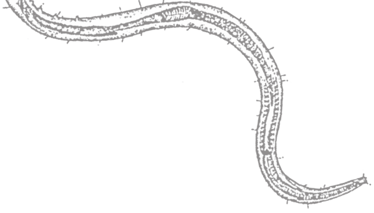

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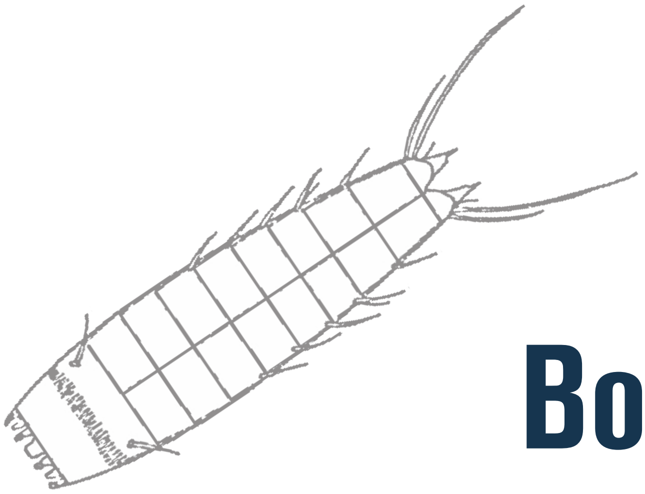

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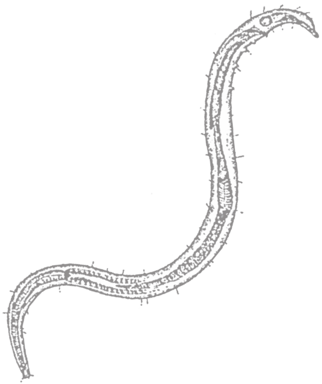

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Preface

MARE-Marine Environmental Sciences Centre, University of Évora together with International Association of Meiobenthologists are proud to welcome the 17th International Meiofauna Conference (SeventIMCO). The SeventIMCO is the major assembly to present and share advances in meiofaunal research and this year-2019 it became a historical meiofauna conference celebrating 50 years (1969-2019) anniversary.

Previous conferences have been held in Tunis, Tunisia (1969), York, England (1973), Hamburg, Germany (1977), Columbia, USA (1980), Ghent, Belgium (1983), Tampa, USA (1986), Vienna, Austria (1989), Maryland, USA (1992), Perpignan, France (1995), Plymouth, England (1998), Boston, USA (2001), Ravenna, Italy (2004), Recife, Brazil (2007), Ghent, Belgium (2010), Seoul, South Korea (2013) and Heraklion, Crete, Greece (2016). The 2019 edition of SeventIMCO, is hosted by MARE - Marine Environmental Sciences Centre - University of Évora, in beautiful cultural heritage town of Évora, Portugal.

This year, 7 keynote presentations, 74 oral presentations and 78 poster presentations are included in the program, which are distributed over 34 countries and 125 corresponding authors. Their contributions are distributed by the following themes, representing emerging topics that meiofauna research:

- Advances in taxonomy, phylogeny and biogeography.
- Meiofauna biodiversity patterns and ecosystem interactions (including Freshwater, Estuarine Coastal and Ocean, Deep sea and Frontiers ecosystems)
- Meiofauna in a changing world: meiofauna response to natural and anthro pogenic pressures.
- Methodologic advances in meiofaunal studies: New tools and analytical and experimental approaches.
- Meiofauna and Science communication to Society

We have also organized an initiative: a roundtable meeting. This is a dynamic encounter aimed at connecting early-career scientists with senior scientists to exchange ideas, collaborate and even identify research priorities for the next decade of meiofauna sciences.

SeventIMCO addresses various challenges that meiofauna research is facing nowadays providing new frontiers and innovative advances in meiobenthology science, to support management decisions of the sustainable use of the oceans, seas and freshwater ecosystems.

Helena Adão
Chair of SeventIMCO

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Part I

Keynote presentations

Invited lectures

ID: 6023

An overview of the ecology of meiofauna in freshwater ecosystems

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Meiobenthic organisms are widespread in habitats like muddy lake bottoms, sandy streambeds, or phototrophic biofilms coating cobbles in rivers, and they also colonize massively ephemeral or disconnected freshwater habitats (like temporary streams). They achieve an important production of biomass throughout the year and there is growing evidence that the meiofauna play a central role in ecosystems by stimulating the mineralization of organic matter by microbial decomposers, or by stimulating photosynthesis through grazing biofilms. Furthermore, the meiofauna seem a significant prey pool for macro-invertebrates and benthivorous fishes. However, our knowledge of the distribution and ecological role of meiobenthic organisms is still minimal in freshwater ecosystems. To some extent, this lack of knowledge might be the result of the difficulty of using the meiofauna in manipulative experiments that have been a stronghold of aquatic ecology. Yet, many meiobenthic organisms possess recognizable functional traits that should make them ideal models for fundamental ecological studies on the interactions between biodiversity and ecosystem functioning. This overview draws a portrait of recent advances in our understanding of the functional diversity of meiofauna in freshwater ecosystems, as well as in our understanding of the diversity of interactions they have with other biota. Given their contribution to secondary production and to the level of connectance in food webs, we argue that meiofauna should not be ignored in concepts and theories about energy flows in ecosystems if we are to meet the challenge of sustaining freshwater ecosystems for the future.

Keywords: Ecological network, secondary production, decomposition, feeding-types

ID: 6070

Quo Vadis, Meiobenthology? Reflections, Perspectives and Conclusions

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Professor emeritus

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The relevant role of meiofauna as mediators between ecosystem processes in contrast to the marginal recognition among biologists and decision-makers has been discussed at the last Meiofauna Conference in Heraklion. This deplorable contrast, neither new nor justified, prompted me to compile the recent meiobenthological literature and put those aspects into the focus that are considered ‘future-relevant’.

Basing on my recent treatise on “Perspectives in Meiobenthology” (Giere 2019) SpringerNature, in press), those directions will be outlined that could bring our research closer to the mainstream, could find notice in general benthology and access to the top-ranked scientific, sometimes even to public media. My focus is on publications from fields of future scientific or even societal potential:

- Importance beyond subject-specific interest
- Pollution and meiofauna – old topics, new hazards
- Future trends in ecological meiobenthos research
- Physiology, biochemistry and meiofauna – a rarely touched terrain
- Towards an integrated triad: Taxonomy, morphology and phylogeny

Based on selected recent literature, only some of these aspects can be outlined here. But the conclusions presented have one underlying concern: the fragile state of meiobenthology in the plethora of benthic or general contributions. My appeal for a future successful research strategy underlines intensive co-operations and use of new technologies to tackle more general aspects of meiobenthology. And it is based on the confidence that future meiobenthology deserves and may attain a greater potential.

Giere, O. (2019): Perspectives in Meiobenthology. Reviews, Reflections and Conclusions. SpringerBriefs in Biology, 80 pp, **https://doi.org/10.1007/978-3-030-13966-7** (in press)

Keywords: Future meiofauna research, out of the ‘dwarf niche’, societal relevance, prospects of scientific progress

ID: 6080

Invisible allies: what can meiofauna tell us about a changing world?

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Marine sediments are by surface the largest habitat on Earth. Interactions between sediment-dwelling meiofauna as well as the interplay between meiofauna and their environment mediate a range of sediment processes, many of which are important on a global scale and are essential to sustain life on Earth. The seafloor has always been changing; current sedimentary ecosystems are the result of millions of years of physical, chemical and biological influences. However, accelerating rates of human-induced changes have led to far-reaching, and in some cases irreversible, degradation of marine sediments. This keynote brings together empirical evidence on the response of meiobenthos to the most dominant and widespread human impacts including climate change, fishing, the introduction of non-native species, and habitat degradation. I will illustrate how meiofauna studies can contribute to the fundamental understanding of human impacts and provide insights into various facets of the threats (e.g. spatial extent, frequency of occurrence, magnitude) such impacts pose to marine ecosystems worldwide.

Keywords: Meiobenthos, marine sediments, disturbance response, human impacts, threats

ID: 6091

New methods for the generation of DNA signatures from marine nematode communities and their application in meiofauna ecology

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High abundances and species diversity suggest that free-living nematodes are important actors in nutrient and biochemical cycling processes in marine sediments. On top of this, a wealth of experimental data show species specific responses to environmental stressors turning nematodes into an important group for ecological impact assessments. Unfortunately, ecological studies are hampered because morphological species identification requires expert knowledge and is time consuming. DNA metabarcoding has been suggested as a way to speed up sample processing for meiofauna communities. We have explored the resolution of different marker genes (18S and COI), of different bioinformatics pipelines (OTU clustering and sequence variants) and of different taxonomic databases to come to a best practice for using DNA metabarcoding in monitoring studies using marine nematodes. The 18S marker gene outperformed COI in terms of taxon diversity, while OTU clustering and sequence variant pipelines of the 18S data showed considerable overlap in the number of species detected. In contrast, little overlap was found when comparing DNA based and morphology based data. This was mainly due to an incomplete reference database. In addition, we also find that the composition of the reference database greatly influences the assignment of sequences to genera. Our results show that 18S metabarcoding data provide higher resolution than morphology based analysis for separating impacted areas from control areas. Metabarcode sequence information can also be used to generate novel insights in species distribution patterns, even from remote and unexplored areas such as the abyssal plain using phylogenetic diversity metrics. Finally, the use of long read Oxford Nanopore data and machine learning are promising avenues for future ecological characterization of marine sediments because they circumvent the use of primers or a reference database.

Keywords: Metabarcoding, metagenomics, reference database, machine learning.

ID: 6117

Biodiversity of marine tardigrades: from intertidal to abyssal depths

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Tardigrades are micrometazoans that occur in a variety of marine, freshwater and terrestrial habitats throughout the world. Marine tardigrades are present in all oceans, ranging from the intertidal zone to abyssal depths, inhabiting a great diversity of sediments (mud, coarse sand, algae and benthic fauna). The research devoted to marine tardigrades is extremely limited and the knowledge of the diversity and geographic distribution of marine tardigrades is still scarce. According to recent estimates, the number of marine tardigrade taxa could exceed that of their limnoterrestrial relatives. However, only less than 220 species and subspecies of marine tardigrades have been described up till now, representing about 16% of all known tardigrade taxa. The diversity of marine forms, highlighting some peculiar morphological traits, will be revisited in this presentation. The main factors responsible for the paucity of knowledge regarding the taxonomy of marine tardigrades, including both methodological aspects and problems inherent to their biology, will be discussed also. This problematic will be exemplified with the results obtained with the research developed in the Atlantic basin on *Batillipes* Richters, 1909, the richest interstitial marine tardigrade genus. Those results clarified the taxonomic status of some species and suggested that cryptic speciation occurs, supporting arguments in favour of endemism against cosmopolitism and contributing to contradict the meiofauna paradox.

Keywords: *Batillipes*, biogeography, cryptic species, meiofauna paradox, taxonomy

ID: 6149

Quantifying the relative impacts of human activities on the coastal systems using free-living nematodes

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The usefulness of nematodes as bioindicators is well documented: they can provide ecologists with a more comprehensive picture of the marine system health status. Since 2011, the community structure, the percentage of certain indicator species and some specific nematode indices have been used to classify the sediments' ecological quality (EcoQ) also allowing to quantify the degree of anthropic disturbance. Although the community structure has proved to be very effective to identify the effects of human impact in Mediterranean basin, the Shannon and Maturity indices appear to be the most suitable tools to be used also to geographically distant areas.Despite these promising results, meiofaunal organisms have not yet been officially included in international monitoring plans. This is because the study of these inconspicuous organisms, requires long analysis times and a good taxonomic experience, which discourages their use in the EcoQ assessment. Therefore, new strategies are needed to enable ecologists to easily use meiofauna for achieving and sharing reliable ecological information. Considering that the morphology of marine nematodes is quite various and generally mirrors the community diversity, some morphological characters have been investigated to test possible community changes induced from natural or human environmental variations. Selected morphological features were the type of buccal cavity, amphid, cuticle and tail, all of that important in the taxonomical identification, but also in a possible adaptive function. We report some preliminary results of a study carried out in an area of Vado Ligure (Ligurian Sea, NW Mediterranean) characterized by a gradient of human impact due to the presence of a commercial port, industrial plants and tourist infrastructures. In particular, the consistence of these morpho-functional traits of nematode species with the diversity and the community structure was tested and the results encourage the use of these nematode features in the monitoring assessment.

Keywords: Marine nematodes, environmental quality, morpho-functional traits, harbour sediments, mediterranean sea

ID: 6174

Not just scratching the surface – Adding deep-sea meiofauna to the bigger picture

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The deep sea covers about 63 percent of our Planet, with an abundance of extraordinary habitats sprawled across its surface. What was once thought of as a monotonous, lifeless expanse vaster than anyone could imagine, we now know to appreciate as a diverse seascape thriving with life adapted to the extreme conditions. Since the first quantitative deep-sea meiofauna study in the early 1960s numerous studies have followed, particularly since the 2000s. These generally characterize the deep sea as rich in meiofaunal diversity, but what else do they show? They give insights on ecological theory, spatial and temporal patterns, biodiversity, environmental impacts, taxonomy and phylogeny, behavior, trophic and other ecological interactions such as symbioses/parasitism, and more recently information on meiofauna contributions to ecosystem functioning and services. Meiobenthologists are employing descriptive methods, but also state-of-the-art technology and novel molecular techniques (age of 'omics') to address questions of scientific importance, but what lies ahead? With Blue Economies in the spotlight, increasing exploration and exploitation of deep-sea habitats, and the emerging impacts of climate change and anthropogenic pollution, questions of wider scientific and societal importance need answering. Deep-sea meiofauna can and should be used to address big picture questions: deep-sea evolution and adaptation, extreme energetics and nutritional limitations, the nature of the 'fabric' of life in the interstitial biosphere including physiology, behavior, and communication, biodiscovery of species and compounds relevant to science, industry, and medicine, etc. Reconciling traditional fields of science with technological advances and societal priorities will enhance understanding of life in the deep sea and promote the intrinsic value of meiofauna to science in general.

Keywords: Meiofauna, deep sea, marine science, blue economy, industry, society, technology

Part II
Oral presentations

1.

Advances in taxonomy, phylogeny and biogeography.

ID: 5791

Deep-sea Kinorhyncha from the US West Coast

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Knowledge about deep-sea kinorhynchs has increased considerably within the last few years. New species of several different kinorhynch genera have been described from the Kuril-Kamchatka Trench, and new species of *Echinoderes* have been described from deep-sea plains around sea-mounts in the East Atlantic and Mediterranean Sea. Furthermore, new and known species of Kinorhyncha have recently been collected and studied from foot of the continental slope off Oregon and California at the US West Coast.

These latter studies resulted in the description of eight new species of Kinorhyncha. In addition, four known species were found at the deep-sea localities, including: *Echinoderes hakaiensis*, known from more shallow water in British Columbia, *E. unispinosus*, known from deep-sea localities in the NE Atlantic, *Fissuroderes higginsi*, known from New Zealand in the SW Pacific, and *Condyloderes kurilensis* known from abyssal plains near the Kuril-Kamchatka Trench in the NW Pacific. The studies furthermore indicated that two new species of *Condyloderes* might co-occur in the deep-sea off California and on the northern continental shelf of the Gulf of Mexico.

Kinorhynch species are usually considered to have a limited distribution, due to their low motile capabilities and lack of pelagic stages. However, the present studies indicate that deep-sea kinorhynchs may show much wider distributional ranges than those of the continental fauna. This suggests that the deep-sea plains may act as dispersal highways for some meiofaunal taxa, and enable much wider, eventually global, distributions.

Keywords: Kinorhyncha, deep-sea, distribution

ID: 5940

Patterns of endemism in marine interstitial microinvertebrates of coastal and shelf areas of the world

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For many years, the spatial distributions of microscopic animals were not explored in depth. Many species are widely distributed and share morphological similarities even though they originate from distant areas. Hence, they have been considered to not show clear biogeographical patterns. Areas of endemism comprise regions in which at least two species have congruent distributional patterns caused by the fauna/flora isolation due to historical or ecological factors. In order to understand the scale of the spatial pattern of distribution and recognition of areas of endemism, we tested marine interstitial microinvertebrate distributions in coastal and shelf areas of the world. Parsimony analysis of endemicity was used to analyze 3034 records and 1084 meiofauna species belonging to Gastrotricha, Kinorhyncha, Polychaeta and Tardigrada. We used provinces and ecoregions as topographic units and congruence core and maximum region of endemism as combined criteria for area delimitation. Also, in order to observe the impact of the inventory incompleteness due to sampling bias between Northern and Southern Hemispheres, we evaluated the relation of sampling effort on the documented species richness and modeled the relationship between species richness and several environmental features for all the ecoregions of the Globe. Twenty areas of endemism were delimited, and the majority of them were found in the Northern Hemisphere. However, our models predicted that the Southern species richness is higher than the actual state of knowledge. Hence, increasing sampling effort, the accuracy of the species delimitation and their geographic range may reveal more areas of endemism in the Southern Hemisphere. In spite of that, the results imply that marine interstitial microinvertebrates respond to events of geographical barriers and abiotic features to explain distributional patterns. Thus, they are not homogeneously distributed throughout the world and can be important study subjects for biodiversity conservation.

Keywords: Parsimony analysis of endemism, meiofauna, Gastrotricha, Kinorhyncha, Polychaeta,Tardigrada

ID: 5957

So different intestine of free-living nematodes

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The midguts of the marine free-living nematodes look in the light microscope very similar in various species. However, various species differ from one another in their diet (bacteriphagous, epigrowth-feeders, predators, etc.). The diets vary in size and solidity of food particles. Also, the species have various stoma constructions using for ingestion of various items. Since of that, we expect the midgut should also vary among species with various modes of feedings and food items. The aim of our study is an attempt to find a connection of intestine fine morphology with either diet or taxonomic position of nematode species. From our study of 12 species from various orders and families and representing different feeding groups (*Bathylaimus arcticus, Oxystomina* sp., *Enoplolaimus* sp., *Paracanthonchus caecus*, *Halichoanolaimus robustus*, *Desmodora communis*, *Draconema ophicephalum*, *Tricoma marisalbi*, *Paramonhystera filamentosa*, Sphaerolaimus balticus, Odontophora *deconinki, Sabatieria ornate* and *Tricoma marisalbi*) and drawing published data on other 33 examined species we come to conclusions that the most variable features of the midgut are apical structures of the microvillar brush and extracellular glycocalyx. Connection the midgut structures with taxonomic position of species is rather weak but nevertheless can be followed in some cases. Connection with size and solidity of food items is more evident though not strong and is expressed in thickness and structural complexity of glycocalyx, and length and density of microvilli. The study is financially supported by RFBR grant N 18-04-00237.

Keywords: Nematode, gut, ultrastructure, ecology, taxonomic

ID: 5979

A supertree of Nematoda: implications for the systematics of marine taxa

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The use of phylogenies has advanced in ecological research aiming to study the role of evolutionary processes in the distribution patterns of many organisms. In this sense, a single hypothesis of the evolutionary history of the target group is commonly adopted. Therefore, this study aimed at constructing an informal supertree of Nematoda, analysing the currently knowledge of phylogenetic relationships from all the valid marine genera,

including the unsequenced ones. The supertree was based on references indicated in the GenBank and the descriptions of taxa considered valid from WoRMS. When phylogenetic information was not available, or it was contradictory among the references, polytomies (uncertainties) were assumed. Only 32% of the marine genera have molecular sequences deposited in the GenBank and were included in phylogenetic studies. Based on cladistic studies and phylogenies from four genes (COI, ITS, 18S, 28S), the supertree ended with thirteen major clades, encompassing 13 orders, including Haliplectida ord. nov. and Axonolaimida ord. nov., and the subclass Dorylaimia. At lower levels, the supertree recognized a new suborder (Comesomatina), 5 new superfamilies (Anoplostomatoidea, Axonolaimoidea, Cyatholaimoidea, Leptosomatoidea, Selachinematoidea) and one new family (Prodesmodoridae). An important proposed change within the families is to consider Enchelidiidae as a subfamily of Oncholaimidae. The supertree showed that polytomies are mainly at subfamilies and genera level due to incipient amount of sequences in public depositories, the paraphyletic conditions in molecular phylogenies and the lack of cladistic analysis. The current supertree serves as a basis to determine phylogenetic relationships among nematodes, to improve systematics classification through the re-examination of taxa, guide future species descriptions and explore the evolutionary relationships in ecological data.

Keywords: Axonolaimida ord. nov., Haliplectida ord. nov., Nematoda, phylogeny, polytomy, systematics

ID: 5982

Are all Kinorhynchs segmented? Evidences from CLSM and 3D reconstruction

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Kinorhyncha is a clade of marine, meiofaunal animals, related with other ‘molting animals’ known as Ecdysozoa. Within the Ecdysozoa, kinorhynchs are nested in the Scalidophora together with loriciferans and priapulids. The kinorhynch body plan consists on a radially symmetrical retractable head, a neck, and a limbless trunk with distinct segmentation. Segmentation within the Ecdysozoa is only present in Panarthropoda (including arthropods, onychophorans and tardigrades) and kinorhynchs, which are closely related to unsegmented phyla. The ancestral body plan of ecdysozoans is unknown but kinorhynchs may provide an important example of convergent evolution of segmentation within ecdysozoans and therefore, the study of their internal anatomy is cru¬cial for understanding the origin of segmentation. Comparative studies on the musculature and the nervous system across Kinorhyncha using immunohistochemistry and confocal laser scanning microscopy have shown that the segmentation patterns may vary and in some taxa (e.g., *Zelinkaderes*) be less distinct. Here, we studied in detail the arrangement of the musculature and the nervous system in two of the most vermiform looking kinorhynch species *Franciscideres kalenesos* and *Cateria styx*, which have very thin cuticle and weak external segmentation. A better anatomical understanding of these aberrant kinorhynchs will help us unravel the evolution of segmentation within Kinorhyncha as well as the relation to non-segmented body plans in Scalidophora.

Keywords: Segmentation, immunohistochemistry, confocal laser scanning microscopy, nervous system, musculature

ID: 6010

Gradual morphological adaptation to deep-sea and pelagic habitats in Aegisthidae Giesbrecht, 1893 (Copepoda: Harpacticoida) inferred from genus level molecular phylogeny

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The family Aegisthidae Giesbrecht, 1893 is known as typical component of deep-sea meiofauna that gradually colonized other marine environments. The phylogenetic relationships within the family, including hyperbenthic, planktonic, benthic and for the first time parasitic Aegisthidae (96 specimens belonging to 60 species and 15 putative genera) were studied here using 2 nuclear genes, small- & large- subunits (18S & 28S) and one mitochondrial gene, Cytochrome c oxidase subunit I (COI). A new classification supported by Maximum likelihood and Bayesian inference is presented, which consists of six monophyletic subfamilies and twelve monophyletic genera. A distinct clade comprising parasitic *Siphonis* Mercado-Salas, Khodami & Martinez Arbizu 2018 cluster as sister to the genus *Cerviniopsis* Sars, G. O., 1903 suggesting a derived branch in which the possession of a stylet-like mandible and an oral cone results in a surprising convergent evolution to Siphonostomatoida Thorell, 1859. Molecular analysis also determined two other new benthic genera to be sister of *Cerviniella* Smirnov, 1946. The two inbenthic genera of this lineage developed adaptations in the swimming legs for digging into the sediments. The planktonic genera *Aegisthus* Giesbrecht, 1891, *Andromastax* Conroy-Dalton & Huys, 1999, *Jamstecia* Lee W. & Huys, 2000 and *Nudivorax* Lee W. & Huys, 2000 form the monophyletic subfamily Aegisthinae Giesbrecht, 1893, sister-group of the hyperbenthic *Pontostratiotes* Brady, 1883. The family Aegisthidae is one of the most basal taxa in the Harpacticoida Sars, M., 1903 tree, but has developed rapid adaptations to the environments colonized by its species in the course of evolution.

Keywords: Harpacticoida, Aegisthidae, molecular phylogeny, 18S & 28S rRNA and COI mtDNA.

ID: 6022

New records of Antarctic meiobentic priapulid larvae

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24 meiobenthic larvae of macroscopic priapulids from north of the Antarctic Peninsula and from Potter Bay, King George Island are reported. They are assigned to four groups according to their lorica pattern, which consists of plates created by ridges. In larvae of the first group the plates in the middle region of the lorica interdigitate in a zig-zag way, this has been described only for *Priapulopsis australis*. Larvae of groups 2 and 3 have more rectangular plates and differ in the presence and abundance of paired versus unpaired plates. The position of

the larval tubuli corresponds to reported larvae of *Priapulus tuberculatospinosus*, but the lorica pattern has not been described in detail for this species. Larvae of group 4 are small and have little lorica structure. They may represent very young larval stages, probably of the co-occurring *P. australis* larvae. The investigations show that much more data are needed about the meiofaunal larval stages of priapulids in order to assign new records to known species or recognize when they represent new species.

Keywords: Priapulida, Antarctic, larva

ID: 6025

Diversity and phylogeny of anchialine cave copepods

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Anchialine habitats are costal water-bodies located within crevicular and cavernous karst and volcanic terrains that extend inland to the limits of seawater penetration. Such systems are characterized by limited primary production; however they are inhabited by rich, diverse and specialized fauna, with high levels of endemism, particularly of crustaceans. Copepod orders Platycopioida, Misophrioida, Calanoida, Cyclopoida and Harpacticoida have successfully colonized anchialine habitats, in which at least one family has been reported as exclusive to these ecosystems. In a recent survey of anchialine caves in the Yucatán Peninsula, Cuba, Lanzarote and Sardinia, so far 63 species belonging to six copepod orders were found including the first record of the order Canuelloida in anchialine ecosystems. Among the most interesting discoveries, we present here for the first time a species of the order Platycopioida in the Mediterranean basin; a new species of the misophrioid copepods genus *Palpophria* from a locality in Cuba is also presented (previously only known from the type locality in Lanzarote). For cyclopoid copepods, a member of the typically deep-sea benthic family Giselinidae is presented, additionally two new species of the family Speleoithonidae from sinkholes in the Yucatán Peninsula are reported. Two nuclear genes fragments from large and small-subunits (28SrRNA and 18SrRNA) and the mitochondrial marker cytocrome c oxidase subunit I (COI) from 56 species have been sequenced in order to investigate the phylogenetic relationships between anchialine copepods. A comprehensive phylogenetic analysis has been performed here including the molecular data of all copepod orders available from Khodami et al. (2017) to reveal the phylogenetic position of anchialine lineages among other copepod habitants. We discuss the close relationship of anchialine cave copepod fauna with the deep-sea species, and the different possible colonization scenarios from deep-sea to anchialine ecosystems.

Keywords: Molecular phylogeny, colonization, meiobenthos, anchialine ecosystems

ID: 6027

Distribution of the genus *Halalaimus* in areas of polymetallic nodules unveiling potential connectivity between different study areas

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Halalaimus is a well-represented genus in deep-sea samples but identifications down to species are not frequently performed. The genus recognition can be easily achieved, but there is no one striking morphological characteristic to identify the species; this is instead done by a combination of characteristics. It is common to have a large number of species, but only few specimens of each species. To date, the genus *Halalaimus* comprises of 98 described species and recent articles describing new species lack an updated list of valid species. The existing revision and identification keys of the species is also outdated. We classified three groups of morphotypes according to the size and shape of the tail: a first group comprising very small and thin specimens with long tail, represented by: *Halalaimus* n. sp, H. aff. *longicollis* Allgén, 1932, H. aff. *monstrocaudatus* Vitiello, 1970 and *H. egregius* Bussau, 1993; a second one of bigger specimens with long tail, represented by *H. praestans* Bussau, 1993, *H. oblongus* Bussau, 1993, *H*. aff. *delamarei* Vitiello, 1970 and *H*. aff. *brimi* Keppner, 1992; and a third one also of bigger specimens but with relatively short tail, represented by *H. abyssus* Bussau, 1993, H. aff. *amphidellus* Vitiello, 1970, H. *oblongus* Bussau, 1993, H. aff. *praestans* Bussau, 1993 and *H*. aff. *turbidus* Vitiello, 1970. The present findings indicate that distant, equally deep nodule-bearing sediments areas are inhabited by similar meiofauna communities, and that the dominant taxa also occur in remote nodule-bearing and nodule-free deep-sea localities. The fact that geographically disparate nodule-bearing, at Clarion Clipperton Fracture Zone - CCFZ exploration areas and abyssal regions, share potentially the same *Halalaimus* species, implies that a wide distribution range may not be limited to higher taxonomical levels. Morphological data suggest potential connectivity between exploration areas in the CCFZ (100s of kilometers apart), and between these CCFZ areas and the Peru Basin (1000s of kilometers apart). However, more molecular data are needed to confirm whether these are in fact the same species or whether they constitute cryptic species.

Keywords: Deep-sea, mining, taxonomy, Enoplida, Oxystominidae

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ID: 6041

Preliminary insights into the gastrotrich community of sublittoral sediments of the Azores Archipelago (Portugal)

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In the course of the BIODIAZ project, a multitude of sediment samples from various depths were obtained during cruise M150 of R/V METEOR in the area of the Azores Archipelago. In order to gain preliminary insight into the community of marine Gastrotricha, a subset of samples was cultivated aboard (vented and stored at 5°C) and meiofauna was subsequently extracted with a 7% aqueous solution of $MgCl_2$ for microscopic investigation and extraction of genomic DNA. This initial study yielded 19 species of the taxon Macrodasyida. Added to the 13 species reported in the 'Global distribution of marina Gastrotricha' (one species probably concordant), we currently know at least 31 marine gastrotrich species (20 genera, Macrodasyida and Paucitubulatina) from the Azores. 14 of these morphospecies are known from different coastal sites on both sides of the North Atlantic Ocean. Among the latter are *Dactylopodola cornuta, D. typhle, Xenodasys riedli, Diplodasys ankeli, D. meloriae,* and *D. minor*, all discovered in our sublittoral samples. The occurrence of widespread morphospecies in remote oceanic biotopes such as the Azores may support the role of such geological formations as 'stepping stones' or 'staging posts' for a trans-oceanic long-distance dispersal of interstitial meiobenthic organisms. Initial analyses of mitochondrial DNA sequence data of the latter three species (*Diplodasys ankeli, D. meloriae,* and *D. minor*) demonstrate a rather high genetic diversity of *D. ankeli* across the whole archipelago. Furthermore, affinities between analysed Azorean specimens of all three species and specimens from different European coastal populations emerged as well. This could indicate past connectivity/gene flow between populations. In order to identify putative source populations or pathways of past colonization of the Azorean sediments, however, comprehensive analyses with more satisfying sampling sizes are essential.

