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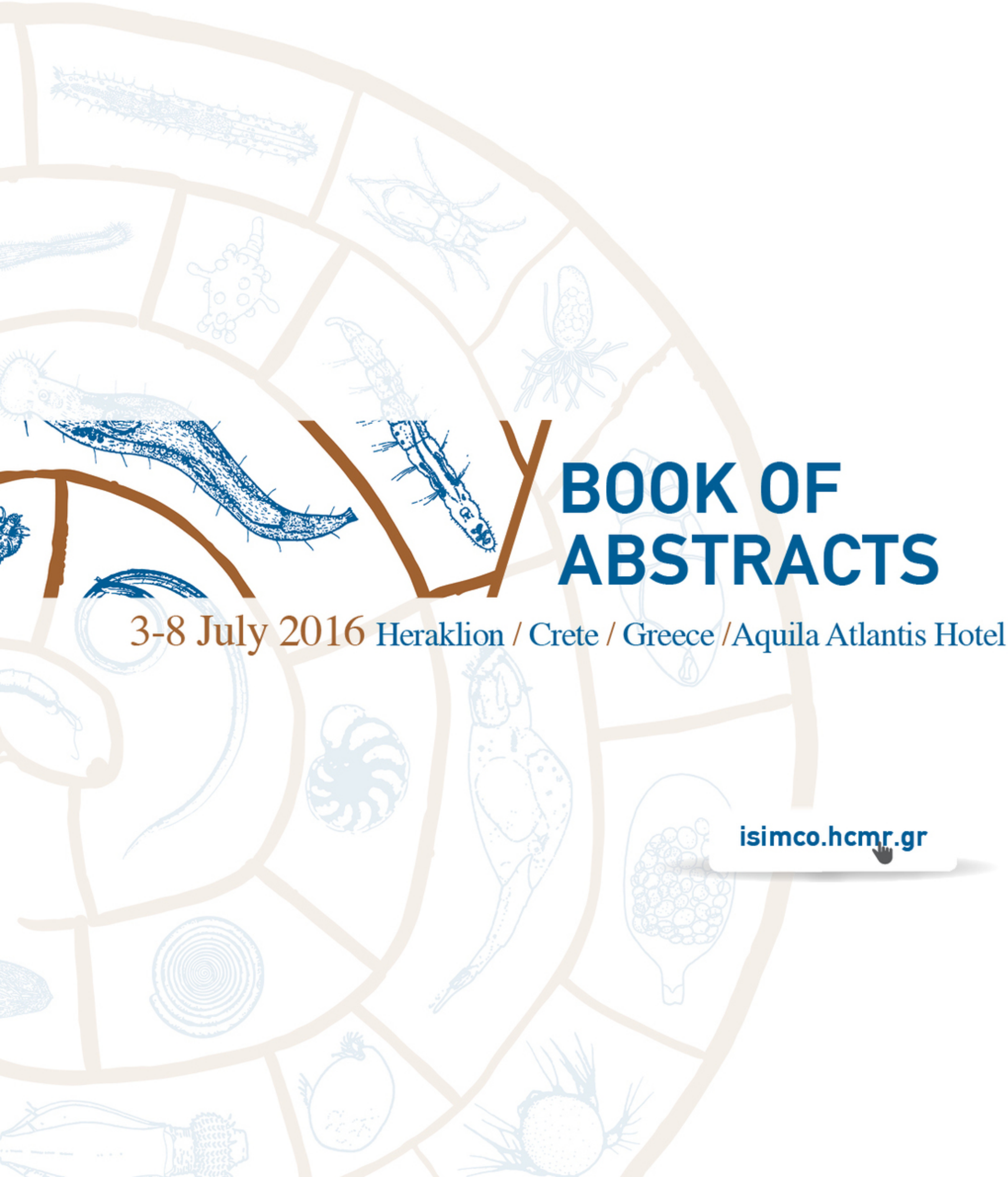
16th International Meiofauna Conference



BOOK OF ABSTRACTS

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Preface

The 16th edition of the International Meiofauna Conference, codenamed IςIMCo, is hosted in 2016 by HCMR, the Hellenic Centre for Marine Research and the Institute of Oceanography in Heraklion, Crete, Greece.

