and dominated by Pandulus shrimps (Pandulus borealis) and fish (mean maximum abundance of scavengers = 22). In comparison, communities in cod-free fjords were dominated by large numbers (mean maximum abundance of scavengers = 1300) of scavenging amphipods (Anonyx spp.) and ophuiroids (Ophiopleura borealis) that quickly reduced the bait to bones. Bait removal rates (g removed per hour) were approximately 10 times lower in cod-influenced fjords ($27.7 \pm 6.5$ g/hr) compared to fjords where they were absent ($284.5 \pm 0.5$ g/hr). This presentation will explore potential mechanisms for the impact of Atlantic cod expansions on scavenger communities in high Arctic fjords using time-series data from these fjords on demersal fish diversity, abundance and stomach content analysis and benthic invertebrate communities. Session: Deep Carbon Flux: sources, processes, and associated communities

## Recovery in the deep sea from trawling: insights from New Zealand

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The recovery dynamics of deep-sea habitats impacted by bottom trawling are poorly known. This paper reports on a 'fishing impact recovery comparison' based on repeated towed camera surveys on six small seamounts east of New Zealand. These seamounts covered conditions where trawling had ceased, where trawling was still active, or seamounts which were untrawled. Surveys were carried out in 2001, 2006, 2009, and 2015 (spanning 15 years). Univariate community metrics of biodiversity (abundance, species richness, diversity) were almost always higher for untrawled Ghoul and Gothic seamounts than the other four. Multivariate community analyses of each seamount at each time-step showed a similar pattern, with the untrawled Gothic and Ghoul seamounts having similar levels and patterns of community structure at one end of the ordination space, the persistently heavily trawled Graveyard seamount at the other

end along with the previously heavily trawled and now closed Morgue seamount, and intermittently trawled seamounts lying in-between. This ordination matches the gradient in commercial fishing effort. Community structure on Graveyard seamount was more consistent than on the other seamounts, with persistently lower faunal richness, possibly due to a regular 're-setting' of the community by disturbance from trawling. Although the analysis over time is confounded by technological changes, there is no evidence that benthic communities on Morgue seamount are recovering following its closure to fishing in 2001. Intact scleractinian coral 'reef' is or was a "climax habitat" on the Graveyard Seamounts, and levels of this habitat on Morgue seamount remain much lower than those on the untrawled seamounts. Implications are that in these situations, management options should not rely upon recovery, but focus on protecting habitat from potential impacts.

## Effects of a seamount protected area on deep-water demersal fishes (Condor seamount, NE Atlantic)

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Seamounts have proved to be extremely vulnerable to fishing. Various measures have been proposed to improve their management, including the protection of some seamounts to enable deeper scientific studies on ecosystem functioning and recovery from anthropogenic impacts. The Condor seamount (Azores, North-East Atlantic) has been a traditional fishing ground for decades, but from 2008 it has been turned into a scientific observatory, targeted by studies on different aspects of seamount ecosystems. This deep-sea seamount was designated as a protected area of the Azores Marine Park for the management of fishing resources, being bottom fishing prohibited in the area since 2010. The experience running at Condor represents a tool to learning lessons about responses to harvesting, recovery and resilience to fishing impacts, by providing data on temporal changes in demersal fish abundance and biomass and their recovery after cessation of fishing. Here we present the results of the annual monitoring survey conducted at Condor between 2009 and 2017, using bottom longline. The effect of the seamount protected area is positive on the blackspot seabream (Pagellus bogaraveo), the most important commercial species in the Azores, which shows a high increase in abundance and biomass, along seven years of protection regime. In other species these indicators fluctuate and considering their average high longevity, it is expected that recovery may be slow. Besides its importance for science, the Condor experience can serve as an example to create other protected areas for management of marine resources.

## Cold-water corals as indicators of anthropogenic impact in the deep sea: lessons learned from the Deepwater Horizon oil spill

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Cold-water corals as indicators of anthropogenic impact in the deep sea: lessons learned from the Deepwater Horizon oil spillAfter the Deepwater Horizon oil spill in 2010, three impacted coral communities were discovered. When the first community was discovered three months after the well was capped, corals were covered in a brown flocculent material

(floc) that contained traces of oil, directly linking the observed damages to the spill. Eleven months later, two other affected communities were discovered. Although corals at these sites were no longer covered in floc, the characteristic patchy impact on the colonies indicated that these corals had also been impacted by the spill. We quantified the impact and assessed the recovery of corals using high-definition photographs. Over 300 individual _Paramuricea_ spp. colonies, well suited for visual monitoring due to their morphology, were imaged and digitized every year between 2011 and 2017. Overall, recovery was slow. Improvements in condition between every consecutive year were negatively correlated with the initial level of impact. Furthermore, branch loss was still significantly higher at two impacted sites in 2017 than at the reference sites. We were also able to measure in situ growth rates and found that impacted corals began to grow faster than healthy corals after 2014, likely to compensate for branch loss. The method we employed allows the detection of small changes in the health of corals that would not be visible with monitoring based on transects. Planar octocoral colonies are well suited to monitor for anthropogenic impact to the deep sea: Natural mortality is rare, they constantly sample the water column to feed and exchange gases, they are normally almost entirely covered with living tissue, making impact detection relatively easy, and they are attached to the seafloor providing a long lasting, spatially explicit, record of damage to a colony. Therefore, we suggest the establishment of image-based coral-monitoring sites to collect baseline data on coral biology, assess the efficacy of Marine Protected Areas, and detect future anthropogenic impact to these vulnerable deep-sea ecosystems.

## Community dynamics at inactive and active vent sites at the 9°N East Pacific Rise after a volcanic eruption

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In early 2006, a major volcanic eruption buried faunal communities over a large area of the 9°50'N EPR vent field. We monitored community dynamics at active and at young inactive vent sites by deploying and recovering settlement substrates (plastic kitchen sponges) one, two and four years after the eruption.In late 2006, we observed that one vent site within the lava-covered area, the black smoker Bio9, was not destroyed by the volcanic eruption. The site contained similar faunal species as observed pre-eruption. In addition, new areas of diffuse venting emerged at several sites (P-Vent, Sketchy, Tica), which were colonized by Tevnia tubeworms. The associated fauna amongst Tevnia included species that could have migrated from the survivor site Bio9 and species that were not known from the area pre-eruption. These early colonizers were abundant in the first year but declined in abundance over time. Four years after the eruption, about 40% of the meio- and macrofaunal species had returned to those tubeworm sites.There was significant ebbing of vent fluid emissions in the years following the volcanic eruption. Two vent sites that were known to be active pre-eruption (Q-Vent and East Wall) showed no sign of venting activity in 2006, probably related to clogging or restructuring of vent fluid channels during the eruption event. Species associated with these decaying megafaunal communities included non-vent species and many typical EPR vent species, including early colonizers. The nascent venting areas at Sketchy and P-Vent became inactive in 2007 and 2009. Arrival of colonizers from remote areas may have had an effect at active and inactive sites. The faunal colonization at active and inactive sites also demonstrated broad habitat range of early colonizers. The young inactive vent sites supported diverse and abundant meio- and macrofaunal communities and shared species with the active vent sites, suggesting that they may provide potential source populations after disturbance events.

## Detecting the effect of scientific drilling on meiofauna with the traditional, metagenomic and image-based methods

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Meiofauna is widely recognized as a useful indicator for assessing the effect of anthropogenic and natural disturbances on deep-sea ecosystems. However, traditional methods of investigating meiofauna, which include individually counting and identifying small-sized meiofaunal specimens under a microscope, are labor-intensive and time-consuming. Alternative methods, which can rapidly process a high volume of meiofaunal samples, are required.In this study, we analyzed the effect of the scientific drilling of D/V Chikyu in the vicinity of the Iheya-Minor Ridge in the Sakai hydrothermal vent field, located in the middle of the Okinawa Trough, north-west Pacific Ocean, on the surrounding meiofaunal assemblages. The scientific drilling of D/V Chikyu was carried out in February to March 2016 at this site (CK16-01 cruise). At the same site, we collected the sediment samples during the research cruises of the R/V Kairei, KR15-17 and KR16-15 in November 2015 and in November 2016, respectively, using a push corer on the ROV KAIKO Mk-IV. Therefore, it is possible to detect the effect of the drill cuttings discharged from the scientific drilling on the surrounding meiofaunal assemblage. Analysis with the traditional method successfully detect the differences in the vertical distribution in the sediment and in assemblage structure of meiofauna between the points where the drill cuttings were deposited and the reference points; namely, the peak of meiofaunal density below 10 cm blow the seafloor and the low N/C ratio were observed at drilling points compared to the reference points. In addition, we examined meiofauna assemblage with metagenomics and image-based methods and assessed the availability of these two methods.

## Persistent impacts of the Deepwater Horizon oil spill on megafauna.

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LUMCON

In scope and severity the Deepwater Horizon (DWH) oil spill in 2010 represented a major environmental disaster with commensurate impacts on the economic and ecological health of the Gulf of Mexico. Although the surface expression of oil and its impacts on coastal ecosystems received considerable public and scientific attention, the far greater part of the spill occurring in the deep ocean and subsequent impacts received considerably less attention. Although studies examined the deep-sea impacts from 2010-2014 and continues for deep-sea corals, a considerable knowledge gap for continued post 2014 impacts on the deep-sea exists. In the summer of 2017 an ROV survey of the Deepwater Horizon wellhead and wreckage documented a significant lack of megafaunal diversity, including the absence of major taxonomic groups common in the deep Gulf of Mexico and the lack of structure associated invertebrates on wreckage. In addition, we observed and quantified substantial organismal damage in several key species including the large mobile crab Chaceon quinquedens. Individuals of this species showed dramatic discoloration, increased ectoparasite loading, carapace and appendage deformities, and missing limbs. Behavioral response of C. quinquedens were also abnormal with most failing to display common defensive postures and retreat at the sight of the ROV. Using historical data prior to the DWH spill and recent evidence from healthy unimpacted areas of the deep Gulf of Mexico, we quantify a dramatic and persistent impact of the DWH event on deep-sea megafauna vicinity of the DWH wellhead and rig wreckage.

## Sponge removal by bottom trawling in the Flemish Cap area (northwest Atlantic): implications for ecosystem functioning

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Bottom trawling is considered unsustainable because it significantly alters seabed characteristics, has low selectivity and decreases overall biodiversity. Sponge aggregations in the deep sea play a key role in the functioning of marine ecosystems but are often found overlapping or in close proximity to important fishing grounds. The objective of this study was to quantify the biomass of sponges removed by the bottom trawling fleet operating on the Flemish Cap area (northwest Atlantic) and to assess the consequences for ecosystem function. We used data from bottom trawl research surveys (2006 and 2010) to estimate total sponge biomass present on the Flemish Cap, Flemish Pass and Tail of the Grand Bank. Two different approaches were used to create these biomass layers: 1) a 5x5km grid with average sponge biomass caught per grid cell; and 2) a species distribution modelling using a random forest machine learning approach. These biomass estimates were overlaid with data on the spatial distribution of fishing effort (based on Vessel Monitoring System, VMS) to estimate total removal of sponge biomass between 2010 and 2013. Finally, information on the function of sponges were compiled from the literature to estimate total loss of key functions provided by sponges (composed mostly by Family Geodiidae, 90%) and conversely the amount of functioning protected under the current closures put in place by the Northwest Atlantic Fisheries Organization (NAFO).

# Natural and anthropogenic disturbance - POSTERS

## Population density of abyssal epibenthic holothurians using fine scale time-series imagery (2007-2017)

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CSUMB/MBARI

Holothurians are one of the most abundant megafauna observed in abyssal deep sea communities. These taxa have been found to respond to fluctuations in organic carbon from surface primary production. Previous studies have determined population density and spatial distribution based on seasonal observations, which cannot detect fine-scale temporal changes. This study examines rapid changes in densities of 16 holothurian species observed at a long time-series site, Station M, in the northeast Pacific during a ten-year period (2007 - 2017) using daily images from a stationary time-lapse camera. Holothurian density, represented primarily by the dominant species Peniagone sp. A, peaked from November 2013 to January 2014. In 2012, Peniagone sp. A density tripled from 0.25 individuals m-2 in June to approximately 0.76 individuals m-2 in September. Sixteen months later Peniagone sp. A reached its peak density of 2.11 individuals m-2. Peniagone sp. A significantly declined in 2017 and was overtaken by Scotoplanes globosa as the most abundant species. Lags between changes in particulate organic carbon flux and rapid holothurian community responses are summarized, demonstrating the advantage of using high temporal-resolution imagery with a long-term presence on the sea floor.

## Phenotypic response and recovery of *Lophelia pertusa* to hydrocarbon and dispersant exposure with the combined stressors of high temperature and low pH

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Lophelia pertusa, a cold-water scleractinian coral, acts as the foundation for deep-sea ecosystems throughout most of the world's oceans, including the Gulf of Mexico. These organisms are under increasing threat due to anthropogenic intrusion into their natural habitats, such as global ocean change and hydrocarbon extraction. While there are numerous studies highlighting the variable effects of climate change factors and oil/chemical dispersant exposure on marine organisms independently, there are very few studies focusing on the combined effects of both climate change factors and oil/dispersant pollution together. This study implemented a series of multi-stressor experiments to assess the effects of variation in pH, temperature, and oil/dispersant exposures and their interactions. Four separate experiments exposing L. pertusa colonies to various environmental conditions (pH: 7.6 & temp: 8°C, pH: 7.9 & temp: 8°C, pH: 7.6 & temp: 12°C, pH: 7.9 & temp: 12°C) and hydrocarbon exposure (oil only, dispersant (Corexit 9500) only, oil and dispersant combined) were performed. L. pertusa's phenotypic response was directly assessed through observations of polyp behavior, mucous secretion, and tissue loss at four time points during exposure and recovery. In all four experiments, regardless of pH and temperature, Lophelia pertusa's average health significantly declined during 24 hours of exposure to dispersant alone but remained relatively constant during 24 hour exposures to oil or oil and dispersant combined. In the first stage of recovery after the initial 24 hours, polyp health quickly returned to the pre-exposure health state under ambient temperature (8°C) even after exposure to dispersants. However, the combination of increased temperature (12°C) and dispersant exposure resulted in a delay in recovery and a few instances of mortality were observed by the end of the experiment (1 week). The next steps for this project are to examine the transcriptomic response between the various treatments to better understand the underlying mechanisms behind the phenotypic responses of Lophelia pertusa to the combined stressors of temperature, pH, and chemical pollutants.

## Mesophotic and deep enviroments of Isla del Coco, Costa Rica, Eastern Tropical Pacific

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Isla del Coco National Park is located 500 km off the Pacific coast of Costa Rica, its enviroments between 50 and 450 m have been explored using the DeepSee submersible. Mesophotic coral ecosystems (MCEs), at ocean depths between 40 and 150 m, have been found throughout the tropics but are different in the Eastern Tropical Pacific (ETP). The ETP is characterized by a shallow thermocline (approximately 50 m depth), reduction in light availability at deeper depths due to the accumulation of particulate matter at the thermocline, cold temperatures, low oxygen concentrations, and low aragonite saturation state (Ωarag) may explain the absence of zoothanthellate corals below 40 m. There is a sharp change in benthic fauna, in both soft and hard bottoms, at approximately 50 m depth. The roccky substrate between 50 and 150 m is densely covered with red algae (down to 90 m), octocorals, black corals, azooxanthellate corals, and calcareous hydroids. Deeper environments consist of sandy bottoms down to 180-200 m at the insular platform edge, where polychaetes predominate and several species of octocorals, gastropods, and fishes are observed. From the platform edge rocky substrates, with sand pockets, drop to as

deep as 3,000 m. This isolated and relatively well-protected National Park has been impacted by anthropogenic and natural disturbances. Litter has been observed, mainly plastics and fishing gear between 200 and 350 m depth. Only one natural disturbance has been recorde in deep waters. The 2015 El Niño warming event caused partial mortality of black coral colonies between 45 and 55 m depth at one of the mesophotic seamounts at Isla del Coco. However, they were fully recovered by October 2017. Studies of deep areas are important for conservation and the advancement of knowledge, especially of Marine Protected Areas such as Isla del Coco National Park.

## Restoration in the deep sea: results of a disturbance experiment

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Our knowledge of the natural dynamics, including colonisation processes, of hydrothermal vent ecosystems is still scarce and limits our ability to predict their resilience to natural (volcanic eruptions, hydrothermal flow changes, etc.) or anthropogenic disturbances (deep-sea mining of seafloor massive sulfide deposits, for example). This fundamental knowledge is a prerequisite to assess the natural regeneration capacity of vent communities. To better document the environmental and biological processes governing the recolonisation of vent mussel assemblages, we designed an innovative experimental project based on an induced disturbance. These assemblages, located near the Montsegur hydrothermal edifice on the Lucky Strike (Mid-Atlantic Ridge), will be monitored in situ during two years following the disturbance. In 2017, a total of 16 quadrats, instrumented with temperature sensors, were deployed. Eight were cleared of all fauna, four were caged to assess the role of predators on recolonization processes and four additional ones were selected as reference sites. In 2018, video cameras will be installed on each quadrats. Different approaches will be carried out. A quantitative description (composition, diversity and biomass) of macrofaunal assemblages associated to the engineer species Bathymodiolus azoricus will inform on faunal recovery in relation to environmental conditions. Then, selected functional traits, such as trophic structure using stable isotopes (δ13C and δ15N), reproductive status of the dominant species and population structure, will be analysed along the ecological succession process. This fundamental knowledge on the resilience of vent communities will help elaborate management and impact monitoring protocols and eventually, to propose active restoration methods to protect these ecosystems and the unique species they harbour.

## OSIRIS: a scenario-tool to explore multiple interacting stressors on a system

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Climate change and increasing anthropogenic interest in the deep sea puts this system under unprecedented stress. How such a system will respond to interacting stressors is unknown, and there is limited ability to do long-term and large-scale experiments to investigate this. Models can play an important role to aid our understanding of system responses. Here we present a new model framework, OSIRIS (Ocean System Interactions, Risks, Instabilities and Synergies), a network model developed to assess the influence of multiple simultaneous stressor effects on the system. System components (species or functional groups), their interactions (e.g. trophic or mutualistic interactions), and specific responses to stressors

(e.g., physiological responses to temperature) can all be flexibly incorporated. Uncertainty in these parameters are incorporated through Latin hypercube sampling, allowing for probabilistic investigation. OSIRIS is a scenario tool that could aid in determining early warning signals, and explore effects of different policies.

## By-catch of deep-sea sponges by bottom trawls and bottom longlines on the Northeast Atlantic

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In the last years, considerable management and conservation efforts has been made to minimize the adverse impacts of bottom fishing on seabed communities and ecosystems, particularly on vulnerable deep-sea sponge aggregations. Nevertheless, more information on the comparative effects of different types of bottom fishing is needed. The objective of this study was to compare and contrast the quantity and composition of sponges caught by bottom trawls and bottom longlines, on selected locations of the Hatton Bank and surrounding areas (NE Atlantic). A compilation of records of deep-sea sponge bycatches, was made from three Science-industry cooperative surveys undertaken by the Spanish Institute of Oceanography in collaboration with fishers (2005-2008 period). Experienced scientific observers travelled onboard the vessels to collect the data. A total of 78 bottom longlines and 172 bottom trawls were studied, at depths ranging from ~300 to ~1600 m. Bottom trawls were generally used on sedimentary seabed, while longlines were deployed on hard rugged terrains. The results show that both bottom fishing gears can produce impacts on benthic ecosystems when their distributions overlap with that of the fishery spatial footprint. We discuss the implications for fisheries management, highlighting the different pros and cons of trawls and longlines. Lessons learned from science-industry cooperation are also presented.