Keywords: Gastrotricha, Macrodasyida, species distributions, molecular taxonomy, COI, Azores

2.

Meiofauna biodiversity patterns and ecosystem interactions (including Freshwater, Estuarine Coastal and Ocean, Deep sea and Frontiers ecosystems)

ID: 5792

Influence of rainfall and salinity intrusion on the meiofauna and nematodes in an Amazonian mesotidal estuarine beach

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Salinity in estuarine environments is one of the most important controlling factors for the distribution of meiofauna. However, few studies have been done on estuarine beaches and those conducted in such environments were done in the nearshore turbid zone of estuaries, where fluctuations in salinity are more similar to oceanic beaches. The present study aimed to verify the response of meiofauna and nematodes to the effects of rainfall and saline intrusion on a mesotidal beach located in the mixing zone of a Brazilian Amazonian estuary. Samplings were carried out bimonthly during one year at four stations in the intertidal zone. At each station, three samples were taken using a corer with 3cm diameter, thrust 10cm into the substrate. The density variation of the meiofaunal community over the months was directly related to the increase of rainfall and decrease of salinity. The highest density of Oligochaeta was found in the months of high rainfall and low salinity. Five genera of marine nematodes were present only in September, month of lowest rainfall and highest salinity. The total richness of Nematoda as well as the brackish genus richness were highest in September and were decreasing until March, month of highest rainfall. The genus *Limonchulus* presented a significant positive correlation with rainfall and a significant negative correlation with salinity. On the other hand, *Metadesmolaimus* had the inverse pattern. *Enoplolaimus*, a typical predator, presented the highest densities in the months of highest rainfall probably due to higher food supply (eg. Oligochaeta). The highest densities of Nematoda occurred at the extreme stations of the intertidal zone in four of the six months studied. Meiofauna and nematodes were strongly influenced by seasonal change of rainfall and salinity. In addition, it was possible to see how seasonal changes in salinity can indirectly influence organisms due to interaction with other groups.

Keywords: Amazon region, meiobenthos, Nematoda, rainfall, seasonality, seawater intrusion

ID: 5825

Meiofaunal communities and nematode diversity characterizing the Secca delle Fumose shallow vent area (Gulf of Naples, Italy)

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Shallow-water hydrothermal vents release gas and hot water, thus creating extreme local conditions. Despite their ubiquitous distribution in tectonically active coastal zones, shallow-water vents have been less explored than deep-sea vents in terms of biodiversity and adaptations to extreme conditions. For the first time, the distribution and diversity of meiofauna and nematode communities inhabiting the Secca delle Fumose (SdF) shallow water vent were investigated. The SdF is a submarine relief consisting of a network of ancient Roman pillars, among which thermal vents discharging hot gas-rich hydrothermal fluids occur.

We selected 4 stations, two characterized by the presence of vent emissions (H=cold emission; S=hot emission) and two controls without vent emission, at comparable water depth. The highest meiofaunal abundance was reported at station S and the lowest at station H. Conversely, station H was characterized by the highest biomass due to the dominance of *Oncholaimus* sp., known to tolerate extreme geothermal conditions and high sulphide concentrations. Nematode and Copepoda were the most represented taxa. Copepods dominated at station H, probably promoted by a higher percentage of coarse grain size and by the intermediate disturbance generated by gas bubbling. Meiofauna and nematode diversity was depressed at station H, but comparable between station S and controls. A high turnover in nematode community composition was reported between all sampling stations. Apparently, each station had a unique nematode community, probably generated by an extreme spatial heterogeneity characterizing the SdF area. The hypothesis that in shallow vents nematodes included a subset of species that lived in control sediments was not confirmed in our study. Even if nematode assemblages were highly diverse, epistrate feeders and carnivores were the most represented trophic groups at all stations, indicating a community of organisms that feed on the available organic resources.

Keywords: Secca delle Fumose, Gulf of Naples, shallow vents, meiofauna, nematodes

ID: 5841

Importance of the microphytobenthos-meiofauna pathway in soft-bottom intertidal food webs highlighted by trophic markers and food web modeling

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Meiofauna play an important role in ecosystem processes in soft-bottom benthic habitats, e.g. food web dynamics, related to their high production, their intermediate trophic position and the energy they transfer towards higher trophic levels. The trophic linkages and flows of organic matter related to the meiofauna remain poorly known or taken into account. To better assess the role of meiofauna, the trophic relationships between food sources and meiofauna were determined in five intertidal soft-bottom habitats (i.e., mudflat, seagrass bed, sandflat) of the Marennes-Oléron Bay, France, and the Sylt-Rømø Bight, Germany.

Meiofauna communities were dominated by nematodes and benthic copepods. Biomass of microphytobenthos and of sediment organic matter were two of the major drivers of community structure. The combination of trophic markers (i.e., stable isotopes, fatty acids) demonstrated that microphytobenthos and bacteria were the major food sources of meiofauna in the five habitats. Information from community structure assessments and trophic marker analyses were implemented in food web models. In all habitats, these models demonstrated that the main flow of carbon to meiofauna originated from microphytobenthos, highlighting negligible changes in meiofauna feeding behavior besides the large differences in availability and productivity of food sources between these habitats. All trophic groups of nematodes, except for selective deposit feeding nematodes, were highly selective and mainly fed on microphytobenthos, resulting in a high production and a short turn-over time of meiofauna. In conclusion, we demonstrated the important role of meiofauna in soft-bottom habitats as well as the importance of the trophic pathway from microphytobenthos to meiofauna in the functioning of these food webs.

Keywords: Free-living marine nematodes, benthic diatoms, bacteria, trophic markers, food web models, intertidal habitats

ID: 5851

Meiofauna versus macrofauna as food resource in a tropical intertidal mudflat

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A better evaluation of benthic marine food webs complexity requires quantifications of organic matter fluxes from meiofauna to higher trophic levels. Meiofauna and macrofauna (tanaidacea) communities from a tropical intertidal mudflat of French Guiana were separately enriched with ^{15}N and ^{13}C. Secondly, those enriched preys were used as tracers during feeding experiments with common predators with different size and feeding mechanisms: a portunidae crab (*Callinectes bocourti*), a penaeidae shrimp (*Farfantepenaeus subtilis*) and a gobiidae fish (*Gobionellus oceanicus*). During feeding experiments all predators except crabs presented feeding rates increasing with the availability of meiofauna and macrofauna food sources. The ability of consumers to selectively ingest their food was evaluated through differences between ratios of macrofauna over meiofauna *i)* ingested and *ii)* available in the environment. Compared to smaller predators, larger ones ingested preferentially macrofauna in accordance with the optimal foraging theory. For large predators, meiofauna would only play a role during first life stage or when large food items are not available.

Keywords: Food web, mudflat, goby, shrimp, crab, tanaidacea, diet

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ID: 5858

When does meiofauna take the lead in benthic functioning? Arctic examples

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Marine soft-bottom zoobenthic communities are usually dominated by macrofauna in terms of biomass and secondary production. However, when biomass of macrofauna is strongly reduced by e.g., decreasing food availability or disturbance (natural or anthropogenic), meiofauna take advantage of reduced predation pressure and competition for food and space. In these situations, meiofaunal biomass can be at a similar level as that of macrofauna, while meiofaunal production can exceed that of macrofauna, as a consequence of inverse relationships

of metabolic rates and size. In the present study we show two examples of zoobenthic communities where meiofauna is a prevailing component in the Arctic: the deep-sea sediments and fjordic basins under influence of glacial disturbance. Firstly, along the bathymetric gradient from shelf to abyssal depths, and decreasing food availability and predictability of food pulses, size of organisms decreases. It is the consequence of higher metabolic efficiency and higher effectiveness of small food particles selection by small organisms. When macrofaunal biomass decreases towards greater depth, meiofaunal organisms became dominated component of zoobenthic communities. Secondly, when natural disturbance occurs, both in shallow water and in the deep-sea, we can observe reduction of the macrofaunal size classes. That causes reshaping of the size spectra of the whole community. In disturbed sediments meiofauna can constitute about 40-50% of the total zoobenthic biomass and over 80% of the secondary production (compared to 4-7 and 35-40%, respectively, in stable conditions). Changes in size structure of the benthic community has further implications on the whole marine food webs and carbon processing.

Keywords: Size structure, disturbance, Arctic, deep-sea, benthic community structure

ID: 5894

A worm's world: Ecological flexibility pays off for free-living nematodes in aquatic sediments and terrestrial soils

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Free-living nematodes are exceptional: they are globally the most abundant metazoans in marine and freshwater sediments, and terrestrial soils, which seems odd given their unusually simple and uniform body plan. We synthesise environmental properties of aquatic sediments and soils and link the composition of nematode communities in each habitat to the distribution of representatives in the 12 major nematode clades (taking into account their generalized biological and physiological characteristics). Several factors (co-)explain the successful ecological proliferation of this ancient and morphologically highly conserved phylum. The capacity of nematodes to adapt to realm-specific environmental conditions is strongly linked to their ability to feed on various food sources in aquatic sediments and soils, the evolution of osmoregulatory functions and reproductive strategies that allow nematodes to proliferate rapidly in a wide range of environmental conditions. The adaptations, roles and behaviours of free-living nematodes have important implications for the resilience of sediments and soils, and for communities that will emerge with continued human alterations to ecosystems worldwide.

Keywords: Free-living nematodes, aquatic sediments, terrestrial soils, ecological success, adaptability

ID: 5915

Meio-and macrofauna of two canyons with contrasting land to deep-sea connectivity on New Zealand's continental margin

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Submarine canyons are often the locus for high primary productivity and can facilitate the transfer of land-derived organic matter (OM) to the deep sea. Differences in the delivery of OM to the seafloor have been evoked to explain differences in benthic communities among canyons, but some studies provide no evidence that variations in OM quantity plays a role in driving these differences. In addition, few studies consider the origins (marine vs land) and quality of sediment OM, which are often modulated by the morphology and location of canyons. In this study, we investigated the meio- and macrofauna of two contrasting canyon systems off New Zealand: Kaikōura Canyon, a steep, short canyon close to the shore, and Hokitika Canyon, a narrow and lower gradient canyon that extends further from the coast. Both meio- and macrofauna abundance and biomass were substantially greater in the highly productive Kaikōura Canyon than in Hokitika Canyon. Stable isotope analyses of sediments show that in Kaikōura Canyon, high proportions of land-derived OM were found in areas near the coast and to 1000 m depth, but very little land-derived material was found further away from the coast (25 km) and deeper in the canyon where marine-derived OM predominated. The nearshore areas with high input of land-derived OM were characterized by high meiofauna biomass. In contrast, sediment OM in Hokitika Canyon was comprised almost entirely of land-derived material, to 2000 m depth and up to 200 km from the coast. Despite the high input of OM from nearby rivers, the infauna biomass was low across the canyon, suggesting that land-derived OM alone is insufficient to support large populations because it is not sufficiently nutritious. Overall, our results indicate that there is a link between land-derived material and infaunal communities within each canyon. However, it appears that variation in marine-derived OM inputs is more important in driving community differences among submarine canyons.

Keywords: Canyons, organic matter, macrofauna, meiofauna

ID: 5930

Nematode-Prokaryote interactions in marine extreme environments

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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 extreme marine ecosystems. The present study aims to unveil nematode-prokaryote interactions in two contrasting extreme environments: shallow water anoxic sediments and deep-sea hydrothermal vents. We selected two of the most abundant thought still overlooked nematode species of Oncholaimidae: *Metoncholaimus albidus* isolated from anoxic sediments of the harbor of Roscoff (Brittany coast, France) and *Oncholaimus dyvae* recovered at the Lucky Strike vent field (1700m water depth, Mid-Atlantic Ridge). Associated prokaryotes were analyzed by microscopic observations (FISH and SEM) and metabarcoding of 16S rRNA. We revealed that both species are very abundant in these extreme environments harbouring a microbial community. In *M. albidus* we distinguished two main morphotypes of bacteria (rod-shaped and filamentous) on the cuticle affiliated to Epsilonbacteraeota and Gammaproteobacteria. *O. dyvae* harbored a microbial community highly represented by sulfuroxidizing bacteria related to Epsilonproteobacteria and Gammaproteobacteria lineages. This study opens the way to the discovery of unexplored prokaryote–eukaryote interactions in marine extreme environments.

Keywords: Oncholaimidae, prokaryotes, extreme environments

ID: 5942

Ecology of meiofauna of the Atacama Trench – bathymetric variation and comparison with the less productive Kermadec Trench

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Hadal regions are the deepest areas of the ocean (>6,000m depth). Particulate organic matter (POM) derived from the primary surface production is the main food supply for the hadal zone, although carrion falls and localized chemosynthetic production also provide resources for some hadal communities. POM flux to the trench floor varies in space and time depending on factors such as local surface primary production and proximity to the coast. Recent investigations of hadal environments have shown that the steep topography of trenches lead to a POM funneling effect resulting in high infauna abundance relative to the adjacent abyssal plain, however several trenches remain poorly sampled. The Atacama Trench is the most southern and deepest trench of the East Pacific Ocean; the first, and until now, only study of Atacama Trench meiofauna, based on core samples from a single station, observed an extraordinarily high density and biomass of meiofauna in comparison to other trenches and the adjacent bathyal region, which led to the "meiofauna hotspot hypothesis". Here, we investigate the spatial variability of meiofauna in the Atacama Trench along the trench axis (six hadal stations classified in three sections: North, Central and South), and three shallower stations (<6000m, one in each section). We also compare the Atacama Trench meiofauna with the less productive Kermadec Trench meiofauna to further test the meiofauna hotspot hypothesis. Preliminary data show high variability of meiofauna density within the axis but not in the shallower stations. While the meiofauna density decreases toward deeper area in the North section, the South section shows an opposite trend. Ongoing analysis will clarify if the surface production controls the meiofauna community in Atacama Trench. Nevertheless, the hadal meiofauna density was not exceedingly high, and the new data not supports a meiofauna hotspot in Atacama Trench.

Keywords: Hadal ecosystems, meiofauna, Nematoda, Copepoda, SE Pacific

ID: 5943

Benthic emergence: an unacknowledged contributor to the ocean's biological carbon pump

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The ocean's biological carbon pump traditionally consists of three phases including euphotic zone carbon fixation, pelagic aggregate sinking and benthic remineralization, but emergence of benthic organisms into the pelagic environment is a potentially unrecognized forth phase. Emergence results in the transport of carbon from sediments or other surfaces into the water column with the capacity to modulate both the flux and transformation of various carbon reservoirs. Many benthic organisms spend part of their life cycle in the water column, but emerging organisms actively swim into the water column often on a diurnal schedule. Harpacticoid copepods are among the most numerous and speciose of emerging benthic taxa. At least one species in >58% of currently identified harpacticoid families has demonstrated active emergence behavior. Varying by habitat and season, studies have documented >30% of the benthic harpacticoid community enters the water column during postsunset periods. Initial seagrass system estimates suggest harpacticoid emergence alone represents from 1.1 to 28.3% of typical carbon settlement occurring over a similar period. Effects on the biological carbon pump will depend on the fate of emerging organisms. The magnitude of possible effects range from limited for emerging organisms that immediately return to the benthos to potentially significant for emerging organisms with prolonged pelagic sojourns. Although few in number, studies on the fate of emerging harpacticoids indicate both extended stays (e.g., long distance dispersal) and interactions with settling particles (e.g., foraging on marine snow) in the water column. Emerging organism foraging in the water column may accelerate carbon settlement and influence remineralization. Occurring in virtually every marine habitat from intertidal to abyssal depths, emergence of benthic organisms into the water column has the potential to influence the biological carbon pump across the world's oceans.

Keywords: Emergence, carbon pump, harpacticoids, benthic-pelagic coupling, marine snow, diurnal

ID: 5944

Kinorhynch diversity around Svalbard: spatial patterns and environmental drivers

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Kinorhynchs, known as mud dragons, inhabit most marine sediments, from the shallow waters to the abyssal depths. However, despite their ubiquitous distribution, information on their taxonomic composition and distribution at the local and regional scale is rare. Particularly for the Arctic region, no comprehensive ecological description of kinorhynch communities has yet existed. To address this gap in our knowledge, we compared kinorhynchs community structure in different localities: north off Svalbard, in the Barents Sea and Svalbard fjords, at 26 stations in total. In the collected samples nineteen species were found. Among them, the most common species were *Echinoderes drogoni* and *E. angustus*, while the most dominant species were *E. eximus*. Patterns of species abundance and shift in their occurrence across the stations were pronounced, with notable distinctions between regions. Three distinct kinorhynch assemblages were observed: 'fjord assemblage' dominated by *E. eximus* and characterized by the highest standing stock and diversity; 'open water assemblage' with *E.arlis* as dominant species and 'north off Svalbard assemblage' characterized by the presence of *E. drogoni* and *E. peterseni*, but the lowest abundance and diversity. We found significant correlation between sediment particle-size diversity and mud dragon diversity, which provides support for the importance of small-scale habitat heterogeneity in the maintenance of local diversity. Variation in kinorhynch communities' structure was also explained by water depth, but this factor was less important in comparison to sediment characteristics. Surprisingly, food-related variables did not contribute significantly to the model, which could suggest that food partitioning did not influence on promoting diversity. However, it is the first study of arctic kinorhynch ecology and further research is needed to get a more comprehensive understanding of the environmental drivers for turnover in mud dragon diversity and distribution.

Keywords: Kinorhyncha, Arctic, diversity, distribution

ID: 5947

Seasonal distribution of marine nematodes in a temperate semi-enclosed bay, China

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In order to study the seasonal changes of marine nematodes, sediment samples at 14 sites were collected in February (winter), May (spring), August (summer) and November (autumn) 2014 in a temperate semi-enclosed bay, China. The species composition, community structure and diversity of marine nematodes and their relationship with environmental factors were analyzed. The volumes of marine nematodes were also measured and their individual dry weight was estimated.A total of 165 species were identified, belonging to 135 genera, 28 families and 3 orders. The average values of nematode abundance in February, May, August, November were (836.93 ± 564.93), (1533.68 ± 612.97), (1036.22 ± 442.07), (2080.48 ± 1011.75) ind./10cm^2, respectively. In winter, spring and summer, *Daptonema biggi, Paradontophora* sp. 1 and *Dorylaimopsis rabalaisi* were the most dominant species, whereas in autumn, *Paradontophora* sp. 1, *Terschellingia longicaudata, Cobbia* sp. 2 were the most dominant species. In terms of trophic structure, epigrowth feeders (2A) were dominant by species number and abundance. Correlation analysis showed that species number had significantly positive correlations with sediment water content and organic matter; species richness index had significantly positive correlation with organic matter; while diversity index, evenness index and dominance index had no significant correlations with any environmental factor. BIOENV analysis showed that the combination of sediment chlorophyll a content, median diameter and silt-clay content could best explain the differences of marine nematode community structure. The body length and width of 1240 nematode individuals at two sites in the four samplings were measured. The average dry weight of nematodes was 0.205 μg/ind. and had high variance. Combined with the present study and previous reports, it is recommended to use a coefficient of 0.2 μg/ind. for the estimation of marine nematode biomass in temperate coastal waters.

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Keywords: Marine nematode, community structure, diversity, seasonal changes, temperate semi-enclosed bay

ID: 5951

Diversity of recent agglutinated Foraminifera in Korean waters: from literature survey

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Foraminifera is one of the most abundant and highly diversified single-celled meiofauna group in marine environments, and more than 9,000 extant species have been reported worldwide. The agglutinated foraminifera is a large polyphyletic group which belongs to three classes – Monothalamea, Tubothalamea, Globothalamea – of phylum Foraminifera, and form their tests with organic or various particles from surrounding environment. In this study, we surveyed the diversity of recent agglutinated Foraminifera taxa reported from Korea. Furthermore, the distribution pattern and dominant taxa of agglutinated foraminifera in Korean waters (East coast, West coast, South coast, and Jeju Island) was also examined. Total three classes, five orders, 16 superfamilies, 31 families containing 68 valid agglutinated genera has been reported from Korea. Genus *Trochammina* appeared most frequently in the Eastern and Western coast, genus Textularia appeared most frequently in Southern coast and Jeju Island region. By considering the limited quantities, methods and areas of the previous researches on biodiversity or ecology of recent Foraminifera in Korea, it is necessary to apply additional research methods and investigate more area.

Keywords: Foraminifera, Korea, agglutinated, biodiversity

ID: 5955

Analysis of seasonal variability of the functional diversity and dynamic of trophic activity-linked traits of micromeiofauna in a freshwater biofilm

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Biofilm-dwelling micromeiofauna – including protozoans, rotifers and oligochaetes – are a primary component of a biofilm, and play an important role in the functioning of microbial food webs by mediating carbon and energy flux from benthos to zooplankton. Micromeiofauna population dynamic varies in function of primary producers and also abiotic factors linked to seasonal cycles, modifying structure and functioning. Because they present life cycle longer than their prey, primary consumer are more sensitive to environmental changes. The trophic characteristics of biofilm-dwelling micromeiofauna were studied at the functional level within the colonization process in a hypereutrophic lake of South West France, in February and April 2017 and in June and November

2018. Samples were collected, using a glass slide method, at the interval of 7, 14, 21 and 28 days. During the whole colonization period, the fast-going bacterivores and generalists were generally the primary contributor to the community in young samples (7-14 days), while the more mature samples (21-28 days) communities were partly dominated by specialist slow-going organisms feeding on larger prey. All seasons appeared to be different in term of functional diversity. Spring samples were richer in functional traits and had more complex traits, while winter samples were more balanced. These results may provide useful information for ecological research on bioassessment in freshwater ecosystem.

Keywords: Colonization, biofilm communities, Hypereutrophic Lake, micromeiofauna, morphofunctional traits, season

ID: 5964

Integrating biodiversity surveys of meiofauna and microbiome for ecosystem biomonitoring

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Animals evolve in a world teeming with microbes, which play pivotal roles in their ecology, health, development, and evolution. Life as we know it would not exist without the profound impact of beneficial host-microbe interactions, and studies of host-associated microbes are critical for advancing our understanding of ecology and developing comprehensive biomonitoring programs. The diversity of meiofaunal community assemblages maximizes opportunities for species-specific responses to individual components of contamination; community changes are also highly specific to the type and severity of contamination, as well as the interaction of the two. Though emerging evidence from invertebrate taxa has underlined the evolutionary and ecological significance of microbiome assemblages, only a few studies have considered the interaction between microbes and meiofauna. This study, driven by recent advances in DNA sequencing technology, represents a potential transformative application of those advances to biodiversity assessment and prediction in changing environments. To investigate microbial community assemblages associated with meiofauna, we have conducted prokaryote 16S rRNA surveys from several individuals across ten meiofaunal phyla collected from different locations in Panama. We then performed statistical analyses to test the presence of assemblage patterns of meiofaunal microbiota constrained to the phylogeny of the host (core microbiota) and assemblage patterns correlated with environmental parameters (accessory microbiota). Additionally, we tested for potential interaction effects between invertebrate and microbial communities on biodiversity measures at different ecological conditions. Results support that changing ecosystems should be assessed by expanding and integrating biodiversity surveys of multiple biological communities.

Keywords: Contaminants, ecology, environmental change, metabarcoding, pollution

ID: 5965

Hydrodynamic exposure decreases the role of environmental filtering over benthic coastal metacommunities

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Species dispersal, habitat heterogeneity, and ecological neutrality determine the biodiversity patterns of metacommunities and the mechanisms influencing their dynamics. Therefore, the roles of environmental filtering and connectivity in metacommunity assembly can be evaluated by understanding metacommunities spatial distributions. Using the elements of metacommunity approach, which evaluates the fit of empirical data to previous-known species distribution models, we accessed the spatial patterns and types of metacommunities for nematode assemblages from three coastal habitats with different degrees of exposure to hydrodynamics (i.e. mangroves, estuarine unvegetated tidal flats, and oceanic sandy beaches) at three different spatial scales (100 km, 100 m, 10 m). Because hydrodynamics directly influences dispersal and habitat heterogeneity, we hypothesized that spatial patterns of soft-bottom metacommunities, represented by nematode assemblages, would depend on the exposure to hydrodynamics. Assemblages each habitat showed distinct patterns of organization. Nematode assemblages from mangroves exhibited a nested pattern with clumped species loss whereas those from tidal flats were characterized by species turnover along the different estuaries, with species having a group response to environmental variations. Both patterns suggest environmental filtering as a principal structuring mechanism at these lower hydrodynamic energy habitats. At sandy beaches, on the other hand, assemblages showed a random pattern where species were not structured by a major gradient. In addition, turnover of the sandy beach metacommunity was lower compared to that observed for mangrove and estuarine tidal flat metacommunities suggesting increased connectivity and a more mass-effect and neutral-based processes shaping community structure. These results indicate that exposure to hydrodynamics is an important driver of metacommunity structure in coastal ecosystems.

Keywords: Metacommunity, biodiversity patterns, hydrodynamics, environmental filtering, coastal ecosystems

ID: 5971

A threefold perspective on the role of cold seeps on benthic fauna assemblages and biodiversity patterns

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Cold seeps are extreme environments characterized by reduced chemical compounds, low oxygen, high habitat heterogeneity and primary production. Despite the harsh conditions several taxa survive or even thrive in the associated habitats. We carried out an ecological research on benthic communities from a pockmark cluster at the Mozambique Channel to understand how the environmental conditions of the seep affected macro-, meiofauna and foraminifera communities; focusing on the dominant taxa of each community, namely Polychaeta, Nematoda and hyaline foraminifers. Intra and inter-stations statistical analyses were conducted to explain changes in richness, abundance and community composition between the pockmark and the adjacent reference site. Elemental Sulphur, dissolved oxygen and organic carbon were used as descriptive environmental factors. Our results showed that all benthic components reached similar richness values both inside and outside the pockmark site, whereas meiofauna and foraminifera had highest abundances at the pockmark with elevated sulphur concentrations, while macrofauna showed higher abundance at the reference site. Moreover, the high meiofauna and foraminifera abundance at the pockmark reflects that some taxa can flourish at these harsh conditions. Conversely, the intra-station analyses showed the normal richness and abundance trends along the vertical profile, being positively correlated with dissolved oxygen and negatively with Sulphur. Polychaetes and nematodes comparison pointed to the same patterns and revealed the presence of polychaetes adapted to hypoxic or sulfide-rich sediments and a clear dominance of the nematode *Desmodora* at the pockmark, which seems to be the better adapted taxa to the conditions of the site. Finally, a high turnover for nematodes may indicate a faster reaction to environmental changes at the pockmark.

Keywords: Cold seeps, pockmarks, biodiversity, meiofauna, macrofauna, foraminifera

ID: 5978

Natural stable isotope ratios and fatty acid profiles of estuarine tidal flat nematodes reveal very limited niche overlap among co-occurring species and a high prominence of omnivory

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The high local-scale species diversity of marine meiofauna, and of nematodes in particular, has puzzled ecologists for decades. Both pronounced niche differentiation and neutral dynamics have been suggested as mechanisms underlying that high diversity. Differential resource use is thé most plausible basis for niche differentiation, yet the vast majority of studies demonstrating that this is prominent in marine nematodes are based on laboratory experiments on single species or highly simplified assemblages. Only a small number of studies have investigated resource differentiation under natural conditions. Here we use natural stable-isotope ratios of carbon and nitrogen, as well as fatty-acid profiles, to assess differential resource use and trophic structure in nine abundant estuarine tidal flat nematode species, comprising different presumed feeding modes (deposit feeders, epistratum feeders, predators, unknown) and resource guilds (herbivores, carnivores, unknown). We demonstrate that resource differentiation is pronounced among as well as within feeding modes and resource guilds. Nematodes comprise up to three different trophic levels (from primary to tertiary consumers), yet with the exception of some herbivores, omnivory is prominent. Bivariate isotopic niche spaces were of similar size among most species, irrespective of their trophic level. Herbivory importantly contributes to the nutrition of herbivores as well as carnivores; it mainly targets diatoms in some species, yet prominently includes dinoflagellates in others. Bacteria, in contrast, appear to be of limited nutritional importance. *Odontophora setosus* is identified as a predator/omnivore with a trophic level in between that of secondary and tertiary consumers.

Keywords: Stable isotopes, fatty acids, marine nematodes, resource partitioning, trophic level, omnivory

ID: 5993

Seasonality in nematodes life cycles and community’s structure in mangroves (Red River, North Vietnam)

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Prominent seasonality were found both in community’s structure and in life cycles of nematodes on mangrove intertidal flat. Seasonal changes in nematodes community were studied on the station situated in the mangrove forest of *Kandelia candel* in the Red River delta, North Vietnam. Quantitative samples were collected seasonally in muddy sediments between mangrove trees (in October, January, April and August). Totally 69 species from 44 genera and 21 family were identified in samples. Total nematodes abundance was rather stable with no prominent pikes, the mean values fluctuate around 600 ind./10 cm^2, seasonal differences were not significant. Species composition is stable during the year and changes appear in relative proportion within the group of dominated species. Two seasonal aspects in community structure described: in autumn and winter *Sabatieria* + *Terschellingia* are most common, while *Ptycholaimellus* + *Metachromadoroides* predominate in spring and in summer. Seasonality in community composition reflects mainly combination of different life cycles of most abundant species. Age structure was described for 11 most common species by seasons. Seasonal changes in abundance found for all the species in different extent, five species reveal strong seasonal changes with maximum in different seasons. Life cycles varied from rather smooth with continuous reproduction along the year to prominent seasonality in reproduction.