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) and Seoul, South Korea (2013).

As has been always the case, IςIMCo will once again provide an opportunity for scientists and students from all over the world to present and discuss the latest developments in our tiny but fascinating meiofauna world within the context of a dramatic global change and the world-wide ever-increasing pressures and uses of aquatic ecosystems and resources.

This year, 69 oral and 94 poster presentations are included in the program, which are distributed over 24 countries and 133 corresponding authors. They cover a wide range of different research fields, such as the response of meiobenthos to environmental changes, climate change and acidification, biodiversity and ecosystem function, morphology, phylogeny and biogeography, amongst many other ‘hot’ topics. They reflect the growing interest and trend in using meiofauna to address larger questions and problems. All in all, IςIMCo is a great opportunity to make our small invisible alien creatures, visible to the outer world.

Nikolaos Lampadariou
Chair of IςIMCo

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Part I

Keynote presentations

Invited lectures

Evolving paradigms: the history of meiofaunal research

K01

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The history of meiofaunal research has been documented in considerable detail by Olav Giere in his book "Meiobenthology" (particularly the second edition which has a more substantial coverage of freshwater meiofauna). Most of the participants at this conference will own this book or at least have access to it and, rather than attempting to summarise it, my presentation will present a quite personal viewpoint that I hope will be provocative and provide some food for thought. Over the years, meiofaunal research activity has been punctuated by technological inventions that have sharpened our understanding; from the mid-1600s with Antonie van Leeuwenhoek's peculiar microscopes to PCR machines developed in the late 1900s. Early research was motivated by the wonder of discovering this new world of microscopic animals, involving faunistics, taxonomy, and describing the particular biological characteristics associated with their small body size (particularly their conservative reproductive adaptations and highly selective feeding behaviour). Subsequently attention turned to descriptive ecology of an academic nature; where do they live, how many are there, how are they influenced by abiotic factors? Increasing awareness of environmental issues then motivated more functional approaches; studies of trophic interactions, production and energy flow, life history, role in benthic ecosystems and impacts of pollution, often involving controlled experiments and manipulations. Most recently, concerns for conservation have demanded the ability to predict the effects of global climate change on species and molecular biodiversity and the broader consequences of such changes, which present meiofaunal researchers with perhaps their greatest challenge. Processes operating over both ecological and evolutionary timescales may be involved, and whilst we can conduct experiments simulating the effects of short term ecological events such as pollution or disturbance, climate changes involving increasing temperature, sea-level rise and ocean acidity are occurring over the much longer term. Since meiofaunal animals have generation times in the order of months, natural selection may compensate for any possible deleterious effects over these evolutionary timescales which, together with the possibility of species replacements, may render the results of short term manipulative experiments meaningless in this context. It is acknowledged that studies of the ecology of freshwater meiofauna have taken longer to emerge as an independent discipline than those of its marine counterpart, and the early literature on this freshwater fauna used terms relating to habitat rather than size. Perhaps this is partly because the term meiofauna originated early in the marine literature that lacked the cognizance of the freshwater community. However, it is undoubtedly also due to the fact that in the sea, despite recent claims to the contrary, animals in the meiofaunal and macrofaunal size ranges comprise recognisably separate ecological and evolutionary units with bimodal size spectra, whereas the freshwater size spectrum is more continuous and the division between the two categories is more arbitrary. The relatively recent scientific and social history of meiofaunal research has been charted in our newsletter Psammonalia, started in 1966 as a 2-page Bulletin "to maintain communication among American psammologists", subsequently becoming the Newsletter of the Association of Meiobenthologists in 1968, with this Association becoming International in 1974. In its heyday from the early 1970s to late 1990s four issues of Psammonalia were published annually, each year averaging around 50 pages and 400 literature citations. Since that period there has been a gradual decline in all these measures. Does this indicate a decline in meiofaunal research activity? Probably not, because internet searches reveal a linear increase in meiofaunal publications from 1970 until now. What we seem to be losing is, to quote the last sentence in Olav's book, "our easy-going way of exchanging news and ideas". We are faced with a stark choice; either we view meiofauna as something special, remain as an effective Association and bring Psammonalia back to its former glory by actively contributing news and ideas, or we accept the views of some that we are becoming too isolationist, integrate with more general ecological research, and abandon the Association altogether.