## Bottom-trawling fisheries influence on macrofaunal assemblages from the West Iberian margin

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The West Iberian margin is one of the most disturbed regions in the European waters by bottom-trawling fisheries at depths greater than 200 m, affecting the seafloor integrity and the associated benthic fauna. To investigate how trawling pressure is affecting macrofaunal assemblages, we compared the standing stocks (abundance and biomass), community structure and taxonomical and trophic diversity in areas subjected to varying trawling pressure along the SW Portuguese upper slope (c.a. 200-600 m). Results indicated that the longstanding trawling pressure presents cumulative effects to the habitat heterogeneity known to characterise the West Iberian Margin fauna. Overall, fishing grounds and adjacent areas showed a depletion of macro-infaunal abundance, as well as taxonomic and trophic richness when compared to not trawled areas. Yet, univariate diversity indices related with community structure typically used in monitoring programmes (i.e. Shannon-Wiener index, Pielou's evenness) failed to detect important compositional changes in the assemblages. Also observed was a decrease in the number of taxa - trophic guilds combinations of the core assemblage (i.e. characteristic, dominant or frequent taxa) with increasing trawling pressure, as fishing grounds were typified by generalist trophic guilds (deposit feeders, detritivores and omnivores) and perceived a loss of trophic redundancy when compared to not trawled areas. These results suggest that these

assemblages are vulnerable to further increases in natural and anthropogenic disturbance and their synergistic effects.Session: Natural and anthropogenic disturbanceType of presentation: Poster

## Vent assemblage on a large sulphide deposit, Niua Volcano, Tonga

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Niua Volcano lies at the northern tip of the Tonga-Tofua Volcanic Arc as part of the complex of volcanoes east of the northern Lau Basin. As such, Niua vent communities are relatively isolated from other vents to the south and west. Two fields of distinctive biological character lie along the summit at about 1150m depth: the sulphur-rich North Field supports a large mussel field, while the South Field hosts many chimneys, both active and inactive, in a small crater. In the South Field, venting in an area 200 m x 180 m hosts extensive low mounds and rubble of massive sulphide with some black smoker spires to 5 m height. We mapped biological indicators using high altitude video imagery acquired during the Virtual Vents cruise in 2016. Across the crater vent fauna was limited to chimneys where provannid snails, shrimp and crabs dominated, and peripheral fauna was scarce. Biomass on most of the 16 colonized chimneys was low; vertical surveys of 12 structures detected high animal concentrations around fluid outlets plus widely scattered shrimp (Lebbeus komaii) and some lithodid crabs. However, on five spires, counts of provannid snails alone exceeded 5000 individuals. This vent assemblage appears simpler than those described on chimneys from south Lau Basin although new surveys in summer 2018 may reveal more detail. Mussels were notably absent in this field while a new large species of paralvinellid polychaete. Only Alviniconcha boucheti was revealed from genetic probes (S. Johnson, pers. comm.), and Chorocaris variabilis was abundant around focussed flows. The nature of flow directed through chimneys, the extensive development of iron oxide overlay on the sulphides, and the lack of volcanic surfaces may deter recruitment of a more diverse macrofaunal assemblage. These results can inform models of regional impacts of mining of seafloor massive sulphides.

# Pelagic systems - TALKS

## Potential complexity of zooplankton responses to deoxygenation: very small oxygen differences matter

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Significant variability in zooplankton abundances and distributions, associated with very small differences in oxygen concentration and temperature, were documented at midwater depths within the strong oxygen minimum zone of the Eastern Tropical North Pacific in Jan – Feb 2017. First, a towed hydrographic profiler, the Wire Flyer, was deployed on ~50 km long transects between 325–650m or 525-850m depths. Locations of midwater features showing oxygen gradients were identified for targetted zooplankton sampling. Horizontally-sequenced zooplankton samples along with hydrographic data were then collected with a MOCNESS net system towed through the feature at a constant depth (either ~430m or ~800m). Day and night vertically-stratified tows were also done for several depth intervals and locations. Species abundances and distributions (copepods, euphausiids, fish), and total zooplankton biomass,

were analyzed relative to depth and oxygen. Horizontally-sequenced tows showed strong differences in abundances of particular species associated with very small changes in oxygen concentration even though the sampling depth remained relatively constant. Vertically-stratified tows provided broader context for the full range of a species habitat including diel vertical migration. Respiration measurements of key species collected live in Tucker trawls at these same locations determined their physiological tolerances (critical partial pressure of oxygen (Pcrit) at selected temperatures) that were related to their distributions. Plots of the Metabolic Index for selected species illuminated physiologically-suitable habitat along these transects. These results suggest substantial unexpected complexity in responses of oceanic organisms and ecosystems to predicted future deoxygenation.

## Exploring the Midwater Time Series of Monterey Bay

Rob Sherlock, Reisenbichler, K.R., Messie, M., Schlining, B., Schlining, K.L., von Thun, S., Walz, K.R., and B.H. Robison
MBARI

The Midwater Time Series (MTS) consists of data from the mesopelagic environment and its inhabitants. At the Monterey Bay Aquarium Research Institute, we have used remotely operated vehicles (ROVs) and high-definition cameras to record video transects that typically begin at 50 m, then run from 100 to 1000 m in 100 m increments. To date the MTS is comprised of over 2000 transects, continuously collected for more than two decades. Transect video is annotated in the laboratory and each annotation then linked using the Video Annotation and Reference System (VARS) to the ancillary data (conductivity, temperature, depth, oxygen and time) collected simultaneously by the ROV. These data reveal a fascinating and diverse fauna; a fauna that is traditionally poorly represented in other types of surveys. Many of the mesopelagic animals exhibit cyclic patterns of seasonal change and many (not all) reach their peak annual abundance in the summer/fall, after upwelling has diminished. Although there is pronounced change in taxa with depth, these patterns are evident even in the deep mesopelagic. Now, because of its longevity, we can begin to use the MTS to identify local factors (upwelling, hydrography, and OMZ) as well as basin-scale phenomena (El Nino events and Pacific Decadal Oscillation) important in structuring the mesopelagic community of Monterey Bay.

## The evolution and diversification of the siphonophore prey capture apparatus

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Siphonophores have the most complex and regularly organized nematocyst batteries of all Cnidaria. These structures are held on the tentacles' side branches called tentilla. Tentilla serve as the principal organs for prey capture, making siphonophores an ideal system for the study of trophic specialization from an evolutionary approach. Modern comparative methods have been applied to study the evolution of siphonophore zooid types, but not yet to the fascinating morphological diversity of siphonophore tentilla. The primary objectives of this work are to describe the morphology and morphometrics of siphonophore tentilla and nematocysts, identify patterns in the evolutionary history of siphonophore cnidoband and nematocyst morphologies, and elucidate the relationships between these and prey selectivity. Specimens were collected by SCUBA divers and ROVs. Morphological data was obtained from 1) the primary literature, and 2) transmission microscopy, and 3) confocal microscopy performed on fixed tentacle specimens. Functional interactions between the measured characters during prey capture were recorded using high speed video on live specimens under a stereoscopic microscope. Dietary

data was extracted from published sources. Most nematocyst complement (cnidome) traits appear to have evolved under simple Ohrnstein-Uhlenbeck processes with single optima, while tentillum shape and size evolution is better represented by models with multiple optima and rates of evolution. Cnidome traits also exhibit a higher rate of evolution than tentillum morphology. Using phylogenetic GLS we identified traits with correlated evolutionary histories, some of which are functionally coupled during prey capture. Size and abundance of nematocysts were phylogenetic correlated with prey type ratios in the diet. These patterns could represent macroevolutionary adaptive responses to prey availability leading to predatory specialization. Understanding the evolution of the prey capture apparatus of siphonophores can help us test hypotheses about the evolution of their predatory habits.

## How fishes create connections in pelagic ecosystems: Lanternfishes (Myctophidae) in the Gulf of Mexico

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Lanternfishes are a highly diverse and globally-important family of fishes, forming 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 commercially-important fishes, seabirds, and deep-living predators, lanternfishes create important trophic linkages between coastal, upper-ocean, and deep-ocean ecosystems, and form an important part of the biological pump. Nonetheless, relatively little is known about the variability of lanternfish 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 vertical and horizontal distribution patterns of the myctophid assemblage in the Gulf of Mexico, including temporal and spatial (relative to mesoscale oceanographic features) variability. The analyses were conducted using depth-stratified data (spanning 0 – 1500 m), collected between 2011 and 2017 across a 200 x 700 km region. Biodiversity analyses suggest that the myctophid assemblage is well-mixed through the northern Gulf of Mexico with a relatively stable species composition over time. However, abundance data show greater variability across spatial and temporal scales. We discuss the implications of these findings for ecosystem structuring and carbon transfer between the surface and deep oceans.

## Are giant larvaceans a missing link in deep-sea food webs?

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MBARI, GEOMAR, Smithsonian

Large larvaceans (e.g. Bathochordaeus, Mesochordaeus) are significantly undersampled by nets and other traditional gear because of their fragility. Direct assessments with either eye or lens are presently the only means of measuring their abundance, and such surveys are rare. Specimens of Bathochordaeus have been reported from both sides of the North Pacific and North Atlantic Oceans, the western South Pacific, the eastern South Atlantic, and the Indian Ocean. They occur in neritic waters, in deep water beyond continental shelves, and in central gyres. Nearly all of these biogeographic records are based on net tows and consequently there is very little information on abundance, but these filter-feeding grazers are clearly widespread on a global scale. In most of the areas we have examined with extended in situ visual or video surveys, large larvacean

houses were a common feature of the midwater landscape. Time series data from the Monterey region show a year-round presence in the upper half of the mesopelagic with seasonal and episodic pulses of abundance. Recent technological advances have enabled reports on the remarkable scale of their potential grazing impact in Monterey Bay and on their latent service as a vertical vector for microplastics. While we have long been aware of the role of discarded Bathochordaeus houses in deep carbon flux, we have recently begun to identify the specific consumers of that carbon in the deep water column and on the seafloor. As we begin to incorporate data on carbon and energy flux into our food web models, it seems clear that large larvaceans must play a very significant but largely under-acknowledged role on a much greater ocean scale than we have surveyed to date.

## Optimizing vision in twilight conditions: the story of the pearlside

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Most vertebrates have a duplex retina comprising two photoreceptor types, rods for dim-light (scotopic) vision, and cones for bright-light (photopic) and color vision. Deep-sea fishes, however, are only active in dim-light conditions hence, most species have lost their cones in favor of a simplex retina composed exclusively of rods. While pearlsides, Maurolicus spp., appear to possess such a pure rod retina, their behavior is at odd with this simplex visual system. Contrary to other deep-sea fishes, pearlsides are mostly active during dusk and dawn close to the surface, where light levels are intermediate (twilight or mesopic) and require the use of both rods and cone photoreceptors. To explore this paradox, we investigated the visual system of two pearlside species. Results show that their previously categorized all-rod retina is in fact composed almost exclusively of transmuted cone photoreceptors. In other words, the pearlside does not possess the usual rods and/or cones, like most animals, but instead possess a third and more efficient type of photoreceptor. In more details, these transmuted cells combine the morphological characteristics of a rod photoreceptor with a cone opsin and a cone phototransduction cascade to form a unique photoreceptor type, a rod-like cone, specifically tuned to the light conditions of the pearlsides' habitat (blue-shifted light at mesopic intensities). Combining properties of both rods and cones into a single cell type instead of possessing two photoreceptor types that do not function at their full potential under mesopic conditions, is the most efficient and economical solution to optimize visual performance in these conditions. This is the first report of photoreceptor transmutation mediating a cone-opsin-based visual system in teleost fishes. These results challenge the standing paradigm of the vertebrate duplex retina and its evolution, and call for more comprehensive evaluations of visual systems in general.

## Northern elephant seals carrying oceanographic tags indicate mesopelagic prey availability in the Northeastern Pacific

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The northern elephant seal (Mirounga angustirostris) is a mesopelagic predator ranging widely in the North Pacific between 3,000 and 5,000 km

offshore during two extended foraging migrations a year. They prey mainly on myctophids and squid between 400 and 600 meters depth. Long-term monitoring and tracking by the University of California Santa Cruz of the breeding population based at Año Nuevo State Park have enabled mapping of seal distribution in their foraging habitat over the past two decades. Recent technological development of miniaturized oceanographic sensors incorporated into satellite tracking tags, such as CTD tags that measure salinity and temperature, have enabled investigation of elephant seals' movement and diving behavior in relationship to oceanographic parameters. In this study, head-mounted CTD tags with integrated fluorometers were deployed on 8 adult female northern elephant seals for three to eight months between 2014 and 2018. A subset of these animals also carried jaw accelerometers to detect prey capture events. Most seals utilized the subpolar-subtropical gyre boundary and showed some affiliation with the Transition Zone Chlorophyll Front during the winter and spring. Elephant seal foraging behavior was determined by transit rate and dive profile shape, and prey capture attempts recorded by the jaw accelerometer where possible. The seals' behavior was used to indicate presence of mesopelagic prey resources and was analyzed in relation to tag-measured water column temperature, salinity, chlorophyll concentrations, and gradients of these parameters. These analyses allow us to investigate utilization of mesopelagic prey in a three-dimensional oceanographic context and determine whether relationships exist between elephant seal foraging regions and oceanographic features such as fronts. With in situ observations of this ecosystem in the remote North Pacific extremely limited, tracking of predators utilizing the mesopelagic zone can provide unique insight into the distribution of organisms in this understudied pelagic system.

## The perils of bad taxonomy for leading edge science: a case study with the genus *Aegina*, and the consequences for Deep Learning

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(1) JAMSTEC; (2) Kitasato Univ.; (3) Tokai Univ.; (4) Minemizu Photo Studio; (5) U. Alaska; (6) U. Guam; (7) Smithsonian

Online biogeographic databases are increasingly being used as data sources for scientific papers and reports, for example, to characterize global patterns and predictors of marine biodiversity and to identify areas of ecological significance in the open oceans and deep seas. However, the utility of such databases is entirely dependent on the quality of the data they contain. We present a case study that evaluated online biogeographic information available for a hydrozoan narcomedusan jellyfish, Aegina citrea. This medusa was considered one of the easiest to identify because it was one of very few species with only four large tentacles protruding from midway up the exumbrella and was the only recognized species in its genus. Online resources such as the Global Biodiversity Information Facility (GBIF) and the Ocean Biogeographic Information System (OBIS) suggested that A. citrea was broadly distributed throughout the world's oceans. However, lack of traceability to information from original providers made it impossible to validate the great majority of records in online resources, casting doubt on species identification. Thus, we conducted a new systematic investigation of A. citrea, integrating morphological and genetic observations of specimens obtained from a variety of different localities. Contrary to the status quo, our morphological and molecular phylogenetic analyses showed that the genus Aegina and the family Aeginidae were polyphyletic. To accommodate for the previously unrecognized diversity in this group, we described two new families, three new genera, and one new species. In light of our integrative systematic study, we found that many past conclusions about the biology of 'Aegina citrea', from life history to ecology to distributions, are compromised

because observations of more than one species were applied to a single name, highlighting how systematics and taxonomy provide the foundation upon which all other biological science is built.We have recently been applying Deep Learning techniques to automate species identifications of gelatinous zooplankton in situ. The effects of training sets compromised by species mis-identifications and skewed taxon sampling are introduced and discussed.

## Reconciling morphology and molecules to explore diversity and distribution of gossamer worms (Polychaeta, Tomopteris)

Karen Osborn, Sarit Truskey, Leann Biancani
Smithsonian National Museum of Natural History

Commonly called gossamer worms, the Tomopteridae are a globally-distributed group of midwater polychaete worms found from the surface down through the bathypelagic depths. With their distinctive delicate, gelatinous bodies and long pair of "whiskers", tomopterids are easily recognizable at the family level and of great interest for their bioluminescence and use in physiological and biomechanical research. Approximately 60 species have been described, based primarily on the presence and arrangement of parapodial glands in fixed animals - unfortunately, most descriptions are incomplete or ambiguous and types not available. Couple these minimal, often contradictory descriptions with tomopterids' simplified morphology and easily damaged bodies and it makes species identification, especially of live animals, particularly challenging. Approximately 350 specimens were collected from the NE Pacific, Gulf Stream, Gulf of California, and Antarctica for this study. We used multiple genes (COI, 16S, ITS1, H3) to explore species diversity and distribution using phylogenetics and a suite of species delimitation methods. We then reconciled morphological characters from both live and fixed animals to species units recovered in molecular-based analyses, providing a clearer picture on characters of use in diagnosing and identifying species and a first step towards the revision of the family. We were surprised to find more than 17 species of Tomopteris off the U.S. Pacific coast alone.

## Appraisal of Microplastic Ingestion in Deep-pelagic Fishes and Crustaceans in the Gulf of Mexico and Straits of Florida

Ryan Bos, Tracey Sutton, and Tamara Frank
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Plastic litter infiltrates aquatic ecosystems globally, the majority of which are microplastics (<5 millimeter). These microplastics have been detected in high concentrations on marine shorelines, surface water of the pelagic realm, deep-sea sediments, and food webs. Prior studies on plastic contamination have examined pelagic and benthic deep-sea ecosystems, yet only one previous study took place in the Gulf of Mexico, home to many commercially important fishery species. That study documented anthropogenic litter in the benthic realm of the Gulf of Mexico, and there remains a gap in knowledge on plastic ingestion by micronekton (water column dwellers) in spite of their importance as major prey items for commercially fished species. The digestive tract of a number of these fish and crustacean prey species, collected in the Gulf of Mexico and the Straits of Florida, were analyzed in the present study. Our results show that microplastics have entered deep-sea (<200 meters) food webs in this ecosystem, as 27% of examined individuals contained plastic in their digestive tracts. Vertically migrating taxa of fishes contained more plastic in their guts than non-migratory species, and the opposite was true for

crustaceans, although these differences were not statistically significant. Species-specific differences were detected for amounts of ingested plastic and differences in color and categorization of plastic were discerned with respect to sampled depth. This study is the first one to show that plastics have infiltrated the deep-sea food webs of the Gulf of Mexico and Straits of Florida, suggesting more scrutiny be given to deep-sea ecosystems globally.

## Now you see me, now you don't: Cephalopod visual ranges and implications for deep-sea visual ecology

Kate Thomas, Sonke Johnsen, Mike Vecchione
Duke University

Sunlight in the ocean exponentially decreases with depth, creating a structured and directional optical environment in the midwater habitat. Because of decreasing light availability, it is thought that the distance over which visual interactions among marine animals can occur decreases with depth. This is thought to have major ecological and evolutionary effects; for example, the lower metabolisms of deep-sea cephalopods have been explained by relaxed visual predation with depth. However, species inhabiting the dim twilight zone are also thought to increase relative eye size with depth to cope with low light levels. We tested this in cephalopods by comparing measured eye sizes and body sizes from species in the Smithsonian collection to species depth distributions and light habitats. We then used these data to model maximum theoretical visual ranges for ecologically relevant visual targets such as predators, prey, conspecifics, and bioluminescence given the depth ranges of each species. Our computational model of contrast attenuation in low-light environments used eye size, water clarity, downwelling light level at depth, and target size in calculating these best-case visual ranges. We will discuss how cephalopod eye investment changes with depth, maximum distances over which vision can be used for various tasks, and ultimately the distances over which visual interactions among animals can occur in the deep pelagic sea.

## New observations of bioluminescent behavior and fluorescence in the deep sea and open ocean

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Methods such as new color low-light cameras, careful collections by ROVs and scuba, and fluorescence excitation sources mounted on ROVs have enabled a new perspective on the biooptical properties and behaviors of planktonic organisms. These include the first observations of luminescence in a diverse range of animals, bioluminescent and fluorescent lures used for predation, unexpected in-situ behaviors, and as-yet-unexplained displays of luminescence. In this talk we will show some of the newly recorded observations which point to a wide range of functions for this ecological trait, underlying its importance as a means of communication in the deep-sea.