Keywords: Nematoda, Vietnam, mangroves, seasonal changes, communities' dynamics

ID: 6014

Is distribution of microcrustaceans (Harpacticoida, Ostracoda) in spring habitats temperature dependent? A comparison from regional and local scale

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Spring habitats are relatively environmentally stable due to the buffering role of groundwater. Nevertheless, there are some temporal fluctuations in water temperature and level in springs, especially at helocrenes even if they are perennial. According to an analysis of the temperature regime at spring fens in the Western Carpathians, the sites largely differ in their temperature stability. However, little is known about how the water temperature affects spring fen microcrustacean assemblages, which include all crenophilic, oligostenothermic, and ubiquist species, and what is the role of small scale heterogeneity and seasonal variation in water temperature at the spring fens.In this study, we documented the response of the whole microcrustacean assemblages and individual species to water temperature in the spring fens on two contrasting spatial scales. 1) On regional scale, we carried out one-shot sampling at 34 spring fen sites and analysed water temperature regime of the individual sites based on two-year continuous measurements of water temperature. 2) On local scale, we sampled four different mesohabitats (pool, mud, tufa, and moss) at three occasions (spring, summer and autumn) to cover the main within-site variation in a heterogeneous but very stable spring fen, and measured water temperature for each sample.We found that water temperature was important for the microcrustaceans at both scales. At regional scale, the effect of high summer temperatures was the most significant for the species composition. At local scale, species distributions were highly patchy, water temperature being the most significant variable; however, seasonal differences in species distributions seemed relatively small, which corresponded with the relative environmental stability of the site. Our study suggests that microcrustacean distribution in spring fens reflects

temperature gradients at different spatial scales, but the seasonal changes are probably small at stable sites.

Keywords: Harpacticoids, ostracods, groundwater-fed habitat, water temperature, stability

ID: 6018

The influence of bioturbatory macrofaunal species diversity on nematode communities

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Infauna in sediments provide important physical and biogeochemical services, but are under increasing pressure from anthropogenic activities, such as benthic trawling. It is known that trawling disturbance has substantial effects on the larger benthic fauna, reducing density and diversity and altering community structure, biomass, production, bioturbation and biogeochemical processes. To investigate the mechanisms by which trawling impacts on the density of large benthic macrofauna may influence the smaller meiofauna, a mesocosm experiment was conducted in which benthic nematode communities from a non-trawled area were exposed to different densities of 7 large (>10 mm) naturally co-occurring, bioturbating species which are potentially vulnerable to trawling disturbance. The results showed that total abundances of nematodes were lower if any one of these large macrofauna species were present, but that no clear nematode community effects could be assigned to macrofauna density differences. It may be, however, that it is not the density of bioturbators that affects the nematodes, but the range of bioturbatory activity. It is interesting to consider, then, whether the diversity of bioturbators, rather than their density, may influence the associated meiofaunal communities. Here we describe results from additional treatments in which the diversity of bioturbators was manipulated.

Keywords: Diversity, macrofauna, trawling disturbance

ID: 6028

Differential effects of resource diversity on taxis to food, population development, and interspecific interactions of cryptic marine nematode species

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Resource partitioning is central to our understanding of the dynamics of species composition and coexistence in biological communities. Based on the principle of competitive exclusion, species occupying the same ecological niche cannot stably coexist due to strong interspecific competition for resources. Niche diversification, for instance, through resource partitioning, may alleviate competition. In addition, there can be tradeoffs between

competitive and dispersal ability. Here, we present data showing the effects of resource diversity on food preference of nematodes using taxis (i.e. a directed movement)-to-food assays, on population development, and on interspecific interactions of four cryptic bacterivore nematode species (Pm I-IV) of *Litoditis* marina that are often found to co-occur in the field. Three resource (bacteria) diversity levels (low, medium, high) were used as food treatments. Results showed that differences in taxis-to-food were present between the cryptic species and between different levels of resource diversity: the cryptic species (except for Pm I) showed higher attraction towards medium food diversity. Interestingly, our data on the population development after seven days revealed that the best population growth was clearly at high food diversity for Pm II and Pm III, whereas only Pm IV showed a tendency for a faster population growth at medium diversity. However, in interspecific experiments, Pm II reached the highest relative abundances among the four cryptic species at all levels of resource diversity (mostly at medium and high diversity), while Pm I and III occurred at very low relative abundances and only persisted in the E. coli treatment. These results suggest that resource diversity has differential effects on taxis-to-food and on nematode population development and can alter the interspecific interactions among the cryptic species of L. marina, indicating that competitive equilibria between species are likely very context dependent.

Keywords: Cryptic species, coexistence, resource partitioning, resource diversity, nematodes

ID: 6030

Characterization of marine nematode associated microbiomes by high-throughput sequencing

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Invertebrate microbiomes may contain information that is relevant to the feeding ecology, fitness, and symbiotic relationships of their hosts. The present study characterizes the spatial (i.e. two stations with contrasting sediment granulometry) and temporal (i.e. three consecutive seasons) variation in the microbiomes of three microphytobenthos biofilm-associated marine nematode species (*Metachromadora remanei, Praeacanthonchus punctatus, Theristus acer)* in relation to the microbiomes of the nematodes' substrates. Only 5 % of the prokaryotic OTUs found in sediments were ever encountered in nematode microbiomes, and only up to 20 % of OTUs from nematode microbiomes were present in sediments. There was also no link between the proportional abundance of specific bacterial taxa in sediments and in nematodes, demonstrating that nematode microbiomes are distinct from those of sediments. Moreover, only just less than half of the OTUs that were shared between nematodes and sediments were also common to all three nematode species, suggesting selective relationships between nematode species and sediment bacteria. These relationships probably involve selective feeding; no clear indications were found for the presence of prominent species-specific nematode-bacteria symbioses. Differences in nematode microbiomes were mostly prominent between *M. remanei* on the one hand and *T. acer* and *P. punctatus* on the other, which likely reflects known differences in their mode of feeding. The microbiomes of sediments and nematodes were strongly context-dependent, differing among stations as well as seasons. A substantial portion (61 %) of the variation in sediment microbiomes, but a much smaller portion of the variation

in nematode-associated microbiomes (7-23 %), could be explained by the spatiatemporal variation in sediment granulometry and in biomass and composition of the microphytobenthos.

Keywords: Microbiomes, marine nematodes, intertidal flat, microphytobenthos, trophic relationships, symbiotic relationship

ID: 6031

Free-living marine nematodes from cold seeps of the Olimpi mud volcano field in the eastern Mediterranean

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The community structure of bathyal meiofauna from 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 was investigated, with a focus on free-living marine nematodes. The Olimpi mud volcano field is a distinctive area of the Mediterranean Ridge accretionary complex, where the occurring mud domes have established close relationships with the existing thrusts, backthrusts and strike-slip faults, which are believed to act as pathways for the upward migration of deep seated mud. The overall aim of the study was to understand geographical patterns and the mechanisms that rule biological diversity, as well as the degree of interconnection between different habitats and areas, a prerequisite to assess the resilience of deep-sea ecosystems and their environmental status. The mud volcanoes were explored during the LEVECO (LEVantine ECOsystem) cruise (2016) with the R/V AEGAEO of the Hellenic Centre for Marine Research. The structure of the meiobenthic and nematode communities is compared with data from adjacent oxic deep-sea sediments, as well as with other cold-seep areas in the eastern Mediterranean. Meiofaunal densities were higher compared to deep-sea basin stations and exhibited high spatial variability, suggesting that certain groups or species may proliferate on chemosynthetic conditions. Nematode communities also varied between mud volcanoes and typical deep-sea sediments, suggesting habitat specificity of meiobenthos. This study contributes to the assessment of the environmental status of the studied deep-sea area prior to the launch of expected socioeconomic activities in the area, such as hydrocarbon exploitation and marine renewable energy production.

Keywords: Deep sea, cold seeps, Mediterranean Sea, community structure

ID: 6043

Meiofauna life on loggerhead and hawksbill sea turtles

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Sea turtles can host a wide range of marine organisms as epibionts. These epibionts range in size from microscopic diatoms and meiofauna (<1mm) to fish that can grow to over half a meter. Here, we present an ecological turtle meio- and macrofauna study based on 19 *Eretmochelys imbricate* (Hawksbill) and 23 *Caretta careta* (Loggerhead) individuals. We found that turtle carapaces can host 10s to 100,000s of epibionts. These epibionts comprise dynamic and fully functional communities. As the turtle breeds, feeds and migrates, it provides a host ecosystem continuously exposed to potential colonizers, enhancing meio- and macrofaunal dispersal, and the geographic distribution of epibiont species. In our study, we investigated epibiotic macro-meio interactions by looking at richness, diversity and community composition. We observed significant positive correlations between meio- and macrofauna diversity, suggesting the presence of mutual facilitating processes and genera enrichment process across size classes and phyla, which may be important for epifaunal recruitment and establishment. Results also suggested that the macrofauna play a bioconstructing role, creating microenvironments that can enhance diversity of nematode assemblages. Furthermore, our study found that turtle nematode diversity exceeded diversity on other hard substrates, but feeding guild, gender and life stage structure did not differ. We therefore suggest that turtle carapaces can be seen as hotspots for nematode biodiversity compared to other epibiotic substrates, but that this is not true for nematode community function. Finally, our study showed that meiofauna community analysis can distinguish between groups of turtle individuals, suggesting that our methods may prove useful in discriminating turtle migration and foraging patterns. The latter results imply that epibiont studies, even if only based on higher-taxa community analysis and reliable identification, may aid sea turtle conservation studies.

Keyword: Nematodes, turtles epibionts, ecological interactions, *Caretta caretta*, *Eretmochelys imbricata*

ID: 6046

Taxonomic Structure of the Meiofauna from Caribbean Mesophotic Reefs

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Biodiversity surveys with emphasis on meiofauna associated with mesophotic coral ecosystems (MCEs) have been conducted as an extension of a long-term research program (Deep Cres) of the Department of Marine Sciences, University of Puerto Rico at Mayagüez from 2007 until present. Mesophotic coral reefs in the Caribbean, one of the most diverse regions in the world, are among the least documented. This study is a research effort aimed to establish a characterization of the meiofauna taxonomic structure that could help to evaluate the biodiversity of this MCEs, and the connectivity between them and their shallow water counterparts. Several mesophotic reefs of Puerto Rico and US Virgin Islands were sampled at different depths (3 to more 100 m) by SCUBA diving during several cruises. Organisms were hand sorted from sediments or after Ludox AM-30 colloidal silica resuspension and a centrifugation step. The total community of organisms were counted and separated into at least the ordinal level. Copepods were the most abundant taxa at all stations, representing 77% of all organisms collected. Acari followed in relative abundance with a 8.7%. Amphipods ranked third in relative abundance (5.61%), and the other orders have relatives abundances lower than 5%. Station El Seco south of Vieques Island represents the place with the highest abundance and the highest diversity of all stations sampled. Significant differences were found among depths and taxonomic groups, the highest densities of organisms were found at the greatest depths sampled and were far more abundant and diverse that shallow and intermediate water depths.

Keywords: Meiofauna, mesophotic coral reefs, Caribbean, Puerto Rico

ID: 6055

Kinorhynch diversity on the Alabama coast

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Recent studies have increased the known diversity and distribution of kinorhynchs in the Gulf of Mexico. Currently, there are 24 named kinorhynch species reported from the Gulf, with additional species that are undescribed. For this study, sediment was sampled from the Alabama coast at shallow depths ranging from 11-26 meters using a multicorer. The 13 stations were positioned to the west and east of the mouth of Mobile Bay as well as at the mouth where the Bay empties into the Gulf of Mexico. A total of 341 animals were collected. Animal densities ranged from <1–66/ 10 cm^2, with an average of 9 animals/10 cm^2.The majority of the identified animals (>70%) belonged to three species in the Genus *Echinoderes*. Animal densities were clustered at the mouth of Mobile Bay, and correlated positively with higher levels of organic matter, silt/clay and most trace metals. Animal density correlated negatively with total sand, surface salinity and depth. These data revealed a surprising low abundance of animals to the east and west of Mobile Bay, suggesting that their populations are heavily influenced by the water entering the Gulf from the Bay, which provides a source for organic matter and other nutrients.

Keywords: Kinorhyncha, community analysis, Gulf of Mexico, taxonomy

3.

Meiofauna in a changing world: meiofauna response to natural and anthropogenic pressures

ID: 5783

Functional diversity of free-living nematodes in river lagoons: Can Biological Traits Analysis (BTA) replace traditional taxonomic-based approaches

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In the framework of the flagship project Ritmare (Ricerca Italiana per il Mare), the functional diversity of free-living nematodes was studied in four Po River lagoons (northern Adriatic Sea) according to five biological traits (feeding type, life strategy, tail shape, body length and shape) considered singularly and combined in a Biological Traits Analysis (BTA). With the exception of the trait ‘Body length’, the ecological information provided by the former approach largely matched with that obtained by the BTA, suggesting that for scarcely biodiverse assemblages such as those of river lagoons the BTA may not be more informative than the analysis of single traits. On the contrary, both approaches may add relevant ecological information when compared to traditional taxonomic-based analyses such as the genera composition of the assemblage, representing therefore a valid alternative in river lagoons monitoring. The analyses of biological traits, in fact, indicated that only the taxonomic change represented by the dominance of *Terschellingia* in Marinetta-Vallona implied also a functional variation. In this lagoon, *Terschellingia* higher abundances entailed a major presence of c-p3 selective-deposit nematodes with elongated tails and slender bodies, while the majority of the genera observed in all the other waterbodies (e.g. *Sabatieria* and *Daptonema*) were c-p2 non-selective deposit feeders that differed for the body length and shape, only. All the distribution patterns obtained (from genera, single and multi traits matrices) seemed driven by flames retardants (PBDEs), whose concentrations in the sediments clearly exceeded their toxicity thresholds in correspondence to the highest abundances of *Terschellingia* and, therefore, to the functional change associated to this genus. Drawing for the first time a link between these emerging pollutants and nematodes biodiversity and function, our findings further confirm the suitability of these organisms as a monitoring tool.

Keywords: River lagoon free-living nematodes, functional groups, Biological Traits Analysis, monitoring

ID: 5794

What promotes the long-term recovery of meiofauna after oil spills?

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The saltmarsh meiobenthic community in Louisiana, USA was monitored with bi-annual collections at reference, moderately and heavily oiled sites following the 2010 Deepwater Horizon oil spill in the Gulf of Mexico. Here we examine environmental factors that influenced recovery over a 4.5-year period beginning 2 years after the spill. The community of 12 taxa began to rebound from oil-induced mortality in < 2 years, but did not fully recover after 6.5 years. The pace and intensity of recovery of nematodes, copepods, annelids, tanaids, bivalves, and amphipods were positively related to the recovery of aboveground plant biomass and benthic microalgae. However, belowground plant biomass was not resilient, indicating that soil quality was insufficient to foster the recovery of the community as a whole. Recovery of the kinorhynch *Echinoderes coulli*, the polychaete *Manayunkia aestuarina*, ostracods, and gastropods was suppressed in association with these factors. Benthic microalgae are an important food source for these meiofauna, and Spartina is a foundation species that enhances habitat quality in the short term and soil quality over the longer term.

Keywords: Oil spill, community analysis, recovery, environmental factors

ID: 5798

Detection of global change with meiofauna and its benthic environment in a shelf sea cold water mass ecosystem

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The marine benthic systems can be affected by global environmental change. The northern Yellow Sea cold water mass (NYSCWM) is locally generated without external intrusion, and relatively independent and sensitive to global change. We utilized multiple scale temporal data (2006-2014) to detect potential impact of global change on meiofauna and its benthic environment in the NYSCWM ecosystem. Time series of bottom water temperature and total organic carbon exhibited increasing trends, while those of meiofaunal abundance, biomass,

sedimentary chlorophyll a and bottom water salinity exhibited decline tendencies. The temporal trends observed in our study were coincident with the global reduction of benthic biomass and increased eutrophication and pollution in response to global change and anthropogenic disturbance. Our study suggested that meiofauna and its sedimentary environment may serve as an integrated indication of potential impact of global change on a shelf sea cold water mass system given that longer-term monitoring data can be accumulated.

Keywords: Meiofauna, sedimentary environment, northern Yellow Sea cold water mass (NYSCWM), temporal change, global change

ID: 5812

Meiofauna in an increasingly stressed Gulf of Mexico: current state and recovery

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The Gulf of Mexico is one of the most important regions for energy resources in the U.S. Offshore federal oil production in the Gulf of Mexico accounts for 17% of total U.S. crude oil production and is expected to continue increasing. But increased economic activity also increases environmental risk, and the Gulf has experienced the two largest offshore oil spills, Ixtoc-1 and Deepwater Horizon, both of which resulted from blowouts during drilling. An understanding of meiofauna community metrics throughout the Gulf of Mexico is important be able to quantitatively assess impacts, response, and recovery of meiofauna from oil production activities. To establish baselines and promote the use of meiofauna as a monitoring tool, six different projects from 1983-2015 were compiled to generate maps of abundance, diversity, and the Nematode: Copepod ratio (NC) for the Gulf of Mexico. Spatial distributions indicate there is a high abundance off the Louisiana coast and high diversity and NC off the Texas and Louisiana coasts. The lowest diversities are in the area impacted by the Deepwater Horizon oil well blowout in the northern Gulf of Mexico. There were fewer samples available for the southern Gulf of Mexico and none along the southwest Florida Shelf. However, analysis of samples in the southern Gulf of Mexico were collected around the Ixtoc-1 oil well blowout and provide an estimate of benthic fauna recovery rate following an oil well blowout. Recovery is estimated to occur once the contaminated sediment is buried below the bioreactive zone of 10 cm depth. Therefore, the area around the Ixtoc-1 oil well blowout will take about 97 more years and the area around the Deepwater Horizon oil well blowout will take about 50 years.

Keywords: Disturbance, diversity, Gulf of Mexico, meiofauna, oil spills, recovery

ID: 5816

The use of nematode assemblages in assessing environmental quality in a semi-enclosed bay

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Free-living marine nematodes are among the most abundant metazoans in marine sediments. They are used as potential indicators of anthropogenic impacts and environmental quality. The present study investigated the attributes of nematode assemblages, including community structure, diversity indices, trophic diversity, feeding types, maturity index and their relationships with sediment environmental variables, especially the concentrations of heavy metals (Cd, Cr, Cu, Ni, Pb, Zn, Co and Mn), at 35 stations in coastal waters of Bohai Bay, China. This study aimed to evaluate the use of nematode assemblage in assessing the benthic ecological quality of a semi-enclosed bay. A total of 77 species of marine nematodes were identified, belonging to 61 genera, 23 families, and 3 orders. The most dominant nematode species were *Dorylaimopsis rabalaisi* (20.65%), *Parodontophora deltensis* (19.58%), *Parodontophora* sp. 2 (17.27%), *Daptonema macrostoma* (12.86%). The species number, Shannon-Wiener index H', and Pielou's evenness J' ranged from 4 to 37, 1.25 to 2.88, 0.54 to 0.97, respectively. The Maturity Index ranged from 1.87 to 2.43. The species with a c-p value of 2 were the most dominant component of the nematode assemblage (81.3%), followed by species with c-p values of 3 (36.5%), 1 (27.9%) and 4 (6.5%). According to the threshold proposed by Moreno et al. (2011), the results of these indices indicated that most stations were classified as poor to moderate ecological quality status. At the same time, the Hakanson's Ecological Risk Index Method was applied to assess the potential ecological risk of the study area. The results of correlation analysis showed that the nematode diversity index H' was not only related to the concentrations of Cr, Co and Mn in sediment, but also had significant relationship with the contamination factors C_f^{Cr}, C_f^{Mn}, C_f^{Co} and ecological risk factors E_f^{Cr}, E_f^{Mn}, E_f^{Co}, indicating that H' can be regarded as a useful descriptor for assessing heavy metal pollution.

Keywords: Marine nematodes, environmental quality, biological indicator, heavy metals, Bohai Bay

ID: 5844

Divergent responses of two intertidal meiofauna communities to CO_2- Induced seawater acidification

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Ocean acidification is changing the carbonate system of the world oceans and posing an ongoing threat to marine organisms and ecosystems. In this study the response of two intertidal meiofauna communities to seawater acidification was examined using microcosm experiment. Fresh sediments inhabiting meiofauna communities

were collected from the extreme low tidal zone of a sandy beach and a silty sandy beach in Qingdao (China). Microcosms were incubated for 0, 7, 14, 28, 56 days in natural seawater (as control) and acidified seawater (pH 7.3, CO_2 concentration: 1900ppm) which simulating the predicted ocean acidification level in 2300 in a carbon dioxide climate incubator. For both sediments the overall response mode of total meiofauna in individual number was similar in 56 days, but the response of individual number of main taxa was completely different. In both sandy and silty sand sediments, nematode number increased in response to low pH in the first two weeks but was not significantly affected in the following weeks, in contrast, the number of benthic copepods was significantly suppressed at pH 7.3 at the end of the experiment. Nauplius number was also significantly suppressed at pH 7.3 at the end of the experiment in silty sand sediment but not in sandy sediment. Community shift of meiofauna occurred at the end of the experiment for both sediments. The community-based microcosm study indicated that seawater acidification could lead to changes in meiofauna communities in intertidal sediments under extreme acidification scenario, but the meiofauna communities inhibited in different types of sediment might response divergently.

Keywords: Ocean acidification, meiofauna, community, intertidal sediment, microcosm

ID: 5852

Ingestion of potentially toxic benthic dinoflagellates by harpacticoid copepods

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Phycotoxins synthesized by benthic dinoflagellates are known to bioaccumulate in macrofauna and constitute a risk for the human health. However, the presence of toxins synthesized by benthic dinoflagellates in smaller marine organisms than macrofauna was overlooked while organisms of this compartment have an important ecological role in the benthic food web. The trophic relationship between benthic dinoflagellates and meiofauna was quantified for the first time in the present study using stable isotopes enriched dinoflagellate during grazing experiments. Harpacticoid copepods were found to graze indifferently on the potentially toxic genus *Ostreopsis* and the non-toxic genus *Amphidinium* even when another food resource like diatom was available. These results suggest that *i)* meiobenthic organisms can constitute an input channel of phycotoxins synthesized by benthic dinoflagellates through the food web and *ii)* meiofauna could consequently concentrate their toxins and then contaminate their predators.

Keywords: Ostreopsis, Amphidinium, grazing rate, isotope, meiofauna, food web

ID: 5862

Species-specific ingestion of microplastics of a free-living nematode community

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Microplastics are hardly biodegradable, they accumulate, rather than decompose in the environment. With decreasing size, secondary microplastics (< 5 mm) as a result of the breakdown of larger plastic items become much more bioavailable for low trophic fauna. In fine sediments, nematodes account for the major share of density and biomass (up to 90 %) of meiobenthic organisms and are considered to have an important position in benthic food webs by connecting lower (bacteria) and higher trophic levels (e.g. macrofauna, fish). Hence, the investigation of the bioavailability of microplastics for nematodes is important for the environmental risk assessment.In this study, the ability of more than 50 free-living nematode species of various feeding types to ingest fluorescent polystyrene microspheres (beads) was tested in direct exposure experiments with natural sediment. Bead diameters (0.5, 1.0, 3.0, 6.0 and 10 µm), bead concentrations (10^4, 10^6 and 10^8 particles ml^{-1}) and exposure time (1, 3, 4, 6 and 10 days) were tested. A total of 690 individuals was analysed and ingested beads were quantified via fluorescence microscopy. Microplastics were ingested by over 30% of the individuals and by over 50% of the free-living nematode species with a maximum of 364 beads in a single individuum at the highest concentration. Suction-feeding nematodes were morphologically unable to ingest any bead sizes via the stylet, confirming that microplastic ≥ 0.5 µm can only be ingested via a buccal cavity. Therefore, about 80% of the non-stylet nematode species ingested microplastics. The carnivorous *Mononchus* was the only genera able to ingest beads > 6.0 µm. A species-specific and particle-size-dependent ingestion could be shown for many individuals and species of nematodes, which may form a basis for a microplastic transfer into higher trophic levels of the benthic food web through predation or indirect uptake.

Keywords: Polystyrene beads, uptake, bioavailability, microcosms, community, meiofauna

ID: 5928

One year natural variability study of meiofauna assemblages and their microbial food among sandy beaches, Alexandria, Egypt

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A total of 1980 sediment samples were collected from November 2012 to October 2013 except for March 2013, from three sandy beaches, El Mex Bay, Abo-Qir Bay and North Western Coast along Egyptian Mediterranean coast of Alexandria that are exposed to different sources of natural and human impacts. Triplicate samples of four profiles with five stations were collected from each beach for meiofauna analysis. A total of 660 sediment samples were sampled for two different bacterial analyses. Samples from November 2012 to April 2013 were used for total bacterial counts. Samples of total Coliform bacterial counts were detected in the period of May 2013 to October 2013. An attempt was done to assess the state of sandy beaches based on natural variability of benthic assemblages in relation to physicochemical and sediment-logical factors. Our results revealed significant temporal and spatial variations among and within sandy beaches in all measured variables. Our expectation was to record higher meiofaunal and bacterial abundance during the period of warm season due to high average of temperature. However, results showed a remarkable decrease in the abundance of both assemblages which is coincident with higher average of water alkalinity. Total bacterial abundance correlated negatively with meiofaunal assemblages at the study areas whereas the relationships between total Coliform bacteria and meiofaunal assemblages differed in signs and magnitudes from one area to another. Results revealed that percent of total organic matter was the best explanatory environmental factors affecting meiofaunal assemblages during cold period whereas the pH was the most important predictor variables during warm period. Our data revealed that the natural variability of benthic assemblages were very sensitive to changes in environmental conditions especially water alkalinity indicating that meiofaunal assemblages could play an important role as biological indicator for natural and human effect.

Keywords: Bacteria, water alkalinity, biological indicator, sandy beach state

ID: 5952

Community structure and variation of meiofauna under environmental change and human activities in Nanji Islands Marine Nature Reserve in the East China Sea

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To study the variation and response of meiofauna under environmental change and human activities, meiofaunal community, abundance, biomass, spatial distribution and seasonal changes were investigated in Huokun'ao sand beach (HKA) and Dasha'ao sand beach (DSA) of Nanji Islands Marine Nature Reserve in four seasons during August 2016 to May 2017. Dasha'ao sand beach is divided into two parts: the experimental zone and core zone. Thirteen meiofaunal groups were classified in this study, the average abundance of meiofauna was 803 ind/10 cm^2, nematodes and copepods are consistently the dominant groups. Compared with the results in 2013-2014, the abundance of meiofauna in HKA increased significantly, and copepod was the most dominant group instead of nematode; abundance of meiofauna in DSA core zone decreased but the biomass increased; abundance of meiofauna in DSA experimental zone was relatively stable. The abundance and biomass of meiofauna were both positively correlated with sediment Pha concentration. The meiofaunal communities were best correlated with the combination of sediment Chl-a and Pha concentration, bottom water temperature, sediment water content, phosphates and nitrates. In Nanji Islands, summer is the peak tourist season and many tourists play, trample and dig on the sand beach in the experimental zone, while no tourists can come into the core

zone. The N/C ratios in DSA experimental zone was slightly higher than core zone in summer. Compared with the core zone, the abundance of meiofauna in 0-8 cm layer in the experimental zone decreased in experimental zone, while the abundance in deeper layer was relatively stable. In autumn, winter and spring, few tourists come to Nanji Islands and the human activities are relatively weak, the community structures of meiofauna in experimental zone and core zone tend to be similar. It can be concluded that human activities have temporary influence on meiofauna in summer in Nanji Islands.

Keywords: Meiofauna, community structure, nematode, China seas

ID: 5967

Influence of sediment organic carbon on toxicity depends on organism's ecology

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Studies which showed the influence of organic carbon on the toxicity of sediment-associated contaminants on benthic invertebrates suggest this was primarily due to its influence on the interstitial water concentrations of the contaminant. A higher organic content offers more binding sites for organic contaminants, which means lower toxicity for organisms whose exposure route is mainly through contaminated pore water. However, a higher organic content in the sediment could mean a higher toxicity for deposit-feeding organisms, which can assimilate the contaminant by ingestion of contaminated particles. To investigate the influence of sedimentary organic carbon content on the toxicity of an organic contaminant on a benthic community, a microcosm experiment was carried out where natural nematode assemblages were exposed to three concentrations of Irgarol in sediments with two different levels of organic carbon for 7 and 35 days. The response of the nematode assemblage to sediment contamination by Irgarol differed between 'rich' and 'poor' sediments. Responses were genus specific and although community composition was the same in both sediments, contamination by Irgarol affected different genera at each sediment type. Also, the differential amount of organic carbon promoted responses of different functional groups. In organic-poor sediments, contaminated treatments showed lower abundances of the genus *Viscosia* and the group of predacious nematodes, which were probably affected by an increased availability of Irgarol in the interstitial water in this treatment. In organic-rich sediments, the group of deposit-feeders were mainly affected, suggesting the ingestion of contaminated food as the main route of contamination in this condition. These results indicate that the bioavailability of toxic substances in sediments is not only determined by their partitioning between the different phases of the sediment but also by the organism's ecology.

Keywords: Sediment contamination, microcosm experiment, ecotoxicology, risk assessment, contaminant bioavailability, Irgarol

ID: 5999

Effects of sediment organic enrichment on a high diversity tardigrade assemblage in the Ría de Muros (NW Spain)

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Canning industry is an important activity of many coastal regions but it is responsible for sediment organic matter enrichment. The response of more relevant meiobenthic taxa (i.e. nematodes and harpacticoids) to organic enrichment is the subject of many studies, but for minor groups is poorly studied. The aim of this study is to explore the response of tardigrade assemblages to organic enrichment. To achieve this, 2 sites located in the Ria de Muros (NW Spain), at both sides of a canning emissary (Sites A and B) were studied as potentially impacted and one site (Site C), the control, about 1 km away. All the 3 sites had biogenic sediment that has showed to harbour diverse and abundant tardigrade assemblages. As sedimentary environmental parameters: total DNA, total organic carbon, nitrite, nitrate, phosphorus and grain size were analysed. Sediment was collected using a van-veen grab. Collected sediment was fixed in formalin (4%) and tardigrades were separated by decantation method, mounted in glycerine and identified to the lower taxonomical level (mainly genus, as many of them are undescribed species). All sites showed a similar grain size (coarse and very coarse sand). Nutrient content was higher at site B than at A and C. Total DNA and organic carbon were also higher at site B than at A and C. Tardigrade diversity showed a clear pattern. At site A 4 species were found (*Batillipes* sp1, *Halechiniscus* sp1, *Florarctus* sp1 and *Halechiniscus* greveni Renaud-Mornant & Deroux, 1976), at site B only 1 species was found (*Florarctus* sp1) and finally at site C 6 species were found (*Corocnartus* sp1, *Styraconyx* sp1, *Tanarctus* sp1, *H. greveni*, *Florarctus* sp1 and *Stygarctidae* indet.). Environmental parameters were not conclusive and only showed some nutrient enrichment at site B but tardigrade assemblage was clearly more diverse at sites A and C while at site B only one dominant species was found. This suggests that tardigrades are sensitive to organic enrichment.