K02

Meiofauna matters: the roles of meiofauna in benthic ecosystems

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Sedimentary habitats cover most of the ocean bottom and therefore constitute the largest single ecosystem on earth in spatial coverage. The benthic ecosystem contributes to human well-being by providing essential services such as food production and nutrient cycling. Although meiofauna are well-recognised as an abundant and ubiquitous component of benthic communities, empirical evidence of their wider role in marine ecosystems is scattered across the literature. Some ecologists and decision-makers thus remain sceptical about what meiofauna can tell us about the provision of ecosystem services. We investigated empirical evidence on the roles of meiofauna in benthic ecosystems using a conceptual model that links the supply of an ecosystem service, the ecosystem processes that contribute to that service (e.g. production, consumption and decomposition of organic matter, nutrient regeneration, energy transfer to higher trophic levels etc.) and the meiofaunal activities (e.g. movement, feeding etc.) that regulate those processes. Meiofauna activities modify a series of physical, chemical and biological sediment properties. They do so often simultaneously by, for example, displacing sediment grains during burrow construction and, at the same time, displacing organic matter and microorganisms within the sediment matrix during feeding. We show that these modifications affect various ecosystem services including sediment stability, biochemical cycling, waste removal and food web dynamics directly and indirectly, positively and negatively, and at various spatial and temporal scales. Meiofauna can mediate ecosystem processes in sediments with little or no macrofauna, thereby increasing the resilience of those benthic ecosystem processes that are essential for the continued delivery of ecosystem services desired by society. This is of growing importance since benthic ecosystems are under increasing anthropogenic pressure. Whilst studies over the past five decades have emphasised the important roles meiofauana play in benthic ecosystems, future studies will need to determine how consistent and widespread these roles are.

The contribution of meiofauna to evolutionary ecology

K03

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Recent technological advances have dramatically enhanced our understanding of the morphology, phylogeny and ecology of meiofauna species. Scanning and transmitted electron microscopy, together with confocal laser scanning microscopy, increased the amount of external and internal morphological information. These advances in microscopy have allowed us to improve the descriptions of species, as well as to understand the morphological adaptations of meiofauna taxa along the evolutionary history. In ecology, the characterization of molecules, such as stable isotopes and fatty acids at the level of populations, have permitted us to infer the trophic position of meiofauna species and enhance our understanding of its functional role in the ecosystem. In parallel, advances in molecular DNA techniques have allowed us to quantify with much higher accuracy population structures, genetic variability within and between species and the phylogenetic position of target meiofauna species. Additionally, techniques on RNA have been used to describe the metabolic response of meiofauna species to environmental changes. Despite these significant methodological advances, techniques have been mainly used within its “knowledge” domains (i.e. taxonomy/systematics, ecology and phylogeny) and there is a need for more interdisciplinary studies. An important step towards interdisciplinarity is to be aware of the challenges and limitations inherent to biodiversity assessments and to each methodological approach, in particular. Interdisciplinary studies face the challenges of improving sampling protocols and preservation methods in order to establish direct relationships between the different datasets. Given the diversity and omnipresence of meiofauna taxa across the globe and environmental conditions, interdisciplinary studies on the group have to be hypothesis oriented and, therefore, based on a clear theoretical framework. In that respect, we introduce the conceptual framework of the evolutionary ecology theory. This framework recognizes that species interactions, environmental filtering, dispersion and drift are the main drivers promoting species coexistence and at the same time speciation and extinction. It is clear that working at the interface between phylogeny, ecology and morphology imposes several challenges and will require creative approaches, but well designed studies making the use of these new methodologies will certainly be at the cutting edge of biological sciences.