# Pelagic systems - POSTERS

## Ecology of the barracudinas (Paralepididae) in the Gulf of Mexico

Richard Jones, Tracey Sutton, April Cook, Jon Moore
Florida Atlantic Univeristy

The Deepwater Horizon oil spill in 2010 prompted an enormous survey effort to assess the under-studied, deep-ocean ecosystems of the Gulf of Mexico. These surveys, supported in turn by NOAA and the DEEPEND research consortium, conducted deep-pelagic (0-1500 meters) trawling from 2010 up to the present year (2018). Data were collected using both an opening/closing net system (10-m2 MOCNESS) and a large-volume, high-speed rope trawl to characterize pelagic fish, crustacean, mollusk, and gelatinous zooplankton assemblages. The resulting samples and datasets afforded a unique opportunity to study the ecology of a poorly known group of mesopelagic fishes, the barracudinas (Aulopiformes: Paralepididae). While these fishes are rarely caught during fisheries-independent sampling, they are frequently documented as prey in the stomachs of pelagic migratory predators, such as billfishes and tunas. Here we address several important data gaps regarding the ecology of the Paralepididae, including: species composition in the gulf, standardized abundances, vertical distribution, and trophic ecology. We documented 19 unique species of barracudina, 3 of which represent first records of occurrence for the gulf. Our samples also included the largest and most numerous specimens ever recorded of the gulf's single endemic barracudina species, which was previously known from only 2 juvenile specimens. Our results indicate that a majority of barracudina species are efficient at avoiding research-sized nets (e.g., rectangular midwater trawls), suggesting that their overall abundance has been historically under-estimated. No barracudina species appeared to be strong vertical migrators, but some diel vertical trends were noted. Notable differences in vertical distribution and diet were observed among the three major sub-groups of the family, with the Lestidiinae and Sudinae sub-families strongly preferring epipelagic depths and a diet of Myctophids, while the Paralepidinae sub-family was almost exclusively mesopelagic, preying upon shrimps. This work provides foundational ecological information about these ubiquitous but understudied predatory fishes.

## Evidence of Crustacean Gut Fullness Contributing to Asynchronous Vertical Migration

Ryan Bos, Tracey Sutton and Tamara Frank
Nova Southeastern University

Diel vertical migration is the largest animal migration on Earth and is exhibited by a diverse variety of deep-sea fauna. The ultimate cause of migration is thought to be predator avoidance, while the proximate cause (the daily trigger) is thought to be the change in the downwelling light intensity at sunset. However, net data have shown that while a portion of any given species assemblage vertically migrates, another portion remains at depth and does not migrate. A longstanding hypothesis for this phenomenon is that the non-migrating individuals of migrating species refrain from migrating if they have full or partially full stomachs from daytime or nocturnal feeding from the previous night. However, the stomach fullness of non-migrating members of a vertically migrating species compared to the migrators has never been studied. The digestive tracts of numerically abundant crustacean species with well-known distributions, collected in the Gulf of Mexico, were analyzed in the present study. Animals were captured during night trawls using a multiple opening and closing net and environmental sensing system (MOCNESS) that sampled discrete depth bins (1500-1200m; 1200-1000m; 1000-600m; 600-200m; 200-0m). Crustacean gut fullness was qualitatively estimated from 0-5 (0=completely empty; 5=completely full), and the gut fullness of migratory taxa caught in shallow-pelagic water (<600m) were compared with conspecifics that refrained from migrating (>600m). The non-migrators that stayed at depth at night had significantly fuller guts than their congeners that had migrated to shallower waters. These findings provide support for the hypothesis that migratory behavior can be modified by state

of satiation, and suggest that further study is needed on the extent at which animals feed at depth.

## A Tool for Classification of Mesoscale Water Mass Structure for Pelagic Community

Rosanna J. Milligan, Matthew W. Johnston, Cole G. Easson, Sergio deRada, Bradley Penta, David English, Tracey T. Sutton
Nova Southeastern University

Mesoscale oceanic features (e.g. eddies) generate considerable environmental heterogeneity in the pelagic oceans, but their chaotic and transient natures make it difficult to generalise their effects on pelagic fauna. Simplifying these complex features according to a biologically-meaningful classification system will be a useful first step in understanding the extent of their influence in structuring open-ocean ecosystems. The Gulf of Mexico (GoM) is a useful location for such a study, as it is a relatively well-studied, semi-enclosed ocean basin, in which the upper circulation (<1000 m) is dominated by the Loop Current (LC) and associated mesoscale eddies. Here, we present a tool to classify the pelagic environment in the GoM using ocean condition data from the 1/25° GOM HYbrid Coordinate Ocean Model (HYCOM). Specifically, we use measures of sea surface height anomaly (SSHa) and temperature at 300 m water depth (T300) to distinguish warm, LC-origin water from the cooler Gulf Common Water (CW). Three "water types" were identified: Anti-cyclonic Rings (AR), CW and Mixed (MIX), where the latter represents an intermediate state that forms as ARs degrade to CW. HYCOM-derived classifications were validated against in situ CTD data collected from 2015 – 2016, which were classified independently using temperature-depth (TD) and temperature-salinity (TS) profiles through the water column; and from microbial community analyses using samples collected from the surface to mesopelagic depths. The HYCOM classifications were refined using the validation data to produce an overall agreement rate of 77% with the TS/TD classifications (44 of 57 stations), and 79% with the microbial classifications (46 of 58 stations). With applicability across a wide range of spatial and temporal scales, the system will provide a useful tool for biological oceanographers and resource managers interested in understanding the effects of major mesoscale features on the pelagic biota of the GoM.

## Potential for color vision in the deep-sea: how widespread are rod opsin (Rh1) duplications among deep-sea fishes?

Fanny de Busserolles, Fabio Cortesi, Justin Marshall
The University of Queensland

Most vertebrates have a duplex retina comprising two photoreceptor types, rods for dim-light vision, and cones for bright-light vision. Color vision is defined as the ability to discriminate between two visual stimuli that differ in their spectral composition. The primary prerequisite for color vision is to possess at least two photoreceptors that are active at the same time and are sensitive to different wavelengths of light i.e. two cone subtypes, or two rod subtypes. Given that vertebrates, including deep-sea fishes, usually only possess a single rod photoreceptor subtype, it is generally assumed that they are color-blind in dim-light conditions. However, recent findings by our team and colleagues challenge this assumption. Retinal transcriptome analysis combined with in-vitro expression of visual pigments in four deep-sea fish species revealed that, due to rod opsin (Rh1) gene duplications and associated functional differentiations, they are likely to have multiple rod subtypes. Hence, at least the basic requirement for color vision seems to be present in these species. Although the deep-sea is characterized as

being one of the dimmest environments on earth, bioluminescence is very common and occurs in several forms, such as flashes, spews and glows that cover a surprisingly wide range of the visible spectrum. Since light signals in the deep-sea vary in spectral composition, we would expect several species to be able to discriminate these different chromatic signals. To assess how widely distributed Rh1 duplications and hence, the potential for color discrimination among deep-sea fishes is, we investigated the retinal transcriptomes of an additional 30+ species representing >20 deep-sea fish families. Our findings and the resulting evolutionary and ecological implications of such adaptations in the context of specific deep-sea fish families are discussed.

## Biochemistry of deep-sea gelatinous luminous animals

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MBARI

Bioluminescence is abundant in the deep-sea among ctenophores, annelids, echinoderms, and many others. However, the chemical mechanisms have been studied only a handful number of species. Remotely operated vehicle (ROV) sampling allowed us to collect organisms in intact and healthy condition. These animals should contains high amounts of bioluminescent materials, since they are not stimulated or disturbed as they are when collected with trawls. Here I will present preliminary results of biochemistry assays on deep-living luminous annelids and echinoderms. The polychaete _Poeobious meseres_ is abundant in the Monterey Bay water column, and emits bright blue-green light. The crude extract contains blue, green, and pink fluorescent compounds, which can be separated by thin layer silica chromatography using organic solvents (MeOH:CHCl3=1:10 + trace of acid). These compound were not detected in other deep-sea luminous polychaetes, _Tomopteris_ sp. and _Flota flaberlligera_, suggesting a potentially unique chemistry of light emission

## Comparative ROV surveys reveal jellyfish blooming in deep-sea Calderas

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Deep-sea calderas and hydrothermal vent sites are known to contain a large amount of mineral resources and simultaneously support unique ecosystems, hence research related to Environmental Impact Assessments (EIAs) for deep-sea mineral mining has become extremely important. Remotely Operated Vehicles (ROV) have allowed us to explore such topologically diverse geological settings where plankton net surveys are near impossible. Non-destructive image-based in situ survey methods have demonstrated that a great variety of fragile gelatinous zooplankton exist at mid-water depths and their importance has been recognized, though information on their community structures is still rare. We collected baseline data on gelatinous zooplankton around deposit sites through comparative ROV observations over the entire water column. In order to identify the drivers behind observed distributions, we took advantage of the fact that water masses inside any particular caldera can differ greatly from those outside. During our study, large concentrations of gelatinous zooplankton were discovered living inside but not outside the surveyed submarine calderas.Two calderas were picked as research sites, one hydrothermally active caldera (Smith Caldera) and one inactive caldera (Kurose Hole), both located within the Izu-Bonin Arc. Investigations at the Smith Caldera were conducted in March by the ROV Hyper-Dolphin, while the Kurose Hole surveys were conducted in September by the ROV

Dolphin-3K. Both calderas possessed extremely different vertical environmental profiles inside and outside the caldera. Outside both calderas a strong North Pacific Intermediate Water signal (low salinity, high oxygen) was detected but inside they were filled with warm water (>10°C). Reflecting these different environmental conditions, extremely different gelatinous zooplankton compositions and vertical distributions were observed. Large abundances of the leptomedusa Earleria bruuni (Navas, 1969) were observed inside both the active and inactive calderas. In contrast, an undescribed species of lobate ctenophore was abundant only inside the hydrothermally active caldera. Details concerning the vertical distribution of other gelatinous zooplankton (ctenophores, cnidarian jellyfish, planktonic tunicates) are also introduced.

### Prey patch distributions in the central North Pacific Subtropical Gyre determined through the diet of longnose lancetfish (*Alepisaurus ferox*)

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University of Hawaii at Manoa

The diet analysis of top predators can augment our understanding of micronekton distributions, particularly by providing high spatial and temporal resolutions compared to shipboard trawling and for mobile species that avoid trawls. A multi-year diet study of the longnose lancetfish (Alepisaurus ferox), a mesopelagic predator, is providing a window into micronekton community dynamics across a large sampling area in the central North Pacific Subtropical Gyre (NPSG). Analysis of 1,880 stomachs collected from 2009-2017 has revealed that some lancetfish ingest unusually high abundances of common prey taxa (defined as "aggregations" using Tukey's rule). These aggregations in the diet should reflect utilization of relatively high-density prey patches in the pelagic. We present an analysis of this diet data that aims to quantify the oceanographic drivers of heterogeneity in micronekton spatiotemporal distributions. We quantified variability in the distribution of lancetfish containing aggregations of mesopelagic fishes (Anoplogaster cornuta, Sternoptyx spp.), hyperiid amphipods (Phronima sedentaria, Phrosina semilunata), and alciopid polychaetes. Prey aggregations appear highest in the northern region of our sampling area for A. cornuta, P. semilunata, and P. sedentaria, following latitudinal trends in the proportional contributions of these groups to overall lancetfish diet. Aggregations of Sternoptyx spp. are well-distributed throughout the sampling region, but the average contribution of these fishes to lancetfish diet is enhanced at high latitudes. The proportion of lancetfish stomachs containing prey 'aggregations' was relatively low during winter (January-March) for all years sampled. Future work will examine the spatial and temporal relations of aggregations with oceanographic features such as eddies and frontal zones to provide insights into dynamic distributions of micronekton. They will further be compared with lancetfish CPUE as a possible indicator for predator utilization of these spatially-explicit prey patches.

# Seamounts and canyons - TALKS

### Identification of ecologically important areas within a large network of seamounts (Northeast Pacific)

Cherisse Du Preez, Tammy Norgard
Fisheries and Ocean Canada

Seamounts are important for the resilience of biodiversity and fisheries, and they are often identified as ecologically and biologically significant areas. There is a large network of seamounts stretching across the deep Canadian Pacific into the high seas, our understanding of which has been hindered by the scale-limitations of individual projects. To guide decision-making concerning the development of seamount management and monitoring plans, both within our national waters and in the high seas, Fisheries and Oceans Canada Science is consolidating existing data and conducting surveys in never before explored areas. This large-scale project constitutes the first assessment of these seamounts as a network and as island-extensions of the continental shelf and slope habitats. By consolidating underwater image and fisheries data, bathymetric maps, and oceanographic models in a seamount classification system, we differentiate five biologically meaningful classes within the seamount network. Results from this assessment are enabling the identification of regionally unique and significant species, communities, and habitats within and among the seamounts (e.g., deep-sea coral and sponge grounds), providing valuable science information required by Canada to meet its national and international marine conservation targets.

### Interdisciplinary approaches for predictive mapping to assist spatial management within submarine canyons

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Marine spatial management, aiming for a sustainable use of marine resources, requires an accurate spatial representation of habitats and biodiversity. Identifying and mapping habitats is recognised by several international organizations as a key activity in protecting natural resources (e.g.: UN vulnerable marine ecosystems, OSPAR threatened and/ or declining species/ habitats and EU Habitats Directive Annex I species/ habitats). The EU Habitats Directive identifies the ability to ascertain the distribution, extent and condition of habitats as a key element of marine conservation. This includes the physical, hydrological, chemical and biological components of the habitat. Predictive mapping offers a powerful tool in the deep sea, where surveys are constrained by cost and technological capabilities.Submarine canyons are associated with increased biodiversity, with cold-water coral (CWC) habitats representing features of high conservation value that are under increasing anthropogenic pressures. Previous deep-sea canyon mapping studies have focussed upon the physical/biological aspects, thereby omitting key information required for effective marine conservation.In this interdisciplinary study, biological, physical and oceanographic datasets were integrated to undertake high-resolution predictions of benthic megafauna diversity and CWC distribution within the Whittard Canyon, which includes the only deep-sea marine conservation zone in English waters. Data were acquired during the JC125 expedition, which was part of the ERC CODEMAP project (Grant no 258482) and the NERC MAREMAP programme. Video analysis was conducted to identify, enumerate and georeference epibenthic megafauna. Environmental variables were derived from bathymetry, the FOAM AMM7 ocean model and a canyon region hydrodynamic model. Generalized regression, classification tree, additive and ensemble modelling techniques were then used to produce maps of diversity and CWC distribution. Model performance varied between methods and was improved with the inclusion of oceanographic data. We advocate the inclusion of oceanographic data into future mapping efforts to ensure biologically representative map creation, enabling more effective spatial management.

## Exploration and Quantitative Sampling in Diverse Deep Water Habitats in Cordell Bank National Marine Sanctuary

Danielle Lipski, Dan Howard, Kaitlin Graiff, Gary Williams, Guy Cochrane, Michael Carver
Cordell Bank National Marine Sanctuary

Recent surveys using remotely operated vehicles (ROVs) have advanced our understanding of deep water habitats and biodiversity in Cordell Bank National Marine Sanctuary (CBNMS) located off the coast of north-central California. In 2017, exploratory benthic surveys were conducted on the deep slope and canyon areas at depths of 860 meters to 2700 meters in CBNMS on board E/V Nautilus using ROV Hercules. Surveys in these previously unexplored areas revealed steep canyon walls with hard substrate and a variety of deep-sea corals, sponges, other invertebrates, and fish, significantly expanding the species inventory for these habitats in the sanctuary. During 76 hours of benthic surveys, new species observations included several bamboo, black, and gorgonian coral species not previously recorded in CBNMS. Also in 2017, quantitative ROV surveys were conducted on Cordell Bank in new and historically sampled areas. Fifteen hours of video was collected using a Phantom ROV on board R/V Fulmar between depths from 60 meters to 150 meters for characterization and long term monitoring of the benthic community. These two missions illustrate the advantages of different tools and platforms used to study the diversity of seafloor habitats at depths of 60 meters to nearly 3000 meters and the challenges and opportunities in research and management of marine sanctuaries. Characterization and monitoring of benthic habitats and communities in CBNMS is critical to provide information to guide management.

## SAIs and Recovery of VME Taxa on Seamounts of the NWHI and Southern Emperors

Amy Baco, E. Brendan Roark, Nicole Morgan, Beatriz Mejia Mercado
Florida State University; Texas A&M University

Seamounts of the far Northwestern Hawaiian Islands (NWHI) and Emperor Seamount Chain (ESC) have experienced some of the heaviest fisheries impacts of any seamounts in the world, including both finfish and coral fisheries. Based on life history characteristics of the deep-sea corals, which often dominate the fauna, it has been hypothesized that seamounts will take decades to recover, if they can recover at all, from fisheries impacts. This hypothesis has not previously been tested on time scales >10 years. The NWHI and ESC offers a unique opportunity to test this hypothesis on longer time scales because a subset of these seamounts has been protected for up to 40 years since the establishment of the US EEZ in 1977. We conducted quantitative video transects from 200 to 700m depth with the AUV Sentry in 2014 and 2015 on 3 seamounts that are still trawled and 4 seamounts that have been recovering. Data are augmented with submersible observations during return visits in 2016 and 2017. Seamount which are still trawled were characterized by vast areas of barren substrate with scars from bottom contact gear, as well as coral stumps and lost fishing gear. However pockets of remnant VME taxa occur on each feature. Recovering seamounts also showed abundant trawl scars, and significant amounts of lost gear are still present on the recovering seamounts indicative of substantial historic fishing pressure. Despite this, some signs of recovery were observed. These include observations of corals growing over trawl scars, and corals growing from fragments. Overall, the recovering seamounts had a higher abundance of benthic megafauna, and a higher abundance of deep-sea corals than still trawled sites. These results suggest that an initial level of recovery of seamount deep-sea coral communities may be possible on 30-40 year time scales.

## Deep-sea Lebanon: A first assessment of the benthic biodiversity of Lebanese canyons

Ricardo Aguilar, Silvia García, Allison L. Perry, Helena Álvarez, Jorge Blanco, Ghazi Bitar
Oceana

Deep-sea ecosystems contribute significantly to the total biodiversity of the Mediterranean Sea, but remain poorly known and protected across most of the region. This knowledge gap is especially pronounced in the eastern Mediterranean, particularly the Levantine Sea, which is characterised by the warmest waters in the Mediterranean and is likely to host distinct deep-sea ecosystems from the better-studied western basin. The deep-sea canyons in the Eastern Levantine have been identified as an Ecologically or Biologically Significant Area by the Convention on Biological Diversity, but previous biological surveys had only been carried out within the first few hundred metres of depth. Here, we present the findings of the 2016 Deep-Sea Lebanon expedition, a four-week research cruise covering the main canyons along the Lebanese coast (Tarablus, Jounieh, St. George, Beirut and Sayniq). Benthic communities were documented visually using a remotely operated vehicle, with a total of 51 dives conducted between 36-1050 m depth, and infauna were surveyed via grab sampling in soft-bottom areas. A total of 622 taxa were identified, of which three are potentially new to science (Axinella sp., Luidia sp., and cf. Anomocora sp.). Other new records included Atlantic species not previously recorded from the Mediterranean (e.g., Hacelia superba) and the first-ever observations of sea pens and gorgonians in Lebanese waters. Among the key communities documented were maërl and coralligenous beds, sponge aggregations, scleractinian communities, gorgonian communities, sea pen fields, and fossil reefs. The canyons surveyed hosted thirteen species that are Red Listed or are protected under the Barcelona Convention (e.g., Dendrophyllia ramea, Funiculina quadrangularis), as well as vulnerable marine ecosystems and habitats that are prioritised under Action Plans developed by UNEP. The relative biodiversity value of the canyons is compared using an index-based approach, and is considered in the context of the wider Mediterranean.