Keywords: Shell gravel, canning industry, *Arthotardigrada*, shallow subtidal, NW Spain

ID: 6008

Effects of oil water-soluble fractions (WSFs) on marine and freshwater nematode assemblages: a microcosm approach

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The water-soluble fractions (WSFs) of oils contain highly toxic compounds, despite their low persistence in aquatic environments. Their effects may be instantaneous or delayed, provoking immediate mortality or sublethal effects, for instance on growth and reproduction. We investigated the effects of crude oil WSFs on both marine and freshwater (FW) meiobenthos, with focus on nematode assemblages, in microcosm experiments lasting up to 15 weeks. Both experiments were performed simultaneously. Nematoda was the most abundant group, comprising ca. 90% of the meiofauna in both marine and freshwater sediments. Oligochaeta (both marine and freshwater), Copepoda (marine), Amphipoda (marine), and Tardigrada (freshwater) almost disappeared from oil WSF treatments. Significant impacts on total nematode abundance, diversity and species composition only became apparent after 15 weeks, indicating that delayed effects are far more pronounced than instantaneous effects. In the short-term, significant oil WSF effects occurred in marine but not in freshwater microcosms: After one week, oil WSFs reduced the number of deposit- and epistrate feeders. In freshwater microcosms, significant effects on nematode feeding types were only detected by differences in the index of trophic diversity, but not by the multivariate comparison of feeding-type composition. Overall, sensitivity was species-specific in both marine and freshwater microcosms, with sometimes opposing responses between even congeneric species. Our results showed that oil WSFs can yield strong effects on both marine and freshwater meiobenthos, and demonstrate the need to assess WSF effects on communities at the species level and over time periods well exceeding the residence time of WSF compounds in the environment.

Keywords: Oil pollution, Nematoda, benthic communities, direct toxicity, experiments, microcosms

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ID: 6017

Meiofauna research to understand the future impact of deep-sea mining in the Clarion-Clipperton Zone

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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 ecology is pivotal in order to provide sound guidelines for environmentally

sustainable mining practices. We therefore studied different aspects of benthic meiofaunal communities as one of the most abundant taxa in abyssal environments such as the Clarion-Clipperton Zone (CCZ) of the east Pacific Ocean. Through a combination of field sampling and in situ experimental approaches both the natural variability in biodiversity and community composition as well as the response to mining related disturbance and its recovery afterwards was investigated. It was shown that despite their success in the abyss in terms of abundances and species richness meiobenthic taxa will be impacted by mining with potentially slow recovery. Through this multimethod approach on meiofauna we aim to illustrate the potential of free-living nematodes as a model taxon to understand drivers and processes of disturbance and recovery in such an extreme oligotrophic environment.

Keywords: Abyssal, nematodes, impact, biodiversity, distribution

ID: 6019

Biomonitoring of freshwater sediments – A comparative assessment using meiobenthic communities and species-based indices

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Nowadays, environmental pollution of surface waters is regarded as one of the most prominent issues, resulting in an emergence of holistic environmental management measures. Soft sediments are known as hotspots of contamination, being of major environmental concern and considerably contributing to the chemical and ecological status of aquatic ecosystems. For this purpose, a thorough eco(toxico)logical assessment of soft sediments can aid in identifying the causes of environmental stress and the implementation of measures to improve the health of this ecosystems. Among the various assessment elements, biological indicators are considered as fundamental due to their overall ecological thoroughness and by providing a holistic measure over time. Regarding suitable bioindicators to assess soft sediment quality, meiobenthic organisms are of particular concern since they are representing very abundant and species-rich components of these habitats. However, they remain under-explored and are not extensively used in routine biomonitoring programs. To contribute to further processes in sediment assessments, surface sediments of Lake Geneva were collected along a contamination gradient and comparatively analysed in this study in terms of chemical and biological parameters. Specifically, structural and functional endpoints of meiobenthic communities were assessed. Additionally, the nematode-based NemaSPEAR[%]-index, and the IOBL, based on oligochaete community analysis, were calculated. Preliminary results revealed distinct responses of meiobenthic organisms to chemical stress, with marked variations in the susceptibility among the various endpoints. Furthermore, the relative distribution of sensitive/tolerant nematode and oligochaete species could also be related to the contamination conditions. Overall, this study provides results allowing for a better sediment assessment of sediment quality and confirmed the importance of looking at the level of meiobenthic communities.

Keywords: Bioindication, meiofauna, nematodes, oligochaetes, contamination, benthos

ID: 6032

Meiofauna as a tool within the framework of European Directives: setting the basis for its use in Greece

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The need to assess and monitor the environmental status of marine ecosystems is growing worldwide due to the cumulative impacts anthropogenic activities have on the seas. For the effective management of the marine environment and its resources, European Directives (*e.g.* Water Framework Directive (WFD), Marine Strategy Framework Directive, Habitat Directive) require an ecosystem-based approach that covers all aspects of marine ecosystems and rests on advanced scientific information and on integrated, multidisciplinary, collaborative approaches. Despite the holistic approach and the vast number of indicators used in environmental assessment, meiofauna have not yet been integrated in monitoring initiatives for a number of reasons, mainly due to gaps in their taxonomy, lack of experts, and the more sophisticated laboratory procedures required for their analysis. However, this will need to change, as the ubiquitous and abundant meiofauna may offer the development of assessment indicators and monitoring tools for a wide range of marine habitats and ecosystems, from where the commonly used macrofauna are scarce, such as the deep sea. Having this in mind, we explore the dynamics of meiofaunal communities from a subset of stations of the Greek WFD coastal monitoring network that covers a wide range of environments and anthropogenic impacts in Greece. Our focus is on the possible use of meiobenthic features (*e.g.* different hierarchical levels and aspects of diversity) and selected key taxa/populations (e.g. kinorhynha, copepod nauplii) as indicators of environmental status that may apply to a range of habitats and types of impacts. First insights on abundance, diversity, population dynamics (*e.g.* sex and developmental stage ratios), their relationship with levels of disturbance, and an attempt to calibrate known indices for use with meiofaunal data will be presented.

Keywords: Environmental assessment, monitoring, anthropogenic impacts, Mediterranean Sea

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ID: 6047

Effects of temperature range changes and interspecific competition to population development and behaviour of marine nematodes

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Global average temperature, frequency of extremes and temperature fluctuations are expected to rise in the future, with many implications for organisms. The amplitudes of temperature variation and the species ability to tolerate thermal stress are crucial for species fitness and survival in rapid changing environments like the intertidal. Sympatric populations of closely related species often compete for mutual resources. Small differences in their life-histories or responses to environmental variation can differentiate their niche breadth and support coexistence. The present experiments examine population fitness and behavioural responses of a free-living nematode, *Halomonhystera disjnucta*, under different temperature regimes in the presence or absence of a competitor. Both stressors (temperature and competition) affected species life-history traits and population development in different ways; *H. disjuncta* showed higher fitness under a daily fluctuating regime and lower under increased constant temperature. The presence of a closely related competitor had a negative effect on population fitness and taxis behaviour of the species. Interaction of competition and temperature stress was apparent and can influence the response of individual species, the stronger effects of competition being under the highest temperature. Thermal stress affects not only species fitness but also species interactions, which in turn will affect species coexistence.

Keywords: Population fitness, interspecific interactions, competition, taxis, thermal stress

ID: 6049

Unraveling fatty acid bioconversion in harpacticoid copepods facing a changing environment

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Global climate change is threatening coastal marine ecosystems by causing changes in oceanographic conditions such as temperature and pCO_2. These shifts affect the physiological performance and productivity of organisms in marine food webs and thus the overall functioning of the ecosystem. A better understanding of the physiological response and adaptive capacity of coastal marine organisms is critical to assess their fate in a rapidly changing ocean. Harpacticoid copepods are a dominant component of estuarine benthic meiofauna, efficient grazers on diatoms, and a major food source for juvenile fish. They are known to contain high levels of polyunsaturated fatty acids (PUFAs), which are essential dietary constituents for fish and humans as the latter can't produce these omega-3 and omega-6 fatty acids themselves. Harpacticoid copepods on the other hand are able to bioconvert PUFAs that originate from primary producers. This capacity might be an essential strategy for harpacticoid copepods to respond quickly to environmental changes, since climate change reduces the amount of PUFAs within primary producers, and thus, their availability for higher tropic levels.Our research aims to uncover the genetic pathways of PUFA bioconversion in harpacticoid copepods and how this mechanism responds to a combination of a reduced PUFA diet and realistic ocean warming. Our species of interest is *Platychelipus littoralis*, a harpacticoid copepod occurring abundantly in the Westerscheldt estuary, the Netherlands. We generated RNA-Seq data and fatty acid profiles from *P. littoralis* subjected to different diet and temperature treatments. Even when fed a PUFA-deficient diet (i.e. the chlorophyte *Dunaliella tertiolecta*), *P. littoralis* maintained similar PUFA levels compared with a control treatment. By means of a

de novo transcriptome assembly and subsequent annotation and differential gene expression analysis, we were able to identify putative genes involved in fatty acid bioconversion. Taken together with the fatty acid profiles, our results hint that the bioconversion capacity of *P. littoralis* could be a potential acclimation mechanism for the species to mitigate the effects of future ocean warming.

Keywords: Transcriptomics, global change, harpacticoid copepods, fatty acid metabolism

ID: 6058

Meio - and nematofauna living inside polymetallic nodules from the CCFZ

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The mining of polymetallic nodules, which occur in abyssal sediments in oligotrophic oceans, is potentially imminent. The Clarion Clipperton Fracture Zone (CCFZ) in the eastern Tropical Pacific, has gained most attention from industries because it is thought to harbor one of the most extensive high-grade reservoirs. Currently, 18 license areas have been delineated in the CCFZ for the exploration of polymetallic nodules. Studies from the 90's in the Peru Basin, south of the CCFZ, reported for the first time the existence of meiofauna living inside the crevices of nodules, which differed from the fauna present in the surrounding sediments. For the CCFZ, published information on the so-called crevice meiofauna is currently lacking. As mining will remove the nodules, it is important to investigate the associated meiofauna to predict future mining-induced losses in meiofaunal diversity. In the present study, nodules were sampled from the license area of Global Sea Mineral Resources in the eastern CCFZ for the analysis of crevice meiofauna with a focus on the nematodes. Per nodule, 2 to 79 meiofaunal organisms were retrieved, most of which belonged to the phylum of the Nematoda. These nodule data were compared with sedimentary data to estimate the contribution of the nodules to the overall meiofaunal and nematode diversity in the area.

Keywords: Deep-sea mining, Nematoda, biodiversity, crevice meiofauna

ID: 6060

Effects of Beach Nourishment: Does Increased Microhabitat Diversity Drive Increased Species Richness?

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Beach nourishment, or the emplacement of dredged sand to mitigate the effects of erosion, has become a standard method of repairing tourist beaches. One long-term effect of nourishment is a coarsening of the beach, as the finer sediments wash away quickly, leaving behind shell-hash. This is of concern, as sediment grain-size is arguably the major abiotic determinant of meiofaunal community structure. Using sieving granulometry to determine sediment parameters and DNA metabarcoding to characterize the meiofaunal community, we have examined two beaches in North Carolina, USA that differ in nourishment history. Our preliminary findings show that there is a significant difference between the two in sediment parameters, with the nourished beach having a significantly greater mean ($p=0.0013$) and median ($p=0.0002$) grain-sizes. Analysis of alpha diversity from the metabarcoding data shows that the nourished beach exhibits significantly higher diversity (as measured by OTU richness) in all three measures used (Faith's PD, Chao1, and number of OTU's). We hypothesize that the increased proportion of habitat heterogeneity in the nourished beach supports higher species richness.

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Keywords: Beach nourishment, metabarcoding, species discovery, species diversity

ID: 6463

Individual and community level responses of benthic nematodes to the environmental estuarine gradient (Sado estuary, SW coast, Portugal)

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Nematodes are among the best candidates for ecological quality assessment due to their ubiquity and sensitivity to abiotic stressors. A background knowledge of how the complex mix of environmental conditions along the Sado Estuary sections affect nematode structural and functional distribution patterns is a prerequisite to develop future bio-assessment tools. Nevertheless, there is less knowledge on how individual species respond to the environmental estuarine gradient when compared to community responses. This study represents the first

data of nematode assemblages and its functional traits (Maturity index-MI, Trophic diversity index - TDI^{-1}) and morphometric attributes (length, weight, L/W ratio and individual biomass) in the Sado Estuary, Portugal. A strong influence of oxygen, temperature, salinity, organic matter content and % of gravel on community structural organization was identified, whereas no significant differences among different estuary "sections" were found for diversity indices, abundance and functional MI, TDI^{-1} indices. Morphometric attributes at the nematode assemblage level were driven by temperature, while at the individual genus level they were mainly associated to salinity, depth and gravel %. Length positively responded to salinity, whereas weight and biomass of most individual genera were positively related to % of gravel and inversely to depth. Significant differences in individual morphometric parameters were found among different estuary sections, although there were no significant differences for diversity metrics and species abundance. This finding suggests that morphometric attributes at the individual genus level better represent differences in abiotic conditions, when compared to community level indicators. These results provide important evidence to support the use of morphometric attributes at the individual genus level as indicators to assess environmental status.

Keywords: Nematode genera, nematode community, estuarine gradient, morphometric attributes, functional traits

4.

Methodologic advances in meiofaunal studies: new tools and analytical and experimental approaches

ID: 5923

Unsupervised meiofauna biodiversity estimation using MALDI-TOF MS data

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Species identification in meiofauna research is still carried out mainly morphologically. Unfortunately, identification of small meiofauna organisms is very difficult and time consuming. MALDI-TOF mass spectrometry is an emerging tool for identification of metazoan species based on a proteome fingerprint. It was shown in several studies to provide a rapid and cost-effective alternative to molecular barcoding, providing quantitative data. However, in areas lacking a good quality reference library, assignment of measured proteome fingerprints to an actual species is barely possible. Nevertheless, it is important to be able to assess biodiversity on species level to allow between-area comparisons. So far, specimen identification using MS data strongly relies on supervised methods using reference libraries. In unsupervised approaches, such as cluster analyses, recognizing species boundaries is difficult as displayed distances can be highly variable and differ between pairs of species. In the present study, we used a MALDI-TOF MS dataset of 34 different harpacticoid copepod species to test which methods provide biodiversity indices fitting the original data best. In more than 30,000 analyses, different combinations of dimensionality reduction methods, data transformations and cluster algorithms were tested. Tests included analyses of different species compositions, typical species distribution patterns and different patterns of species abundances. The results are in good concordance with, and frequently identic to, the original data. Hence, a method is provided to rapidly assess biodiversity quantitatively based on a combination of MALDI-TOF MS and automatic cluster recognition in areas lacking reference libraries.

Keywords: MALDI-TOF MS, rapid biodiversity assessment, biodiversity, Harpacticoida, species identification

ID: 5936

Nutritional sources of hydrothermal vent meiofauna revealed by natural-abundance radiocarbon and stable isotope analyses

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Deep-sea hydrothermal vents host unique marine ecosystems, which rely on organic matter produced by chemoautotrophic microbes together with phytodetritus. Although meiofauna can be abundant at such vents, studies on meiofaunal nutritional sources are limited due to their small size. Here, we investigated dietary sources of meiofauna at hydrothermal vent fields in the western North Pacific using stable carbon and nitrogen isotope ratios ($\delta^{13}C$, $\delta^{15}N$) and natural-abundance radiocarbon ($\Delta^{14}C$). The $\delta^{13}C$ and $\delta^{14}C$ values of dirivultid copepods, endemic to hydrothermal vent chimneys, were -11‰ (on average) and -661‰, respectively, and were similar to the bacterial mat ($\delta^{13}C$: -14‰, $\Delta^{14}C$: -614‰) and hydrothermal vent-endemic *polychaete Paralvinella* ($\delta^{13}C$: -11‰, $\Delta^{14}C$: -678‰). Those isotopic compositions were distinct from those of near-by non-vent sediments ($\delta^{13}C$: ~-24‰) and water-column plankton ($\Delta^{14}C$: ~40‰). In contrast, $\delta^{13}C$ values of nematodes from vent chimneys were similar to those of non-vent sites (ca. -25‰). Our results suggest that dirivultids relied on vent chimney bacterial mats as their nutritional source, while vent nematodes did not obtain significant nutrient amounts from the chemolithoautotrophic microbes. The combination of stable and radioisotope analyses on hydrothermal vent organisms provides valuable information on their nutritional sources and, hence, their adaptive strategy to inhabit chemosynthesis-based ecosystems.

Keywords: Dirivultid copepods, hydrothermal vent, nutrition, natural-abundance radiocarbon, stable carbon and nitrogen isotope ratios

ID: 5966

Confocal laser scanning microscopy (CLSM) and 3D visualization: An imaging workflow to study meiofauna

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Recently confocal laser scanning microscopy (CLSM) has been used to image different groups of meiofauna, providing detailed information about their internal and external morphology. Pioneer studies imaged small crustaceans and selected copepods as model organisms to describe treatments for mounting and preparing specimens for CLSM visualization. In this presentation, we will discuss a workflow including the description of the pre-processing steps of material preparation (staining and mounting), confocal laser scanning microscopy basic settings for meiofaunal groups, data visualization and isosurface rendering using open-source programs (ImageJ and Drishti) and 3D printing output. The methodology presented here for the data visualization used representatives of Acari, Copepoda, Nematoda, Ostracoda, Kinorhyncha, Isopoda, Tardigrada and Tantulocarida.

Keywords: Data visualization, Drishti, ImageJ, Blender, 3D printing

ID: 5968

Unity makes strength: high contribution of intertidal benthic foraminifera to sediment reworking

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Although benthic foraminifera are one of the most abundant components of the meiofauna, their role in intertidal ecosystems functioning has been largely overlooked. Specifically, benthic foraminifera may contribute to bioturbation process by sediment reworking. Whether this contribution is significant remains, however, to be assessed. The aim of this study was to quantify the sediment-reworking rate (SRR) of 5 foraminiferal species characteristic of European temperate mudflat: *Ammonia tepida, Haynesina germanica, Cribroelphidium williamsoni, Milliammina fusca* and *Quinqueloculina seminula*. Sediment surface was gently scrapped-off to collect living benthic foraminifera for the experiment. In the laboratory, individuals were gently sorted and spread over a thin layer of sediment in a beaker filled with seawater. Movements of all individuals were subsequently recorded every 10 min using a digital camera for 24h. The volume of reworked sediment was calculated considering the total distance travelled and the surface of the test for each species. For the 5 studied species, the SRRs ranged from $3x10^{-3}$ $cm^3.d^{-1}$ (*M. fusca*) to $16x10^{-3}$ $cm^3.d^{-1}$ (*Q. seminula*). Considering

a community of those 5 species with a typical total abundance of 60 ind.cm^{-2}, the volume of sediment mixed per surface unit (1 m^2) is 8.34x10^3 cm^3.d^{-1}. As a comparison, a population of Heteromastus filiformis, a polychaete inhabiting the same ecosystem as the studied foraminifera, can mix up to 1.44x10^3 cm^3.day^{-1}. These results unambiguously show that sediment reworking by benthic foraminifera is not to be neglected, and it stresses the need for further experimental work to furthering our understanding of the role of benthic foraminifera in bioturbation processes (*i.e.* particle reworking) but also the related biogeochemical fluxes at the water-sediment interface.

Keywords: Benthic foraminifera, bioturbation processes, experimental approach, species and community scales

ID: 6006

Genetic barcoding in marine nematodes - promises and pitfalls

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Correct identification of marine meiofauna organism is crucial for ecological as well as for phylogenetic studies. Genetic barcoding and metabarcoding have become important and often used tools for fast and less time consuming identification of marine meiofauna. Here we compare classical PCR and metagenome barcoding approaches using members of the marine nematode order Desmodorida and highlight the importance of carefully curated and reliable databases using full length gene sequences. We compare the performance of two highly used marker gene sets (18S rRNA and COI) in correct taxonomic identification and phylogenetic studies. Depending on the marker gene and primer set classical PCR based approaches can be the source of many mistakes and therefore metagenome based tools are more reliable and less error prone with a high potential not only for one or two but a whole set of multiple marker genes or even genomes.

Keywords: Metagenome, genetic barcoding, marine nematodes, Desmodorida

ID: 6012

Inter-and intraspecific competition influence the resource utilization and niche width of closely related nematode species

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Nematode assemblages have high abundances and a high species diversity, where many species, including functionally very similar ones, coexist. This challenges competition theory, since competition should be most

severe between species with a high ecological equivalence. Species may alter their diet in response to competition, following either niche pre-emption or dominant plasticity. In the former, the superior competitor(s) can 'monopolize' a preferred food source, forcing weaker competitors to switch resource. In the latter, superior competitors exhibit resource plasticity and change niche width as a function of the competitive environment, be that inter- or intraspecific. Hence, competition can reduce the resource niche width of individuals, while at the same time increasing interindividual variation, thereby widening the niche width at the population level.
A microbiome represents the collective genomic content of the microbiota of a host, including bacteria ingested as food. Here, we test whether intra- and interspecific competition influence the microbiome composition of two cryptic species of *Litoditis marina*. We know that when Pm I and Pm III are combined, the former can outcompete the latter. However, in the presence of Pm IV, both Pm I and Pm III are inferior competitors. We performed a monospecific experiment in which the starting densities of Pm I and Pm III were varied to assess intraspecific competition; and an interaction experiment combining Pm I with Pm III, in presence and absence of Pm IV, to evaluate interspecific competition. Nematodes were fed bacteria for two days, after which we analysed the microbiomes of 10 specimens per species using next generation sequencing of the 16S rRNA gene on an Illumina MiSeq. The microbiome of Pm III was mostly affected by interspecific competition, indicating the niche pre-emption theory. Differences in composition, diversity and biomarker taxa of the microbiome were found. The microbiome of Pm I mainly reflected a contracted individual niche width in the presence of both intra- and interspecific competition (dominant plasticity). This result indicates that individuals may mitigate the effects of competition by reducing niche overlap with both conspecific and heterospecific competitors.

Keywords: Competition, intraspecific, interspecific, nematodes, microbiomes, coexistence

ID: 6016

New multivariate approaches to access and predict metacommunity patterns

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Ecological communities are characterized by many coexisting species, which patterns are dictated by several structuring and interacting abiotic and biotic variables, which in turn rule over at multiple spatial and temporal scales. Metacommunity adds a new layer of analytical complexity, since deals with interconnected communities in space and time. Metacommunity is therefore one of the most challenging entity to be analyzed and predicted. Today analytical tools to explore a metacommunity can be separated in two groups depending whether includes or not the "a priori" categorical factors among the predictors. Till now the "a posteriori" approach lack significance tests. A posteriori tests are however particularly valuable when species distributions are discontinuous and were not considered in the sampling design. In order to explore whether there is a significant discontinuity in a data set, we introduce two methods: the kernel density estimation (KDE) and the segmented redundancy analysis (segRDA). The KDE is based on the principle of mapping the density probability function of a multivariate scatterplot and set the 95% interval as the threshold between communities. The segRDA was designed

to find one or more breakpoints in the data set and run a multivariate regression analysis separated for each part (piecewise RDA). Thus, the segRDA returns a breakpoint, a R² and tests whether the combined model explains more than the original model without a break. While the KDE is more appropriate to find discontinuities in multiple dimensions, it does not give us a predictive model. The segRDA, instead returns a predictive model but is restricted to how the dataset is ordered. These two methods are promising tools to navigate in the complex realm of metacommunities.

Keywords: Ecology, community, kernel density, simprof, piecewise redundancy-analysis

ID: 6024

Integrating simulations and experimentation to predict community responses to disturbance and immigration regimes

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The present article tests the ability of discrete-event simulations to predict the response of free-living marine nematodes to events of disturbance and immigration. We used inverse parameterization techniques to model the hypothesis that disturbance associated with low immigration rates decreases abundance and diversity, whereas disturbance associated with high immigration result in a more abundant, diverse and evenly distributed assemblage. Experiments were conducted in microcosms, where each replicate corresponds to an experimental unit. Simulations included five assumptions of species equivalence: across (1) all species; (2) a same feeding type; (3) a same trait group; (4) a same abundance group and; (5) non-equivalent at all. Contrary to expectations, the results showed no differences between control and low immigration treatment, whereas high levels of immigration decreased significantly both the abundance and richness of species, while increasing evenness. Simulations suggested ecological equivalence among nematode species whose life history traits exhibit similar adaptations for colonizing and persisting in the system. Under this assumption, simulations mimicking the treatments predicted the effects of disturbance associated with low immigration levels but failed in predicting the effects of high immigration level. However, after recalibrating the carrying capacity parameter (the most influential factor on the parameter space), simulations were able to predict both microcosms treatments. Together, our results suggested that nematodes assemblages remain near the carrying capacity of the microcosms. In our simulations, this parameter can be interpreted as a factor that affects the equilibrium of the assemblages. Increased immigration events may alter this equilibrium state by increasing the asymmetry of competition.

Keywords: Simulation, microcosms, free-living nematodes, pattern-oriented-modeling

ID: 6034

Update on Nemys/WoRMS – An evolving online database with taxonomic and ecological information on nematodes

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Nemys is an online Taxonomic database that was created in the 1990's to help students and researchers with the identification of marine nematodes. In 2014 Nemys was integrated with WoRMS (World Register of Marine Species) to provide a broader access platform. The progress of Nemys in the last four years involved, among other activities, the inclusion of new editors. The editor's team grew from 10 to 15, adding mainly experts on continental (terrestrial and fresh-water) nematodes. This move expanded the scope of Nemys by providing taxonomic and ecological expertise and information across a wider range of ecosystems. The editors' workshops in 2015 and 2018 provided an opportunity to discuss ongoing issues and ways to improve the usefulness of the database to researchers and end-users. The list of missing authorities and environment, for each species, was completed; new taxa have and are continuously being uploaded; the database is being expanded to include soil, plant- and animal parasitic nematodes; information on type material, original description and distribution are also being updated. The importance of complete and accurate morphological descriptions was also discussed and a manuscript with a review of morphological characters used for species descriptions and their presentation in taxonomic papers is being drafted (see also poster by Mokievsky et al.). Our aim is to enhance the use of Nemys for ecological studies and as a tool for biomonitoring of marine and freshwater sediments in addition to its taxonomic usefulness. The Nemys database remains a work in progress, and in order to help us improve the database in the future, we encourage users to provide their feedback or queries directly to the editors who will be happy to help.

Keywords: Nematoda, taxonomy, taxonomic descriptions, distribution, marine, freshwater, terrestrial

ID: 6039

Improved Mitochondrial Metagenomic Methods for Analyzing Meiofaunal Communities

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Mitochondrial DNA persists as a pivotal tool for investigating speciation events, patterns of population demography, and biogeography. Recently, the technique of bioinformatically extracting complete mitochondrial genomes from environmental samples (coined mito-metagenomics or MMG) has recently been demonstrated in diverse animal communities, however, the technique has not been applied to meiofauna (benthic metazoans < 2mm). Despite a major effort to publish mito-genomes from diverse lineages, current databases remain biased towards select branches of the animal tree (vertebrates, insects), while many other important clades, including many meiofaunal groups, have been historically underrepresented or missing altogether. This leads to an inability to classify many of the sequences produced from environmental samples. Here we develop a bioinformatic tool for binning mitochondrial reads (both taxonomically and gene wise) from metagenomic datasets using only distantly related reference sequences. We also investigate the applicability of mito-metagenomics for broad surveys of meiofaunal populations by exploring simulated and novel metagenomic datasets. Specifically, we test how variable levels of reference database completeness can affect the ability to classify a given environmental sequence. Furthermore, we describe a novel method of enriching mtDNA from next generation sequencing libraries, which results in an average of ~450x fold enrichment over standard sequencing. Together these methods reduce the computational resources needed for processing mito-metagenomic data and provide more accurate classification of mtDNA sequences from environmental samples.

Keywords: Metagenomics, mitochondria, bioinformatics, biodiversity, environmental

ID: 6048

Microbiome partitioning of coexisting nematode species in shared microhabitats: insights of a metagenetic analysis

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Local species diversity and coexistence of ecologically similar species can be attained through differentiation of their ecological niche. Resource partitioning is a potential mechanism for niche differentiation and, along with different tolerances to abiotic conditions, can facilitate species coexistence. In this study, we characterise the microbiome of 10 marine bacterivorous nematode species of different phylogenetic relatedness, which co-occur in nature in intertidal habitats, using high- throughput sequencing. We investigate microbiome diversity and composition of nematodes collected from 6 types of phytal substrates – microhabitats (including 3 algal species and cordgrass, fresh and decomposing) in the field. A large microbial diversity and a high intraspecific variability of the nematode microbiomes was revealed. The microbiome of species sharing their microhabitats showed a significant overlap, suggesting that resource differentiation within a microhabitat is rather limited at a single moment in time. Microbiomes were also not strongly related with the microhabitat. But temporal divergence in resource use may occur, as suggested by temporally divergent microbiome composition of nematodes associated with *Ulva* sp. Potential ecological interactions of nematodes and bacterial or archaeal taxa belonging to their microbiome may also play a role in niche differences, either by facilitating resource utilisation or by affecting tolerances in abiotic conditions, their role deserving further study.

Keywords: Microbiome, next generation sequencing, metagenetics, resource partitioning, coexistence

ID: 6068

On the use of artificial substrates to evaluate environment differences using meiofaunal communities

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Meiofauna organisms are important components of coastal benthic systems and because meiofauna are strongly influenced by surrounding abiotic factors, changes in this trophic level, due to different environmental changes or impacts could become an important threat to the ecosystem. However, one of the major difficulties in the detection of environmental perturbations is to separate natural variations from anthropogenic impacts. To circumvent this difficulty, artificial substrate units (ASUs) were proposed and have been used at least during the last 40 years. ASUs provide standardized microhabitats that may be used at different points within a spatial scale therefore, any difference found is not attributable to habitat features. However, few studies tested or used ASUs focusing meiofauna communities. During the last years our team tested several types of ASUs and selected among them synthetic grass as it mimics the turf algae that cover hard substrates in different tropical ecosystems like coral reefs and mangroves. ASUs have been used in both the laboratory and in situ experimental studies. Here we synthesized several published and unpublished meiofauna studies showing that: ASUs significantly reduces meiofauna community variation compared to that of natural substrates; ASUs colonizing meiofauna communities enable the detection of significant differences among environments submitted to differential anthropic impacts even in naturally stressed environments like estuaries; ASUs enable the settlement of a diverse and abundant meiofauna community and Harpacticoida assemblage for assessing anthropogenic impacts associated with climate change in laboratory experiments. Meiofauna colonizing ASUs are thus suggested as important tools both in observational and manipulative experiments concerning anthropogenic impacts in tropical environments.