K04

Experimental elucidation of meiofaunal trophic interactions: from radioactive tracer techniques to next generation sequencing

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Nematodes are by far the most numerous and often also the most species-rich metazoans in aquatic sediments. They affect various ecosystem functions through a variety of trophic and non-trophic interactions. However, our understanding of the importance of nematodes in benthic ecosystem processes remains limited because a) qualitative information on the mechanisms and diversity of trophic interactions involving meiofauna is still very incomplete, and b) most interactions and processes remain poorly quantified. In addition, assessments of the potential contribution of nematodes to carbon flows still heavily rely on a black-box approach, which assigns nematodes to a limited number of feeding guilds and assumes that the trophic interactions of all members of a particular guild are at least qualitatively similar. Here, we present a brief overview of several decades of research on the roles and trophic positions of nematodes in benthic food webs, and of our continuing struggle with some fundamental qualitative and nearly all quantitative questions. We point at large discrepancies between studies highlighting a significant contribution of nematodes to benthic carbon processing and studies showing exactly the opposite. This discrepancy has remained despite methodological advances. We argue that in order to substantially advance our understanding of nematode feeding ecology, we have to move away from the mere use of morphology-based feeding guilds and shift our focus to a) species-specific and b) context-dependent approaches, where possible encompassing inter-individual variability in resource use. We use natural stable isotope ratios to demonstrate that confamiliar species (belonging to the same feeding guild) can differ substantially in resource use and even trophic position in one and the same food web, and that the same genus in different food webs may exhibit differences in feeding ecology. We then use next generation sequencing (NGS) to analyse the microbiomes of individual nematodes and demonstrate that even cryptic nematode species, belonging to the same morphospecies complex, display species-specific resource use, and that individuals of the same species can vary substantially in their resource use. In addition to NGS, we point at novel stable-isotope approaches (NanoSIMS) which allow analysis of trophic interactions at the level of individual meiofaunal organisms.

Part II

Oral presentations

The response of meiobenthos to environmental changes

How do physical dynamics of the seabed at subtidal sandbanks combine to determine the number and type of available niches for meiofaunal nematodes?

O01

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Conservation objectives for subtidal sandbanks generally demand that, subject to natural processes, the extent and distribution of sandbank habitats, their faunal structure and function, their gross morphology and the supporting processes on which sandbank habitats rely, are maintained or recovered. In order to be able to measure the success or otherwise of such management goals, detailed investigations of the links between the sedimentary habitat and the biota are essential. We combined sediment and faunal data to explore the role of the sedimentary regime in shaping the distribution of subtidal sandbank environments and the associated meiofaunal nematode communities in the southern North Sea. A variety of sediment transport processes occur in the area, differing in the frequency and magnitude of sediment mobility, and the continuum between erosion, translation and sediment accumulation. Based on sedimentary bedforms and grain size analysis, sedimentary facies were delineated which were analysed for their relationships with the meiofauna. The sedimentary facies fell clearly into groups of facies, respectively representing high, moderate and episodic sediment mobility. For those sedimentary facies where daily movement of sediments and bedforms occurred, the resulting spatially homogeneous environments were dominated by a functionally impoverished nematode community comprising small deposit feeders and large predators. Resistance to sediment movement and the ability to exploit alternative food sources were prominent functional features of the successful colonisers. Those facies characterised by relatively infrequent sediment mobility comprised a heterogeneous suite of benthic habitats, containing taxonomically and functionally diverse assemblages of nematodes of various sizes, feeding types and reproductive potential. Faunal distribution patterns here indicated trade-offs between the resistance to sediment movement, environmental tolerance and competitive abilities. Our focus on diverse assemblages of organisms with high turnover times, inhabiting highly dynamic sedimentary environments, has revealed new animal-sediment relationships of relevance to pure and applied science.

O02

Varying patterns on varying scales: a metacommunity analysis of nematodes in European lakes

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Ecological community patterns are often extremely complex and the factors with the greatest influence on community structure have yet to be identified. In this study we used the elements of metacommunity structure (EMS) framework to characterize the metacommunities of freshwater nematodes in 16 lakes located in northern Germany and southern Sweden. Lakes varied in their trophic state. The analysis was applied at four geographical scales (radius ranging from 80 m to 360 km). The site characteristics associated with site scores indicative of the structuring gradient were identified using Spearman rank correlations. The metacommunities of the 174 nematode species included in this analysis mostly had a coherent pattern. The degree of turnover increased with increasing scale. Ordination scores correlated with geographical variables on the larger scales and with the trophic state index on a regional scale. The association of the structuring gradient with spatial variables and the scale-dependent increase in turnover showed that nematode dispersal was limited. The different metacommunity patterns identified at the increasing geographical scales suggested different, scale-related mechanisms of species distribution, with species sorting dominating on smaller and mass effects on larger geographical scales. This study shows that meiobenthic organisms provide great benefit for metacommunity analysis due to their high abundance and diversity on small and large scales of analysis.