## Topographic Effects on Bait-Attending Fauna: Examining the Effect of Abyssal Hills Using Baited Cameras

Astrid Leitner, Jennifer M. Durden, Craig R. Smith, and Jeffrey C. Drazen
University of Hawaii, Manoa

Talk Abstract for Session Seamounts and Canyons:Topographic Effects on Bait-Attending Fauna: Examining the Effect of Abyssal Hills Using Baited CamerasAstrid Leitner, Jennifer M. Durden, Craig R. Smith, and Jeffrey C. DrazenUniversity of Hawaii ManoaAbrupt topographies in the ocean such as seamounts and canyons have been demonstrated to have important impacts on ecology and various oceanographic processes. Abyssal hills are small seamounts whose heights range from 100 to 1000 m. Despite their small size, these structures can alter flow, change sediment grain size and biogeochemistry, increase particulate organic matter, increase sessile megafaunal biomass, and change sessile benthic megafaunal community composition. However, their impact on highly mobile animals has not been extensively tested. Here we present baited camera data from abyssal plains, abyssal hills, and seamounts across the central and eastern North Pacific. Baited cameras are ideal tools for studying the highly mobile, low density top predators of abyssal ecosystems since these animals are frequently undersampled by other techniques such as ROV and AUV surveys. Using relative position (benthic position index) and a variety of

other oceanographic predictors (eg temperature, habitat type), we analyzed the effect of bathymetry on abyssal bait-attending fauna across the region. Our analyses provide evidence that topography influences abyssal bait-attending communities, specifically by increasing species richness and changing community composition. Abyssal hills and seamounts together are the most abundant geological feature in the largest habitat on our planet. Thus, we need to continue to build our understanding of the role of these features in structuring deep-sea communities, especially in the light of the ever-increasing anthropogenic footprint in the deep-sea.

## Multiscale variability of Mozambique Channel seamount megafauna, oceanographic and geological drivers

Karine Olu, M. Boulard1, E. Miramontes2, L. Corbari3, I. Van den Beld1, G. Jouet2, S. Jorry 2
1 Ifremer, Centre de Bretagne, REM/EEP, Laboratoire Environnement Profond, Plouzané, France. 2 Ifremer, Centre de Bretagne, REM/GM, Laboratoire Géodynamique et Enregistrements Sédimentaires, Plouzané, France. 3MNHN (Muséum National d'Histoire Naturel

Seamounts support ecosystems historically viewed as unique, diverse and productive, but potentially threatened by human activities, such as the exploitation of mineral and/or biological resources (e.g.: polymetallic crusts and fishing). Ecological paradigms need to be supported by more extensive studies particularly in under-sampled areas, at regional scale and taking into account the heterogeneity of habitats (Rowden et al. 2010). The Mozambique Channel, between the eastern African margin and Madagascar, is characterized by several modern isolated carbonate systems forming the Eparses islands, and flat top seamounts corresponding to ancient carbonate platforms subsequently affected by tectonic and volcanism. Seamount tops, and terraces along slope islands, all between 300 and 800m depth, have been surveyed by a deep-towed camera. Megafauna community structure varies in density and composition between seamounts at regional scale, along the investigated latitudinal gradient (11°S to 21°S) and according to the distance from the coast. Species turnover at seamount scale is influenced by seamount geomorphology and high substrate heterogeneity. Oceanographic regimes and water masses characteristics are also potential drivers of biodiversity patterns at different spatial scales. Although diversity and endemism level need a greater sampling effort to be properly estimated, this first ecological study on the Mozambique Channel seamounts suggests that the complex oceanography and the long term evolution of carbonate platforms drive here a high diversity of benthic communities by a nested scale environmental control. This research was co-funded by TOTAL and IFREMER as part of the PAMELA (Passive Margin Exploration Laboratories) scientific project.Cited reference: Rowden AA, Dower JF, Schlacher TA, Consalvey M, Clark MR. 2010. Paradigms in seamount ecology: fact, fiction and future. Marine Ecology 31: 226-241

## Submarine canyons provide link between river catchments and remote deep-sea ecosystems off New Zealand

Daniel Leduc1, Scott Nodder1, Max Gibbs1, Andrew Swales1, Andrew Kingston1, Ashley Rowden1, Fabio De Leo2, Craig Smith3, Joshu Mountjoy1, Brittany Graham1, Arne Pallentin1
1 NIWA, New Zealand; 2 University of Victoria, Canada; 3 University of Hawai`i at Manoa, USA;

Canyons can facilitate the transfer of land-derived organic matter to the deep sea. The extent to which canyons connect coastal and deep-sea ecosystems depends on factors such as the shape of the canyons and their position relative to the coast. We studied contrasting canyon systems off New Zealand: Kaikoura Canyon, a steep canyon close to the shore, and Hokitika Canyon, a narrow and lower gradient canyon further from the coast. Bulk stable isotope and compound-specific isotope analyses were used to determine the source of the organic matter in sediments. In Kaikoura Canyon, high concentrations of land-derived organic matter were found in areas near the coast and down to 1000 m, but very little land-derived material was found further away from the coast (25 km) and deeper in the canyon - where marine-derived organic matter predominated. The nearshore areas with high input of land-derived organic matter were characterized by high biomass of benthic fauna. In contrast, sediment organic matter in Hokitika Canyon was comprised almost entirely of land-derived material, down to 2000 m and up to 200 km from the coast. Despite this relatively high input of organic matter from nearby rivers, the biomass of benthic fauna was low across the entire canyon, suggesting that land-derived organic material alone may be insufficient to support large populations because it is not as nutritious as marine-derived organic matter. We used the results of this study, together with a morphometric and environmental classification of the 273 canyons that surround New Zealand, to model the regional extent of the connectivity provided by canyons between the land and deep ocean.Opportunistic analysis of samples taken from Kaikoura Canyon after a large earthquake which caused a canyon-flushing event, indicate that such events can alter the amount and source of organic matter available for canyon communities.

## Do environmental drivers of benthic assemblages in submarine canyons scale spatially in heterogenous seascapes?

Thomas Schlacher, Franziska Althaus 2, Alan Williams 2, Vanessa Lucieer 3, Ben Gilby 1, Phil Alderslade 2, Mark Green 2; Andrew Olds 1
1 - The ANIMAL Research Centre, University of the Sunshine Coast, QLD, Australia; 2 - CSIRO Oceans and Atmosphere Flagship, TAS, Australia, 3 - Institute for Marine and Antarctic Studies, TAS, Australia.

Submarine canyons have been treated as high-priority features in the design of Australia's network of offshore Marine Parks, chiefly because they are widely considered that their complex geomorphology and varied seabed terrain enhance fauna diversity and abundance. It is, however, plausible that not all canyons, or parts of canyons, consistently form high-quality habitats for benthic animals. Importantly, there is limited understanding of the spatial scales at which their benthic assemblages are structured by habitat features. Here we address this question, analysing image-based seabed transects of megabenthos in canyons off Tasmania (Australia), matched with advanced terrain metrics derived from multibeam sonar bathymetry and backscatter data. Variation in megabenthic composition and density is apparently driven by the combined effects of depth range (primarily) and changes in seabed properties (mostly substrate type). A strong effect of seabed heterogeneity is evident at smaller scale, embedded in broader drivers of seascape features most likely operating at larger scales. Whether the observed scaling of environmental determinants of seabed canyon fauna is hierarchical, or combines uniquely in different canyon systems, is a testable hypothesis for these and other submarine canyons globally.

## Ecological communities and drivers of biodiversity within the transverse ridge of the Vema Fracture Zone

Lissette Victorero, Emily Sym, Laura F. Robinson, Michelle L. Taylor, Daniel O.B Jones, Veerle A.I. Huvenne
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Fracture zones (FZ) are currently poorly studied deep-sea ecosystems, which have recently become highlighted as a result of growing interest in their potential as sites of deep ocean mineral extraction. While they have been identified to be important pathways for deep and bottom waters, our knowledge of their biology and ecology, and their potential role as biogeographical pathways between ocean basins, remains speculative. One of the largest FZ in the Mid-Atlantic Ridge, is the Vema FZ, which is a major conduit for the Antarctic Bottom Water and North-Atlantic Deep Water between the western and eastern basins. Here based on three ROV-dives across the summit, flank and deep slope of a transverse ridge within the Vema FZ, we present the first biological characterisation of these habitats. The ridge habitats range from sediment plains, volcanic plateaus to vertical walls and pinnacles, which were found to host 46,300 individuals across 172 different morphospecies. These included vulnerable marine ecosystems (VMEs), such as cold-water coral gardens consisting of Enallopsammia sp. and sponge gardens of the Poliopogon sp. The pinnacles were colonized by multi-species coral assemblages, such as Primnoids and Chrysogorgids. In order to understand patterns of biodiversity and its drivers within the ridge, we modelled changes in species richness, diversity (H') and abundance in response to topographic and oceanographic variables using generalized additive mixed models (GAMMs). Preliminary results suggest that greater depth and broad-scale local elevation of the seabed significantly increases species richness and diversity in the ridge. Abundance reduces with greater depth, but was highest at intermediate slopes and at slightly elevated sites. This study suggests that the dynamic oceanography and complex geomorphology of the Vema ridge system supports ecologically important and diverse communities. These communities are likely to play a biogeographical role in faunal connectivity between deep-sea habitats across the Atlantic basin.

Seamounts and canyons - ABSTRACT 95
MONDAY MIdday • 13:45 • San Carlos Room

## The Benthic Communities of the New England and Corner Rise Seamounts

Abby Lapointe, Les Watling
University of Hawaii at Manoa

The New England and Corner Rise seamount chains in the Northwest Atlantic extend approximately 1700 km from the continental slope southeast of George's Bank to the vicinity of the Mid-Atlantic Ridge. The benthic communities on 17 seamounts, ranging in depth from 713 to 3262 m, were analyzed using species data compiled from 605 collected specimens, 38,433 in-situ images, and video footage obtained during the NOAA Ocean Exploration "Mountains in the Sea," "Deep Atlantic Stepping Stones," and "CanyBal" cruises conducted on the New England and Corner Rise Seamounts from July 2003 to October 2005, as well as the Okeanos Explorer "New England Seamount Chain Exploration" in 2013 and "Our Deepwater Backyard: Exploring Atlantic Canyons and Seamounts" in 2014. Hierarchical cluster analysis by seamount using presence/absence data produced three main groups: Group 1 consisting of the three deepest seamounts, Mytilus, Physalia, and Atlantis, all sampled below approximately 2400 m; Group 2 consisting of the New England Seamounts Manning, Retriever, Gosnold, Balanus, Kelvin, and Rehoboth; and Group 3 consisting of the Corner Rise Seamounts Verrill, Yakutat, Kukenthal, and Milne-Edwards. Bear (on the continental shelf), Goode, Picket, and Nashville do not fall into any group, most likely due to the narrow depth ranges sampled. Additionally, the benthic communities show distinct variation with depth, with the highest diversity and density between 1700 and 2200 m, and faunal breaks at 900-1000 m and 2200 m. We hypothesize that the differences in benthic communities, both within and across seamounts, are correlated most strongly with the characteristics of the water masses in which they reside.

Seamounts and canyons - ABSTRACT 27
MONDAY MIdday • 14:00 • San Carlos Room

## The Meso- and Bathypelagic Fish Community in a Submarine Canyon

Trevor Kenchington, Daphne Themelis, Shannon DeVaney, Ellen Kenchington
Bedford Institute of Oceanography

During 2007–10, four midwater trawl surveys were conducted in The Gully, a very large submarine canyon incised into the continental slope off Nova Scotia, most of which is a Marine Protected Area. Sampling extended to depths of >2,000m. We here present multivariate community analyses and examination of single-species spatio-temporal distributions and length frequencies for the 19 principal fish species caught (of ≈250 recorded). The major patterns were those expected for the meso- and bathypelagic zones in the open ocean outside the canyon's mouth, the community comprising one dominant myctophid (Benthosema glaciale), seven additional myctophids and a mix of other species, all of them commonly seen in the northwest Atlantic. Only Melanostigma atlanticum, which spawns in seabed burrows, could be a "canyon specialist". The distributions of the 19 were primarily controlled by oceanic drivers: depth, water masses, diel and seasonal cycles, plus inter-annual variability. However, most species showed both an elevation of depth distribution and a reduction in abundance up-canyon, the latter especially marked among smaller individuals. It is suggested that fish at the canyon mouth are entrained in the known up-canyon flow and carried towards the head, while suffering losses to squid predation and, for diel migrants, displacement over adjacent banks at night. The flux of fish biomass through the canyon is on the order of 10t per day in summer.

# Seamounts and canyons - POSTERS

POSTER 161 - Seamounts and canyons
TUESDAY Evening • 17:45 • Serra Ballroom

## Ligurian seamounts: unveiling deep biodiversity and new Mediterranean VMEs

Bo Marzia, Coppari Martina, Betti Federico, Canese Simonepietro, Costantini Federica, Massa Francesco, Bavestrello Giorgio
Dipartimento per lo Studio del Territorio, dell'Ambiente e della Vita, Università degli Studi di Genova

About 250 seamounts have been recently identified in the Mediterranean Sea. Despite this numerosity, however, very few data are available on the benthic assemblages of these structures with consistent information only for a dozen of mounts. The Ligurian Sea embraces six large underwater structures, five of whom have been investigated by means of ROV for the first time within the BioMount-SIR Project: Ulisse, Penelope, and Janua seamounts, representing the Genoese triad (tops at 500-800 m depth), and St. Lucia and Occhiali (tops at 150-500 m depth) along the Tuscan side of the basin. The aim of the study was to depict the megabenthic biodiversity, connectivity and vulnerability to fishing effort of the communities found on the top of these underwater structures. This was particularly relevant since the Ligurian Sea is a highly exploited basin, embracing the so-called Whale Sanctuary, and is considered a sentinel for climate changes linked to tropicalization. The explored seamounts host ecosystems dominated by relevant structuring species whose composition is driven by the different depth of the tops of the structures. Assemblages include a well-diversified black coral community on the shallowest peak and a mixed community of small Cold-Water Corals and sponges, mainly of Atlantic origin, on the 500 m depth tops. Outstanding, instead, is the Janua Seamount hosting black corals (a new Parantipathes species), gorgonians (among which the enigmatic Chelidonisis aurantiaca) and hexactinellids (Farrea sp.) never reported before in the Ligurian or Mediterranean Sea. Significant amounts of lost fishing gears (mainly long lines) were found on St. Lucia and Ulisse

seamounts. A high frequentation by professional and recreational fishermen is known for the shallowest peaks since the 1970s. In this regard, the co-occurrence of long living, slow growing, rare and fragile species represent important criteria for the definition of Vulnerable Marine Ecosystems in need of protection.

## Structure of the deep-sea fish assemblages on Necker Island, Northwestern Hawaiian Islands

Beatriz Mejia-Mercado, Nicole B. Morgan, E. Brendan Roark, Allison Metcalf, Kelly Klein, Amy R. Baco
Florida State University

Some seamounts harbor a high abundance and diversity of fishes. However, evidence is emerging that within any given seamount, these attributes may vary strongly depending on variability in the physical, chemical or geological conditions, as well as from the influence of human activities, such as fishing. Necker Island is the second smallest of the Northwestern Hawaiian Islands (NWHI), but includes a diversity of deep-sea habitats. Unlike locations further west in the NWHI, this seamount has not been subject to commercial trawl fisheries. This site is also currently protected from fisheries activities as part of the Papahānaumokuākea Marine National Monument. The relatively pristine nature of this site allows for baseline studies of deep-sea fish assemblages that can improve our understanding of the distributions of fishes on seamounts as well as inform management of sites throughout the Hawaiian Archipelago.Using 52,098 AUV photos we identified 18,515 fishes from three sides of Necker Island at depths of 200-700 m. The dominant fish orders identified were Stomiiformes, Aulopiformes, Gadiformes, Myctophiformes and Perciformes. Species richness showed significant differences among depths, side of the seamount, and their interaction. Relative abundance was significantly different among sides, whereas Shannon diversity and Simpson dominance showed differences among depths and their interaction with sides. The highest richness was found at 500 m, in which diversity was also very high with low dominance. The highest values of dominance were observed at 250 and 700 m. Community structure was different among depths, sides, and their interaction, with a variation along a depth gradient. At deeper depths pelagic fishes were dominant, whereas shallower depths were dominated by benthic fishes. Based on DISTLM, fish community structure was most strongly correlated with depth and POC.

## Fine scale benthic invertebrate megafaunal assemblage structure on the North Pacific seamount Mokumanamana

Nicole B. Morgan, Savannah Goode, E. Brendan Roark, Amy R. Baco
Florida State University

Changes in megafaunal assemblage structure have been found across gradients of environmental variables for many deep-sea habitats, including seamounts. To assess the scales of variability in benthic communities on the smaller scale of within a single seamount and to assess environmental drivers of assemblage changes, replicate 1 km transects were conducted at 50m intervals from 200-700m depth using the AUV Sentry from multiple sides of 10 seamounts in the Northwestern Hawaiian Islands and Emperor Seamount Chain. From these we selected Mokumanamana, in the Papahānaumokuākea Marine National Monument, as the seamount of focus because it is a site with no known trawling history that had the most even transect coverage. Megafaunal abundance and substrate parameters were obtained from 26,119 total images from replicate transect on 3 sides of the seamount. Water column data was also collected by the AUV Sentry.

The dominant megafaunal taxa were sponges, sea pens, and corallimorpharians. Octocoral and scleractinian cup corals were also abundant. Assemblages varied by substrate type, with soft substrates being somewhat less diverse than hard substrate areas. Overall, abundance of megafauna increased with depth. NMDS and cluster analyses of assemblage structure suggested three main clusters defined by "shallow" (200-350), "mid-depth" (400-500), and "deep" (550-700). Within the mid-depth and deep groups there were also different assemblages when comparing the north side to the south and west sides of Mokumanamana. The deep group had a higher overall diversity while the mid-depth group was lowest. DISTLM indicated that depth and percent sand cover were the main factors correlated with assemblage structure. These results suggest that microhabitats on seamounts can promote unique assemblages to occur along depth gradients as well as on different sides of the feature, and this diversity may be easily overlooked without fine-scale sampling.

## Benthic communities on encrusted deep-sea seamounts located in the largest oceanic desert

Juliette Delavenne, Keszler, Louise; Castelin, Magalie; Lozouet, Pierre; Maestrati, Philippe; Samadi, Sarah
Muséum National d'Histoire Naturelle

Three deep-sea cruises were organized to explore the upper bathyal zone in French Polynesia and produced many new species descriptions and species catalogues. We used this material to analyse the pattern of biodiversity of benthic communities in relation to depth, geography, topography and the presence of polymetallic crusts. We inventoried 472 species among which 169 were newly described using the sampling of these three expeditions. Presently mainly the molluscs and decapods have been examined and a large part of the sampling of these cruises remained unidentified. Nonetheless, these data allow us to show that in French Polynesia, the deep-sea benthic communities are structured by depth, habitats and geography. We specifically show that the presence of polymetallic crust influences the structure of benthic communities. Moreover, we show for molluscs that the spectrum of body size differs among surveyed habitats. Notably the range of shell size is smaller on encrusted seamounts than on island slopes. The low abundancies of organisms coupled with the small size of the organisms in habitat targeted by the exploration for new mineral resources should be taken into account when evaluating the impact of mining activities on biological communities.