Keywords: Coral reefs, mangroves, environmental impact, climate change

5.

Meiofauna and Science communication to Society

ID: 5788

Is Meiofauna better than Macrofauna for environmental assessment?

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Environmental assessments and monitoring are fundamental studies in applied ecology, and form the basis of science-based decision making. Biodiversity and community structure is a very sensitive metric to detect change or disturbance for the simple reason that sensitive species are reduced or disappear, and tolerant species remain or are enhanced. Yet, most managers do not accept meiofauna as a bioindicator, and many scientists still do not appreciate the importance of meiofauna as a component of ecosystems. However, during the last 30 years when I have measured both meiofauna and macrofauna, I have demonstrated that meiofauna metrics are more sensitive to detect change where there is hydrocarbon exploration and production, oil spills, and alterations of salinity when environmental flows are reduced by climate variability or human activities. In spite of these findings, I am still challenged to use meiofauna because they are not charismatic and not well known to many management stakeholders. The solution has to be in education using 3-D printing, communicating results via social media, and a more proactive IAM.

Keywords: Assessment, biodiversity, disturbances, environmental flows, monitoring, oil spills

ID: 5901

Predicting deep-sea meiofauna abundance on large geographic scale in the Clarion Clipperton Fracture Zone (CCZ)

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There is an increasing economic interest in the polymetallic nodules covering the abyssal plains of the Clarion Clipperton Fracture Zone (CCZ). Mining activities will severely impact the deep-sea environment and there

fore appropriate preservation and protection zones are urgently needed. In the past, such areas have mainly been installed based on expert opinion or sparsely available environmental data.

To integrate the meiofauna community into the definition of such areas, a distribution modelling approach is applied. Meiofauna abundance, as well as richness and diversity on high taxonomic level, was modelled in a 63.500 km^2 area with random forest regression based on bathymetry, backscatter signal and the abundance of polymetallic nodules. The resultant continuous spatial predictions were combined with all available environmental parameters and used for habitat mapping based on k-means clustering.

Although no environmental variables with direct influence can be used for prediction, it is possible to compute sufficient models for meiofauna distribution. Predicted distribution varies between individual taxa, overall abundance, diversity and richness.

To evaluate predictions, random forest regressions were additionally computed with 1000 replicates integrating varying numbers of sampling positions and parallel samples. Higher numbers of parallel samples are especially useful to smooth the influence of the outstanding variability of meiofauna on a small scale. However, a high number of sampling positions that integrate a greater diversity of conditions into the model is even more important.

Keywords: Deep sea, preservation zone, random forest, polymetallic nodules, bathymetric features, distribution modelling

Part III

Poster presentations

1.

Advances in taxonomy, phylogeny and biogeography.

ID: 5796

Six new species of the Genus *Krithe* (Krithidae) from Kuril-Kamchatka Trench (Hadal Zone)

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Deep-sea is classified as an extreme environment, due to the various physical and biological factors such as high pressure, the absence of sunlight, and a small amount of organic material. The hadal zone is the deepest areas of the ocean the ranges are 6,000 to 11,000 meter (Wolff 1960). Our samples collected from Kuril-Kamchatka Hadal depths. Following the previously paper only 15 Ostracoda species known from the Hadal zone including unidentified species (Beliaev 1989, Hartmann 1985, Jamieson 2015, Maddocks 1969, Rudjakov 1961). The Genus *Krithe* named by Brady, Crosskey & Robertson in 1874, type species is *Krithe praetexta* (Sars, 1866) collected from Christianafjord in Norway, sediment type is the muddy bottom, this genus is usually discovered all around the world (intertidal zone to deep sea area). But from Hadal zone there are only one species described: *Krithe setosa* Rudjakov, 1961 from Java Trench (6,487m). Most species of the genus *Krithe* with smooth ornament and subrectangular shape of the carapace, this simple characters makes confusing when identification. Mostly taxonomic paper of the genus *Krithe* without detail soft parts descriptions, only use carapace pattern. It called anterior vestibulum, which positioned carapace anteriorly. Following Coles et al 1994 they distinguished species use that pattern that research is good for distinguishing to dead carapace and fossil ones, but living specimens need to check soft parts. Here we described five new species from Kuril-Kamchatka Hadal Trench with detail illustrate and phylogenetic tree data.

Keyword: Taxonomy, Ostracoda, Krithidae, deep-Sea, Kuril-Kamchatka

ID: 5823

World-wide distribution of marine benthic harpacticoids: role of geographical and environmental factors

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Some theoretical models (e.g., Finlay 2002) postulate the two different types of large-scale distribution depending on organisms' size: unicellular taxa are not limited in their dispersal, have purely environmentally-driven distribution, low endemicity and mainly ubiquitous; while larger-sized macro-organisms are more likely to be geographically restricted and thus have "classic" biogeographies, i.e. spatially-structured distribution patterns with high levels of endemicity. The ubiquity-biogeography transition is believed to be located in the species size range 1 to 2 mm, that is the typical size of micrometazoa, including meiofauna. The "borderline state" of meiofauna is seemingly corroborated by existence of many widespread or even cosmopolitan species ("meiofauna paradox", Giere 2009). However, geographical patterns of their diversity and composition are unclear, and the relative role of various factors in structuring these patterns is poorly known due to lack of empirical data. We studied the world-wide distribution patterns of the harpacticoid copepods, the key group of marine meiobenthos, basing on the comprehensive database (3350 species × 21 region) compiled from many sources. About 55% of harpacticoid species are regional endemics, which is comparable with endemicity level for macro-organisms. They also demonstrate rather predictable pattern in distribution, with 40% of compositional variations explained by geography (spatial distance and geographical isolation), indicating the considerable role of dispersal limitation, while only 6% - by environment (average sea surface temperature, its annual variation and salinity), and 5% - by spatially structured environmental variations. This pattern is typical for "classical biogeography" of other metazoan taxa. This research was supported by the Russian Foundation for Basic Research [grant numbers 17-04-00337, 18-04-00206, 18-05-60228 and 19-05-00128].

Keywords: Large-scale distribution, Harpacticoida, biogeography, dispersal limitation

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ID: 5843

Updating the high-level classification of marine nematodes

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Over the last two decades, molecular phylogenetic analyses have greatly improved our understanding of nematode classification and evolution. Since the last comprehensive treatment of the phylum in the Nematoda Handbook

published in 2014, phylogenetic analyses based mainly on SSU sequences have led to several major changes in marine nematode classification. As a result of recent research, the nematode phylogenetic tree needs to be updated. For example, SSU phylogenetic analyses provide no evidence for a close relationship between the Desmodoroidea and Microlaimoidea, which until recently comprised the Desmodorida. This result, added to the lack of morphological synapomorphy linking the two superfamilies, has led to the erection of the order Microlaimida to accommodate the Microlaimoidea. SSU phylogenies also indicate that the classification of parasitic benthimermithids, and of the genera *Raptothyreus, Molgolaimus, Paramicrolaimus* and *Africanema,* should be changed. Studies of New Zealand Tripylidae also indicate that *Trischistoma* and *Tripylina* should be classified with the largely marine family Trefusiidae (Enoplida).Overall, molecular phylogenetic analyses show that many morphological features have evolved independently in different groups of nematodes, i.e., convergent evolution is common. They also have led to a re-think about which morphological features are taxonomically informative, and which ones less so. Despite these new insights, SSU phylogenies have not enabled us to disentangle deep relationships among basal Chromadorean orders or to identify the branching order at the base of the nematode tree. Other approaches such as phylogenomic methods will be required in order to answer outstanding questions on the classification of the phylum.

Keywords: Molecular phylogenetics, evolution, taxonomy, classification

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ID: 5845

New *Helmutkunzia* species (Copepoda, Harpacticoida, Miraciidae) from intertidal sandy beach of Xiamen, China

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A new species of the genus *Helmutkunzia* Wells & Rao, 1976 (Miraciidae) is described from specimens recovered from intertidal sandy beach of Xiamen, Fujian Province, China. *Helmutkunzia sinensis* sp. n. differs from its congeners by the presence of pseudoperculum. The new species is similar to *H. variabilis* Wells & Rao, 1987 but remarkably differs from it by the shape of P5 in both sexes.

Keywords: Copepoda, Harpacticoida, *Helmutkunzia sinensis* sp. n., China

ID: 5933

Two new species of the genus *Tigriopus* Norman, 1869 (Copepoda: Harpacticoida: Harpacticidae) from Chonburi province, Thailand

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Two new species of the family Harpacticidae Dana, 1846, *Tigriopus namsaiensis* sp. nov. and *T. wannapaensis* sp. nov. were found at Namsai and Wannapa beaches in Chonburi province, Thailand. There are currently 14 known species in this genus, and two of which, *T. thailandensis* Chullasorn et al., 2012 and *T. sirindhornae* Chullasorn et al., 2013 were also discovered in Thailand. The two new species will be added to this list, making a total of 16 species. Sexual dimorphism is expressed in the A1, A2, P2, P5, P6, and urosomites. The two new species share several characters with other species in this genus, for example, a cyclopiform body shape, A1 with 9-segmented in the female, A2 allobasis with 3-segmented exp, male lacking an abexopodal seta, male P2 enp-2 with distinct outer spiniform apophysis, both baseoendopod and exp of female P5 with five setae. However, both species are distinguishable from *T. kerguelenensis* and *T. kingsejongensis,* which have an abexopodal seta on A2 allobasis in the male, one knob-like structure on P2 enp-2, and tip of apophysis round in the male. *Tigriopus namsaiensis* and *T. wannapaensis* are closely related to *T. thailandensis* and *T. sirindhornae*, as they have the following characters: fewer sensilla; 2-segmented mandibular exp; Mx1 praecoxa more spinulose, Mx2 with spinules on three syncoxal endites, Mxp with spinules on outer margin, and P4 exp-3 with 2 inner setae. *Tigriopus namsaiensis* closely resembles *T. sirindhornae*, which has 7-segmented A1 in the male. Besides, the new species is characterized by one tiny pore on P3 enp-1, P4 exp-2 and exp-3. *Tigriopus wannapaensis* is similar to *T. thailandensis*, which has 8-segmented A1 in the male. Moreover, the two new species also have different structures with setae on A2 exp-1; exp-2; and exp-3. These characters are suggested as autapomorphies of the new species.

Keywords: Harpacticoida, *Tigriopus*, taxonomy, morphology, Thailand

ID: 5938

New *Zosime* species (Copepoda: Harpacticoida: Zosimeidae) from the South western Gulf of Mexico

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As a part of ongoing efforts for monitoring benthic ecosystem in the Gulf of Mexico, Harpacticoid copepods were collected from the south western Gulf of Mexico in a survey during from August 3 – 6 2015. The sampling depths varied between 179 m and 1440 m depending on each survey site. Among them we report four new *Zosime* species. Each new species has superficial similarity with congeners including *Zosime typica*, *Z. Major*, *Z. mediterranea*, and *Z. incrassata*. However they can be distinguished from congeners based on the seta formation in the legs 1 to 5, the length/width ratio of caudal rami, and body ornamentations. This is the first report on the genus *Zosime* from the Gulf of Mexico.

Keywords: Deep-sea, Gulf of Mexico, Zosimeidae, *Zosime*

ID: 5941

The pharynx in Stilbonematinae (Nematoda, Desmodoridae): Adaption to a symbiotic life-style?

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Stilbonematinae, a subfamily of the Desmodoridae, is remarkable for its symbiosis with chemoautotrophic sulfur oxidizing bacteria that cover nearly the entire body surface of their symbiotic partners. Stilbonematinae have become model systems for symbiont-host interactions, however, the question of whether they feed on their own bacterial symbionts is still under debate. In several genera of Stilbonematinae the pharynx shows a tendency towards the development of an enlarged muscular anterior-most part (corpus) and a glandular terminal bulbus with only weak musculature. This is in contrast to most nematodes, which have a predominantly glandular corpus with weak musculature and a prominent muscular bulbus that acts as a suction pump. This indicates a take-over of the suction function from the posterior bulb towards the anterior corpus. Using modern morphological methods (immunostaining in combination with confocal laser scanning microscopy and histological ultrathin sectioning in combination with transmission electron microscopy), we analyse the stilbonematine pharynx to shed light on whether its reorganization evolved multiple times independently and whether the change in proportions of the pharynges in different genera can be related to the symbiotic life-style, in particular to the shape and arrangement of their bacterial symbionts.

Keywords: Nematoda, Stilbonematinae, Pharynx, evolution, adaptation

ID: 5946

Species diversity of Harpacticoida in the Palau, with description of the new species in the genus *Rhyncholagena* Lang, 1944 (Copepoda: Harpacticoida: Miraciidae)

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Palau is known to be biologically diverse due to the influence of two currents (North Equatorial Current and Kuroshio Current) passing through the area. Several studies on coral reef, planktonic copepods and benthic foraminifera have been conducted in Palau. However, very little research has been done on the Harpacticoida. In October 2018 and January 2019, meiofauna samples were collected from Palau by SCUBA diving. The species diversity of benthic copepods inhabiting the Palau coast has been identified. For eight collection sites, the differences in the species composition according to the collection season were investigated. During this research, a new species belonging to the genus *Rhyncholagena* Lang, 1944 was discovered. We examined the morphological characteristics of this species and obtained the 18S ribosomal DNA and MT-CO1 sequences. The new species is morphologically similar *R. littoralis* Por, 1967. The most prominent feature of the new species is the development of long lateral spinous process at the end of the anal somite. This is the tenth species of the genus *Rhyncholagena*.

Keywords: Palau, Harpacticoida, Miraciidae, *Rhyncholagena*

ID: 5948

Redescription of five species belonging to the family Thoracostomopsidae (Nematoda: Enoplida) from Jeju Island, South Korea

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Jeju Island of South Korea is a volcanic island formed from eruption approximately two million years ago. Considering its origin and location closer to the subtropical waters, the difference in make-up of biodiversity has always been topic of interest to many experts. Five most naturally maintained beaches were selected from pre-examination and sediments were sampled using filter method. Results indicated nematodes belonging to families Chromadoridae, Desmodoridae, Xyalidae and Thoracostomopsidae were most abundant. For this study, five species belonging to the family Thornmjacostomopsidae Filipjev, 1927 discovered from the survey are redescribed. Of the five species, two belong to the genus *Enoploides* Saveljev, 1912, rest belong to *Enoplolaimus* de Man, 1893, *Mesacanthion* Filipjev, 1927 and *Paramesacanthion* Wieser, 1953 respectively.

New morphological details missed from the original descriptions are described from scanning electron micrographs. Description of the five species, diagnosis of its respective genera, and emended pictorial key to valid species are provided.

Keywords: Thoracostomopsidae, redescription, free-living, sandy-beach

ID: 5950

A study on the phylogeny of Siphonophorae (Cnidaria: Hydrozoa) using multiple genomic markers

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Siphonophore have been conducted relatively often. However, only few data are available on ITS regions (the provision of ITS-1, 5.8S and ITS-2 rDNA) rDNA sequences, which are known to be significantly meaningful to the species-level identification. In this study, we first secured a sequence of ITS from Siphonophores in Korean coastal waters and Kuroshio extension and compared the phylogeny tree with the results from seven data sets (16S, COI, ITS, 16S+COI, 16S+ITS, COI+ITS and 16S+COI+ITS). All results generally yielded similar phylogenetic tree, however, there were some differences in the details. To identify the better phylogenetic marker, we compared the results based on morphological factors (shape and number of nectophores, hydroecium, ostial teeth and mouthplate). As a result, we found that most of the morphological factors excluding hydroeciem were more consistent with 16S+COI+ITS and COI+ITS results than using other data sets. The phylogeny of Siphonophorae cannot be determined with one marker, and the concatenated sequence of at least COI and ITS markers must be used to achieve high reliability. We expect that present result is applicable for the barcoding and phylogeny of meiobenthic hydrozoans.

Keywords: Hydrozoa, Siphonophorae, phylogeny, genomic markers, concatenated sequence.

ID: 5954

Descriptions of two deep-water copepods of the genus *Leptotachidia* Becker (Harpacticoida, Pseudotachidiidae) from the north-western Pacific

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The monospecific genus *Leptotachidia* Becker, 1974, belonging to the family Pseudotachidiidae Lang, 1936, was previously known from only the deep-sea of the Atlantic. During an expedition of the research vessel RV ISABU of the Korea Institute of Ocean Science and Technology (KIOST) in November 2017 from the north-western Pacific, second and third members of *Leptotachidia* were collected from abyssal sediments. The two new species, *L.* n. sp. 1 and *L*. n. sp. 2, are described herein based on the female specimens. They exhibit significant generic features: the female antennule five-segmented, with a Brodskaya organ on the distal segment and the second exopodal segment of second to fourth legs without inner setae. Outstanding character of both Pacific species is the reduced armature of thoracic legs in contrast to that of type species, *L. iberica* Becker, 1974. In addition, *L*. n. sp. 1 and *L*. n. sp. 2 have a unique setal armature in the genus such as the female P5 with six elements instead of five and the antennary exopod bearing a single seta instead of two on the proximal segment, respectively. This is the first record of *Leptotachidia* species in the Pacific and a key to the species of *Leptotachidia* is provided.

Keywords: Abyssal harpacticoids, biodiversity, deep-sea, Pacific basin, *Paradanielssenia* group

ID: 5956

Three new records of halocyprid ostracods from Korea with molecular phylogeny of Myodocopa inferred from 18S rRNA

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So far, a total of 88 ostracod species have been reported from Korea, but only few belong to the family Halocyprididae. As a part of an ongoing study of ostracods in Korea, samples were collected from the south coast in April and September, 2018. Among other species, we found three previously unrecorded halocyprids: *Archiconchoecia striata* Müller, 1894; *Mikroconchoecia curta* Lubbock, 1860; and *Proceroecia microprocera* Angel, 1971. They were initially identified based on morphological characters using light microscopy and SEM photographs. In addition, we successfully amplified partial mtCOI sequences, and 18S rRNA. Based on the K2P distances calculated between our mtCOI sequences and those of the same species available on GenBank, sequences of *A. striata* from Korea differ by 9% from those on GenBank, while the other two species differ by only 1%. These results may indicate the existence of cryptic species among populations of *A. striata*. We use 18S rRNA sequences of the three species to preliminary infer phylogenetic position of the family Halocyprididae within the subclass Myodocopa.

Keywords: Halocyprida, molecular phylogeny, mtCOI, 18S rRNA, South Korea

ID: 5958

Alimentary tract structure of *Halichoanolaimus robustus* (Chromadorida, Selachinematidae)

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Halichoanolaimus robustus is a peculiar predatory nematode. Its alimentary tract is characterized by a voluminous complicated stoma equipped with solid rhabdions, muscular pharynx and conspicuous brown blind intestine lacking rectum and anus. This species feeds on other nematodes swallowed whole. In our research we study stoma and gut ultrastructure. Buccal cavity (pharyngostoma) consists of two compartments, anterior cup-shaped chamber and posterior narrow cylindrical part. Walls of the anterior chamber are reinforced by six longitudinal rhabdions terminating posteriorly with small sharp teeth. Walls of the posterior chamber are made with three thick rhabdions. A prey nematode is evidently grasped by the teeth and then swallowed down into the pharynx lumen and intestine. Midgut cells may differ even on the same cross-section. In the anterior intestine, two cell types occur differing in that which function predominates, absorption or secretion. Cells of presumable predominating absorbing function possess a developed microvillar brush and abundant inclusions while the cells of presumable secretory function have sparse microvilli, many dictyosomes and many small vesicles. Absorbing cells outnumber the secretory cells in the medium region of the intestine. Intestine epithelium of the posterior region is made up of only absorbing cells containing numerous electron-dense inclusions. Lumen of the posterior midgut can be filled with undigested remnants including such well-identified parts as copulatory spicules or buccal armatures of the ingested preys. By absence of rectum and anus, these remnants can be stored there throughout the life of the predatory nematode. However, enterocytes of *H. robustus* do not differ principally from those of species with normal through alimentary tract, possibly because of the short life span. The study is financially supported by RFBR grant N 18-04-00237.

Keywords: Predator nematode, alimentary tract ultrastructure, Halichoanolaimus

ID: 5972

Comparison between the inner and outer sides of Ría de Foz, Galicia (NW Iberian Peninsula)

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Ría de Foz is situated in the north of the province of Lugo (43º34'N, 7º14'W). The entrance of the estuary opens to the northwest, following southwest-northwest orientation. Its morphology is narrow (its width ranges are between 450 and 2250 m) and elongated (4250 m), although its coastal development is equal to 5600 and 8000 m for the eastern and western margins respectively. Moreover, it belongs to Masma-Foz Site of Community Importance (SCI, Natura 2000). The studied material consists in two samples that were taken in *Ría de Foz*, one in the inner part of the estuary (43º33'35N, 07º15'04''W), and the other one in the outer part (43º 33' 08''N, 07º 15' 22''W). To extract the meiofauna present in the samples, they were washed first with $MgCl_2$ and then with tap water filtered. Then, the nematodes were picked up from the rest of the meiofauna. We found a total of 4519 specimens, which belong to 15 different families and 26 different genus.

Keywords: taxonomy, free living marine nematodes, Nematoda, Galicia, Ría de Foz

ID: 5973

The use of micro-CT in the study of the organization of Foraminifera shell: *Lobatula lobatula* (Walker & Jacob, 1798)

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Foraminifera are organisms with a single cell protected by a shell of different nature, calcareous, siliceous or made by grains of sand or other particles that the cell itself obtains in the environment. This shell is formed by a series of successive chambers and its external morphology as well as its internal organization have a high taxonomic value. The external morphology can be studied in detail using scanning electron microscopy, but not the internal organization of the chambers, their relative dimensions and their modifications throughout the ontogeny of the cell.The present communication is the result of the beginning of the study of the shell orga-

nization of foraminifera present in the Galician coasts, choosing one of the most common species, *Lobatula lobatula* (Walker & Jacob, 1798) and using for it the micro-computed tomography (micro-CT) that, by means of X rays, allows the observation of the interior of the chambers. From the obtained 3D reconstructions, we study the morphology of the chambers, the relationships between them, as well as the dimensions of their interior and the volume that each one represents in the shell as a whole.

Keywords: Foraminifera, micro-CT, *Lobatula lobatula*, shell organization

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ID: 5974

Nematode composition in two tropical sandy beaches of Salvador (Bahia, BRAZIL)

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Nematoda is an important component of meiofaunal benthic environments. In Brazil, however, few groups have been developing research in this field. The present study characterizes the nematode composition in the intertidal zone of two beaches in Salvador (BA): Itapuã (12°57’ S/38°21’ W) and Ribeira (12°55’ S/38°30’ W), located in the open Atlantic coast and Todos os Santos Bay, respectively. Samples were collected in November 2014 and February 2009, at low tide, in the intertidal zone of the beaches, using cores of 30 cm length and 3.5 cm diameter, being divided into three strata. They were then fixed in 10% neutral saline formalin, and processed with meshes (500 and 45 µm) for specimen extraction. The nematodes were sorted, diaphanized, and mounted on standard glass slides for identification. The nematofauna community in Ribeira and Itapuã beaches consisted of 9 orders, 25 families, and 66 genera. Chromadorida (27.8% - 18) was the most representative order, with greater genus richness, followed by Enoplida (23.3% - 17) and Desmodorida (16.7% - 11); together, they account for 69.7% of all richness observed. Both beaches presented a different number of exclusive families: Ribeira beach (26.2% - 8), with Xenellidae, Enchelidiidae, Ironidae, Leptosomatidae, Oxystominidae, Tripyloididae, Haliplectidae, and Rhabditidae; and Itapuã beach (11.4% - 4), with Rhabdodemaniidae, Tarvaiidae, Camacolaimoidea, and Microlaimoidea. Some families presented exclusive genera for Itapuã or Ribeira beaches, respectively, as Chromadoridae (*Euchromadora, Rhips,* and *Neochromadora; Actinonema, Endeolophos,* and *Innocuonema)* and Desmodoridae (*Eubostrichus, Desmodora, Chromaspirina,* and *Paradesmodora; Acanthopharyngoides, Metachromadora, and Molgolaimus*). Ribeira beach showed greater genus richness (47.0% - 31) than Itapuã beach (36.4% - 24), and few genera (16.7% - 11) occurred simultaneously in both places. This distinction is probably due to differences in hydrodynamism, granulometry, and salinity, which benefit some groups.

Keywords: Intertidal, benthic, meiofaunal, nematofauna, richness

ID: 5975

Meiofauna community structure of a tropical sandy beach affected by sediment erosion and deposition, with emphasis on nematode community

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Beach environments are constantly changing, mainly due to natural forces such as wind, waves, currents, and tides. Erosion occurs when sediment is removed from a location, and deposition when sediment is added to it. This study characterizes the meiofauna community structure of a beach affected by natural sediment erosion and deposition (Armação beach, northeastern Brazil), with emphasis on nematode community. Previous studies were conducted in Armação beach and the author verified that the beach is constantly changing mainly by the forces of the wind, carrying sediment from one end of the beach to the other. This means that when erosion occurs in one side of the beach, deposition occurs in the other side. Sediment samples were collected in the intertidal zone of the beach in 11 different dates between August 2007 and January 2008, in the same station. This sampling covered both erosion and deposition conditions. Samples were taken through cores of 30 cm length and 3.5 cm diameter, divided into three strata, 0-10, 10-20, and 20-30 cm related to sediment depth, and subsequently fixed in 10% formalin-seawater. The meiofauna was extracted, counted, and then some nematodes were sorted out to be mounted on glass slides. A total of 59.855 animals were counted and 11 groups were found: Ostracoda, Copepoda, Nematoda, Nauplius, Oligochaeta, Foraminifera, Turbellaria, Isopoda, Polychaeta, Acari and Mollusca, in relative abundance order. The highest meiofauna densities were found in the 10-20 cm and 20-30 cm strata. The analysis of similarities (ANOSIM) showed that meiofauna community structure in erosion is different from the one found in deposition. Copepoda was the most abundant group during erosion, while Nematoda was the most abundant during deposition. The Nematoda group exhibited an inverse migratory pattern, migrating to deeper strata during erosion and to shallower strata during deposition. Regarding Nematoda, 18 genera were identified, belonging to 6 orders and 12 families. Nematode community differed between erosion and deposition.

Keywords: Brazilian coastline, intertidal, meiobenthos, Nematoda

ID: 5976

Composition of the meiofauna and nematofauna from a tidal cycle in Itapuã beach - Salvador - Bahia - Brazil

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Meiofaunal composition and distribution are associated with several biotic and abiotic factors. The tide is an element that influences the composition and the horizontal and vertical distribution pattern of meiofauna in the sediment. This study characterizes the meiofauna and nematofauna from a tidal cycle in Itapuã beach, Salvador, Bahia, Brazil. The samples were collected at two points in the intertidal region, at four times in a tidal cycle. At each time and point, three cylinders of 30 cm depth were subdivided into three layers, (A) 0-10, (B) 10-20, and (C) 20-30 cm. The samples were fixed in 5% neutral saline formalin, washed with manual elutriation, and filtered using sieves with mesh sizes of 0.5 and 0.045 mm. The animals were counted, diaphanized, and mounted on slides for identification. Seventy-six percent of the samples were analyzed. The meiofauna consisted of Copepoda, Nematoda, Oligochaeta, Polychaeta, Turbellaria, Acari, Ostracoda, and Isopoda. Copepoda is the most representative group, with 76.9% of the abundance of all samples, followed by Nematoda, representing 11.4%. There was greater meiofauna representation at the second time (high tide), except for polychaetes and isopods, which had their highest occurrence at the third time (low tide). Copepods presented a larger record in stratum C at all tidal times, while nematodes had greater representativeness in stratum C at high tide hours, whereas at low tide the highest values varied between A and B. Ostracods had greater occurrence in stratum B. The following Nematoda genera were recorded: *Oncholaimellus, Trissonchulus, Marylynnia, Haliplectus, Enoploides, Thalassironus*; and species: *Trileptium ribeirensis* and *Cynura cerambus.*

Keywords: Meiobenthos, nematodes, beach, taxonomy

ID: 5984

The disjunct distribution of *Echinoderes ohtsukai* (Kinorhyncha) explained by human-mediated dispersal across the Pacific Ocean

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The dispersal ability of kinorhynchs, like many other meiofaunal groups, is inferred to be limited because they are endobenthic direct developers (i.e., without planktonic larval stages). However, the distribution of certain species of kinorhynchs extends over vast geographical areas, for example in *Echinoderes ohtsukai*. This species was originally described from Japan, but is has also been found in several localities in the northeastern Pacific Ocean (British Columbia). To evaluate the unexpected biogeographical pattern in *E. ohtsukai*, we sequenced two mitochondrial genes (*Cytochrome* c oxidase subunit I, COI; and *Cytochrome* b) and one nuclear gene (Ribosomal internal transcribed spacer, ITS) in 95 isolates from three different populations in Japan, including the species type locality in the Seto inland Sea, and three populations off the British Columbia coast. Haplotype networks and phylogenetic trees show that most individuals collected from Japan and British Columbia share the same haplotypes at all three molecular markers, and only few mutations separate diverged haplotypes in individuals separated by the Pacific Ocean. We interpret this high sequence similarity as the first evidence of a highly disjunct geographical distribution in kinorhynchs that is consistent with human-mediated dispersal. The coast of British Columbia has historically had a high level of maritime traffic from the coast of Japan, thus we infer that aquacultural related activities could have played a key role in transporting kinorhynchs across the Pacific Ocean.