O03

Habitat preference analysis of fresh water copepods from the tropical forest of the Yucatan Peninsula, Mexico

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Free living copepods are customarily treated as aquatic in general limnological literature. In comparison with the multitude of studies on aquatic systems, the number of studies on copepods in semi-terrestrial habitats (STH) and phytotelms is limited (especially in North and Central America) and their presence in such environments is generally conceived as a coincidence. The present study was carried in two natural protected areas of the Yucatan Peninsula and was aimed to understand the diversity (morphological and genetic) of copepods and its habitat preferences. Herein we included samples from different habitats (open water bodies, leaf litter, moist soil and bromeliads) and biotopes. Nineteen species of Cyclopoida, two of Calanoida and five of Harpacticoida were found. Open water bodies' diversity included all members of Cyclopoida and Calanoida recorded in the study and two species of Harpacticoida. Around 30% of the bromeliads sampled were colonized by copepods: *Phyllognathopus vigueri, Epactophanes richardi, Remaneicaris* sp. 1 and one member of the family Ameiridae were recorded. The two former species were found in

three different species of bromeliads (*Aechmea bracteata, Tillandsia dasyliriifolia, T. fasciculate)*, *Remaneicaris* sp. 1 was only found in soil bromeliads of the species *T. dasyliriifolia* and the Ameiridae was reported only in bromeliads associated with mangroves (*Tillandsia* sp. 1). Less than 9% of the samples of moist soil and leaf litter contained copepods; only cyclopoid copepodites and *Remaneicaris* sp. 1 were recorded in such environments. From the 26 species listed in this study only *Remaneicaris* sp. 1 was found in all habitats studied showing a high habitat specificity of the taxas studied. Variables such as the high and the distance of the bromeliad and the STH to the water body were included in order to test if there is a pattern of colonization among habitats. Results showed that both tested variables do not have influence on the diversity of the habitats studied. In the case of the bromeliads, such environments represent small islands with their particular diversity of copepods and other invertebrates which should be included in the strategies for the conservation of the tropical forest.

Meiofaunal community composition along Western Antarctica examined by high-throughput approaches

O04

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Meiofauna community composition around Antarctica has not been readily examined mainly due to the remote location. Previous research examining the distribution of meiofaunal taxa within this geographic region has focused on the Antarctic Peninsula or the Ross Sea areas. Assessment and understanding of the distribution and variation of these key ecosystem functioning players is imperial, especially as the climate begins to alter the environment within this region. Sediment cores were sampled along a 5500 km portion of Western Antarctica from the Ross Sea to the tip of the Antarctic Peninsula during two research expeditions in 2013. The top 0−2 cm fraction was isolated from the cores, sieved, and environmental DNA was extracted from the resulting sieved sample. Using high-throughput Illumina amplicon sequencing approaches, meiofauna community composition was determined by targeting the eukaryotic specific hypervariable V9 region of the small subunit ribosomal RNA gene. Taxonomic presence and abundance along with diversity metrics (alpha and beta) were calculated for the regions examined. High proportions of annelid and nematode taxa were present throughout the dataset. Difference in community composition was observed between locations along the Antarctic Peninsula and the remaining Western Antarctic region surveyed. Examination of correlations of community composition with sediment characteristics is currently being conducted. Metabarcoding approaches allow for a more holistic examination of meiofaunal communities in a faster time frame than traditional methods. Because traditional methods rely on considerable microscopy time and taxonomic expertise, researchers general focus on a few select taxonomic groups (e.g., nematodes, copepods, annelids) during their study, limiting the ability to extrapolate trends in the

community as a whole. Metabarcoding approaches are limited by the quality and extent of properly identified taxa in available databases. However, they have been proven useful for rapid assessment of these communities and therefore could serve as a highly beneficial tool in ecological monitoring and impact assessment research.