## Mapping community structure of canyons and seamounts of the Northeastern US Atlantic Margin and the environmental factors that influence their distributions

Jenn Dijkstra, Kristen Mello1, Mashkoor Malik2 Derek Sowers2, and Larry Mayer1
1The Center for Coastal and Ocean Mapping, University of New Hampshire, Durham, New Hampshire; 2National Oceanic and Atmospheric Administration, Office of Ocean Exploration and Research, Silver Springs, MD

The deep sea communities along the continental margin of the Northeastern United States and the New England Seamount Chain are biologically diverse systems in which little is known of their distribution and the factors that influence their distribution. In the present study, we examined the distribution and structure of benthic communities along and between ROV tracks and examined relationships between abiotic factors and habitat structure. We analyzed full underwater video footage of 5 canyons and 5 seamounts spanning depths between ~550 m and 2500 m. Tracks were collected by ROV Deep Discoverer during three cruise legs of

the 2013-2014 NOAA vessel Okeanos Explorer expeditions along the Atlantic Continental margin. During each dive, a CTD recorded temperature, dissolved oxygen, salinity and depth. We then combined ROV coordinates with CTD, sediment and biological data to map the distribution of benthic communities and their associated environments. To standardize video interpretation, each track was divided into 50 m longitudinal X 50 cm segments widths and were analyzed for substrate type and organisms. Our findings indicate both coarse and fine-scale difference in community structure between canyons and seamounts, with greater abundance of organisms in canyons and greater evenness and diversity associated to seamounts. Our correlations of abiotic factors and community structure indicate that dissolved oxygen and salinity concentrations were linked to greater evenness and dissolved oxygen concentrations with diversity of organisms for both canyons and seamounts.

## Geographic variation of bacterial communities in a seamount with cobalt-rich ferromanganese crusts

AKIRA IGUCHI, Miyuki NISHIJIMA2, Yuki YOSHIOKA1, Atsushi SUZUKI3, Yuichiro TANAKA3, Hideki SUGISHIMA4, Takaaki MATSUI4, Nobuyuki OKAMOTO4
1Department of Bioresources Engineering, National Institute of Technology, Okinawa College, 2Kaiyo Engineering Co., Ltd., 3Geological Survey of Japan, National Institute of Advanced Industrial Science and Technology, Japan, 4Japan Oil, Gas and Metals National Corporation (JOGMEC), Japan

Cobalt-rich ferromanganese crusts have attracted attention as an important seafloor resource for metals. It is believed that microorganisms have contributed to the formation of cobalt-rich crusts, but the details are still unknown. There are six seamounts off southeastern Minami-Torishima Island in the north Pacific, in which cobalt-rich ferromanganese crusts exist and International Seabed Authority (ISA) licensed for the exploration. In 2016, we collected sediment samples around Xufu Guyot (the JA06 Seamount) among these six seamounts. To attempt to comprehend geographic variations of bacterial communities around the seamount, we performed metabarcoding analysis of sediment samples from the crest and base areas of the seamount and of one sample from the digestive tract of a fish collected during our biological sampling. We extracted DNA from the samples and targeted the 16S rRNA gene sequence in our metabarcoding analysis. We obtained short-read data by using the Illumina MiSeq platform. After selecting high-quality data, we processed the data by using the QIIME pipeline software MacQIIME (removal of chimeric reads, extraction of Operational Taxonomic Units (OTU), and annotation of each sequence). We performed community analysis by using R software. We found that the bacterial composition of the sample from the fish stomach was clearly different from those of the sediment samples. Cluster analysis showed two main clusters corresponding to the crest and base areas of the seamount. Network analysis also supports the existence of two groups, suggesting that bacterial community composition may be influenced by water depth. In addition, we identified some hub species which bridge these two groups based on betweenness centrality. We discuss the characteristics of bacterial communities found in our study and previous studies in cobalt-rich crusts.

## Beyond the vents: Megafauna of the mid-Atlantic Ridge

Lenaick Menot, Fanny Planchette, Catherine BorremansIfremer, Centre de Bretagne, REM/EEP/LEP
Ifremer, Centre de Bretagne, REM/EEP/LEP, France, Ifremer, Station de Sète, UMR MARBEC, France, Ifremer, Centre de Bretagne, REM/GM, France, University of Plymouth, United Kingdom

In the French exploration area for Seafloor Massive Sulfides, two cruises with the HOV Nautile and one cruise with the ROV Victor 6000 have been carried out in 2014, 2017 and 2018. The BICOSE1 cruise (2014) and Bicose2 cruise (2018) focused on the two vent fields TAG and Snake Pit while during the HERMINE cruise (2017), the exploration contract was explored from south (21°N) to North (26°N). The megafauna and geomorphological have been annotated from HOV- and ROV-videos. The seafloor is dominated by hard substrates, mainly basalts, locally interspaced by patches of soft-sediments. Most the dives were carried out at depth deeper than 3000 m. At those depths, and beyond the influence of hydrothermal vents, which gradually decreases within a hundred meter of the most active sites, the megafauna is sparse but yet diverse. On a seamount reaching 1200 m depth however, an unusual ground of a yet unknown sponge have been observed. At first glance, the sponge can be easily be confounded with an octocoral. This large branched sponge differs from Sarostegia oculuta but similarly mimics coral gardens.

## Amphipods in a seamount with cobalt-rich ferromanganese crusts in the north Pacific

Miyuki Nishijima1, Akira IGUCHI2, Yuki YOSHIOKA2, Ryuich MIWA1, Atsushi SUZUKI3, Yuichiro TANAKA3, Takaaki MATSUI4, Yoshiaki IGARASHI4, Nobuyuki OKAMOTO4
1 Kaiyo Engineering Co., Ltd., 2 Department of Bioresources Engineering, National Institute of Technology, Okinawa College, 3Geological Survey of Japan, National Institute of Advanced Industrial Science and Technology (AIST); 4Japan Oil, Gas and Metals Industry Association (JOGMEC), Japan

Cobalt-rich ferromanganese crusts have attracted attention as an important seafloor resource for metals. There are six seamounts off southeastern Minami-Torishima Island in the north Pacific, in which cobalt-rich ferromanganese crusts exist and International Seabed Authority (ISA) licensed for the exploration. In 2016, we collected amphipods by using baited traps from three sampling sites around Xufu Guyot (the JA06 Seamount) among these six seamounts. Total genomic DNA was extracted from pleopods of each specimen and determined cytochrome oxidase I (COI) gene sequence according to the method described in the ISA Technical Study No. 13 (ISA, 2015). In order to estimate belonging taxon of specimens, molecular phylogenetic analysis was conducted using sequences of specimens and their closely related species. Total 37 amphipod specimens collected from each sampling site belonged to the Superfamily Lysianassoidea based on the COI gene sequence analysis. Based on the phylogenetic analysis result, collected specimens were separated into 11 groups. The Group 1 (18 specimens) was included the specimens collected from all three sampling sites. We found that this group was included in almost the same lineage with specimens collected from New Hebrides Trench of genus _Abyssorchomene_. Then, to derive the genetic connectivity pattern of marine organisms around the JA06 Seamount, haplotype network analysis targeting one of the representative amphipods (Group 1, _Abyssorchomene_ sp.) was performed using software ape (Paradis et al., 2004) and pegas (Paradis, 2010) packages by R programming language. From the result of the haplotype network analysis, the Group 1 and its related formed one cluster, suggesting that these haplotypes belonging to a single species. Analysis of molecular variance (AMOVA) detected a non-significant genetic structure (P = 0.1638), suggesting that connectivity was maintained among sites.

## Deep Benthic Ecosystems in an Antarctic Fjord Reveal High Export Flux and Sensitivity to Climate Warming

Craig R. Smith, Andrew K Sweetman2; Clifton Charles Nunnally3; McKenna Lewis1; Emily Young1, Maria Vernet4; and Amanda F Ziegler1

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The West Antarctic Peninsula (WAP) has an extensive system of deep (>500 m) rapidly-warming fjords with tidewater glaciers, providing hotspots of pelagic and benthic biomass/biodiversity. However, the drivers of fjord productivity, and their sensitivity to climate warming, remain poorly known. Our FjordEco Project integrates field/modeling studies in Andvord Bay, a WAP fjord, to address: (1) What physical, glaciological and biogeochemical processes enhance fjord productivity and biodiversity? and (2) How sensitive are these processes to increased meltwater and sediment inputs expected from climate warming? We conducted oceanographic studies in Andvord Bay from early summer to early fall, 2015-2016, to elucidate down-fjord patterns of productivity/export flux. "Snapshots" of chl-a and primary production indicated intermittently high water-column production throughout the fjord; however, the location of highest seasonal export flux could not be resolved from these measurements. We use benthic ecosystem parameters from fjord basin floors to integrate summer seafloor POC flux (food for benthos) and identify fjord areas of highest summer export flux. Sediment inventories of chl-a were low throughout the fjord in Dec 2015, but were 10-fold greater in Apr 2016, with highest levels unexpectedly in the inner fjord only 1 km from fast-flowing glaciers. Seafloor carbon respiration showed similar large increases between early summer and fall, with highest rates near tidewater glaciers. Benthic megafaunal abundance matched the patterns of "food" availability with an inner fjord peak, while macrofauna peaked in mid fjord, ~10 km from rapid glaciers. We hypothesize that macrofauna are more sensitive than megafauna to burial stress in the inner fjord due to lower mobility and smaller body sizes. Our results suggest that export flux is especially high deep inside WAP fjords near tidewater glaciers, and that climate warming and enhanced meltwater/sediment inputs will alter these inner-fjord hotspots of productivity/biodiversity.

POSTER 170 - Seamounts and canyons
TUESDAY Evening • 17:45 • Serra Ballroom

## Internal tides affect benthic community structure in an energetic submarine canyon off SW Taiwan

Chih-Lin Wei, Jian-Xiang, Liao; Guan-MingChen; Ming-Da, Chiou; Sen Jan
Institute of Oceanography, National Taiwan University

Gaoping Submarine Canyon (GPSC) connects to a small mountain river (SMR) originated from mountainous areas in southern Taiwan. The erodible lithology, heavy seasonal precipitations and steep topography of the SMR drainage basin mean that the GPSC is prone to high sediment load and frequent turbidity currents. The tectonic active margin of the SW Taiwan also means that the GPSC is subjected to frequent underwater earthquakes and thus the subsequent sediment mass wasting in the canyon. More importantly, the GPSC is next to the world's largest internal waves in the Luzon Strait. The internal wave energy originated from underwater ridges and banks propagates into the GPSC to drive strong bottom intensified currents, likely causing long-term, recurrent and negative impacts on the local benthic communities. Through repeated sampling the GPSC and adjacent slope since 2014, we demonstrated that the strong bottom currents driven by the internal tides might erode the sediment and negatively affect the densities, diversity, body sizes and alter the composition of meiobenthos and macrobenthos. The bottom shear likely re-suspended and prevented the organic-rich particles to settle and thus reduced the food supply to the benthic communities. Despite the majority of submarine canyons are hotspots of benthic abundance, biomass, and diversity, the GPSC was apparently an anomaly due to strong bottom currents and occasionally destructive sediment mass wasting. Our finding suggests that the GPSC is an ideal natural laboratory to examine the effects of disturbance on deep-sea communities and maybe a new paradigm in the study of submarine canyon ecology.

# Technology and observing systems - TALKS

## Subseafloor observatories reveal microbial deep biosphere in oceanic crust

Beth N. Orcutt
Bigelow Laboratory for Ocean Sciences

Over the past decade, major progress has been made in understanding the form and function of a microbial deep biosphere hosted within the rocky subseafloor. This progress resulted from the installation and expansion of subseafloor observatories hundreds of meters into oceanic crust, accessing the hydrothermal circulation of altered seawater. The two largest observatory systems are installed in warm and anoxic basaltic crust on the eastern flank of the Juan de Fuca Ridge and in cool and oxic basaltic crust on the western flank of the Mid-Atlantic Ridge south of the Kane Fracture Zone. Through microbe-mineral colonization experiments, fluid monitoring, and repeated sampling over several years, we have learned about the dynamics of structure and function of subseafloor crustal microbial communities, about the connectivity of these ecosystems to the deep ocean, and about the drivers that shape community structure in this hydrothermally altered ecosystem. This presentation will provide an overview of these findings while highlighting some of the technologies that have made them possible.I'd also like to submit a second abstract to Deep ocean stewardship session on "assessing the microbial ecosystem service impacts of deep sea mining", but not enough space here.

## Observing the Deep-sea Ecosystem with a Continuously Monitoring Instrument Suite

Alana Sherman, Paul McGill, Richard Henthorn, John Ferreira, Christine Huffard, Ken Smith, Jr.
MBARI

The deep ocean covers two-thirds of the earth's surface, but this vast ecosystem is difficult to study because of the technical and financial challenges of sampling at great depth with adequate temporal resolution. Continuous long-term monitoring of the deep sea is critical for assessing the impact of climate change on this environment. With this goal in mind, a suite of instruments have been developed and deployed over the past three decades to measure the biological and chemical processes at a long-term time-series study site in the NE Pacific. The currently deployed ocean observing systems include a time-lapse camera system, a seafloor rover, and an imaging-based sedimentation sensor. The time-lapse camera system comprises two cameras: a "far-field" camera, which images an area of 20 m2; and a "near-field" imager, which captures a close-up of the sea floor (approximately 3 m2). The Benthic Rover transits from site to site collecting still images and sediment community oxygen consumption measurements. Finally, the Sedimentation Event Sensor uses macro imaging rather than sample preservation to determine the sediment flux near the seafloor for comparison with concurrently deployed sediment traps. Each of these instruments is deployed at the 4000 m monitoring site, Station M, for a period of one year between servicing. In recent years, a Wave Glider equipped with an acoustic communication system has been sent from shore quarterly to communicate with the Benthic Rover, reporting

position and status information between annual servicing cruises. This presentation will cover the technological advances and data collected by each of these systems, and how the increased temporal resolution of the resulting measurements provides us greater insight into deep-sea ecosystem function.

## Introducing GOSSIP (General Ocean Survey and Sampling Iterative Protocol)

Lucy C. Woodall1,2, Dominic A. Andradi-Brown1,3, Andrew S. Brierley4, Malcolm R. Clark5, Douglas Connelly6, Rob A. Hall7, Kerry L. Howell8, Veerle A.I. Huvenne6, Katrin Linse9, Rebecca E. Ross8, Paul Snelgrove10, Paris V. Stefanoudis2, Tracey T. Sutton11, Michelle Taylor12, Thomas F. Thornton1, Alex D. Rogers1,2

(1) University of Oxford, UK; (2) Nekton Foundation, UK; (3) World Wildlife Fund-US, USA; (4) University of St Andrews, UK; (5) National Institute of Water & Atmospheric Research, New Zealand; (6) National Oceanography Centre, University of Southampton, UK; (7) University of East Anglia, Norwich, UK; (8) University of Plymouth, UK; (9) British Antarctic Survey, UK; (10) Memorial University of Newfoundland, Canada; (11) Southeastern University, USA; (12) University of Essex, UK

In marine science there are almost as many sampling methods as there are researchers. Our individual research questions are fundamental to how we conduct our research and the data we collect; however, understanding the patterns of diversity of ocean life over different temporal and geographic scales requires extensive data both biological and environmental. Therefore, to address these questions, extensive collaboration and comparable data are required. GOSSIP (General Ocean Survey and Sampling Iterative Protocol) is a multidisciplinary framework for generating globally comparable data for biological communities, which has been designed as a guide on how these data can be collected. In this presentation we will share the 20 parameters that have been chosen, explain why each is considered important and how the framework could be utilised. GOSSIP is intended to change over time as technology and techniques evolve. Alongside this recently published paper, we have produced a technical guide that simply pulls together data on current protocols and indicates where further information can be found.

## Expanding deep-sea observation through access to industry infrastructure

Andrew R. Gates, Peter I. Macreadie, Dianne L. McLean, Paul G. Thomson, Julian C. Partridge, Daniel O. B. Jones, Mark C. Benfield, Shaun P. Collin, David J. Booth, Luke L. Smith, Erika Techera, Danielle Skropeta, Tammy Horton, Charitha Pattiaratchi, Todd Bond, Ashle

National Oceanography Centre, University of Southampton Waterfront Campus, Southampton, SO14 3ZH, UK

Industries that operate in the deep sea collect observations across a range of activities such as environmental baseline survey, impact assessments and routine inspections of subsea assets. For example, baseline surveys regularly collect large benthic sample sets and industrial ROVs collect millions of observations of our oceans each year. These data have the potential to fuel scientific discoveries. We assembled a group of international experts from both academia and industry to reflect on some of these discoveries and, more importantly, to identify key questions relating to our oceans that can be supported by access to industry data and infrastructure through collaboration with companies that use them. From a long list, we narrowed down our top ten questions. These questions covered the viewpoints of opportunity (e.g. what is the resource value of the oceans?) to the impacts of global change (e.g. which marine ecosystems are most sensitive to anthropogenic impact?). Looking ahead, we provide recommendations for how data collected by industry can be maximised by higher levels of collaboration, resulting in beneficial outcomes for both academic and industrial sectors. What is clear from this work is that the potential for greater collaboration with industry, unravelling the mysteries of our oceans is only just beginning to be realised. This is particularly important as the oceans are subject to increasing impacts from global change and industrial exploitation including traditional and novel industries. The coming decades will represent an important time for scientists to partner with industry to expand the network of deep-sea observations to inform our knowledge of the changing ocean and ensure evidence-based management of anthropogenic activities.

## Observing the deep ocean using submerged echosounders

Stein Kaartvedt, Thor A. Klevjer, Anders Røstad, Ingrid Solberg
University of Oslo

The remote and inaccessible nature of deep-sea habitats has largely precluded direct observations of their inhabitants. Acoustic studies have normally been conducted from moving vessels, using hull-mounted transducers. However, submerged echosounders can be used for telling quite new stories and provide information on organismal behavior and ecosystem processes at mesopelagic depths and beyond. This comprises assessments of abundances and size distributions in the deep sea, but also involves revealing movements of individuals traversing the acoustic beam both horizontally and vertically, making it possible to establish the in situ swimming behavior of macroplankton, fish and squid. By deploying autonomous echosounders which may be battery powered or cabled to shore for power and transmission of data, ecosystem processes and organisms can be studies at timescales of seconds to years, and even cm-sized individuals and their potential predators can be assessed in their undisturbed natural environment. Here we present results from acoustic studies on individual behavior and predatory prey interactions in the deep sea. Echosounders can also be used in assessing impacts from human activities and we suggest ways that echosounders can be used for assessing effects of deep-sea mining.

## Identification of benthic epifauna from images using computer vision

Nils Piechaud, Christopher Hunt; Kerry L. Howell
Plymouth University

The development of new robotic and autonomous technology may significantly enhance our ability to study the deep-sea environment, bringing down the cost of data gathering, while increasing the volume of information we can collect. AUVs are increasingly use by ecologists to study seafloor biology using photography and image based sampling. AUVs are capable of collecting vast image datasets in a single deployment. At present these images have to be manually annotated, which is a slow process, and creates a bottleneck in the data acquisition process. Automated image classification, or computer vision (CV), offers a cost-effective, consistent and faster alternative to manual annotation. For a long time, these methods remained difficult to implement without extensive knowledge of informatics and programming. However, more recently the availability of user-friendly annotation software, remote computing facilities and Neural Networks (NN) training software's, such as TensorFlow, now make these tools more usable to non-specialists. Yet, deciding to abandon tested and functional, albeit slow, working protocols in favour of automated alternatives involves compromising on flexibility, control and error source traceability. Moreover, as precious few practical examples have been published, the necessities and potential gains of such a shift in methodology are difficult to estimate. In this study, we used trained NN to identify (or classify) deep benthic species from the North-east Atlantic, in

images collected by an AUV. This study attempts to address questions typically appearing when considering the automation of an image analysis process: 1) How the amount of training material affects the classifier's performances; 2) How the number of classes affects the performances and 3) How the classifier deals with newly encountered species. The results presented provide a practical example of what can be expected from CV in benthic sampling and we aim to help inform ecologists considering implementing this method for small scale projects.