Keywords: Kinorhyncha, human-mediated dispersal, Pacific Ocean, molecular markers

ID: 5985

There are still dragons out there: new insights into the kinorhynch biodiversity of the Caribbean

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The coastal Caribbean region is a large, marine, tropical ecosystem that encompasses a global marine biodiversity hotspot. So far, only three Caribbean localities have been studied with focus on the meiofaunal phylum Kinorhyncha: the coral reef ecosystem of Carrie Bow Cay (Belize), Bocas del Toro (Panama) and the Mochima Bay (Venezuela), bringing a total of 31 valid species for the whole area. Dr Robert P. Higgins collected, during over three decades, a total of 114 samples of sediment from many different localities of the Caribbean Sea, including the continental shore (Mexico, Belize, Honduras, Panama, Colombia and Venezuela) and the Antilles (Cuba, Jamaica, Puerto Rico, Haiti, Dominican Republic, Guadeloupe, Barbados, Tobago and the Leeward Antilles). Many of these samples have been already processed, yielding new species to science of the allomalorhagid genera *Cristaphyes, Dracoderes* and *Fujuriphyes*, and the *cyclorhagid* genera *Echinoderes* and *Triodontoderes*, suggesting that the kinorhynch biodiversity of this area is far higher than previously known. Additionally, the studied samples also yielded new records for the Caribbean Basin of already known species, so the geographical distribution of the Caribbean kinorhynchs could be more extensive than previously thought. The present study, currently ongoing, will enable the Caribbean Sea to become in one of the best studied hotspots of kinorhynch diversity worldwide.

Keywords: Biodiversity, Kinorhyncha, Caribbean, New species, Taxonomy

ID: 5994

Deep-sea desmoscolecid nematodes of the Angola Basin in SE Atlantic Ocean

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DIVA-I expedition (July-August 2000) provides very rich material on meiofauna and nematodes including desmoscolecids from the Angola Basin (depth 5400-5500 m). The desmoscolecids altogether comprise 221 identified specimens (6-7.4% of all nematodes from two stations). The specimens belong to three genera, *Desmoscolex* is most species-rich of them (16 species) while *Protricomoides* and *Tricoma* are presented by an only species each. Only two species have been described earlier, *Desmoscolex obscurus* Bussau, 1993 and *Protricomoides noctuabundus* (Bussau, 1993) both were originally found in the remote site, DISCOL-area, SE

Pacific (4100-4200 m deep). First species presents a notable case since it was also described from quite contrast habitat, sandy sediment of Great Barrier Reef by Decraemer (1975). All the specimens from three remote sites coincide in all morphological details. All other species are considered new for science. Some new characters for species differentiation are introduced such as formalized ratios of head, terminal ring, position of terminal setae. All the specimens examined have no content in the intestine. No females with ripe eggs were found. The study is financially supported by RFBR grant N 18-04-00237.

Keywords: Deep-sea, Desmoscolecida, taxonomy

ID: 5995

Tardigrades of intertidal sandy watts of Jeju Island, South Korea

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Five tardigrade species have been found in frame of exploration intertidal sandy watts of Jeju Island situated between southmost Korean Peninsula and Japan. *Orzeliscus* sp. is close to *O. asiaticus* Lee et al. 2017 differing in more prominent body punctations and possibly in shape of sense organs of legs IV. *Angursa* sp. is similar to *A. clavifera* Noda 1985 but lacks evident secondary clavae and spines on legs II and III. *Quisarctus yasumurai* fits well to the original description of Fujimoto 2015. The genus *Batillipes* constitutes majority of tardigrade specimens and is presented by two species, *B. orientalis* Chang & Rho 1997 and *B.* aff. *similis* Schulz 1955 (the latter species has some differences from the original diagnosis in shape of lateral body processes). *B.* aff. *similis* occurs on only lower part of watt while *B. orientalis* is confined to only medium watt; both species don't occur together. Other species are distributed rather evenly from medium to lower intertidal watt. The study is financially supported by RFBR grant N 18-504-51026.

Keywords: Jeju, Tardigrada, watt, taxonomy

ID: 5996

Morphological species descriptions of free-living nematodes: measurements, characters and their presentation in taxonomic papers

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Morphological characters remain the core markers for species identification and differentiation. More and more morphological characters being included in descriptions and diagnoses of species. Since 1998, over 1000 new descriptions and re-descriptions of species of free-living aquatic nematodes have been published (including over 200 from freshwater habitats). However, not all meet the required standards of description of nematodes, making their identification problematic and separate species status – questionable. Therefore, a modern review of taxonomically significant characters and recommendations for species description are necessary. To update and consolidate the character lists, facilitate new descriptions of nematodes and encourage their comparability, we provide an updated list of characters for description of free-living aquatic nematodes and summarize contemporary approaches for species description and diagnosis based on our experience as Nemys/WoRMS taxonomic editors. We reiterate the basic requirements for descriptions and suggest a minimal set of characters to be used in description of new species of nematodes. We also suggest ways to make descriptions more broadly comparable and standardized in format so that species can be more easily compared. Basic requirements for new species description and presentation of morphological characters and measurements in taxonomic papers are discussed.

Keywords: Nematoda, identification, taxonomic descriptions, character list, measurements, nemys

ID: 5998

The missing piece in the puzzle: using a collaborative integrative taxonomy to disentangle the diversity of Cyatholaimidae (Nematoda)

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The free-living marine nematodes are one of the most abundant and diverse group of the meiofauna, however the knowledge on their biodiversity is still scarce. The high phenotypic plasticity and the lack of conspicuous morphological characters are some of the limitations that raise this shortfall. Integrative taxonomy associated with reconstruction of the ancestral state through statistical tests are a promising way of overcoming these issues. Allied with this approach, the data sharing between researchers may be the key to increases sample size and statistical power. Our intends are to evaluate morphological and molecular data, by means of statistical analyses, in order to find homologous characters in the family Cyatholaimidae, one of the most abundant and diverse of free-living marine nematodes. Also, we plan to form partnerships on the Conference to specimen sharing and broaden the scope of this work. So far, sampling was carried out in beaches and estuaries along the coast of the São Paulo State, Brazil, and 56 samples have been taken from 12 localities. More than 100 individuals from 10 morphospecies were found on the North coast of the state. At least two of them are new species for science. The collected species are being evaluated morphologically with optical and scanning microscopes and the molecular data will be obtained by sequencing regions of 28S and 18S genes. From the molecular phylogeny obtained, different methods of reconstruction of the ancestral state will be used to trace the evolution of definite characters and to evaluate the relative importance of the same to the classification. Particularly will be tested the importance of cuticle features, buccal structure and male reproductive system for defining phylogenetic relationships within the family. A collaborative research may accelerate the acquisition of knowledge not only for the nematode taxonomy and systematics, but also on the evolutionary processes that are shaping the group.

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Keywords: Taxonomy, molecular phylogeny, ancestral state reconstruction, 18S, 28S

ID: 6002

Two new species of the genus *Agauopsis* (Acari: Halacaridae) from Korea

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Two halacarid species of the genus *Agauopsis* Viets, 1927, which are tentatively new to science, are reported from Jeju Island and southern coast of the Korean peninsula. They were collected by washing coralline algae, barnacles on intertidal rocks, and subtidal sediments. *Agauopsis* sp. 1, belonging to the *ornata* group, is allied to three congeneric species in bearing one pectinate seta on tibia II: *A. pseudoornata* Bartsch, 1985, *A. calidictyota* Bartsch, 2007, and *A. zanzibari* Chatterjee, Pesic, Chan & De Troch, 2009. However, *Agauopsis* sp. 1 is characteristic and distinguished from them by bearing six setae/spines of telofemur of leg II. *Agauopsis* sp. 2, belonging to the *brevipalpus* group, most resembles *A. novaezelandiae* Bartsch, 1986 in sharing the short frontal spine, the shorter rostrum than gnathosomal base, the fourth dorsal seta on the posterior dorsal plate, three pairs of perigenital setae in the female, and 36-37 perigenital and five pairs of subgenital setae in the male. However, *Agauopsis* sp. 2 is distinguished from it by the different chaetotaxy of leg II, that is, five setae/spines on genu and six on tibia (versus six and seven, respectively, in *A. novaezelandiae)*. We provide description of the two species from Korea with detailed illustrations, and make systematic accounts of them, based on the tabular keys for each of the two species groups. A key to halacarid species of the genus *Agauopsis* hitherto known from the northwest Pacific is also prepared.

Keywords: *brevipalpus*, description, halacarid mite, northwest Pacific, *ornata*, tabular key

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ID: 6005

A new species of the genus *Paramesochra* Scott, T., 1892 from marine interstitial water in Goseong, Korea

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The genus *Paramesochra* is established by Scott, T. (1892) with *P. dubia* as the type species. Since Scott, T. (1892) erected the genus, 20 species are described within four different species groups. Among them, four species are recorded in Korea waters. They are: (*acutata*-group) *Paramesochra taeana* Back & Lee, 2010; (*dubia*-group) *P. bisegmenta* Back & Lee, 2013, *P. mirabilis* Back & Lee, 2013, and *P. parasimilis* Back & Lee, 2013. We collected a new *Paramesochra* species from a sandy habitat in Goseong, Korea. The new species has the apomorphic characters of *acutata*-group that is the absence of the inner seta on the proximal segment of third and fourth leg. This new species is closely related to *P. acutata* Klie, 1964 and *P. taeana* by following characters:

strongly developed beseoendopod of fifth leg; the number of setae on exopod of fifth leg; shape of the caudal rami. However, the new species can be easily distinguished from these species by following characters: 1) the antennule of *P. acutata* is 7-segmented, but 8-segmented in the new species and *P. taeana*; 2) free body somites with distinct hyaline lappets in P. taeana, whereas without lappets in another two species, 3) baseoendopod with one seta in *P. acutata* and *P. taeana*, however the new species with two setae.

Keywords: Harpacticoida, paramesochridae, meiofauna, morphology

ID: 6011

An updated phylogeny and classification of the Cyclopoida (Copepoda)

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The cyclopoids are the most abundant group of copepods in fresh water. They are also widely distributed in marine habitats being predominantly benthic and planktonic including many parasitic members. The family level phylogeny of the Cyclopoida has been an issue of ongoing discussion. Here we provide a detailed phylogenetic relationship of the Cyclopoida using DNA sequences of 28S, 18S rRNA and COI mtDNA, comprising 17 families including the key families such as the Erebonasteridae, Gisellinidae, Schminkepinellidae and for the first time Thaumatopsyllidae. The family Thaumatopsyllidae has been formally placed in the Monstrilloida, the Cyclopoida and even in its own order, the Thaumatopsylloida. Within Cyclopoida 16 families are supported to be monophyletic by both Maximum Likelihood and Bayesian inferences; however the Cyclopidae is shown to be paraphyletic. Thaumatopsyllidae is supported to be nested in Cyclopoida sister to the marine Speleoithonidae. The Cyclopicinidae is the first monophyletic offshoot of the cyclopoid tree, followed by two derived clades. The first monophyletic clade which contains the Schminkepinellidae + Giselinidae is sister to a clade including all poecilostome families with monophyletic Erebonasteridae as the most basal lineage within poecilostomes. In the second clade marine Euryteinae is sister to two well-supported clades encompassing Eucylopinae + Cyclopinae and unexpectedly parasitic Lernaeidae + Halicyclopinae, making the Cyclopidae paraphyletic. The other clade of families comprises 12 monophyletic families, including the Pterinopsyllidae (first offshoot), the Smirnovipinidae sister to the Hemicyclopinidae + Psammocyclopinidae, the Thaumatopsyllidae + Speleoithonidae, an undescribed family sister to the Archinotodelphyidae + Notodelphyidae and the Cyclopinidae sister to the Oithonidae + Cyclopettidae.

Keywords: Cyclopoida, Thaumatopsyllidae, molecular phylogeny

ID: 6040

A new, chimera-like species of Gastrotricha discovered in deep sublittoral sand off Flores Island (Azores) and affiliated with integrative taxonomy

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In the course of the BIODIAZ project, a multitude of sediment samples from various depths were obtained during cruise M150 of R/V METEOR in the area of the Azores Archipelago. In order to gain preliminary insight into the community of marine Gastrotricha, a subset of samples was cultivated aboard (vented and stored at 5°C) and meiofauna was subsequently extracted with a 7% aqueous solution of $MgCl_2$ for microscopic investigation and extraction of genomic DNA. This initial study yielded 19 species from 13 genera of the taxon Macrodasyida. Amongst these, there was a peculiar specimen from a species so far unknown to science. This exceptional morphotype looks like a chimera of two known genera. Its front end possesses characteristic features of the genus *Ptychostomella* such as a funnel-shaped mouth opening formed by an oral hood, sensory papillae and an unarmed cuticle. The posterior trunk is distinctively shaped as an elongated, unpaired appendage featured with characteristically arranged paired posterior adhesive tubes like in species of *Dendrodasys*. A cladistics analysis of a fragment of the 18S rRNA gene definitely places the new morphotype among other sequenced species of the genera *Ptychostomella* and *Tetranchyroderma* (Thaumastodermatidae). Hence, the new species will be described as a member of *Ptychostomella* while its *Dendrodasys*-like rear trunk is a nice example of convergent evolution within Gastrotricha. An additionally sequenced fragment of the mitochondrial COI gene will guarantee a secure identification of this new species during future biodiversity surveys using standard procedures as well as metabarcoding approaches.

Keywords: Gastrotricha, Macrodasyida, new species, integrative taxonomy, Azores

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ID: 6059

Internal Systematics of Monocelididae: Three New Species Help Resolve Outstanding Taxonomic Issues (Platyhelminthes: Proseriata)

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The Monocelididae are the most diverse family in the species-rich Platyhelminth Order Proseriata. Although recent internal molecular phylogenies of Proseriata largely concur, those focusing on the family Mononcelididae (~200 spp) have revealed conflicts with the current taxonomy for over two decades. Molecular studies have allowed some clarification, such as erection of a monophyletic subfamily Monocelidinae, characterized

morphologically by a conjuncta-simplex male organ. However, recent molecular phylogenies of the family as a whole continue to reveal paraphyletic subfamilies and even genera. Here, we describe three new early-branching species of Monocelididae with simplex copulatory organs, provide an updated molecular phylogeny for the family, present a revised taxonomy, and suggest where improved taxon sampling for molecular phylogeny and detailed morphological studies of the male copulatory organ might further revise help to revise taxonomy within this family.

Support for JPSSIII and MA was provided by grant P20GM103499 (SC INBRE) from the National Institute of General Medical Sciences, National Institutes of Health.

Keywords: Platyhelminthes, systematics, phylogeny, functional morphology

ID: 6067

Chaetonotidae (Chaetonotida, Gastrotricha) – Hollow Curve Distribution' phenomenon or systematics artefact?

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Gastrotricha, with nearly 850 described species, is a phylum of small aquatic invertebrates that are both ubiquitous and abundant. Gastrotrichs are grouped into two orders: almost exclusively marine Macrodasyida and mostly freshwater Chaetonotida. According to traditional systematics, chaetonotid gastrotrichs are classified into two suborders: Multitubulatina, consisting of one monogeneric family Neodasyidae, and the more species-rich suborder Paucitubulatina. The family Chaetonotidae appears as the most diversified and evolutionarily successful chaetonotidan lineage comprising of 16 genera. It contains more species than all the remaining families combined and includes freshwater, brackish, and marine species. The Chaetonotidae family was established on the basis of very common and frequently occurring features like minute body size with bilateral symmetry, a head region separated and more or less covered by 'cilia' and 'long hairs,' together with straight intestine with mouth and anus opening and presence in freshwater. The family diagnosis was expanded by about 20 detailed morphological characteristics, but many of these features are present in the majority of remaining chaetonotids. Conflicts also exist between current gastrotrich systematics in which the family rank of Chaetonotidae is still valid and evolutionary hypotheses based on morphological and molecular analyses showed that this group is paraphyletic in relation to Dasydytidae and Neogosseidae and is not a homogenous group. The problem of paraphyletic and polyphyletic Chaetonotidae is commonly known and postulated but up today a formal change of taxonomy was not proposed. My morphological and molecular data confirm that within Chaetonotidae independent evolutionary lines are nested and should be isolated as separate families. In my presentation I will show the proposition of establishing three new families, and I outline a new view on Chaetonotida systematics in the light of integrative taxonomy.

Keywords: Gastrotricha, integrative taxonomy, systematics, molecular analyses, new families, new species

2.

Meiofauna biodiversity patterns and ecosystem interactions (including Freshwater, Estuarine Coastal and Ocean, Deep sea and Frontiers ecosystems)

ID: 5795

A meiofaunal chicken and egg question; Do temporary meiofauna influence the number of macroinfauna or do macroinfauna influence the number of temporary meiofauna?

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How do the temporary meiofauna (juvenile stages of benthic metazoans that pass through a 0.5 mm sieve) and macroinfauna (animals that are retained on a 0.5 mm sieve) correlate? The juvenile stages of meiofauna may be most abundant where adult macroinfauna is present and abundant, or adult macroinfauna abundance may be a function of the presence and abundance of temporary meiofauna. Studies rarely examine the temporary meiofauna and macroinfauna from the same samples to be able to address these questions. Over 300 sediment samples from saltmarshes in Barataria Bay, Louisiana were examined, and the numbers of various taxa retained on 0.5- and 0.063-mm stacked sieves were compared. Adult and juvenile tube-dwelling amphipods, tanaids, and polychaetes were highly correlated, and the abundance of one size fraction was predictive of the other size fraction. However, for species that either grow to a large adult size or reproduce by larval dispersal (errant polychaetes, gastropods and bivalves), correlations between numbers on each sieve fraction were very low. Reproduction and recruitment are likely seasonal for many such species and adults may occur a different microhabitat compared to recently settled post-larval stages reducing co-occurrences.

Keywords: Temporary meiofauna, juvenile macroinfauna, correlations, tube-dwelling

ID: 5824

Harpacticoida (Crustacea, Copepoda) of the East Siberian and Chukchi Seas in comparison with the adjacent Arctic seas

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A thorough analysis of harpacticoid biogeography is hampered by the lack of sufficient data, especially from the Arctic regions. In particular, very little is known of the harpacticoids of the East Siberian and Chukchi Seas. We present the results of preliminary analysis of the material collected during several surveys in 2018 at the depths ranged from 0 to 800 m. Over twenty species new for the region and over ten species seemingly new for science have been revealed. Check-list of marine harpacticoids known from these seas is compiled, and compared with other Arctic seas. Basing on these data, the biogeographic pattern of the Arctic seas is quantified, and is compared with the subdivision systems based on the oceanographic characteristics and on associated macrofaunal communities.

This research was supported by the Russian Foundation for Basic Research [grant numbers 17-04-00337, 18-04-00206, 18-05-60228 and 19-05-00128].

Keywords: Arctic, East Siberian Sea, Chukchi Sea, Harpacticoida, biogeography

ID: 5842

Effects of beach structure and sediment characterization on meiofaunal community diversity along the California coast

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Due to their small size and taxonomic obscurity, meiofauna remain a fundamentally understudied group despite their important position at the base of the sandy-beach food web and close association with the surrounding environs. This study aims to characterize meiofaunal community diversity in California across various spatial scales using next generation sequencing techniques and to assign potential abiotic drivers through the analysis of sediment samples using grain size analysis and X-ray powder diffraction (XRD) for mineral composition. Hypotheses suggest that (1) meiofauna will adhere to patterns established by the latitudinal diversity gradient (LDG) and known biogeographic breaks such as Point Conception, (2) meiofaunal communities will change as a function of beach profile (from reflective to dissipative), (3) meiofaunal communities will differ based on their tidal orientation (low-medium-high), and (4) communities will change based on sediment characteristics such as grain size and mineral composition. Analysis of this dataset continues –and will be complete prior to

SEVENTIMCO– but preliminary results have found that communities tend to be more diverse in the southern sites (in keeping with the LDG), that significant differences in community composition exist as a function of tidal height, and that sediments vary significantly between sites with respect to mineral composition and grain size analysis. Ultimately, the results of this study will provide a detailed description of meiofaunal composition and abundance along a highly variable and biodiverse coastline and help to bolster meiofaunal sequence representation in molecular databases.

Keywords: : Illumina MiSeq, meiofauna, community structure, coastal California, metagenetics, 18S rRNA Gene

ID: 5854

Role of meiofauna in the diet of the heart urchin *Abatus cordatus* in the Kerguelen Islands (Southern Ocean)

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Deposit-feeders derived their nutrition from the particulate organic fraction of sediments. Most of this organic matter is non living and unpalatable. In sandy sediments where organic matter is rare, deposit feeders need to process large amount of sediment to reach their food requirement. Selective feeding represents a good strategy to limit the waste of energy in sediment processing. Meiofauna represents a good food source with high nutritional value. The aim of the present study was to evaluate the selective feeding behaviour of the burrowing spatangoid, *Abatus cordatus* in the sub-Antarctic Kerguelen Islands (Southern Ocean). In order to evaluate the selection of meiofauna over other food sources two approaches were simultaneously used with measurement of ^{15}N and ^{13}C isotopic composition of ingested food in *i*) natural conditions and *ii*) after isotopic enrichment in two types of sediment with different organic matter content.

Keywords: Food web, deposit feeding, diet selection, sub-Antarctic, spatangoid

ID: 5861

What shapes nematode community structure in unpolluted river sediments?

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Nematodes are one of most abundant and diverse metazoan groups in freshwater sediments and play a key role in benthic food webs. They are acknowledged as suitable bioindicators to assess the toxic potential of polluted sediments with specific indices (e.g. NemaSPEAR) helping to evaluate the ecological quality of freshwater systems. However, chemical pollution is of course only one of many environmental factors that determine the structure of nematode communities. As one example, the geophysical structure of sediments influences the complex pore space where meiofaunal organisms live and thus also determines the composition of the biota that moves and feeds in this habitat. Moreover, the connectivity of sites, especially along the watercourse reflects the dispersal frequency of nematodes and plays an important role in structuring communities. Therefore, we analyzed a large data set (>12,000 identified nematodes sampled at 60 sites from 40 different rivers) on the composition of nematode species in river sediments, that had been collected together with chemical data and geo-physical properties at various sites in different German river catchments. Only sites that showed low anthropogenic contamination were selected to analyze the cooccurrence of nematode species and traits (feeding type, body size) with specific sediment properties compared to its spatial distribution.

Keywords: Nematodes, freshwater sediments, species composition, traits, sediment structure

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ID: 5892

Diversity and functional traits of deep-sea nematodes in a high energy canyon off SW Taiwan

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Gaoping Submarine Canyon (GPSC) off SW Taiwan is a high energy canyon connected to a small mountain river and known for frequent mass wasting events and strong bottom currents driven by the internal tides. To understand the effects of these extreme conditions on marine nematodes, we sampled the surface sediments of the upper GPSC and adjacent slope (200-1100 m) using a multiple corer in August and November 2015. We found that the meiofauna abundances, nematode species and functional diversity dropped significantly in the GPSC. The non-selective depositing, fast colonizing nematodes (*e.g.*, *Sabatieria, Daptonema, Axonolaimus,* and *Metadesmolaimus*) dominated the canyon, whereas the non-selective deposit feeders (*Setosabatieria* and *Elzalia*), epigrowth feeders (*Craspodema)* and omnivores/predators (*Paramesacanthion*) predominated the slope. Our results suggest that the strong bottom currents in the GPSC not only affected the local meiofauna

community but also removed the organic-rich, fine-grain sediments; therefore, only the durable or fast recovering nematodes could survive. The high species turnover with depths and between the canyon and slope suggest strong environmental filtering processes in structuring the nematode community assembly in the dynamic submarine canyons.

Keywords: Nematode, submarine canyon, continental slope, community structure, functional groups, biodiversity

ID: 5934

Small-scale horizontal distribution patterns of nematodes in deep NW Mediterranean surface sediments (DYFAMED-BENTHOS 2003)

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The three-year time series survey of meiofauna conducted at the DYFAMED-BENTHOS station (2347-m depth) in the Var Canyon (NW Mediterranean) revealed that 58% of the observed variability in nematode abundances was temporal (seasonal and interannual), while 27% was spatial at the centimeter scale (Guidi-Guilvard and Dallot, 2014 ; DOI:10.1016/j.dsr.2014.07.003). To further investigate the small-scale horizontal distribution patterns of nematodes at this station, in 2003 three multiple-c orer tubes (9.8-cm inner diameter) were each subsampled with 44 contiguous mini-cores (0.9-cm inner diameter) arranged in a honeycomb pattern, at two different seasons (early spring and early summer). A total of 8781 nematodes were counted in the resulting 6 x 44 (= 264) mini-cores. Density per mini-core varied between 12 and 77 individuals. Overall, mean nematode density did not differ significantly between seasons, i.e. 463±63 and 581±66 ind.10cm^{-2} in April and July, respectively. However, spatial patterns analyzed by autocorrelation (Moran's I statistic) showed that aggregation was more pronounced in April than in July. In April, patches were present in all 3 cores, varying in size from 2-3 cm^2 to more than 10 cm^2. In July, patches were not always present. When they were (in 2 out of the 3 cores), they were small (2-3 cm^2) and occasionally followed a threadlike pattern. A possible driver for these different patterns could be the local patchiness of deposited food that probably differed between seasons. Indeed, particulate matter fluxes (i.e. food for the deep-sea benthos) measured with sediment traps in the water column at the DYFAMED station, were ca. 6 times larger in early spring than in early summer, and could have led to different aggregation patterns in the surface-sediment nematodes.

Keywords: Deep sea, meiofauna, submarine canyon, patchy distribution, aggregation

ID: 5960

Impact of subterranean estuaries on the diversity of copepods in the intertidal of the central Wadden Sea

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Coastal ecosystems located in the intertidal are characterised by strongly fluctuating environmental parameters (salinity, temperature, grain size, nutrition flow) and therefor just contains organisms capable to tolerate this kind of stress. Salinity can be influenced by precipitation/evaporation or through escaping ground water, like in subterranean estuaries. This changing salinity might be a local phenomenon from which we hypothesise that it has an effect on the composition of the meiofaunal community. We investigated the diversity of copepods within the intertidal zone of two neighboring areas, of which one is characterised by groundwater springs. The study sites are situated in the central Wadden Sea of the southern North Sea and are affected by semi-diurnal tides. The measured salinity varied between 0-15 in one area, and 10-32 in the other study site. Mainly fine sand occurred in the areas with average grain size from 68 µm to 104 µm and at one sample with an average of 148 µm. Eleven different species were determined. *Tachidius discipes* and *Microarthridion fallax* were the most abundant species through all samples. These taxa are characterised by their osmoregulatory function of their integumental windows. Our study revealed that some taxa are indicator species for a specific site. *Platychelipus littoralis* counts as an indicator species for the groundwater site, whereas *Delavalia palustris* represents one for the sites with normal salinity conditions. Species evenness is significantly correlating with the salinity and the sediment temperature. Our investigation revealed that solely euryhaline copepods characterise the subterranean estuaries habitats.

Keywords: Meiofauna, groundwater discharge, environmental gradient, tidal flat, southern North Sea

ID: 5961

The influence of pH and Redox on the meiofauna assemblages in the fjords and channels of northern Chilean Patagonia

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With the exception of a few taxonomic studies, the meiofauna of Chilean Patagonia have scarcely been studied. We report the initial results of an extensive sampling (16 stations) of the fjords, channels and continental shelf

of northern Chilean Patagonia. At each sampling station, in addition to quantitative and qualitative meiofaunal samples; water depth, sediment temperature, sediment pH and sediment redox potential were also recorded. Meiofauna were extracted from the sediments using the Ludox floatation technique and subsequently mounted in glycerol within a wax ring on a large microscope slide. The samples analysis was made using a compound microscope. The meiofaunal assemblages were dominated by nematodes, but the following groups were also present: harpacticoid copepods, foraminiferans, ciliates, turbellarians, gastrotrichs, kinorhynchs, tardigrades, priapulidans, ostracods, amphipods, tanaidaceans, cumaceans, isopods, halacarids, bivalves, polychaetes and oligochaetes. Nematode abundances ranged between 53.4 ind./$10cm^2$ and 3221.6 ind./$10cm^2$; and harpacticoid abundances between 0.8 ind./$10cm^2$ and 157.8 ind./$10cm^2$. There were no significant correlations between the variables water depth, sediment temperature, sediment pH and sediment redox potential. Multiple regression analysis indicated two significant associations. First pH had a significant effect on meiofaunal abundance, with meiofaunal abundance decreasing with increasing pH. This was due to one site in the Aysén Fjord where sediment pH was significantly higher (8.52) than at other sites (mean 7.60). This may be due to volcanic vents in the area emitting substantial amounts of CO_2. The second more general association indicated that meiofaunal abundance decreased with decreasing sediment oxygen concentrations. Redox potential values ranged from 186.70 mV to -169.68 mV. These results were broadly supported by the multivariate analysis.

This research was supported by project CIMAR-Fiordos CONA C24F 18-07.

Keywords: Chile, fjords, patagonia, pH, redox, nematodes

ID: 5969

Ecological connectivity and functional links between deep sea hydrothermal active and inactive sites in view of potential sulphide mining

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Hydrothermal vents are oasis of productivity and biomass compared to the surrounding deep sea. Mining SMS (seafloor massive sulphide) deposits will remove all benthic organisms inhabiting the substratum, but also provoke high-turbidity and potentially toxic sediment plumes, which will likely impact benthic communities downstream. The recovery of faunal communities at SMS deposits disturbed by mining activities will depend on recolonization from neighboring populations. However, very little is known about the connectivity and spatial distribution of the fauna at inactive sites. Our objectives are to: 1) assess the benthic communities inhabiting inactive sediments in the surrounding of an active vent field; 2) investigate the connectivity between SMS deposits, neighboring populations and active vent sites; and 3) determine the influence of environmental constraints on the structure of benthic communities. For our purpose, we sampled sedimented sites along a gradient of influence of hydrothermal input, from active areas to reference sites away from the area of influence of the vent, and including intermediate stations (near inactive or slightly active areas). Sediment samples were collected on the Mid-Atlantic Ridge during the BICOSE2 cruise on board the RV *Pourquoi-Pas*?, both in active and inactive sites of the TAG and Snake Pit vent fields (part of the French exploration permit area), using the HOV Nautile. Benthic fauna, macro- and meiofaunal organisms, is identified and analyzed using a combination of classical (taxonomy) and molecular (barcode) techniques, in order to describe the benthic community inhabiting sediments along the gradient and characterize the ecological connectivity in the area.

Keywords: Deep-sea mining, hydrothermal vents, connectivity, macrofauna, meiofauna

ID: 5988

Effect of salinity and habitat on rotifer communities from the United States and description of two new species

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Thalassic rotifers are poorly investigated, especially in the New World. This study shows the results of a faunistic survey in saline waters from six sites located in the Northeastern states and one in California. We characterized samples by different salinity values and habitats (such as open waters, temporary flooded marshes, and circumscribed ponds) and compared community compositions to test for possible ecological correlations. Results indicate significant correlations between rotifer communities and both salinities and habitats, supporting that the biodiversity of small species provides fundamental information for ecosystem biomonitoring. During the survey, we identified two species never described before: here we describe and formally name *Encentrum melonei* sp. nov. and *Synchaeta grossa* sp. nov. This investigation also leads to a refined description of *Encentrum rousseleti* (Lie-Pettersen, 1905). Finally, we provide a comprehensive review of the diversity and distribution of thalassic rotifers in the United States.