O05

What drives marine nematode species distribution across various spatial scales in Antarctic continental shelf sediments? Insights from community and population genetic analyses

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Understanding the processes that explain organisms' distribution patterns across the globe is a major goal in community ecology, but at the same time forms the subject of much debate. Traditionally, many studies have focused on local species-environment interactions as drivers of community composition. But what if this direct effect of environment on local communities is overrated and we merely detect a correlation between an environmental and faunal matrix because they share the same underlying spatial structure? In other words, how important are more regional large-scale processes in explaining distribution of species? And how connected are populations over larger spatial scales? Especially in the marine environment, which presents few barriers for free dispersal of organisms, such questions remain difficult to answer. This study therefore assessed community composition and genetic differentiation of free-living endobenthic nematodes at shelf depths in the Antarctic Weddell Sea, at various spatial scales. Through a combination of i) the application of some general concepts in community ecology and ii) assessment of gene flow within and between species and populations of two genera, we investigated to what extent spatial scale and environment are able to explain differences in community composition and distribution of species. Results show that in spite of the endobenthic lifestyle and associated dispersal limitation in free-living nematodes, large-scale links (> 2000 km) are present for some species, while others exhibit strong spatial patterns and population genetic structure, even at smaller geographic distances. Furthermore, in addition to a strong horizontal divergence between communities at the eastern and western side of the Weddell Sea, there was a clear vertical segregation of species between surface and deeper sediment layers. Our findings suggest that surface communities are more prone to passive transportation by means of bottom currents and hydrodynamics, responding to local environmental cues and resulting in larger contribution of species-environment relationships. Alternatively, communities buried deeper in the sediment are more restricted in their dispersal and are thus mainly structured by large-scale spatial processes.

Using the randomForest modeling approach to predict meiofauna in Icelandic waters

O06

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Sediment samples were collected with the multicorer in Icelandic waters onboard the RV Meteor (M85-3) from August–September 2011 within the IceAGE1 (Icelandic marine Animals: Genetics and Ecology) project. We investigated the meiofauna community of 21 stations taken in the Iceland Basin, Irminger Basin, Denmark Strait and the Norwegian Sea at water depths between 300–3000 m. This research aims at identifying environmental variables structuring the meiofauna community, dispersal and abundance. A total of 632,346 individuals from 18 taxa were sorted using a dissecting microscope. Density ranged from 3185–187 individuals per 10 cm^2. Nematodes were most dominant followed by copepods in all four regions studied (77–97% and 1–7%, respectively). Differences in meiofauna densities were observed between the Norwegian Sea and the Irminger Basin. The *envfit* function in R identified water depth, sediment granulometry, temperature and food availability as the main factors structuring the meiofauna community. To predict meiofauna on a larger spatial scale randomForest regression models were applied to the eight main meiofauna taxa using 23 predictor variables, 2,000 random trees (ntree = 2,000) and eight random variables (mtry = 8). Species distribution modeling was applied to evaluate the distribution of selected harpacticoid copepod species in Icelandic waters. Highest meiofauna abundances were predicted in the Norwegian Sea, where sediments are dominated by silt, and in the shallow regions. Tardigrada were predicted in high abundances in regions with coarser sediments of the Iceland Basin and the shallower Irminger Basin. Our study showed that the differences in the meiofauna community structure could be well explained by environmental variables. The main controlling factor might be sediment grain size. It gives the interstitial space for the inhabiting fauna and this variable may be a proxy for current activity, sedimentology, chemical and physical conditions.

Deep-sea meiobenthos temporal fluctuations in the NW Mediterranean (DYFAMED–BENTHOS 1993–1995) and impact of a major flood of the Var River

O07

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Between 1993 and 1995, a temporal survey of the metazoan meiofauna was conducted in the deep basin of the Var Canyon (DYFAMED–BENTHOS station; 43° 24.62′ N – 7° 51.68′ E) in the NW Mediterranean. Surface sediment was taken at 2347 m depth with a multicorer at an average frequency of 1.3 months. Total organism abundance in the top 10 cm of the 170 sediment samples collected over the