## The Ocean Observatories Initiative: A Long-Term, Deep-Sea Time Series in Real-Time

Michael Vardaro, Leila Belabbassi, Lori M Garzio, Friedrich Knuth, Michael J Smith, Charles Sage Lichtenwalner, John Kerfoot, Michael F Crowley
Rutgers University

The Ocean Observatories Initiative (OOI) is a multi-decadal, NSF-funded program that provides long-term, real-time cabled and near real-time telemetered measurements of climate variability, ocean circulation, ecosystem dynamics, air-sea exchange, seafloor processes, and plate-scale geodynamics. The OOI platforms consist of seafloor sensors, fixed moorings, and mobile assets containing over 700 operational instruments in the Atlantic and Pacific oceans. These include an HD Video system at Axial Seamount, passive and active acoustics, and fluid sampling at hydrothermal vents and cold seeps, as well as a core set of oceanographic measurements throughout the water column. The OOI website (oceanobservatories.org) serves as a hub to access the other sites for the project, and highlights the science themes and instrumentation of the OOI project. The OOI Data Portal (ooinet.oceanobservatories.org) facilitates access to OOI data for research and education, including the ability to plot and download datasets and associated metadata. Additional access is provided via the Raw Data repository, the Analytical Data page, and the Live Video page. The OOI Ocean Education Portal (education.oceanobservatories.org) enables the development of educational data visualizations and translation of OOI science into pedagogical resources and data explorations. Finally, the OOI ERDDAP servers provide a simple, consistent way to download subsets of OOI datasets in common file formats, and make graphs and maps. The tools built on top of the core system enable greater access and utilization of the data, both as an open-access dataset for research and education, and as a baseline to compare to additional experimental instruments added over time.

## Chasing larvae and microbes: the project LO3CAted

Luciana Génio, Clara Rodrigues; Nikoleta Bellou; Ana Hilário; Craig M. Young; Marina R. Cunha
1. Departamento de Biologia & CESAM, Universidade de Aveiro, Portugal; 2. Institute of Oceanography, Hellenic Centre for Marine Research, Greece; 3. Oregon Institute of Marine Biology, University of Oregon, USA.

Chasing larvae and microbes: the project LO3CAtedDistribution and population dynamics of deep-sea species are largely unknown, and consequently resilience and recovery of deep-sea communities from natural and anthropogenic threats are yet immeasurable. Sustainable management of deep-sea resource exploitation requires improved knowledge on population connectivity to advance our understanding of source-sink dynamics in deep-sea ecosystems. As most benthic species have biphasic life cycles, larval dispersal is vital for colonization of new habitats and exchange of individuals among sub-populations. Yet, understanding deep-sea connectivity is presently hindered by knowledge gaps in both physical and biological processes regulating larval dispersal

and settlement. LO3CAted - Larval Occurrences in Open Ocean: Connectivity studies in the East Atlantic and West Mediterranean - aims to substantially contribute towards filling some of these gaps by obtaining sustained observations on vertical distributions and settlement of deep-sea larvae in open ocean. We developed a new modular device that consists of a colonization frame hosting biogenic substrates attached to passive larval tube traps. This modular platform was deployed at bathyal and abyssal water depths using mooring arrays of three Atlantic (PAP, ESTOC and CVOO) and one Mediterranean (PYLOS) observatories of the FixO3 network. Deployment periods ranged between 6 and 18 months. Here we present results of microbial and metazoan assemblages found across geographic and depth gradients.

## New technology reveals the structure and function of deep-sea, giant larvacean mucus houses

Kakani Katija, Alana Sherman, Rob Sherlock, and Bruce Robison
MBARI

The midwater region of the ocean (below the euphotic zone and above the benthos) is one of the largest ecosystems on our planet, yet remains one of the least explored. Little- known marine organisms that inhabit midwater have developed life strategies that contribute to their evolutionary success. Larvaceans (Class Appendicularia) are found throughout the world's oceans, and feed across trophic levels via elaborate mucus feeding structures they create. Larvaceans swim tethered to their mucus house, forcing fluid and particles through filters that eventually lead to their mouth. Once filters become clogged, the house structure is abandoned, sinks, and eventually the particle-rich structure reaches the seafloor. It is estimated that larvaceans are responsible for the deposition of a third of the particulate that reaches the seafloor in Monterey Bay. Despite having such an important ecological role, little is known about the structure and function of giant larvacean (Bathochordaeus stygias) houses. To address this need, we developed DeepPIV, an instrumentation package that incorporates a high-powered, continuous laser and optics, which is deployed on board remotely operated vehicles (ROVs) and a dye/particle injector. This instrumentation enables investigation of various biological and physical phenomena from the surface down to 4000 m. Using DeepPIV and image processing algorithms, we are able to reveal the structure of mucus houses, measure filtration rates, and conduct in situ feeding experiments. In addition to midwater animal-physical interactions, future measurements using DeepPIV include particle-feeding interactions with deep-sea benthic communities.

## A pilot design of an autonomous plankton pump for assessing deep-sea coral and sponge zooplankton communities in the western Gulf of Alaska

Rachel Wilborn, Chris Rooper, Pam Goddard
NOAA-AFSC, Lynker Technologies

Evidence supporting the ecological importance of cold-water coral and sponge (CWCS) habitats continues to grow, particularly in temperate and subpolar regions of the world. Zooplankton and ichthyoplankton communities in the water column above seafloor habitat have been sampled using towed nets, but in situ, stationary collections of plankton assemblages associated with CWCS and the seafloor have proven difficult to implement in deep waters. In situ sample collections provide small-scale, habitat specific species assemblages that can be used to assess the importance of coral and sponge habitat to benthic community diversity,

when compared to samples collected on habitat-free seafloor. This pilot study takes a novel and cost-effective approach to zooplankton sampling in remote locations at depth. An autonomous plankton pump design allowed for advanced programming of pump speed, collection duration, and camera image collection of surrounding habitat. This study found a diverse community of zooplankton, dominated largely by copepods, in and among CWCS. The autonomous pump design used for this project may be useful for other important data collection such as examining benthic prey fields and energetics of near-bottom fishes in a variety of deep-water habitats.

## Water column exploration from the surface to the abyss: community recommendations for a collaborative observing network

Amanda N. Netburn, Anni Djurhuus, Bruce Robison, Marsh Youngbluth, Enrique Montes
NOAA Ocean Exploration and Research

With a few notable exceptions, the last several decades of ocean exploration efforts have been driven by seafloor and epipelagic priorities. The habitats defined by circulation and stratification processes in the vast oceanic realm between these sectors have received far less attention. Efforts to understand ecological changes that regulate diversity, distribution, abundance, and behavior of pelagic organisms, especially fauna that prevail in deep-water habitats, remain rudimentary. To develop a coordinated approach to enhance understanding of biological, physical, and chemical processes in the water column, a group of scientists, engineers, and program managers convened on March 4-5, 2017 in Honolulu, HI, during the NOAA Office of Ocean Exploration and Research led workshop From Surface to Seafloor: Exploration of the Water Column. The main scientific questions and knowledge gaps pertaining to the water column were distilled into five themes: (1) Diversity, behavior, and evolution of pelagic fauna, (2) Vertical structure of the water column and organismal responses to shifts in environmental regimes, (3) Anthropogenic impacts on populations, (4) Lack of baseline data to formulate hypotheses, and (5) Inspiring public interest in the water column. Recommendations from this workshop include the combined use of sensors, instruments, and techniques for the simultaneous collection of biological observations with physical and chemical parameters throughout the water column using ship-based, autonomous, and animal-based platforms. The approach would include use of environmental DNA assessments such as those being tested by the US Marine Biodiversity Observation Network (MBON) project, and would be synergistic with the Deep Ocean Observing Strategy of GOOS, the Ocean Biogeographic Information System (OBIS), and other relevant programs. Achieving the vision of a comprehensive, multi-institutional, and interdisciplinary water column exploration program will require investment now in novel technologies, strong interagency coordination, and innovation and maintenance of an exploration fleet comprised of various seagoing and autonomous assets.

## Vertical migration's why and when revisited with new technology

Kelly Benoit-Bird, Mark Moline, Brandon Southall
MBARI

Each day, animals in high biomass aggregations called 'deep scattering layers' migrate vertically from the deep sea, comprising the largest net animal movement on earth. This migration is thought to be a result of the competing needs of feeding in energy rich surface waters and avoiding predators in the dark refuge of the deep. Previous work using a newly adapted autonomous vehicle to measure individual characteristics in scattering layers provided the first measures of the internal layer structure,

demonstrating off Southern California that, deep scattering layers are made up of many topologically-scaled, mono-specific aggregations, or 'schools'. Follow up measurements show these groups remain coherent during dusk migration, allowing us to examine the timing and ordering of migration from the deep sea. We found that groups of smaller animals began migrating sooner each night than larger individuals, likely due to their relatively lower visibility to visual predators. However, when individual size was accounted for, we also found a correlation with swimming capabilities with squid migrating first, followed by fish, and finally crustaceans, suggesting that the ability to avoid predators once they were encountered also plays in a role in the patterns of migration observed. The presence of squid predators, Risso's dolphins, however, altered this pattern, making the largest squid remain at depth for approximately 45 minutes longer. This non-visual predation risk was apparently assessed by the squid and appropriately responded to as their risk of predation by this air breathing predator is decreased at depth. Understanding the timing of individual migration patterns provides insights into the bioenergetic and predator-prey processes in the deep sea that are critical for understanding their ecological and biogeochemical impacts of these high biomass layers in the ocean.

# Technology and observing systems - POSTERS

## The Station M time series study turns 29: A retrospective and outline of new directions

Christine L Huffard, Alana D. Sherman, Paul R. McGill, Rich G. Henthorn, John G. Ferreira, Linda Kuhnz, Henry A. Ruhl, Kenneth L. Smith Jr.
MBARI

The Station M time series sits under the highly productive California Current in the eastern North Pacific (4000-4100 m). Station M was established in 1989 and remains one of the longest running and most comprehensive abyssal research sites. Early goals were to understand the influence of seasonal particulate organic matter flux to the sea floor on changes in benthic boundary layer processes. Subsequent work identified links between changes in animal communities, particulate organic matter flux, surface ocean conditions, and climate. The initial instrumentation suite included sequencing sediment traps moored in the benthic boundary layer and a time-lapse camera system taking hourly photographs of the seafloor. These time series were supplemented with seasonal seafloor respirometry, and photo-transect measures of animal communities. Over the years technology development has prioritized high-temporal-resolution data collection by fully autonomous instruments deployed for long durations. The current suite includes three time-lapse cameras, two sediment trap arrays, the Benthic Rover, and the Sedimentation Event Sensor. These instruments yield hourly to weekly imagery, fluorescence, respiration, carbon flux, and particulate matter composition during deployments of up to a year. These continuous data are allowing more robust analysis of the timing, patterns, and processes associated with deep sea carbon flux and ecosystem responses. Continued efforts are underway to understand the fundamental biological and ecological mechanisms that underpin community change, which can inform deep-sea resource industry impact assessment. Work also continues to understanding the influence of high-magnitude, ephemeral carbon deposition events to inform efforts to improve carbon budget and sequestration models used in predictive global climate change assessments.

## Functional responses of a canyon ecosystem to organic pulses: an experimental strategy to monitor transient climate-sensitive processes

Nadine LE BRIS, Erwan Peru, Dimitri Kalenitchenko, Franck Lartaud, Gilles Vétion, Pierre Galand, Audrey Pruski

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Canyons, seamounts, hydrothermal vents or methane seeps form a vast network of habitats that are crucial for maintaining the unique biodiversity and ecosystem functions of the deep ocean. Assessing the suitability of these habitats to ecosystem key players in the design of protection or management plans, also requires anticipating disturbances generated by climate change. Yet, we critically lack of understanding of how various combinations of stressors affect these hotpots. A particularly important gap relies on the effect of short-term environmental dynamics on the seafloor that could lead to synergetic or antagonistic effects. To explore this question, we have developed an experimental strategy in the Lacaze-Duthiers submarine canyon (Western Mediterranean Sea), included in the Marine Protected Area of the Gulf of Lion. Canyons experience hydrodynamic phenomena, like dense shelf-water cascades, storm-induced downwelling or eddies, that drive surface waters and organic materials down to the depths. These massive pulses of organic resource, under the form of particles or coarse debris, are major drivers of deep-sea biodiversity. We explored how habitat building/engineer species interplay with these events, by focusing on two main functions supporting benthic diversity in the canyon: the growth of cold-water coral and the colonization of coarse wood debris. The experimentation site at c.a. 500 m depth host large cold-water coral structures was visited by ROV on an annual or seasonal basis. The experiments revealed transient steps supporting high rates of energy transfer to benthic biota, as illustrated by a marked seasonal signature of coral growth and by the rapid conversion of wood into chemosynthetic habitats supporting symbiotic bivalves. These results show that short-term hydrodynamic phenomena have the potential to propagate climatic disturbances on the seafloor more rapidly than predicted from regional models, encouraging the continuous monitoring of ecological functions to address these transient phenomena in future deep-sea observing and experimentation strategies.

## MBARI Media Management

Brian Schlining, Nancy Jacobsen Stout, Lonny Lundsten, Linda Kuhnz, Kyra Schlining, Susan von Thun

MBARI

The Monterey Bay Aquarium Research Institute's (MBARI) Video Annotation and Reference System (VARS) has been used for creating and managing video and image annotations for over fourteen years. The central tenants of VARS--using a controlled vocabulary and a centralized archive of annotations--have proven extremely effective for generating quantitative and qualitative information from images and video. Over 400 peer-reviewed publications have been written using data from VARS. MBARI is currently transitioning from videotape recordings to file-based formats. As part of this transition, we have developed a new software stack designed around a microservice architecture that communicates via standard web protocals. Each component is relatively small and independently deployable. This type of design allows for the evolution or replacement of individual services over time and gives researchers tremendous flexibility in developing special-purpose annotation and video applications. MBARI is releasing these tools as open-source for external researchers and organizations for managing their own video assets and to faciliate the development of new, custom video analysis applications.

## Food supply mechanisms to Norwegian cold-water coral reefs using the LoVe cabled ocean observatory

Tom Van Engeland (1), Olav Rune Godø (2), Espen Johnsen (2), Gerard C. A. Duineveld (3), Dick van Oevelen (1)

1 NIOZ Royal Netherlands Institute for Sea Research, Department of Estuarine and Delta Systems, and Utrecht University, Yerseke, The Netherlands 2 Institute of Marine Research, Bergen, Norway 3 NIOZ Royal Netherlands Institute for Sea Research, Depa

Ocean observatories allow for a detailed characterization of the local marine environment by automated and real-time data collection at high frequency over longer periods of time. We investigated the seasonality in food supply mechanisms to a cold-water coral (CWC) reef situated in a glacially-deepened trough (±250 m deep) on the Norwegian continental shelf using data from the cabled LoVe observatory that was equipped with Acoustic Doppler Current Profilers (ADCPs), echosounders, and sensors for chlorophyll, turbidity and hydrography in the benthic boundary layer (BBL). Tidal currents of the order of cm s-1 dominated water column hydrodynamics, but residual currents were weak (~10 cm s-1) suggesting a phytodetritus supply from local primary production and prolonged retention within the trough. Modes of organic matter food supply varied seasonally. Surface-derived organic matter (OM) was quickly mixed into the BBL during the spring bloom, but temperature stratification in summer reduced this surface-to-bottom connectivity. A qualitative assessment of acoustic backscatter intensities from the ADCPs (600 kHz, 190 kHz) and echosounder (70 kHz) suggests that zooplankton vertical migration may compensate for the deteriorating quality and quantity of the phytodetritus supply after the spring bloom. Nocturnal feeding by zooplankton in the upper water column and subsequent zooplankton migration down to the reef sustains downward OM transport independent from water column mixing and may serve as a nutritional upgrade of the CWC diet while the phytodetritus in the BBL loses its nutritional quality. Our findings suggest seasonal changes in the diet and modes of food supply to reef communities. It is hypothesized that future climate scenarios with intensified temperature stratification may increase the contribution of zooplankton in the CWC diet. This study shows the added value of permanent ocean observatories to research based on dedicated campaigns and regular monitoring.

## Seasonal overwintering of *Neocalanus* spp. (Copepoda, Calanoidea) in Barkley Canyon, NE Pacific, revealed from a deep-sea cabled observatory: insights into particulate organic carbon flux.

Fabio Cabrera De Leo1,2*, Bruno Ogata2,3, Akash R. Sastri, 1,2, Martin Heesemann1,4, Steve Mihály1,5, Moira Galbraith5, Michael G. Morley1

1 Ocean Networks Canada, University of Victoria, PO Box 1700 STN CSC, Victoria, BC, Canada V8W 2Y2 2 Department of Biology, University of Victoria, PO Box 3080, Victoria, BC, Canada V8W 2Y2 3 Biosciences Institute, São Paulo State University (UNESP)

Many submarine canyons are known hotspots of pelagic and benthic biodiversity and productivity. Despite a very limited knowledge of the ecology, biodiversity and ecosystem function of Canada's West Coast canyons, Barkley Canyon is becoming a relatively well studied system, particularly after the installation of the NEPTUNE seafloor cabled observatory in 2009. Video observations of large densities of overwintering calanoid copepods drifting near the bottom at 970 m in the axis of Barkley Canyon motivated our interest in investigating the temporal dynamics of their ontogenetic migration cycle. Large calanoid copepods, and especially Neocalanus plumchrus, comprise up to 50% of the mesozooplankton biomass in the subarctic NE Pacific, being considered a keystone species

in the trophodynamics of pelagic ecosystems in the region. Here we used ~21-months (May 2013-Jan 2015) of seafloor video imagery combined with acoustic Doppler current and backscatter time-series data from the NEPTUNE observatory to identify the precise timing and seasonal and inter-annual variability in the deep ontogenetic migration of Neocalanus spp. in Barkley Canyon. A total of 33,486 still images were extracted from 1,674 x 5-min videos, captured at two-hour intervals, and used in an automated image analysis protocol designed to estimate Neocalanus spp. densities near the seafloor. The results from the entire time-series revealed close correspondence with the described developmental and reproductive cycle for Neocalanus, with the highest densities of copepodite-5 and adult individuals present at depth from late fall through winter. The concomitant high-frequency ADCP backscatter time-series nearly mirrored the patterns obtained from the video imagery, and highlighted a clear inter-annual variability. Low and high-frequency ADCP current data demonstrated an along axis mean flow near the bottom and an up-canyon mean subsurface flow from 70 to 300 m above the seabed, suggesting a recirculation cell likely trapping the Neocalanus migrant biomass. We estimated that 35-215 tons of carbon reach Barkley Canyon's seafloor yearly over an area of approximately 24 Km2 due to Neocalanus ontogenetic migration. Future studies should aim to further constrain the role of submarine canyons in transporting and concentrating deep zooplankton migrating biomass, as there are at least another 230 submarine canyons in the subarctic NE Pacific.

## Longterm deployments of stationary echosounders reveal individual fish behaviour

Svenja Christiansen, Josefin Titelman, Øystein Langangen, Leif Asbjørn Vøllestad, Stein Kaartvedt
University of Oslo, Department of Biosciences

Stationary echosounders can be used for observing population and individual behaviour of pelagic organisms on different time scales. Continuous acoustic recording allows for relating observed behaviour to environmental conditions. One major type of behaviour in the pelagic ocean is diel vertical migration (DVM). While DVM of mesopelagic acoustic scattering layers is commonly documented, the small scale and individual behaviour of mesopelagic organisms is relatively unexplored. We deployed three upward-facing echosounders of different frequencies (200 kHz, 120 kHz, 38 kHz) at different depths (90 m, 270 m, 400 m) in Masfjorden, a 400 m deep fjord at the west coast of Norway, over a period of ten months. The aim of the study was to characterize the behaviour of mesopelagic organisms from the individual to population level. Here we show the first results on the individual behaviour of the pearlside Maurolicus muelleri, a small, ubiquitous, mesopelagic fish that forms distinct acoustic scattering layers in Norwegian fjords. We characterize different types of swimming behaviour and quantify behavioural changes on a diel to seasonal time scale. We explore the development of juvenile M. muelleri "step-wise" swimming behaviour over the course of one winter and relate our observations to changes in light conditions. The use of submerged echosounders can be applied to the deep ocean and allows for observing behaviour of deep sea fauna over extended time periods.