Keywords: Brackish, marine, meiofauna, microscopic invertebrates, North America, taxonomy, thalassic

ID: 5991

Meiobenthos and nematode fauna of Hainan mangroves (China)

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As part of a project to study mangrove meiobenthos associations in various geographical regions of southeast Asia, mangrove associations of Hainan Island, South-China Sea were investigated in November 2014. Small

mangrove alongshore littoral loci (about 0,04 km^2) in Gaolong bay near Wenchang (19°51.805'N; 109°32.690'E) was selected for comparison with a similar mangrove areas in Vietnam. Two sites (dense *Rhizophora apiculata* mangroves and the muddy-sand intertidal) were sampled. Nematodes accounted for 96-99% of the total meiobenthic density. Nematode density was slightly higher in *Rhizophora* mangroves (2678 ind / 10 cm^2) than at the non-vegetated intertidal (1193 ind / 10 cm^2). 37 species of free-living nematodes were found during the survey. The nematode families Desmodoridae and Comesomatidae had the greatest species diversity. Representatives of these families, as well as the Xyalidae, also dominated in numbers. The faunal composition of the muddy littoral in areas free of mangroves and in the thickets of rhizophora had a number of common species and genera, but was markedly different in terms of the set of leading forms. *Hopperia* sp. dominated in both biotopes. *Spirinia* sp. was also among the dominant species in the mangrove thickets. *Metadesmodora* sp. and Daptonema sp. were numerous in the non-vegetated areas. A certain similarity between the nematode taxonomic composition of *Rhizophora* thickets of the eastern coast of Hainan and the northern Vietnam was observed. In particular, representatives of the genera *Ptycholaimellus* and *Anoplostoma* were noted in the community. They are represented by species similar or identical to that described by us from the mangroves of Vietnam.

Keyworlds: Nematoda, South-China Sea, mangroves, *Rhizophora apiculata*

ID: 5997

Echinoderes dujardini Claparède, 1863 a frequent kinorhynch of phytal meiofauna along Portugal. Distribution and temporal variability

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As part of a wide project to explore the meiofauna associated with macroalgae along the rocky shores of continental Portugal, different species of native and non-indigenous intertidal macroalgae were sampled. The presence of *Echinoderes dujardini* Claparède, 1863 as member of the phytal meiofauna was reported from the north to the south of Portugal. All the studied macroalgae, including those non-native, harboured individuals of *E. dujardini*. However, the most complex macroalgae *Cystoseira tamariscifolia* (Hudson) Papenfuss and *Stypocaulon scoparium* (Linnaeus) Kützing harboured a higher abundance of *E. dujardini* than other macroalgal species with a simpler morphology. Unexpectedly, two individuals of *E. dujardini* were found from water samples collected on rocky shores.In north Portugal, the abundance of *E. dujardini* on the three main macroalgae from rockpools (*Sargassum muticum* (Yendo) Fensholt, *Bifurcaria bifurcata* R. Ross and *Chondrus crispus* Stackhouse) was studied at four dates along the year. Results showed that *E. dujardini* was more abundant on *S. muticum* and *B. bifurcata* than in *C. crispus*. The temporal variation of *E. dujardini* showed the same pattern in the three studied macroalgae. In spring samples, noindividuals of *E. dujardini* were found and their abundance increased in summer reaching its maximum during autumn and decreasing again in winter.

Keywords: Rocky shores, Atlantic Ocean, macroalgae, plankton, seasonality

ID: 6000

Chemoautotrophic food availability influences benthic copepod composition at deep hydrothermal vent sites on NW Pacific volcanic calderas

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We investigated spatial variation in benthic copepod composition and its association with environmental parameters, including food quality, at hydrothermal vent sites on chimney structures in the calderas of three neighboring sea knolls (Bayonnaise Knoll, Myojin Knoll, and Myojin-sho Caldera) in the Izu-Ogasawara arc in the western North Pacific Ocean. At the vent sites, spatial differences in copepod composition were significantly correlated with the stable carbon isotopic signatures ($\delta^{13}C$) of organic matter in the detritus, which reflects the relative contribution of carbon substrates around vent spots. Dirivultidae, a copepod family endemic to vents, dominated at the sites with higher $\delta^{13}C$ values on active chimneys. Most of the dirivultids at those sites were composed by *Stygiopontius senokuchiae*, the first dirivultid species described from the study area. On the other hand, the relative abundance of harpacticoids showed a negative associations with the values of $\delta^{13}C$ around chimneys. The results suggest that the availability of vent fluid carbon may have been a primary and common factor controlling copepod assemblage composition around the hydrothermal vents in the calderas of the three sea knolls, although the assemblages were spatially separated from one another by the caldera walls.

Keywords: Deep sea, Chemosynthesis, community composition, copepod, Dirivultida, Stygiopontius

ID: 6001

Correlation analysis of meiofaunal biomass and macrofauna community in the water around Korean Peninsula

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Meiofauna play an important role in the energy flow of marine benthic ecosystems and are also known to influence the composition of higher trophic level organisms. In this study, we analyzed the correlation between the biomass of meiofauna and macrofauna community. Meiofauna biomass was calculated by measuring their length and maximum width with image analysis software. Results of macrofauna community were obtained from published report of "National investigation of Marine Ecosystem in Korea". For the analysis, we compared sample results of 297 stations collected from 2015 to 2016. As a result, meiofauna biomass showed a significance correlation in abundance and biomass of macrofauna. We also analyzed the correlation with some macrofauna species which dominated during each survey, and three polychaete species (*Ampharete arctica, Mediomastus californiensis* and *Magelona johnstoni*) were found to have a significant correlation with meiofauna biomass. This comparison confirms that meiofauna community functions as important food sources in the marine ecosystem. If more data are accumulated throughout collaborative study with relative researchers, ecological study of meiofauna in the waters around Korean Peninsula would be established at a more detailed level.

Keywords: Meiofaunal biomass, macrofauna, correlation analysis, Korea

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ID: 6007

Meiofaunal assemblages in horseshoe crab habitat in an intertidal zone, China

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In China, horseshoe crab *Tachypleus tridentatus* populations have been declining sharply in recent years. Habitat destruction, environmental pollution and overfishing are the main reasons for the decline of this species, which usually inhabits the upper intertidal zone of pristine sandy beaches. In order to learn the meiofauna assemblages in horseshoe crab habitat, we began to investigate the meiofaunal assemblages in high, middle and low intertidal zones in horseshoe crab habitat of Eyu Islet in Tong'an Bay, Xiamen from October, 2018, and plan to investigate this area for four seasons. In October 2018, meiofaunal density was highest in the mid-intertidal zone, followed by high, then low intertidal zone (mean density of 856, 778 and 700 ind. 10 cm^{-2}, respectively). Average nematode density ranged from 600 to 810 ind. 10 cm^{-2}. Average copepod density increased from the high intertidal zone to the low intertidal zone (16, 35 and 82 ind. 10 cm^{-2} respectively). A total of 47 nematode genera were recorded, but only eight (*Daptonema, Dorylaimopsis, Metachromadora, Metoncholaimus, Neochromadora,*

Ptycholaimellus, Sphaerolaimus and *Terschellingia*) that occured in all the samples. *Tripyloides* was only found in the high intertidal, whilst *Bathylaimus, Laimella* and *Paramesacanthion* were only found in the mid-intertidal zone and *Quadricoma, Vasostoma* and *Syringolaimus* only in the low intertidal zone. *Sabatieria*, a tolerant genus had low percentage in the study area but was the dominant genus in other intertidal zones in Tong'an Bay, indicating that the study area provides better environmental quality for horseshoe crabs. ANOSIM analysis indicated that nematode assemblages of high, middle and low intertidal zone did not differ significantly from each other. The relationships of nematode assemblages and environmental factors such as temperature, salinity, sediment granulometry, chlorophyll-a content, TOC, PAHs and trace-metals will be discussed.

Keywords: Meiofauna, horseshoe crab, intertidal zone, environment factors. China

ID: 6020

Collaborative opportunities with the Plymouth Marine Laboratory

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The Plymouth Marine Laboratory (PML) has a long history of meiofaunal research. The laboratory holds two sets of valuable samples which are currently in storage. The first was collected in collaboration with the International Association of Meiobenthologists in the early 1990s. Standardised packs of artificial substrate units (ASUs) were sent to scientists around the world. The ASUs were deployed on shallow sublittoral hard substrates. Following a colonisation period the ASUs were collected using an agreed protocol. ASUs were returned to PML for processing. The fauna from the ASUs was extracted and meiofauna and macrofauna were stored separately. The data represent an opportunity to examine global and latitudinal variation in meiofaunal community structure. The second consists of meiofaunal samples collected in the Western Channel Observatory (www.westernchannelobservatory.org.uk). PML has been sampling regularly off Plymouth for over 30 years, building up world-class long-term datasets. Initially the focus was on the pelagic system (plankton, nutrients, physics). A benthic programme was initiated more than 10 years ago, initially focusing on regular (bimonthly) samples from 4 sites with contrasting sediments. The programme has evolved, and now consists of regular (monthly) samples from the focal site at L4 and a nearby site influenced by dredging disposal. An extended survey takes place annually. The samples offer opportunities to examine meiofaunal variation through time at a range of scales, and how that variation is influenced by environmental variation. Owing to the nature of the WCO each sample comes with a wealth of supporting information ranging from physics to fish. We are interested in discussing collaborations with other organisations which may wish to analyse some or all of these samples.

Keywords: Plymouth Marine Laboratory (PML), meiofaunal research, collaboration discussions

ID: 6033

Relationship between the free-living marine nematodes and microphytobenthos (benthic diatom) from the tropical mangrove ecosystem, Andaman & Nicobar Islands, India

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For the first time, interaction between the free-living nematodes and microphytobenthos has been studied from the mangrove ecosystem of Andaman Islands. The sampling was carried out in mangrove sediments of south Andaman and classified into three seasons. From the 65 species recorded, six dominant genera represented almost 70% of the assemblage in the mangrove sediments of south Andaman. Among them, the most dominant genera were Sabatieria (10%), Daptonema and Terschellingia each contributed 9%, followed Chromadora (8%), Sphaerolaimus (6%) and Metalinhomoeus (5%). In mangrove sediments, the dominant nematode families were Linhoemoeidae (18%), Chromadoridae (16%), Comesomatidae (13%) and Xyalidae (12%) while the diatoms family were mainly dominated by Bacillariaceae, Naviculaceae, Pleurosigmataceae, Diploneidineae, Coscinodiscaceae, throughout the study. Non-selective deposit feeders (1B) and epigrowth feeders (2A) accounted 37 % and 30 % of the total nematode population density, respectively. The feeding strategies of the dominant genera, particularly non-selective deposit feeders (1B) and epigrowth feeders (2A) are discussed and assessment made based on the nematode abundance and microphytobenthic biomass and diatom density. Nematodes grazing rates were compared with the nematode abundance and MPB diatoms. ANOVA revealed significant ($p < 0.05$) difference on the sediment characteristics (Chlorophyll *a*, organic matter, silt/clay) between seasons. Total sediment organic matter content and silt/clay percentage was maximum during summer while the Chlorophyll *a* content found least concentration ($0.98\ \mu g/cm^3$) in summer. A total of 76 species belonging to 31 genera and 23 families were benthic diatoms. Some of the dominant genera *Nitzschia, Navicula, Gyrosigma, Pleurosigma* and *Diploneis* are the pennate diatoms that present in the mangrove sediments of south Andaman. The seasonal difference revealed the nematodes abundance were higher during summer while the diatom density found lower. The study showed a significant relationship with the population density of nematodes and their suspected food MPB diatoms in mangroves. The high grazing rates of nematodes on MPB diatoms makes it important and should be taken into consideration while structuring a trophic model in the mangrove ecosystem. However, this results provide the baseline information on their distribution and the trophic level importance in mangrove sediments of Andaman & Nicobar Islands. Further studies should be extended to build a trophic food web for the nematode compartment to know their potentiality in the trophic level.

Keywords: Nematodes, pennate diatoms, mangroves, microphytobenthos, Andaman Islands

ID: 6035

Maërl beds meiofauna from the Bay of Brest (Brittany), a quantitative and qualitative first insight

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Maerl beds are threatened by several types of anthropogenic activities, such as large-scale commercial extractions, reduction of water quality by discharges, eutrophication, dredging and bottom trawling activity, aquaculture and invasive alien species. Beside their ecological importance a complete species lists for maerl biotopes do not exist yet and meiofaunal data are completely lacking. Meiofauna, protists and small multicellular metazoans between 1000 µm and 32 µm, holds a key position in the benthic food web playing a significant role in ecological processes and ecosystem function. Among meiofaunal metazoans, nematodes represent one of the most abundant and diverse taxa inhabiting all kind of sediments therefore they can represent a very useful tool for biological monitoring. To date, only few studies were conducted on maerl meiofauna. This study aims to characterize the meiofaunal abundance, distribution and community structure of a maerl area in the Bay of Brest (Brittany), investigating the structural and functional diversity of maerl nematodes and comparing meiofauna from a maerl area with meiofauna from a close sandy beach. Nematodes were always the most represented taxon in both environments. A total of 97 species belonging 78 genera of nematodes were identified from the maërl station vs 27 species belonging to 21 genera from the sandy beach. The total meiofauna abundance recorded in the present study appeared consistent with available information from other site of north Brittany (France), at similar depth with the highest abundance value concentrated in the first 2 cm of sediment layer and then progressively decreased with increasing depth. Among 13 taxa identified, nematodes were the most abundant and present at all depth intervals (81-97%). Copepods and nauplii instead, are concentrated in the upper maerl and 0-1 cm. All together our data represent an important step towards the knowledge of meiobenthic biodiversity of maerl beds.

Keywords: Biodiversity, meiofauna, Maërl beds, Bay of Brest

ID: 6063

Biocoenosis of Meiofauna in a high-latitude glacial Arctic fjord (Kongsfjorden, Spitsbergen) with attributes on selected fauna

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Kongsfjord (79ºN, 12ºE) is an open glacial fjord on the west coast of Svalbard, located northwards of Norway. The meiobenthic samples collected as a part of Summer Phase, Indian Arctic Expeditions 2011, 2015 and 2016 forms the basis of this study. The dominant meiobenthic groups observed during the studies were Foraminifera (48%) and Nematoda (37%). These major meiofaunal groups were dominant towards the outer basin where the sediment disturbances caused by increasing sediment re-suspension due to glacial activity is low. The abundance and diversity of both nematodes and foraminiferans were also high in the outer basin. During the expeditions 80 nematodes belonging to 26 families were identified in which *Dorylaimopsis* sp. (39.55%) and *Terschellingia longicaudata* (12.53%) had the highest relative abundance. Out of the 72 foraminiferans belonging to 8 sub orders, *Nonionella labradorica* (18.30%) had the highest relative abundance followed by *Cassidulina teretis* (8.85%). Among nematodes Chromadorids and Araeolaimids had a tendency to distribute in the inner fjord while Enoplids and Monhysterids in the outer fjord. The feeding guild analysis showed the dominance of Epistrate feeders (2A) (66%) and particulate feeders (IA) (10%) in Kongsfjorden. Carbon sequestration studies indicated that nematodes are the key contributor of carbon sequestration in Arctic benthic system, where *Anticoma eberthi* (14.06 µg) subsidised the highest carbon, followed by *Marylynnia complexa* (12.94 µg). The foraminiferan species namely *Cribrostomoides jeffreysii* (0.074 µg) and *Globobulimina auriculata* (0.071 µg) structured the maximum amount of carbon. The net carbon sequestrated by the nematodes and foraminiferans were higher in the outer fjord as compared to inner fjord of Kongsfjorden. Sediment organic matter, silt content and pH were the best matching variables (BEST) for the distribution of meiofauna. In the context of emerging global climate change the studies on the benthic faunal abundance and diversity might be useful for future sustainable management of Arctic system.

Keywords: Arctic, Kongsfjorden, meiobenthos, Foraminifera, nematoda

ID: 6065

Mite(y) journey on the back of caddisfly (Trichoptera) for ca. 45 000 000 years

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Amber is a resin that has been polymerized and fossilized for millions of years. Sticky sap dripping from the branches and trunks was a trap for many small invertebrates, whose remains have survived to this day. Through good preservation, these organisms are available for research in an almost unchanged morphological form. Furthermore, intra- and interspecies interactions that provide insight into the structure and composition of extinct ecosystems are often discovered. The largest amber deposit in the world, located on the Sambian Peninsula (Russia) and in the vicinity of the Gulf of Gdansk (Poland), contains Eocene Baltic amber, known to people for thousands of years. Despite its popularity, new findings are made almost every day. Mites (Acari) are a group of diminutive arachnids inhabiting the majority of land and some aquatic environments. Their vast morphological, ecological, behavioural etc. diversity is a measure of their evolutionary success. Despite their ubiquity and abundance, mites remain the least studied group within all arthropods. Inclusions in amber are the main (and exclusively for most groups) source of the fossil record of these animals. Detailed examination of such small inclusions is problematic and requires prior grinding and polishing treatment. Due to the extensive interactions that mites have created with various invertebrates, larger inclusions (e.g., of insects) are also in the concern of paleoacarology. During the exploration of the inclusion collection in Baltic amber, a specimen of the caddisfly (Trichoptera) was discovered along with a dozen parasitic larvae of water mites (Hydracarina) attached by the chelicerae on the dorsal part of the abdomen of its host. Adults of water mites are free-living predators in freshwater reservoirs but their larvae parasitize on insects associated at least at some time in their development with water. This is the first finding of Hydracarina associated with caddisfly in the fossil record.

Keywords: Amber, paleobiology, water mites, interspecific interactions, new record

ID: 6081

Nematodes of the three Arctic Seas

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The nematode fauna was studied at 54 stations in the three Arctic Seas - Kara, Laptev and East Siberian. We used data on fauna of 500-600 km latitudinal transects from the Yenisey bay, Lena, Indigirka and Kolyma deltas to shelf to describe taxonomic composition and abundance in relation to environmental factors. The stations located in the open central sea, characterized by marine conditions and the most southern stations were influenced by

runoff from the big Siberian rivers. A total of 11000 nematode individuals were identified, representing 130 genera. High taxonomic similarity was recorded for Arctic shelf. Whereas nematode taxonomic composition at stations influenced by runoff was slightly different from adjacent Arctic shelf. Abundance and diversity of nematodes are affected by the depth, hydrodynamics, grain size and organic matter content.

The reported study was funded by RFBR according to the research project № 19-05-00128 A.

Keywords: Nematode, Arctic, taxonomic composition, diversity, distribution

ID: 6453

Biodiversity of Copepoda Harpacticoida in a submarine canyon and its adjacent slope area in the Southwest Atlantic (Campos Basin, Brazil)

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Copepoda Harpacticoida is the second largest group of meiofauna in most benthic habitats, including the deep sea. Despite the large number of species, the taxon Harpacticoida is not properly known, especially in areas of submarine canyons. The aim of this study is to assess the diversity of Harpacticoida in the Almirante Câmara Canyon and the Adjacent Slope Area including four isobaths (400, 700, 1,000 and 1,300 m), in the Campos Basin, Rio de Janeiro, Brazil. Samples were slice in different layers (0-2 and 2-5cm). In this study, 23 families, 108 genera and 115 species were found. Among them, Ectinosomatidae was the most abundant (22%), followed by Argestidae (19%) and Cletodidae (14 %). The harpacticoid density tended to decrease with increasing depth, but this tendency was not observed for diversity indexes. In addition, the most superficial layer showed significantly higher values of density and diversity. Simper analysis indicated that families Argestidae, Ectinosomatidae, Ameiridae, Miracidae (and their respective genus) showed major contributions for similarities among isobaths in both areas (Canyon and Adjacent Slope).

Keywords: Meiofauna, Deep Sea, Atlantic Ocean, marine ecology

3.

Meiofauna in a changing world: meiofauna response to natural and anthropogenic pressures.

ID: 5819

Foraminiferal assemblages at a former deep-sea experimental disturbance site in the Clarion-Clipperton Zone (subequatorial NE Pacific)

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In April 1995, sediment at an abyssal site in the eastern part of the Clarion-Clipperton Zone (CCZ, subequatorial NE Pacific) nodule field was experimentally disturbed to produce and study effects mimicking those generated by nodule mining. Following the disturbance, the abyssal seafloor within the 1.5 km x 2 km test site was divided into three zones: tracks left in the sediment by the disturbing device (= impacted zone), the adjacent area covered by re-deposited sediment stirred up by the disturbance (= re-sedimentation zone), and the unimpacted area (= control zone). Twenty years later, in April 2015, the test site was resampled during the SO 239 cruise of RV SONNE. We examined benthic foraminifera present in the uppermost sediment layer (0-1 cm) collected with a multiple corer at stations located in each of the three zones. We compared the composition and abundance of assemblages in the three zones in order to: 1) contribute to knowledge of CCZ foraminifera, which are predominantly monothalamids, a ubiquitous but poorly known group of deep-sea protists; and 2) establish if foraminiferal assemblages in the impacted, re-sedimentation and control zones exhibit differences that potentially reflect the impact of the disturbance.

The SO 239 cruise of RV SONNE was a part of the JPIO Pilot Action project “Ecological Aspects of Deep-Sea Mining”. The research presented is supported by the Polish National Science Centre grant No. UMO-2014/13/B/ST10/02996.

Keywords: Deep-sea, CCZ, Foraminifera, disturbance

ID: 5853

Nanoplastic contamination of mangrove meiofauna communities

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The PEPSEA project (Nanoparticles of plastic in the environment: source, impact and prediction) evaluates the life-cycle of microplastics and nanoplastics (MNP) in Guadeloupe (French West Indies) in two mangroves differently contaminated by plastic from *i)* North Atlantic gyre or *ii)* local waste production. Reduced water circulation between mangrove tree roots potentially contributes to contaminant sedimentation providing the opportunity to estimate the impact of MNP in the local benthic biota. Due to its small size and sediment habitat, meiofauna can accumulate MNP and represents a path of contaminant transfer to higher trophic levels. The objective of the study was to evaluate contamination of meiofauna community in mangrove sediment. Nanoplastic particles were identified using pyrolysis-GCMS. Mass spectrometry of meiofauna samples shows smaller and more abundant peaks of small size commercial plastics potentially due to aged plastic with PVC plastic type proportionally more abundant in sample.

Keywords: Benthic, sediment, contamination, Guadeloupe, meiofauna, nanoplastic

ID: 5863

Do microplastics affect population growth rates of different nematode species?

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Apart from global warming, microplastic pollution is currently one of the biggest environmental concerns. Since plastic debris is not biodegradable, it accumulates, rather than decomposes in the environment. Secondary microplastics are a result of the breakdown of larger plastic items caused by weathering via mechanical action, oxidative weathering or biological degradation. Microplastics (<5 mm) that have been generated in this way and sedimented by biofouling processes, are much more bioavailable to low trophic fauna. In fine sediments, nematodes account for the major share of abundance (up to 90%) of meiobenthic organisms and are considered to have an important position in benthic food webs by connecting lower (bacteria) and higher trophic levels

(e.g. macrofauna, fish). Therefore, the investigation of impacts of microscopic particles on the population growth for nematodes is important for the environmental risk assessment of microplastics.

Preliminary studies showed that two nematode species, *Caenorhabditis elegans* and *Poikilolaimus regenfussi*, are affected by 1.0 µm polystyrene (PS) beads reflecting in lower numbers of individuals as well as lower population growth rates. The aim of this study is to assess impacts of lowly (10^3 beads ml^{-1}) and highly (10^7 beads ml^{-1}) concentrated PS beads of 1.0 µm in size on the population growth rates of different nematode species (e.g. *C. elegans, Pristionchus pacificus, Plectus aquatilis, Panagrolaimus cf. thienemanni*). If different nematode species may be negatively influenced by microplastics, it will be having impacts on the benthic food web.

Keywords: Microplastics, population growth, nematodes

ID: 5931

Mangrove meiofauna as bio-indicator for the monitoring of coastal and transitional waters in French Guiana

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Mangroves forests, inhabiting the intertidal area between land and sea at low latitudes, represent one of the most productive ecosystem of the world. Being frequently polluted by the wastewaters, they play a buffer role between these interfaces. Since 1986 several coastal laws protect worldwide mangroves, but it's still necessary to quantify and limit the anthropic pressures on this unique ecosystem regarding as the human densities increasing in the intertropical regions. Meiofauna organisms are highly sensible and show rapid responses to natural environmental alterations or anthropogenic impacts. Meiofauna is very abundant in mangroves and can be a good candidate to characterize the quality of this environment. In French Guiana, mangroves account for 80% of the littoral and are still weakly disturbed by human pressure. In this study, we explored meiofauna community, with a focus on nematodes, aiming to develop potential biological indicators to monitor French Guianese mangroves. We investigated abundance, biomass and diversity of meiofauna community (taxa level) and more specifically of the nematodes populations (genus level) in three stations according to a pollution gradient from the Cayenne city (polluted, moderately polluted and not impacted) along the Cayenne River (French Guiana). Meiofauna abundance and biomass showed the lowest value in the most impacted site. Opportunistic genera such as *Desmodora* were observed only in polluted sites, while the genus *Pseudocella*, very sensitive to anthropogenic impacts, was found only in the reference site located in downstream. Furthermore, in the two impacted sites we observed the presence of *Suctoria* ciliates attached to the cuticle of several *Desmodora* specimens. This parasitism could be explained by a possible diminishing of nematode fitness and defense in polluted sites. These preliminary results suggest that meiofauna, and in particular nematodes, can be a good biological indicator of anthropogenic impacts in Guianese mangroves. Further studies of mangrove meiofauna from a large range of geographical locations are essential for strenghthening our conclusions on the use of this group as bio-indicator.

Keywords: Pollution, mangroves, biological indicators, French Guiana, meiofauna, nematodes

ID: 5935

Spatiotemporal variations of meiofauna assemblages in relation with environmental factors in two contrasting nearshore habitats

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This study aimed to investigate the spatial-temporal pattern of meiofaunal assemblages and the environmental variables that determined the variability and distribution of meiofauna in two different nearshore habitats. Biotic and abiotic data were collected seasonally at six sites in each two different localities, one in semi-enclosed bay in south coast of Korea (Jinhae bay) and the other in open sea area in East Sea, Korea (Samcheok coast) over three years, including 12 consecutive season from 2013 to 2016. Our result showed that organic matter, dissolved oxygen, mean grain size and water depth were significantly different between two study areas. The meiofauna assemblages also showed clear difference between two study areas, among seasons, and among sites within each area. The estimated variations of meiofauna assemblages among sites was higher than among seasons and between areas variations. Such spatial meiofaunal differences among sites were significantly influenced by the local environmental factors such as grain size, organic content, sea-water temperature and depth. This high spatial variability showed clear inner-outer site difference and might indicate that natural variability is affected by anthropogenic pressures in some sites of the study area. Those site-specific variabilities of meiofauna assemblage highlighted the usefulness of meiofauna in ecological quality assessment.

Keywords: Meiobenthos, benthic community structure, spatio-temporal distribution

ID: 5939

The impact of temperatures, salinity levels and Chitosan concentrations on the survival and production rates of Harpacticoid Copepod, *Tigriopus* sp.

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This study aims to observe survival and production rates of Harpacticoid Copepod at different temperatures,

salinity levels and Chitosan concentrations. An ovigerous female Harpacticoid Copepod *Tigriopus* sp. was collected in Chonburi province, Thailand, and reared at Ramkhamhaeng University. The copepod offspring were brought to conduct two experiments. The first experiment was carried out by culturing the copepods at the temperatures of 25° C and 30° C, and salinity levels of 5, 10, 20, 30, 40, 45 ppt for 15 days. The results showed that the temperatures and salinity levels significantly affected survival rates of the copepods ($P<0.05$). The copepods cultured at the temperature of 25° C and salinity level of 30 ppt had a survival rate of 85.04% with 11 copepodids and 31 adults, while those cultured at the temperature of 25° C and salinity level of 20 ppt had a survival rate of 82.56% with 6 copepodids and 31 adults. At salinity levels of 5 ppt and 45 ppt, the number of survived copepods was the lowest. It took 6 days for the copepods to develop from nauplius to copepodid stages, and 5 days from copepodid to adult stages at the temperature of 25° C and salinity level of 30 ppt. Thus, the temperature of 25° C and salinity level of 30 ppt are the optimum conditions for copepod culture. The second experiment was conducted to evaluate the effects of Chitosan concentration on the production of *Tigriopus* sp. Four groups of 20 ovigerous female copepods were fed with microalgae, *Tetraselmis* sp., and Chitosan solution with 0.01%, 0.1% and 1% concentrations in 500 ml seawater. One of these groups was a control group without Chitosan. The production rates were measured every 5 days for 25 days. The group with Chitosan concentration of 0.01% yielded the highest production rate of 1,406 inds./100 ml, while the one with Chitosan concentration of 1% had the lowest production rate of 945 inds./100 ml. Therefore, the concentration of Chitosan solution did not have a significant impact on copepod production rates, compared to the control group ($P<0.05$).

Keywords: *Tigriopus* sp., temperatures, salinity levels, Chitosan solutions

ID: 5945

The impact of sea ice regime on nematode communities: structural and morphometric approach

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Eight stations located in the seasonal sea ice zone north of Svalbard (Yermak Plateau, Nansen Basin, Northern Svalbard shelf) were investigated during 'TRANSSIZ' cruise within Arctic in Rapid Transition initiative. Sample locations covered a wide depth gradient (300-2200 m), different sea ice concentrations and subsequent bloom stage. Our study provides previously unavailable data on nematode diversity and morphometry for this Arctic region during ecologically important spring to summer transition time. 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. Therefore, we compared standing stocks, diversity, and 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 obtained results suggest that nematode community differences are attributed to prevailing environmental conditions, ice-edge related bloom-phase. Three distinct nematode assemblages were observed. Nematodes standing stock and diversity was the lowest at stations where pre-bloom phase occurred. Conditions at stations with already developed bloom promoted enhanced abundance and biomass of nematodes and almost two time higher number of nematode genera in comparison to pre-bloom stations. Stations with early-bloom conditions appeared as transitional, with conditions in which relatively high number of genera with different life strategy can co-exist. Moreover, a clear division of nematode size and shape indicates that the morphological attributes of nematode assemblages are useful in demonstrating differences in the environmental conditions of the Arctic sediments. 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, as well as community structure.