3-year period ranged from 133 to 770 ind. 10 cm^{-2} (mean 380 ind. 10 cm^{-2}). The community comprised on the average ~89% nematodes, 4.7% copepods, 4.3% nauplii, 1.1% annelids and 0.5% least common taxa. Temporal statistical analyses of the time series including estimates of sampling effect, showed that temporal fluctuations were significant for most of the meiobenthic taxa/groups (Guidi Guilvard and Dallot, 2014, DSR I 92: 127-140 ; DOI:10.1016/j.dsr.2014.07.003). The temporal fluctuations appeared to be mainly driven by the recurring sea-surface derived food pulses. In November 1994 however, a major flash flood of the Var River (situated 52 km upstream from the sampling station) generated a turbidity flow intense enough to deposit a 0.5-cm-thick layer of fine foreign sediment at 2347 m depth. This occasional physical disturbance induced strong short- and long-term reactions in the different taxa/groups and largely influenced the general food-induced interannual abundance patterns. In order to clarify the impact of the deposition event on the fauna, an additional set of sediment cores larger than the ones used in the study cited above (i.e. 75-cm^2 cross sectional areas *vs.* 6-cm^2), and that had been sliced into 6 layers down to 5 cm, were analysed. Examination of the vertical profiles showed that the sediment deposition changed the composition of the community and caused profound modifications in the nematode assemblage as suggested by the occurrence of transitory sub-surface peaks in abundance and median body length. While nematode numbers dramatically decreased during the following year, the copepods (with nauplii) that remained concentrated in the surface layers were the only taxon/group to recover and even increase their reproductive effort (nauplii) four months after the disturbance.

O08

Meiofaunal communities in the Levantine Basin (Eastern Mediterranean): the effect of depth and distance-to-coast on distribution patterns

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The Mediterranean Sea is an unusually oligotrophic marine system with the eastern Levantine basin representing its extreme. Being in a land-locked sea, Mediterranean deep-sea ecosystems are not only dependent on pelagic production but are also influenced by inputs from the surrounded lands. LEVAR expedition (Levantine Basin Biodiversity Variability) carried out on board R/V METEOR during December 2006 – February 2007 aimed at exploring biodiversity patterns and the underlying factors and processes in the Levantine basin. One of its main goals was to investigate the relationships of benthic fauna with environmental variables, in particular with depth and distance to coast. For that purpose, meiobenthic samples were collected from two areas southeast of the island of Crete: Area 1 (Ierapetra Basin) is located close to the island and is deeper than 4000 m, whereas Area 2 (Pliny Plain) is more distant but shallower (2700 m). Several multiple-corer deployments at three stations within each area and the vertical sectioning of the sediment samples allowed the detailed study of horizontal and vertical meiofaunal distribution. Data analyses indicated differences between the two studied areas and among sediment horizons when richness and community structure at major taxa level were used, but these patterns do not stand for overall metazoan meiofaunal abundance. Nevertheless, nematode and copepod standing stocks follow diversity community patterns that could even indicate differences among stations of the same area. The results of this study suggest that meiofaunal richness and community structure are rather related to depth than distance to coast, exhibiting the well-known decreasing bathymetric trend even in an enclosed, event driven system.

Deep-sea harpacticoid copepods: habitat heterogeneity at the 10-km scale on the continental rise off California

O09

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At the time when the sediment-covered, deep-sea floor was discovered to be inhabited by vast numbers of species, it was thought to be environmentally homogenous. To resolve this apparent paradox, deep-sea ecologists have been searching for ecologically important environmental heterogeneities. We studied harpacticoid copepods from two sites at ~3150 m depth on the continental rise. One was in the mouth of a submarine canyon, and one was on an escarpment. The sites differed significantly in multivariate faunal similarity. At the canyon site, absolute abundance, the ratio of subadult copepodites to adults, species density, the proportion of the harpacticoid species that emerged, and the proportion that lived in tubes were significantly less than at the escarpment site. These marked differences imply that ecologically important environmental heterogeneities exist at each site. We speculate as to the identity of these environmental differences.