## Deep Sea ID v1.3: a field guide to the marine life of the deep sea

Adrian Glover, Higgs, ND [2], Horton, T [3], Porrer, A [4]
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Deep Sea ID, is a field guide interface to the World Register of Deep-Sea Species (WoRDSS) that currently stores on your device (for offline access) the taxonomic information for over 20,000 deep-sea species, over 750 high-resolution photographs of deep-sea specimens as well as links to online taxonomic tools, sources and important references. Here we present for the first time, the new version 1.3 with enhanced features and greatly increased image database. The app is designed to improve access to taxonomic information for researchers and contractors working at sea, in the field or in the laboratory as well as educators and science communicators who wish to learn more about the remarkable diversity of deep-sea life. At this poster and demo I will explain why we made this app, how we did it, the importance of open data and take you on a visual tour through some of the amazing creatures of the deep sea.

## Exploiting and conserving deep-sea genetic resources

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Started in September 2016, the 5-year Science Foundation Ireland project "exploiting and conserving deep-sea genetic resources" focuses on biodiscovery research in Irish deep-sea Cnidaria and Porifera. The aims are three-fold. Firstly, previously and newly collected samples of these two Phyla will be analysed to characterise their chemical diversity. Crude chemical extracts will be used in various biological screenings such as antibiotic or cancer assays to identify new chemical compounds and/or new activity in known compounds with pharmacological potential. Libraries of crude extracts and isolated compounds will be built to facilitate access to the material by other screening programs. Secondly, the economic potential of deep-sea Irish waters in relation to Porifera and Cnidaria bioactive compound production will be analysed. This analysis requires the: 1) development of a method to define the bioactivity of natural products, a critical step as few natural products have been tested in a comprehensive series of bioassays, but rather too often limited to a particular group of diseases; 2) prediction on the likelihood of families and genera of Cnidaria and Porifera of producing bioactive / drug-like marine natural products knowing the bioactivity of natural products found in these phyla and phylogenetic relationships between species; 3) estimation of the economic potential of Irish Atlantic margin using the above and records of both Phyla in the North East Atlantic. Thirdly, predictive maps of biodiscovery potential in Irish offshore waters will be created based on georeferenced records of species obtained from ROV video annotation, predictive modelling and the above economic studies. Results will inform conservation planning software to determine biodiscovery hotspot clusters. Overall, the project will develop informed bioprospecting approaches to maximise the chance of finding pharmaceutical active natural products in difficult environments to sample such as deep-sea ecosystems.

## Deep-sea biodiscovery: An untapped resource for biomedical application

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The oceans cover 70% of the Earth's surface, with 95% of those oceans being deeper than 1000 m. Despite this vast habitat, marine metabolites of deep-sea origin only account for 2% of the described marine metabolites. With the development of new technologies we can now access and collect in these biodiverse and species-rich habitats. Currently, there are six drug of marine origin on the market for treatments ranging from severe pain to

metastatic breast cancer. All these metabolite derived drug were sourced from shallow waters, highlighting the untapped potential of biodiscovery from the organism that inhabit the deep-seas. In this presentation we would like to highlight our efforts to collect, screen and ultimately isolate and describe these bioactive deep-sea metabolites from the Irish deep-sea canyons. To date we have collected over 500 samples of deep-sea fauna, including demosponges, hexactinellid sponges, bamboo corals, gorgonians, soft corals, sea pens, and black corals, with future collecting expeditions funded and scheduled. Screening assays to identify bioactive deep-sea marine invertebrates are targeted at range of human afflictions such as drug-resistant colorectal cancer, MRSA and malaria. Extracts identified as biologically active will be fractionated and rescreened to identify the active fraction. Bio-guided fractionation will be used to obtain spectroscopically pure bioactive secondary metabolites. In one such study, a screen for inhibitors and activators of the apoptosome, (a protein complex responsible for programmed cell death) identified an extract from an unidentified zoanthid which grows on Aphrocallistes beatrix. Initial chemical evaluations have begun to yield a series of brominated metabolites.

## Mesobot: A new autonomous underwater vehicle for tracking and sampling animals and particles in midwater

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MBARI, UTRGV, Stanford, WHOI

We are designing and building a new autonomous underwater vehicle (AUV) to address critical knowledge gaps on the biodiversity, ecology, and biogeochemical cycling in midwater. This vehicle, called the Mesobot, will be rated to 1000 m and will have the ability to track slow-moving midwater targets like zooplankton, fish, and particle aggregates using a stereo imaging system. In addition to tracking midwater targets, the AUV will be equipped with hardware to collect pump-filter samples for small zooplankton, environmental DNA, and particles. Typical midwater imaging targets will include migrating fish and zooplankton (e.g. salps, jellyfish, crustaceans), non-migrating zooplankton (e.g., larvaceans), and particle aggregates. The vehicle will acquire these targets under teleoperated control through a tether, after which the vehicle will autonomously track targets guided by the stereo imaging system without a tether. For targets like diel-migrating animals, the goal will be to track continuously for up to 24 hours.Here we present our efforts to address a single scientific use case: tracking motile midwater targets for 24 hrs. In order to do so successfully, we have to address technical challenges that include minimizing hydrodynamic effects that could disturb targets including flows induced by the vehicle body and thruster wash, avoidance and attraction by animals due to lighting and acoustic noise, and reacquisition of fast-moving targets in the stereo imaging system. We will present our preliminary results, tracking jellyfish in Monterey Bay, using the Mesobot's stereo imaging hardware and algorithms on ROV Ventana.

# Trophic ecology - TALKS

## Food-web dynamics and isotopic niches within two deep-sea canyons and adjacent slope habitats

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Submarine canyons are dynamic environments, where complex morphology, intense currents, and variable nutrient conditions influence food quality and quantity fluxing to the seafloor. However, few studies have examined the trophic pathways of deep-sea canyon communities relative to those on the adjacent slopes. In this study, we sampled fish and invertebrates, sediments and water for stable isotope analysis (SIA) and utilized standard ellipse areas (SEA) to examine food-web structure and trophic niches in Baltimore and Norfolk canyons and their adjacent slopes along the U.S. mid-Atlantic margin. Mixed-effect models were developed to identify which factors, including depth, seafloor terrain (e.g., slope, rugosity), feeding group, system (canyon or slope), and/or site (Baltimore or Norfolk) were driving the patterns in the isotope data. Results revealed that communities were composed of isotopically diverse feeding groups, encompassing ~ 5 trophic levels, with phytoplankton-derived carbon providing the basal food resource. Canyon consumers were significantly depleted in 13C relative to consumers on the adjacent slopes. Niche widths (SEA) varied among feeding groups, with little overlap between paired groups found in canyons compared to slopes, possibly due to differences in food selection and habitat association. Distinct isotopic niches quantified from canyon suspension feeders may be due to assimilation of a discrete food source, including fresh organic matter. In contrast, benthic feeders were enriched in 13C relative to suspension feeders, consistent with the consumption of older and more refractory organic material. Benthic feeders were isotopically diverse, potentially because they select food from a mixture of sources, including sediment, infauna, and epibenthos. The large spread in consumer δ13C values indicate that the isotopic composition of particulate organic matter changes, which may be a function of location within canyon and slope environments. Ongoing analyses will elucidate how seafloor terrain, habitat, and location along the margin influence the food-web structure these deep-sea environments.

## Shifts in deep-sea food webs linked to climate and food supply

Rachel M Jeffreys, David S.M. Billett, Brian J. Bett, George A. Wolff
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Shifts in deep-sea benthic communities detected in time-series data at the Porcupine Abyssal Plain (PAP) in the NE Atlantic have been linked to climate-driven variation in particulate organic matter (POM) fluxes. The effect of decadal variation in POM flux on food web dynamics in the deep sea is unclear. We investigated the trophic structure of the benthic megafaunal food web using stable nitrogen isotope analysis at the PAP from 1989-2005. The δ15N composition of six key species was determined including: the holothurians, Amperima rosea, Oneirophanta mutabilis, Pseudostichopus aemulatus, Psychropotes longicauda, the anemone Iosactis vagabunda, and the asteroid Hyphalaster inermis. Bulk δ15N isotopic compositions ranged from 7.8‰ in A. rosea to 16.3‰ in H. inermis, revealing clear differences between feeding strategies. Significant inter-annual differences were observed for A. rosea, P. aemulatus and H. inermis. This suggests a change in either the quality or δ15N composition of POM through the time-series coupled to differences in feeding strategy of consumers at the PAP. We used compound-specific stable isotope analysis of amino acids (δ15N -AA) to disentangle the relative effects of δ15Nbaseline (i.e. δ15NPOM) over trophic fractionation on deep-sea consumers' δ15N composition. δ15NPhenylalanine, an amino acid representative of the base of the food web was relatively consistent across the six species throughout the time series at ~5‰. Conversely, δ15NGlutamic, an amino acid indicative of trophic position varied between different consumers and across the time-series, ranging from 15 to 30‰. These data illustrate that deep-sea food webs exhibit significant variation in trophic status over decadal time-periods. This appears to be driven by shifts in community composition, leading to changes in trophic position, rather than shifts in the isotopic composition of POM. Temporal shifts in

deep-sea food webs are underpinned by climate-driven variation in POM, which results in changes to the structure of the consumer community.

## Methane seep ecotones: sphere of trophic influence on carbonate macrofauna

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Methane seeps are increasingly disturbed by direct human activities and climate change, and, because they provide key ecosystem services, we need to understand their resilience to disturbance and how these ecosystems adapt and recover from such stressors. Seeps are usually accompanied by precipitation of carbonate rocks, which host microbes and a diverse fauna, and play an important role in carbon sequestration. When seepage activity slows or ceases, those structures remain, attracting background species. The rocks then promote an interaction between seep and background communities that may last for long periods forming an ecotone. Here, we present four different approaches to study the sphere of trophic influence of methane seeps. (1) By sampling in situ carbonate rocks with increasing distance from active seepage, we observed a shift in community composition and seep-derived isotopic signatures, although methane-derived carbon was evident at transition sites of lesser seepage. (2) Rock, wood and bone substrates deployed for 7 years at active and transition sites revealed similar fauna and isotopic signatures, supporting the hypothesis that seeps and organic falls can function as metacommunities and possibly metaecosystems. (3) Shipboard incubation experiments using 13C labeled methane documented use of methane in Kiwa puravida and arborescent foraminifera suggesting affiliation with aerobic methanotrophic bacteria. Such taxa may represent important intermediaries in transfer of methane-derived carbon from the seep to the surrounding deep-sea community. (4) A large scale transplant experiment examining community response to the activation or cessation of seepage is underway. These four approaches offer a revised picture of seeps, not as isolated patches, but with multiple interactions with the surrounding community matrix, functioning as source of food and fauna to background and other chemosynthetic communities close by and vice-versa. Understanding these interactions is crucial for management and valuation of its services, and for predicting consequences of climate change.

## Red, Hot, Dexterous Devils: Influence of environmental variability on diet of Humboldt squid (*Dosidicus gigas*) in the Gulf of California, Mexico

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Over the past two decades, the Guaymas Basin of the Gulf of California (GOC) has experienced four El Niño events and a tropicalization, observed as increased sea surface temperature, subsurface warming, and a redistribution of primary productivity during summer (July-October). Concurrently, there has been a drastic reduction in mantle length of mature Humboldt squid (from 75cm to 20cm) to a phenotype typical of this squid in the tropical portion of its range. However, it is unclear how these oceanographic changes affected the midwater organisms that squid feed on, limiting our ability to assess the relative effects of temperature and food

availability on the phenotypic response of Humboldt squid to the environmental variability of the GOC. We quantified the diet of D. gigas in the GOC during the 2015/2016 El Niño and examined whether its trophic ecology varies with respect to body size and environmental variability by comparing our data to past diet studies from the GOC. Diet composition varied significantly and predictably with respect to temperature and chlorophyll-a concentration in the GOC, and we suggest diet can be used to infer prey availability with respect to environmental variability. To further examine interannual changes in prey availability we used acoustic data collected from 2005-2017 to describe the response of nighttime acoustic scattering in the upper 200m of the water column to El Niño and subsurface warming. Mean volume backscattering in the central GOC varied significantly in both basin and shelf habitats with respect to climatic conditions and was sensitive to the subsurface warming observed 2014-2017. This work provides a unique glimpse into the response of a midwater forage community to oceanographic variability, and the effects of forage variability on the trophic ecology of a pelagic predator.

## Trophic structure of deep-pelagic micronekton as revealed through bulk and compound-specific stable isotope analysis

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Recent evidence suggests that small suspended particles can represent an important carbon source for deep-pelagic zooplankton and micronekton. Estimation of suspended particle contributions to micronekton biomass is a significant insight into the structure of deep-pelagic food webs, warranting further examination. Here, using a combination of bulk stable isotope (SIA) and amino acid compound-specific stable isotope analyses (AA-CSIA), we further test the hypothesis that species-specific variation in vertical distribution/migration of micronekton drives differential reliance on suspended particles in deep-pelagic food webs. A suite of seven fishes with similar diets (zooplanktivores) but contrasting vertical migration and depth distribution patterns were collected over two years (2015-2016) in the Gulf of Mexico. Additionally, at each sampling location, samples of particulate organic matter (POM) were taken within the epi-, meso-, and bathypelagic zones to delineate baseline isotopic signatures. Bulk isotopic signatures of POM samples (N=104) were significantly different across depth zones and displayed a general pattern of enrichment in 15N with increasing depth. Mean δ13C values of micronekton (N=402) were similar among species, ranging from -18.29‰ to -19.86‰, while mean δ15N values ranged from 8.05‰ to 10.58‰. Despite similarities in diet, the deepest dwelling, non-migratory bathypelagic species, Cyclothone obscura, was significantly enriched in 15N compared to other taxa, suggesting increased reliance on deep-suspended POM. Vertical migration type (migratory; non-migratory) and depth did not perfectly correlate with bulk 15N signatures, as two non-migratory meso- and bathypelagic species were characterized by bulk δ15N values that were significantly depleted relative to shallower-dwelling migratory species. Ongoing AA-CSIA will further identify potential trends determining the utilization of deep-suspended particles by micronekton in the Gulf of Mexico.

## Trophic structure of two co-occurring species of deep-sea sharks

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Two of the most species-rich fish communities in Icelandic waters are found at the southwest and southeast parts of the continental slope. In

these areas, two deep-sea sharks of the family Etmopteridae; black dogfish (Centroscyllium fabricii) and great lanternshark (Etmopterus princeps), are frequently caught in groundfish surveys at depths of 400-1200 m. As a part of a larger ongoing research on the trophic structure of the deepwater ecosystems, the aim of this study is to analyse feeding habits and estimate trophic positions of the two species. According to stomach content analysis (SCA), fish were the main food of both species by weight, numbers and frequency of occurrence of prey categories. The proportion of fish prey by weight was about 70% for black dogfish but 50% for great lanternshark. The proportion of euphausiids and shrimps in stomachs of black dogfish was high, but great lanternshark appears to prey relatively more upon cephalopods. Jellyfish were found in relatively high abundance in both species. The two sharks, as well as their potential prey, were also analysed for stable isotopes of nitrogen (δ15N) and carbon (δ13C) to get a complementary information on diet, as stable isotope analysis (SIA) gives information over longer time periods than SCA. According to δ15N values, great lanternshark occupied a slightly higher trophic position than black dogfish, still the values for black dogfish were highly variable and partly overlapped those of great lanternshark. The stable isotopic signatures of the sharks and their prey will be used to determine the relative contribution of different prey, using mixing models.

## Trophic ecology - POSTERS

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### Benthic macrofaunal trophic structure and organic carbon flux at deep vent and seep systems of the Southern Gulf of California (Pescadero and Alarcon Rise)

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Deep-sea hydrothermal vents and hydrocarbon seeps communities are based on chemosynthesis. Their dietary carbon sources and their unique trophic structure can be examined using stable isotopes. We analyzed the carbon, nitrogen and sulfur stable isotope ratios of the dominant species collected in three contrasting sites in the Southern Gulf of California: hydrocarbon seeps at 2,400 m depth (PFT) and hydrothermal vents at 3,700 m (PB), found in Pescadero, and hydrothermal vents at 2,300 m in Alarcon Rise (AR). In Pescadero, including both chemosynthetic ecosystems, the δ13C values ranged from -40.8‰ (vesycomid Calyptogena costaricana) to -12.1‰ (siboglinid worm Oasisia aff. alvinae). This wide range in δ13C values indicates a variety of dietary carbon sources, including methane (in PFT), and the presence of macroconsumers that use two different carbon fixation pathways: rTCA and CBB. The δ15N values fluctuated from -12.5‰ (C. costaricana) to 18.3‰ (Actiniaria 3), suggesting the existence of at least four trophic levels. The δ34S values ranged from -36.2‰ (worm Lamellibrachia barhami) to 15.1‰ (Actiniaria 3). The most enriched δ34S values observed in the non-vent Actiniaria 3, along with its enriched δ15N values, were useful to detect a relative contribution of photosynthetic carbon to the system. Additionally, δ34S values contributed to clearly distinguish among vent and seep fauna, the latter having the most depleted values. In AR, δ13C values ranged from -36‰ (Calyptogena magnifica) to -8‰ (worm Alvinella pompejana). The δ15N values fluctuated among -7.9‰ (C. magnifica) and 18‰ (sponge Caulophacus cyanae and a holothurian). The δ34S values ranged from -14.5‰ (C. magnifica) to 15.6‰ (holothurian). The δ34S values allowed the detection of photosynthetic input in this locality. The intervals of all isotopes values were wider in Pescadero than in Alarcon, suggesting that different chemical conditions between both sites influence the composition, distribution and trophic structure of the macrofauna.

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### Ecological roles and trophic diversity of the cephalopod assemblage near Bear Seamount in the Northwest Atlantic Ocean

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Cephalopods comprise a vital component of marine food webs worldwide, yet their trophic roles remain largely unresolved. This study used stable carbon and nitrogen isotopes to describe the trophic structure, ontogeny, and isotopic niche overlap of major cephalopod groups from pelagic and demersal habitats near Bear Seamount in the Northwest Atlantic Ocean. Beak tissues from 225 specimens (13 families; 27 species) were analyzed. The majority of samples were collected during a deep-sea biodiversity cruise conducted in 2012 by the National Marine Fisheries Service. Significant differences in mean δ15N and δ13C values were detected among all families, and among species within the families Ommastrephidae, Histioteuthidae, Mastigoteuthidae, and Argonautoidea. Inferred trophic positions ranged from 2.7-5.0 across all community members, with top positions held by the families Mastigoteuthidae, Joubiniteuthidae, Vampyroteuthidae, Chiroteuthidae, and the species Illex illecebrosus and Histioteuthis reversa. Cephalopod families exhibiting the greatest isotopic niche widths and most diverse niches overall included Ommastrephidae, Cranchiidae, and Octopoteuthidae. Groups with the narrowest isotopic niches included Joubiniteuthidae, Onychoteuthidae, and Vampyroteuthidae. Trophic position increased significantly with mantle length across all individuals sampled, and ontogenic shifts in δ15N values with increasing body size were detected within the species Abraliopsis morisii, Octopoteuthis sicula, Taonius pavo, I. illecebrosus, Ornithoteuthis antillarum, Ommastrephes bartramii, and Sthenoteuthis pteropus. The continuous gradient and broad spectrum of isotopic values measured across families, species, and body sizes suggests an unstructured assemblage within the region. Results provide some of the first quantitative trophic metrics for many poorly known species, and advance our understanding of the diversity of cephalopod ecological roles in marine ecosystems.