Keywords: Nematoda, diversity, morphometry, Arctic, sea ice, spring time

ID: 5959

Breakwaters as beach habitat modifiers: a case study of meiofauna in southwestern Spain

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Maritime infrastructures such as breakwaters can modify the hydrodynamics and biotic composition of coastal sandy habitats. These disturbances can impact meiofaunal communities. The spatial variation of meiofauna was analyzed along a disturbance gradient established by the presence of a breakwater in an intertidal sandy beach (Punta Umbría, SW Spain). Six zones were sampled at low tide at different distances from the breakwater (0, 50, 100, 200, 400 and 800 m). In each zone 3 tide levels were established in relation to low tide level, taking 3 samples/level. The variation in granulometry and other abiotic features was also studied. Samples were taken with a PVC core of 3.6 cm diameter and 10 cm length. The meiofauna was extracted by decantation and sieved through 0.5 mm and 30 µm sieves. The material was preserved in 4% formaldehyde with Bengal rose. Over 30,000 individuals belonging to 13 taxa were identified: Turbellaria, Nematoda, Tardigrada, Gastrotricha, Polychaeta, Oligochaeta, Gastropoda, Bivalvia, Nauplii, Copepoda, Ostracoda, Cumacea and Acari. Nematodes were numerically dominant, followed by turbellarians, nauplii and copepods. The composition and taxonomic structure of the meiofauna was relatively homogeneous within the first 100 m from the breakwater. Changes in the composition and abundance of the dominant groups seemed to occur further from that zone. Nematodes presented abundance peaks close to the breakwater, and then fluctuated within a lower range. Turbellarians showed maximums from 200 m, while the nauplii and copepods (adult forms) exhibited peaks of abundance from 400 m. The tide level had a significant effect on the composition and abundance of meiofauna, especially of nematodes that were, more abundant in upper tidal levels. The combination of the gradient of proximity to the breakwater and the tidal level in the profile of the beach are determining factors in the meiofaunal community.

Keywords: Meiofaunal communities, breakwater, sandy beach, SWSpain

ID: 5970

Deep Metal: Deep-Sea Kinoryncha from the Polymetallic nodule fields of the CCFZ

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Polymetallic nodule areas are currently in the spotlight due to their potential commercial and strategic interest for metals such as nickel, copper, cobalt and rare earth elements. It is expected that nodules will be mined in the near future in order to face the growing demand of these metals. The polymetallic nodule fields occur in deep-sea bottoms with low sedimentation rates, where nodules lie on the soft sediment increasing the heterogeneity of the environment (hard and soft substrates). These areas are beyond national jurisdiction and its regulation is handled by the International Seabed Authority (ISA), for whom it is needed to identify the fauna associated with the areas of nodules to make accurate environmental impact predictions and stablish mining regulations before the concession of the exploitation. Our study is focused on the Kinorhyncha diversity and abundance in the BGR license area at the Clarion-Clipperton Fracture Zone (CCFZ) in order to assess how meiofaunal organisms may be affected by seafloor mining activities, which not only will remove the nodules (decreasing the heterogeneity and habitat availability) but also resuspend sediment that otherwise keeps very stable. Therefore, we identify the kinorhynch community at the exploration area, contributing to fill the knowledge gap of deep-sea kinorhynch diversity in general, mostly unexplored and particularly at the nodule fields, and providing a detailed geographic distribution of kinorhynch species in the area which is crucial for their effective preservations. Finally, our research allows to investigate whether or not some taxa are specialized in a specific area or habitat (nodules/soft sediment) and, if so, to predict the potential impact of nodule mining on kinorhynch diversity and on the whole meiofauna community to some extend too.

Keywords: Clarion-Clipperton Fracture Zone, Kinorhyncha, meiofauna, deep-sea mining, diversity, distribution

ID: 5986

Meiofauna communities from an eroded tropical sandy beach (Pernambuco, Brazil)

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Sandy beaches represent one of the most extensive Brazilian coastal environments and thus constitute important buffer zones between the terrestrial and marine environments. Due inhabited in a disorderly way and other influences, as the erosive process, those environments are frequently in change. Nematoda is the main group among the various meiofauna representatives. The aim of this study was to analyze the structure and spatial distribution of meiofauna and nematodes communities present in an eroded tropical sandy beach (Praia de Gaibu – PE) and correlate these communities with the granulometric parameters. The meiofauna was composed of Nematoda, Copepoda, Tardigrada, Oligochaeta, Polychaeta, Ostracoda, Turbellaria and Bivalvia. The highest and the lowest density of meiofauna occurred in the lower mesolittoral (1,556.77 ind/10cm^2 and 13.80 ind/10cm^2, respectively). Representatives from five orders, sixteen families and forty-five genera composed the nematodes community, and Xyalidae was the most abundant one. The genera that stood out in terms of abundance were *Daptonema, Bolbolaimus, Mesacanthion* and *Theristus*. The biggest representativeness, from the trophic point of view, was the "non-selective deposit feeders", type 1B, reflecting the high abundance of *Daptonema* and *Theristus* genera. The Spearman test showed significant positive correlations of Nematoda with fine sand and with the mean grain size, and negative correlations with medium sand. Turbellaria also had positive correlations with fine and very fine sand. Only 20 out the 45 Nematoda registered genera were correlated with the granulometric characteristics, demonstrating with this result that in addition to sediment, other factors are co-responsible for the distribution and composition of the nematodes community in this environment.

Keywords: Sandy shores, meiobenthos, ecology, marine environment

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ID: 5987

Biomonitoring of Egyptian Mediterranean Sandy beaches by using free living nematode assemblages and functional biological traits, Alexandria Egypt

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Free living benthic nematode assemblages were investigated among three sandy beaches along Egyptian Mediterranean coast of Alexandria during March 2014.The abundance, composition, species diversity, sex ratio, trophic guilds and tail type were determined from core samples (4.9cm^2 and 11 cm long). Total organic matter and grain size were analyzed in accordance. Duplicate samples were taken from 4 profiles and 5 stations per each beach. The current study provides the first taxonomic identification of benthic nematode assemblages of Egyptian Mediterranean sandy beaches of Alexandria in addition to functional biological traits as a biomonitoring tool. Results revealed that the highest nematode abundance and species richness were significantly recorded at the most hotspot sandy beach (El-Mex). Community structure consisted of thirteen species and dominated with 5 species among studied sites. Sex ratio recorded a shift towards male individuals. Juvenile stage 3 dominated two beaches whereas Juvenile stage 4 dominated the hotspot beach. Trophic guilds revealed the dominance of predator and scavenger nematodes at the relatively cleanest beach and at the hotspot beach respectively. Conical tail was the dominant type; however, long tail nematodes were recorded at the lowest disturbed beach. Diversity indices revealed significant variations among beaches and within stations nested profiles with few exceptions. Functional trophic trait of trophic guilds responded strongly to sedimentological parameters. Although of the significant variations among sandy beaches in most of the studied biological traits and taxonomic identifications, results of the current study were surprising. The highest abundance and species were recorded at the hotspot probably due to prevalence of coarse grain size. However results of sex ratio, predator and scavenger could be used as biomonitoring tool for aquatic ecosystems.

Keywords: Taxonomic identification, hotspot beach, sex ratio

ID: 5990

Nematoda genera assemblage's along continental shelf in Santos Basin, Southeast Brazil: State of the art for a monitoring program)

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A monitoring program in order to characterize the environment of Santos Basin, throughout shelf and shelf brake, in Southeast Brazil, will begin in 2019 (PETROBRAS). In this basin, oil drilling activities are developed. That characterization will help in the understanding of the dynamics of the area and in the environmental management. Nematoda genera assemblage's previous data of the shelf are here analyzed in order to provide the state of the art of its knowledge. Sediment samples were obtained with a box corer on board of the R. V. "Prof W Besnard". Meiofauna samples were collected with a core of 2.5 cm diameter and 10 cm high. Environmental variables were also obtained. In Cabo Frio shelf (CF), two stations were sampled around 40 and 100 m depth, in the summer and winter 2001. In Ubatuba (UB) two stations were samples around 40 and 100 m depth, in the winter 2001 and summer 2002. In Santos shelf (SA), six stations were sampled between 16 and 100 m depth in the winter 2005 and summer 2006.Along the continental shelf were found 197 Nematoda genera. This number represents a high diversity and 53% of the total genera recorded for marine environments in Brazil, according to Venekey (2017). *Sabatieria* was dominant. Along Ubatuba and Cabo Frio, the station at 40 m depth off CF was separated from the other stations by the presence of *Daptonema, Amphimonhystrella* and *Paramonhystera*. Sediment chlorophyll a biomass was higher than at the other stations. Although stations at 100 m in CF and

UB, and at 40 m in UB were not clearly separated, *Aponema* was dominant in sandy sediment at CF 100m, and *Viscosia* and *Linhystera* were dominant in fine sediments at UB 100m. Along Santos shelf, stations at depths > 50 m had high percentage of *Sabatieria* and *Desmoscolex* in fine sediments. Stations around 30 m depth had sandy sediments and *Ptycholaimella* and *Chromadorita* were dominant. The shallowest station, around 16 m depth, had high chlorophyll a biomass and *Microlaimus* was dominant.

Keywords: Continental shelf, Nematoda, diversity, monitoring program, Southeast Brazil

ID: 6013

Composition and abundance of meiofauna in shellfish protected area compared to non-protected area on a sandy beach in the Andaman Sea

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Sandy beach ecosystems are at the ecotone between marine and terrestrial ecosystems and are mostly recognized as low primary productivity areas because of less abundance of algae in the intertidal zone. Meiofauna is an important group of benthic invertebrates and plays a major role in marine food webs. High abundance of the wedge clam *Donax scortum* has been reported at Hat Pak Meng, a sandy beach in Trang Province, the Andaman Sea coast of Thailand. A management strategy for *D. scortum* conservation at Hat Pak Meng is establishment of a shellfish protected area. This study aimed to examine composition and abundance of meiofauna in a shellfish protected area compared to non-protected areas on a sandy beach at Hat Pak Meng in 2018. The meiofauna samples was collected from the study sites in the shellfish protected area and some non-protected areas by using PVC meiocores of 3.5 cm diameter. Meiocores were randomly inserted into the sediment down to a depth of 10 cm, with four replicates for each study site. Nine major groups of meiofauna were found, and the dominant groups were Foramminifera, Bivalvia, Ostracoda and Nematoda. Higher diversity and density of meiofauna was found at the shellfish protected area compared to the shellfish non-protected areas. The densities of Foramminifera, Copepoda and Bivalvia were much higher in the shellfish protected area. Our results imply that establishment of shellfish protected areas may enhance diversity and abundance of some meiofauna groups on the sandy beach ecosystems.

Keywords: Protected area, meiofauna, foramminifera, copepoda, Andaman Sea

ID: 6021

Effects of changing ice cover on Artic meiofaunal assemblages

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In polar seas ice cover effects light and nutrient availability which subsequently affects the organic matter available to sediment fauna, whilst providing extra organic matter through the presence of algae under the ice. The Arctic Ocean is experiencing rates of warming amongst the highest globally, and in Northern Latitudes this is exhibited through retraction and thinning of the ice shelf. The resultant changes to organic matter, carbon and nutrient availability affect the communities in the sediment below and the ecosystems they sustain by utilisation and storage of these resources. NERC has funded the Changing Arctic Ocean Seafloor project (ChAOS) to investigate the influence of the ice shelf on the Arctic Ocean's biological communities, processes and ecosystems. Sediment samples were taken from stations along an N-S transect, encompassing the edge of the summer ice shelf and also that of the winter ice shelf in the Barents Sea. This is an area affected by drastic changes to the ice shelf, experiencing pronounced retreat of the summer sea ice, but still covered by ice in the winter. Benthic meiofauna samples are being analysed to characterise the community structure under different ice cover scenarios and preliminary data will be presented.

Keywords: Ice shelf effects, benthic meiofauna, ice cover scenarios

ID: 6026

Abundance of foraminifera on coral communities in Mu Ko Chumphon, the Gulf of Thailand

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Foraminifera is an important group of meiofauna and can be found in all marine habitats. Scientific data on the ecology of particular foraminifera species lead to the determination of foraminifera as an important bioindicator for understanding about oceanographic status and biogeochemical processes. Previous studies have focused on relationships among species or communities and the environmental factors of the seawater and marine sediments. However, studies on foraminifera from coral reefs are very limited, particularly in the South-east Asian countries. This study examined the abundance of foraminifera on coral communities in Mu Ko Chumphon, the Western Gulf of Thailand in 2017. The samples were collected at 3-5 cm below the sediment-water interface by SCUBA divers at sixteen study sites, then stained and sieved through 63µm mesh net in a laboratory. The total densities of foraminifera were significantly different among the study sites. The low densities of foraminifera were found at Ko Mattra, Ko Kula, Ko Lawa, Ko Rang Kachiu, and Ko I Raet while the highest one was recorded at Ko Maphrao. The influences of river discharge, organic matter and turbidity may contribute to foraminiferal communities on coral reefs in Mu Ko Chumphon. This research is the initial study on foraminifera which was carried out on the coral communities in the Gulf of Thailand and provides important baseline data of marine biodiversity in this region.

Keywords: Coral community, foraminifera, meiofauna, abundance, environment

ID: 6092

Is there a relationship between diversity and density in nematode community after a beach nourishment process?

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Meiofauna communities are known for playing an important role regarding energy use in aquatic systems. Within the meiofauna, Nematoda is the most abundant and diverse group, sometimes representing 90% of the fauna. For spending their whole life cycle in an intimate relationship with the sediment, they are important bioindicators of anthropic impacts and environmental quality. This study aimed at evaluating the influence of a beach nourishment process on nematodes communities of Piedade Beach, Jaboatão dos Guararapes, Pernambuco-Brazil. We determined points along the benthonic limits: superior, medium, and inferior mid-intertidal zone, and low intertidal zone. In each point, four samples were collected using a *corer* with an area of $10cm^2$ before the nourishment, and in a sequence of one, seven, 15, 30, 60, and 90 days after. 36 genera were found, belonging to 13 families. A decrease in the whole nematode community occurred after the process. Before the nourishment, Nematoda dominated 80% of the meiofauna but, just one day after the process, represented only 20%. Before the process, non-selective deposit feeders represented 75% of the community, decreasing to 16%, while epistratum feeders became the most expressive group throughout the sampling days. Regarding nematode families, Xyalidae was the most abundant, while Thoracostomopsidae and Microlaimide had little expression. Among the 36 genera found, *Stylotheristus*, *Ceramonema*, *Chromadorida, Neochromadora, Coninckia,* and *Paracyatholaimus* standout for being found merely before nourishment. By diagnosing the nematode community, we can correlate the nourishment process to the reduction of nematode populations, as well as to the change in community diversity, thus enabling the occurrence of groups previously never reported. Monitoring the results of this process is crucial for understanding coastal engineering constructions effects on marine biodiversity, as well as in the benthic dynamics of the littoral environment.

Keywords: Nematoda, erosion, ecological succession, sandy beach

ID: 6452

Effects of acidification on the functional structure of free-living marine nematodes from coral reefs: an experimental approach

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The present study assessed the potential effects of decreasing seawater pH, which could be driven by global climate change, on functional indicators of a nematode community from tropical coral reefs. Four Artificial Substrate Units (ASUs) were randomly selected to characterize the trophic nematode structure before the beginning of the experiment. ASUs were randomly allocated to four treatments (control, 0.3, 0.6 and 0.9 units of pH), two ASUs were placed in each of the 16 tanks. The control was maintained with local ambient seawater without manipulation (pH= 8.1) No food was provided during the course of the experiment. ASUs were maintained in the tanks for 3 days before exposure for acclimatization. From each tank, one ASU was collected at 15 and 30 days post-placement. Nematode functional structure from the pH treatments showed a clear pattern of separation between the two sampling moments (15 and 30 days) in the MDS analysis. There was no clear pattern of differentiation for functional structure among pH levels for samples collected at 15 days. However, for samples collected after 30 days, two groups were evidenced one for control samples and another for all pH treatments. PERMANOVA results confirmed the MDS pattern showing significant differences in the trophic nematode structure between samples collected after 15 and 30 days and for the interaction term (time and pH), but no difference were found for the decreasing pH. On the other hand, there was no difference for trophic diversity and maturity indexes between control and pH treatments. Our result indicate that the trophic structure responded to experimental decreasing pH and it might be an useful tool to evaluate pH changes on coral reefs.

Keywords: Meiofauna, functional ecology, trophic diversity, maturity index

4.

Methodologic advances in meiofaunal studies: New tools and analytical and experimental approaches

ID: 5896

Do nematodes tell the truth? On the robustness of the NemaSPEAR[%]-index in the quality assessment of fine sediments

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Commonly used methods to assess the ecological status regarding the benthic invertebrate fauna (*e.g.* according to the EU Water Framework Directive) are solely based on the monitoring of macrofauna organisms. These methods are potentially limited for the quality assessment of fine sediments as in those habitats usually the number of macrofauna organisms are by far outweighed by the number of meiofauna organisms. As fine, cohesive sediments considerably contribute to important ecosystem services of aquatic systems and are often hotspots of chemical contamination, the NemaSPEAR[%]-index was developed as a monitoring tool for the assessment of those sediments by using freshwater nematodes, one of the most abundant and species richest meiofauna group in benthic habitats. In the present study, the informative value of the NemaSPEAR[%]-index in relation to macrofauna-based indices was assessed. We synchronously monitored the macrofauna and the nematode communities at six locations at different streams. Chemical analysis of the sediments revealed that the chemical pollution status of those six locations ranged from unpolluted to highly polluted. Moreover, we performed a synchronous monitoring of macrofauna and nematodes over the course of one year at a reference stream with very low chemical loading. Those two settings allowed us to meet statements on how robust the NemaSPEAR[%]-index is along a chemical pollution gradient as well as against seasonal variations and how it relates to macrofauna-based indices. Additionally, a molecular analysis of the nematode community of every location was implemented to validate if the NemaSPEAR[%] can also be assessed by innovative methods (*e.g.* barcoding or metabarcoding) and if similar results can be achieved.

Keywords: Macrofauna, meiofauna, bioindicator, metabarcoding

ID: 5932

Meiofauna Outreach: 3D printed models

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A common problem in working with meiofauna is describing what they look like to individuals of all ages. Some people cannot see clearly through a microscope. To help with outreach, five three-dimensional (3D) models have been created. Files that enable 3D printing of an ostracod, kinorhynch, harpacticoid copepod, nematode, and polycheate are available for printing on the sculpeto website (https://www.sculpteo.com/). These printouts have been used with prepared microscope slides to help teach people about meiofauna.

Keywords: Meiofauna, outreach, 3D printing, 3D model

ID: 5937

Variations in 3-D cytoplasmic structures of foraminifera (protistan meiofauna): microfocus X-ray CT and TEM observations

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Benthic foraminifera, meiofaunal size protists, inhabit a broad environmental range of the seafloor, and are particularly common in hypoxic sediments. Because hypoxic environments are expected to increase in a future, the biology and ecology of benthic foraminifera are key to understand benthic ecosystems and biogeochemical cycles. Here we investigated the cytoplasm and ultrastructural features of 8 bathyal foraminiferal species using combined techniques of microfocus X-ray computed tomography (CT) and the osmium-based cytoplasm-staining methods. Osmium binds to organic membranes, proteins, and nucleic acids, rendering them visible by X-rays due to their high X-ray attenuation and enabling their reconstruction as 3-D images. The obtained 3-D model further allows us a volumetric calculation of cytoplasm and vacuoles. The micro-X-ray CT revealed the different distribution patterns of cytoplasm and vacuoles between chambers suggesting that the roles and/or contents of vacuoles are different between shallow and deep-infaunal species. Large vacuole-like structures are observed below the aperture of *Globobulimina affinis*, and the large vacuole were surrounded by peroxisome-mitochondria clusters based on the subsequent TEM observations. These clusters were not observed in older chambers of the cytoplasm near small vacuole, suggesting the large vacuoles connecting to aperture have special roles in their adaptation to oxygen-depleted sediments. On one hand, another deep-infauna, *Chilostomella ovoidea*, showed completely different cytoplasm morphology from *Globobulimina* or shallow

infauna, indicating there are some different adaptive mechanisms to oxygen-depleted environments among benthic foraminifera.

Keywords: Foraminifera, microfocus X-ray CT, cytoplasm, 3-D, hypoxic condition

ID: 5963

Ultrastructure and possible role of the epidermal gland system of *Tetranchyroderma suecicum* Boaden, 1960 (Gastrotricha: Macrodasyida)

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Marine Gastrotricha are microscopic, interstitial protostomes that exhibit several adaptations to their interstitial habitat. Among those are differentiations of the epidermis like cushioning cells, a strengthened and often sculptured cuticle, or adhesive glands that facilitate a sticking to the sediment grains. The epidermis of most species of the Macrodasyida furthermore contains conspicuous glandular structures, the epidermal glands. As yet, there is no coherent hypothesis on the functional role of this organ system and there is only a single transmission electron microscopic (TEM) investigation of epidermal glands of *Turbanella cornuta* plus scattered data of few further species. We investigated the epidermal glands of the species *Tetranchyroderma suecicum* by means of serial sectioning and TEM as well as scanning electron microscopy (SEM). Aligned images were three-dimensionally analysed and reconstructed. *T. suecicum* has up to 50 pairwise arranged epidermal glands. Each gland consists of a single huge merocrine glandulocyte with a basal nucleus and an apical appendage carrying the chimney-like cell pore. The cell comprises an anastomosing cistern with granular content and has a rather electron-dense cytoplasm. The density probably results from molecules with carbon chains and C=C double bonds that are synthesized by the glandulocyte. Inside the cistern, these molecules are possibly transformed to the final secretion that is released through the apical cell pore. Each gland is associated with a ciliary sensory cell. Different roles of the epidermal glands are possible. Since no traces of mucus-like substances were observed on the specimens investigated by SEM, we suppose a water-soluble nature of the secretion. Hence, it could either represent a pheromone for intraspecific communication or an allomone that is, for instance, used as a repellent against predators such as flatworms. These hypotheses shall be tested subsequently with experimental setups.

Keywords: Gastrotricha, epidermal glands, ultrastructure, chemical communication

ID: 5983

Microbiome profiling of small marine invertebrates

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Metazoans commonly harbor essential microbial communities – microbiomes – in their gut, on their skin, and often within some of their organs. The microbiome associated with many large and commercially important animals, from cattle to bees, have been thoroughly investigated and shown to have highly integrated metabolic networks that complement their hosts' and complex coevolutionary histories. However, the vast majority of metazoan diversity is understudied, and we know next to nothing about the microbiomes of most non-model organisms. One large black box is represented by relatively small marine invertebrates (meiofauna and larger organisms <2-3 mm), which play critical roles in ecosystems across the globe. There is considerable evidence that small invertebrates commonly harbor bacteria, archaea, protists or combinations thereof, but no extensive survey across major lineages has ever been performed. We are attempting to fill this gap in knowledge by investigating the microbiomes of small marine invertebrates in the coastal waters of British Columbia (Canada) and the Caribbean (Curaçao). We have collected more than 1000 specimens belonging to 21 phyla, recorded their main morphological features with photos and videos, and extracted their DNA; we are currently profiling their associated prokaryotic and eukaryotic microbiomes using the hypervariable V3-V4 region of the SSU rRNA gene. We are concurrently characterizing background microbial communities from the same habitats (sediment, water column, and macroalgae) in order to identify the taxa that are specifically associated with the animals. Our data will allow us to describe the microbiome of specimens covering the entire spectrum of the metazoan tree and address fundamental questions: do these small metazoans harbor microbiomes as complex as those of large animals? Does microbiome composition correlate with host phylogeny? If so, at what level? What level of microbiome variability exists within each species?

Keywords: Meiofauna, microbial communities, ecology, morphology, taxonomy

ID: 6029

Structural and functional response of meio- and microbenthic fauna under different organic matter settling scenarios - case study from the Baltic Sea

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The Baltic Sea is one of the world's largest brackish water system, supporting over 85 million people. Today, it is particularly affected by climate change and modifications in hydrographic conditions are likely to affect phytoplanktonic communities, inducing a decline in diatom-dominated spring bloom and a prolonged cyanobacterial summer bloom. In aphotic sediments of the Baltic Sea, benthic organisms rely primarily on organic matter (OM) sedimentation as a food source. The extent to which changes in phytoplankton communities will affect meio- and microbenthic communities and the processes that they mediate remain largely unknown. We conducted a mesocosm experiment using sediment cores from the Stockholm archipelago, where we simulated 5 scenarios of OM input from phytoplankton, ranging from 100% diatoms to 100% cyanobacteria. The experiment lasted for 4 weeks, after which we assessed the community composition of active microeukaryotes and bacteria using DNA metabarcoding on 18S and 16S rRNA genes. Effects on microbial activity were measured *via* qPCR on genes involved in Nitrogen-cycling. Our results show a significant difference in community composition of microeukaryotes after 4 weeks. Such changes likely reflect differences in how microeukaryotic taxa utilize the 2 types of microalgae as a food source, affecting their fitness and survival. These structural effects of OM inputs to the benthos were accompanied by functional changes. We notably observed that denitrification gene expression positively correlated with increasing proportions of cyanobacteria input to the sediment. Results concerning the bacterial community structure are currently being processed and will give us a more holistic view on the impact of OM input on taxonomic and functional groups. Altogether, these results suggest that future changes in settling OM will have important implications on both the composition and function of microbenthic communities in the Baltic Sea.

Keywords: Benthic-Pelagic coupling, Microeukaryotes, Baltic Sea, DNA metabarcoding, Denitrification

ID: 6037

Climate change pressures on sandy beach nematodes: preliminary results from an ex-situ experiment

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According to the Intergovernmental Panel of Climatic Changes, the increasing surface sea temperature is one of the climate changes and the increase of submersion time of intertidal zones can be a direct consequence of the sea level rising, which occurs due to the movement of the waterline towards the continent. We aim to assess the response of intertidal sandy beach nematodes to the increase of temperature and submersion time by means of an ex-situ experiment. In this approach, the midlittoral nematode assemblage was submitted to a high temperature (30°C) and a longer submersion period (7h) and compared to a control situation (normal temperature-26°C and submersion period-4h). The experimental design consisted of 20 experimental units placed in 4 different mesocosms: (1) normal temperature and normal submersion-NTNS, (2) normal temperature and increased submersion-NTIS, (3) increased temperature and normal submersion-ITNS, (4) increased temperature and increased submersion-ITIS, which were acclimated for 7 days. After this period, tides were simulated twice a day in two different conditions: 8h of emersion vs 4h of submersion and 5h of emersion vs 7h of submersion for normal submersion and increased submersion mesocosmos, respectively. Three replicates of each mesocosmo were removed in the begging of the experiment (day 0) and after 15, 30 and 45 days post-placement. Differences in the nematode density between treatments and time were tested by a two-way ANOVA. Our results indicated a highest significant difference (666±69.55 ind./10cm²) for ITNS treatment at day 0 and a lowest density (7.67±7.17 ind./10cm²) for NITS treatment at day 45. These results suggest that the submersion is more harmful to sandy beach nematodes rather than the temperature increase, and it may be caused by the depleting O_2 supply under increasing submersion periods since the experiment was performed in the absence of waves, a common hydrodynamic condition always present on sandy beaches.

Keywords: Climate changes, ex-situ experiment, nematodes temperature, submersion

ID: 6300

COPAS VISION flow cytometer analyzes and captures brightfield images of meiofauna and dispenses selected subsets

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We have developed a flow cytometer that can capture brightfield images of meiofauna in flow. Adding imaging capability to a flow cytometer greatly enhances the phenotyping of samples by providing morphological and spatial information of the sample constituents, information that is not collected by conventional flow cytometers. Researchers can survey the population of meiofauna in a sample and determine the numbers of each type of organism. Traditional measurements of size, optical density, and fluorescence, as well as Profiler data, are also collected, and these measurements are used for making sorting/dispensing decisions. The collected images and flow cytometry measurements are synchronized so that objects dispensed to wells of multiwell plates can be traced back to their corresponding image. Our COPASTM VISION technology platform is designed for large particles making it ideally suitable for sample types like meiofauna. We have tested samples collected on the Atlantic shores and show representative data. Our data from the COPAS VISION shows proof-of-principle support for increased level of phenotyping of these types of samples.

Keywords: Meiofauna, imaging flow cytometer dispenser

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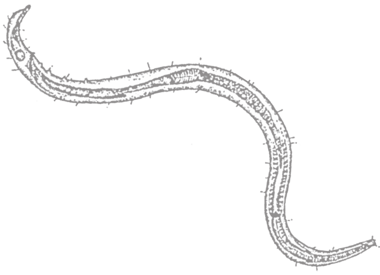

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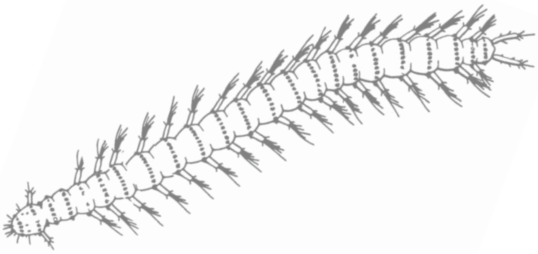

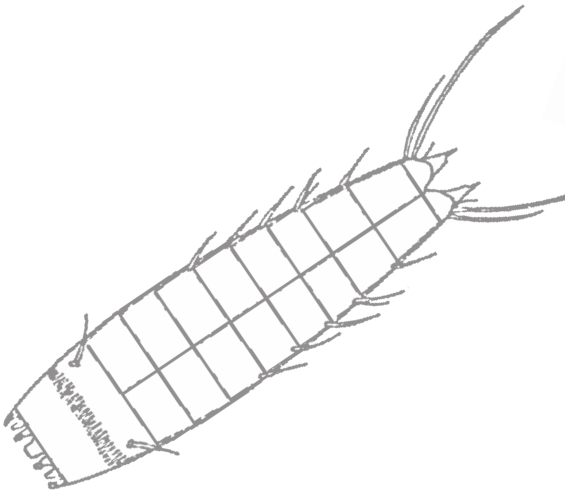

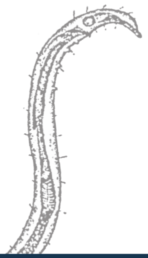

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