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### In-situ observations of an intact natural whale fall in Palmer Deep, Western Antarctic Peninsula

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In early 2017, an intact whale fall was discovered by manned submersible in Palmer Deep, off Anvers Island in the Western Antarctic Peninsula. The skeleton of a ~9m Antarctic minke whale (_Balaenoptera bonaerensis_) lay on a steeply sloped, muddy substrate at 963m and was observed to be in the late enrichment–opportunist stage of decomposition. The skeleton remained largely articulated, with several caudal vertebrae scattered upslope and a disarticulated jaw and baleen plates downslope. The community of organisms present was filmed in HD for approximately two hours; observed fauna included representatives of at least ten phyla, and comprised at least ten OTUs directly associated with the bones (with the polychaetes _Osedax_ and _Vigtorniella_, plus several amphipod species, being most abundant), and a further 15 OTUs considered incidental (with _Notolepis coatesi_ and _Salpa thompsoni_ most abundant). The

observed faunal distribution suggests patterns consistent with planted whale falls and supports the oil gradient hypothesis. This discovery represents the highest-latitude natural whale fall reported to date.

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## Labial Cartilages - more to it than meets the eye

Claudia Klimpfinger, Jürgen Kriwet
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Labial cartilages are two to three paired structures located at both sides of the jaws in elasmobranchs (sharks, rays, skates), though not all species posess them. Information about these structures is scarce since they are often overlooked even when it comes to anatomic species descriptions. Suggestions about their possible function are wide-spread. Some suspect them to have a restricting function on the volume of the mouth cavity, which would be benificial for the efficiency of suction feeding in cartilogenious fishes. Others rather interprate them as an additional stabilization to the corners of the mouth when opening it very wide, as in the family of Chlamydoselachidae, the frilled sharks, who are assumed of being capable of caturing and seizing very large prey. Are those different adaptations of the same structures or is one of these theories a misconception? What is their function in extant species and what can be concluded for extinct species? And where did those structures derive from? A summary of species holding this structures and their styles of living as well as the anatomical characteristics of the labial cartilages in different species could give a clue on some of the many questions.

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## Molecular analyses of *Solenogaster* gut contents to investigate the diversity of food sources

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Trophic interactions among the benthic invertebrate community in the deep sea are generally poorly understood. Solenogaster molluscs are mainly minute predators of the deep-sea benthos, but knowledge about their biology and role in the benthic community is scarce: Direct feeding observations are rare, yet most Solenogastres were assumed to be cnidariovorous based on the frequent encounter of cnidocysts in the midgut via histological investigations. In the present study, we analysed a dataset of approx. 150 specimens of bathyal, abyssal and hadal Solenogastres belonging to more than 40 different morphospecies, from several cruises to the Northwest Pacific (NWP, i.e. Sea of Okhotsk and Kuril-Kamchatka Trench and surrounding plains). We used a universal set of nuclear 28S rRNA primers, known to fail on Solenogastres themselves but to successfully amplify a broad range of gut content 'contamination' and applied BLAST searches to classify the retrieved sequences to best taxonomic level. In approx. 60% of the samples, we retrieved sequences of potential food sources. Remarkably, our data shows that the diet of the NWP deep-sea Solenogastres is highly diverse, clade-specific and not restricted to cnidarians, but revealing nemerteans, polychaetes, and other molluscs as other potential food organisms. We plot the potential food sources onto a molecular phylogenetic tree of NWP deep-sea Solenogastres together with morphological data on the digestive system (i.e., configurations of the foregut glandular organs and radula type). This provides insights into the evolution of Solenogastres and their specific trophic niches and reveals prey-predator relationships in the deep-sea benthos. (*spelled: itadakimasu, translated "let's eat", is a term used in Japanese culture before starting to eat)

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## Scavenging processes on jellyfish carcasses across a fjord depth gradient

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Gelatinous zooplankton populations have increased in some regions, specifically Norwegian fjords, which has likely increased the occurrence of dead jellyfish aggregations on the seafloor (jelly-falls). The importance of scavengers in the redistribution of organic material from jelly-falls and their biogeochemical influence on the benthic environment has been demonstrated. However, scavenger responses to jelly-falls across environmental gradients have not been studied, but would significantly advance our understanding of the impact of jelly-falls on benthic communities and processes in different regions. This study examined scavenging ecology on jelly-falls across an upper-bathyal depth gradient in a boreal oxygenated fjord using baited time-lapse camera lander deployments. The mean maximum abundance of scavengers increased with depth (eight individuals at 250 m, 10 at 600 m, and 18 at 1250 m) and at shallower depths more scavenger species fed on the bait (six species at 250 m, five at 600 m, and four at 1250 m). Mean scavenging rates (841.5 g d21 at 250 m; 667.7 g at 600 m; and 883.7 g at 1250 m), however, did not vary significantly with depth. The lack of detection of a significant depth effect in this study may result from steep fjord topography enhancing food supply to deep waters reducing food limitation at the seafloor. Significant temporal changes in scavenging dynamics were primarily caused by changes in the dynamics of lyssianassoid amphipods. This study demonstrates that scavengers can rapidly remove jellyfish carcasses at the seafloor across a range of upper bathyal depths, potentially reducing the effects of jellyfish decomposition in fjord benthic environments.

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## Food web functioning in Oxygen minimum zones: insights from worldwide isotopic data

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Oxygen minimum zones (OMZs) are defined as water masses where O2 concentrations are <0.5 mL L-1 (<22mM). Permanent OMZs cover over 1 million Km2 of seafloor and intersect the continental margins of the Pacific, Indian and Atlantic Oceans. OMZs are predicted to expand in response to global warming. OMZ expansion has implications for food webs and ecosystem function through reorganization and compression of faunal communities. Understanding faunal responses and ecosystem processes in permanent OMZs is becoming increasingly important given the undetermined and potentially adverse consequences of OMZ expansion and increasing ocean deoxygenation. Naturally occurring OMZs provide an excellent in situ laboratory to test hypotheses, which can be related to increasing ocean deoxygenation and OMZ expansion.Stable isotopes provide a powerful framework for studying metabolic and nutritional pathways in food webs. This is because both carbon and nitrogen isotopes have distinct isotopic values associated with different metabolic pathways. OMZs are microbial biogeochemical reactors with complex and diverse microbial communities utililsing a variety of metabolic pathways. In this study we used stable isotopes to investigate the trophic structure of

infaunal benthic food webs across OMZs in the: Indian, Pacific and South East Atlantic Oceans. We compare these results with food webs at continental margins, which are not impacted by OMZs. Our data reveal a broad range in mean consumer $\delta^{15}N$ values ranging from: 4‰ - 14‰ for OMZ margins and 7.9‰ to 11.6‰ for other margins. Ranges in consumer $\delta^{13}C$ values were smaller, ranging: -15.6‰ to -19.9‰ for OMZ margins and -19.5‰ to -22.7‰ for other margins. We calculated sample size corrected Bayesian food web metrics to analyse trophic niche width. OMZ food webs had larger trophic niche widths compared to other margins. This suggests the presence of a diverse range of food sources and metabolic pathways in benthic OMZ food webs.

TUESDAY Evening • 17:45 • Serra Ballroom

## Trophic ecology of hydrothermal-vent communities in Juan de Fuca Ridge

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Hydrothermal vents host dense assemblages of endemic species supported by local chemosynthetic microbial production, sustained through the oxidation of reduced elements present in the hydrothermal fluid. While the relationships between vent faunal assemblages and habitats have been relatively well described around the globe, our knowledge on trophic ecology and biotic interactions is still limited. Faunal communities associated with active sites along the Juan de Fuca Ridge are dominated by the chemoautotrophic symbiont-dependent tubeworm Ridgeia piscesae. Stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope ratios coupled with biomass and abundance data of many species were used to investigate the food web structure of six R. piscesae assemblages, corresponding to different successional stages, collected on the active Grotto edifice, and to identify the main energetic pathways of this vent ecosystem. Although symbiont-bearing invertebrates R. piscesae represented a large part of the total biomass, the low number of specialized predators of this potential food source suggests that its primary role lies in community structuring. Although trophic structure complexity increased with ecological successional stages, showing a higher number of predators in the last stages, the food web structure itself did not change across assemblages. We suggest that environmental gradients, provided by the biogenic structure of tubeworm bushes, generate a multitude of ecological niches and contribute to the partitioning of nutritional resources, releasing communities from competition pressure for resources, thus allowing the coexistence of species with potentially overlapping niches.

TUESDAY Evening • 17:45 • Serra Ballroom

## Distribution of $\delta^{13}C$ and $\delta^{15}N$ of deep-sea crabs and invertebrates on the Hupo Bank of East Sea (Sea of Japan)

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A combination of stable isotopic measurements was used to study food web structure of Hupo Bank in East Sea (Sea of Japan), an important snow crab fishing ground. Stable carbon and nitrogen isotope ratios of various macrobenthic invertebrates and their potential food sources, such as suspended particulate organic matter (POM), sinking particle, sediment and meiobenthos were identified. We examined stable carbon and nitrogen isotopic signatures of 3 crabs and 11 invertebrate taxa common to the Hupo bank and Ulleung basin slope food web. A total of 21 individuals from 3 crab species (Chinoecete opilio, C. japonicas, Erimacrus isenbeckii) were analysed, and exhibited a broad range of $\delta^{13}C$ (19.3~17.0‰) and

$\delta^{15}N$ (12.0~14.8‰). The food sources, pelagic particulate organic matter (POM) ($\delta^{13}C$=−21.7‰, $\delta^{15}N$=3.0‰) and sediment ($\delta^{13}C$=−21.5‰, $\delta^{15}N$=3.6‰), were not significantly different. Values of meiobenthos (nematode, copepods) ranged between 20.1‰ and 25.6‰ for $\delta^{13}C$ and 6.0‰ and 14.6‰ for $\delta^{15}N$, may reflect diet-related differences in bioenergetic status. Isotope values of macrobenthic invertebrates showed two different food level groups. These data provide the first assessment of deep-sea food web structure in the East Sea (Sea of Japan), and suggest inherent complexity associated with deep-sea slope and basin ecosystems.

TUESDAY Evening • 17:45 • Serra Ballroom

## Carbon and nitrogen stable isotope signatures of macrobenthic nematodes from the Kuril-Kamchatka Trench (Pacific Ocean)

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Free-living deep-sea nematodes are typically smaller than 1 mm and considered in studies of the meiobenthos (fauna retained on 32-μm sieves). At the same time, deep-sea nematodes are often found in the macrobenthic size fraction (retained on ≥300-μm mesh sieves) and have sometimes been recorded in high densities. In general, large nematodes appear to be common inhabitants of at least some deep-sea communities, although the biology of these species remains unclear. High densities of nematodes (up to thousands of individuals per m2) were obtained in macrobenthic sampling efforts during the joint German-Russian KuramBio II (Kurile Kamchatka Biodiversity Study) expedition at water depths of 5146-9539 m. In this study, we investigated the trophic ecology of several macrobenthic nematode species (belonging to 7 families) in the Kuril-Kamchatka Trench by means of stable isotope analysis. We observed high isotopic signature variability of nematodes among individuals, species and study sites. The nematode $\delta^{13}C$ signatures ranged from -25.5 to -17.0‰, and the $\delta^{15}N$ signatures ranged from 6.5 to 19.0‰. Among species, the variability in isotopic signatures within one site reached ranges of 3.6‰ for $\delta^{13}C$ and 5.8‰ for $\delta^{15}N$. The variability in the $\delta^{13}C$ and $\delta^{15}N$ values in individuals of the same species from one site had ranges of 2.8‰ and 1.3‰, respectively. We did not reveal significant differences between the isotopic signatures of females and males. At the same time, there was a prominent bathymetric gradient in stable isotope signatures within Kuril-Kamchatka Trench.

TUESDAY Lightning Talks • 08:30 • Serra Room

## Towards a stable isotope database for deep-sea foundation species

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In the absence of light, communities associated to deep-sea hydrothermal vents and cold seeps strongly rely on habitat and food resources provided by chemosynthetic symbiont-bearing foundation species. However, due to the lack of studies encompassing the vast heterogeneity of seeps and vents environments, factors globally influencing trophic ecology of those animals are still unclear.To tackle this issue, we have established an international database of stable isotope ratios of C, N and S of bivalve molluscs and siboglinid worms from deep-sea vents and seeps. The data acquisition strategy comprises of two approaches: 1) analysis of available literature and 2) new valorisation of specimens already sampled during past cruises.The compiled database will be used to understand, through global, large-scale analysis, how environmental and biological factors (sampling location, depth, fluid composition and emission intensity,

substrate nature, presence of other foundation species, etc.) can drive ecology of foundation species.Moreover, we aim to provide the deep-sea and stable isotope research communities with a freely available data analysis tool that can be used in the context of future ecological research. In deep-sea vents and seeps, stable isotope ratios of symbiont-bearing invertebrates can indeed provide indirect estimates of the isotopic baseline of food webs, in an analogous way as suspension feeders are used in coastal marine ecosystems. By making our database accessible online through the IsoBank repository (www.isobank.org), we will therefore help deep-sea researchers to use stable isotope markers at their full efficiency.To maximise the scope of the database, we are currently looking for new partners that would be willing to contribute to the project by sharing suitable data or samples. If you match this description, or are in contact with people that do, please get in touch during the 15th Deep-Sea Biology Symposium.

## Assemblage structure and trophic ecology of the tubeshoulders (Osmeriformes: Platytroctidae), a biomass-dominant bathypelagic fish family

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Tubeshoulders' (Platytroctidae) are circumglobal and are one of the few fish families centered almost solely within the bathypelagic zone. Due to the lack of specimens this taxon has received little focused attention, despite recent evidence suggesting its predominance in the bathypelagic biome. Within the Gulf of Mexico (GoM), a highly diverse deep-pelagic system, only four species had been reported prior to this study. An extensive bathypelagic trawl series in the GoM allowed a detailed examination of this family, including species composition, abundance, distribution, and trophic ecology. A total of 16 species were collected, 12 being new records for the GoM. The five most-abundant species collected were Mentodus facilis, Platytroctes apus, Barbantus curvifrons, Mentodus mesalirus, and Maulisia microlepis. All platytroctids were collected from depths below 700 meters. Platytroctids appear to be capable of actively avoiding standard research-sized midwater trawls, evidenced by higher catch rates using a large, high-speed rope trawl. Gut content analysis revealed that the dominant platytroctids are generalist zooplanktivores, consuming a wide variety of prey such as, gelatinous taxa, chaetognaths, copepods, euphausiids, ostracods, and occasionally consumption cephalopods. The majority (~70%) of platytroctids examined had empty stomachs, suggesting infrequent feeding. This study represents the first investigation into the diet of this fish family, and adds to the sparse community data of the bathypelagic zone by identifying alternative nutrient pathways (e.g., the fish-jelly link) that connect the deep and upper oceanic ecosystems.

## On parasitism in mesopelagic fishes as a function of trophic ecology and vertical distribution

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Mesopelagic fishes are important consumers of zooplankton and are prey of oceanic predators. Some mesopelagic fishes (e.g. myctophids and stomiids) undertake a diel vertical migration where they ascend to the near-surface waters during the night to feed and descend into the depths during the day to avoid predators. Other mesopelagic fishes (e.g. Sternoptyx spp.) remain at depth throughout the day. While in the epipelagic zone, vertically-migrating fishes become prey to upper-trophic level predators, such as tunas and billfishes. Benthic fishes (e.g. macrourids) often vertically-migrate as well, ascending to feed on pelagic organisms. Although fishes of different depths experience different food environments, vertical migration patterns likely lead to overlap, linking surface, deep-pelagic, and demersal/benthic food webs. The study of gut contents and trophically transmitted parasites can yield insights into ecological processes occurring within these assemblages. We examined the gut contents and parasite communities of 26 mesopelagic fish species in the Gulf of Mexico. Based on gut content analyses, we identified six distinct feeding groups within this assemblage: copepodivory, predation centered on copepods and other zooplankton, predation centered on copepods and euphausiids, gelativory, generalist predation, predation centered on decapod shrimps, and upper-trophic-level predation. The parasite assemblage differed significantly among host feeding groups. For example, generalists feeding on more diverse prey items (e.g. non-migrating hatchetfish, Sternoptyx spp.) had more diverse parasite assemblages, whereas larger upper-trophic-level predators feeding on squids and fishes (e.g. snake mackerel, Nealotus tripes) hosted abundant infections of single taxa, typically tetraphyllidean larvae. Fishes with a mixed diet of copepods and euphausiids contained high abundances of anisakid nematodes and trypanorynch cestodes, whereas those feeding strictly on calanoid copepods exhibited low infection rates of digenean larvae. These data are being used to develop and refine models aimed at understanding ecosystem structure and resilience.

## Nutritional interactions in a midwater community off Southern California inferred from stable carbon and nitrogen isotope ratios

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The two primary mechanisms suggested for the movement of organic matter through the water column are through a chain of predator/prey interactions and through sedimenting of material from shallower depths. In studying the trophic structure of midwater communities, isotopic methods offer the advantage of integrating feeding over a longer period of time rather than depending upon stomach content analysis. We analyzed the 13C/12C and 15N/14N isotope ratios in protein extracts from 179 individual midwater animals representeding all the major midwater phyla. All samples were captured by midwater trawling over a 4-day period at depths from the surface to 1400 m in the 2000-m water column of San Clemente basin off Southern California. Overall δ13C values ranged from -18.5‰ to -23.5 ‰ and δ15N values ranged from 7‰ to 18.5‰ with neither showing a significant depth trend across the entire dataset. However, there are clear increases in δ15N with depth in some groups of animals and the highest δ15N values are at greater depths. At the same time, there appear to be animals at low trophic levels at all depths in the water column. We interpret these data to indicate that both sources of organic matter are important to the midwater community and that it utilizes sedimenting matter extensively.

## The structure of food webs in the Mariana and Kermadec trenches from stable isotope analysis

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Hadal trenches may serve as hotspots for biomass and community activity because their V-shaped structure facilitates food concentration. However, trench food web structure, which could provide insight into such processes, are poorly described. We used stable isotope (δ15N, δ13C) analysis to evaluate food web structure, nutritional sources and animal trophic levels in the Kermedec and Mariana trenches. Sediments from each trench were used as baselines to estimate trophic level. In the Kermedec Trench, samples were collected from 4,000-8,100m. The δ15N values ranged from 5.8‰ in trench sediment to 17.5‰ in the giant amphipod, Allicela gigantea, substantially higher than fishes at ~15‰. The detritivores (holothurians) had δ15N values much higher (~6‰) than expected in comparison to sediment, their putative food source. The difference in δ15N values between deposit feeders and predatory fish was ~3‰, suggesting a range of ~2 trophic levels. The δ13C values ranged from -21.4‰ in sediment to -17.3‰ in the brittle star Ophiolimna sp., and did not co-vary strongly with δ15N values. The most extensively sampled taxa were amphipods and their isotope values showed no relationship with increasing depth. In the Mariana Trench, only fishes, amphipods and sediments were analyzed from 4,000-10,250m, and the δ15N values were similar to those from the Kermedec Trench (sediment δ15N values were 1‰ higher and A. gigantea values were lower at 15‰). However, the δ13C values were slightly higher. These results suggest that there is a compressed food web which spans about two trophic levels. The substantial enrichment in 15N from sediment to detritivores, and the variability in δ13C values suggest multiple food inputs to the system, which could include carrion, phytodetritus, and microbially reworked material from turbidity flows. Compound specific isotope analysis of amino acids provides additional insights on nutritional sources and trophic levels and these data also will be discussed.