A multifaceted approach to understanding spatial turnover and connectivity in the deep sea

O10

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Productivity at the surface waters, together with the flux of organic matter to the seafloor and disturbance effects are considered to structure benthic communities dwelling the deep seabed. Nevertheless, it is still unclear to what extent these processes control benthic local and regional biodiversity. In this study, by means of an integrative approach, we examined ten stations at the Western Iberian Margin located within two isobathic parallel transects. The shallower transect was situated at the shelf break (∼300 m) and deeper transect at the mid-slope (∼1000 m). We tested whether food resources and hydrodynamic effects at the seafloor similarly alter nematode resource utilization at different depths. Moreover, we examined the role of connectivity as a result of potential nematode dispersal between different depth zones. By applying integrative taxonomy using molecular and morphological approaches in combination with environmental factors, this study intended to explain spatial turnover and connectivity in relation to depth in the deep sea. Results revealed that high variability in resource availability is directly linked to high alpha diversity and spatial heterogeneity. Moreover, communities dwelling in deeper regions showed to be able to use resources complementarily and promote species coexistence. Our study also demonstrated that higher hydrodynamics at the shallower habitats near the shelf break, as inferred from the high sediment heterogeneity, promoted higher beta diversity compared to the mid-slope. Lastly, phylogenetic relationships revealed no evidence for depth-endemic lineages or isolation per habitat, indicating regular interchanges across different depths.

O11

Metazoan meiofaunal distributions and environmental parameters in the bathyal sediments affected by the 2011 off the Pacific coast of Tohoku earthquake and tsunami

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We investigated the abundances and vertical distributions of metazoan meiofauna in sediments after the disturbances caused by the 2011 off the Pacific coast of Tohoku earthquake and tsunami. We collected surface sediment cores from eight bathyal stations off Tohoku in March 2012, November 2013, and November 2015, and examined meiofaunal abundances, sedimentological and geochemical parameters. Copepods always showed peak densities in the sediment surface layer. Nematodes densities, on the contrary, were lower in the surface event-deposit layers compared to those in deeper sediments at most of the investigated stations. Nematodes at these area originally showed peak densities at the surface sediments in general before the earthquake, suggesting the subsurface peak in our study were rather unusual distributions. Based on multivariate analysis, the subsurface peak of nematodes were mainly explained by NH_4^+ concentrations, while copepods density were explained by both NH_4^+ and O_2 concentrations. The subsurface peaks of nematodes were continuously observed in the samples collected in November 2013, suggesting that episodic sedimentation events on scales of several centimetres have a large effect on meiofauna inhabiting sediments.

Starving in the trenches: is there a link between terrestrial productivity and communities of food-limited hadal habitats? O12

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Large vascular plant debris provides a plentiful, though localised and unpredictable, food source for a wide range of specialist and opportunistic deep-sea fauna. Fine terrestrial organic matter could also make a significant contribution to carbon budgets of deep seabed communities, particularly in offshore areas where aeolian input of organic matter to the oceans is comparable to the flux of marine-derived organic matter to the sediments. However, no studies have yet been conducted to test the latter hypothesis. In the present study, we describe the meiofaunal communities of the Kermadec and Tonga trenches in the Southwest Pacific (6000–10800 m depth), and investigate potential environmental drivers of abundance, biomass, diversity and community structure. Our results indicate that a variety of food sources, ranging from fresh microalgal detritus to pollen, are available in trench sediments. Pollen of pine (*Pinusradiata*) was particularly abundant and likely originated from forestry plantations in northeastern New Zealand, several thousands of kilometres away from the trenches. Pine pollen appears to be utilised by at least some components of the meiofauna (e.g., gromiids) and pollen concentrations in the sediments was positively correlated with meiofaunal abundance. These results suggest that there could be a significant contribution from long-range aeolian transport of terrestrial organic matter to food-limited hadal (and abyssal) communities. It is also consistent with recent findings showing the presence of wood-digesting enzymes in trench amphipods. Further research is required to quantify this terrestrial organic matter subsidy from large forests of wind-pollinated trees to the deep sea.

O13

Population dynamics and species interactions of marine nematodes under climate change

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Although changes in average environmental conditions can have serious consequences, the main impacts of global climate change on populations and communities may well result from changes in short-term climate variability. Those may affect different levels of ecological organization: from the individual to the ecosystem, including changes in reproductive success, population dynamics, species interactions and community structure. The present study focuses on the effects of diurnal temperature fluctuations on the fitness of free-living marine nematodes. We focus on different levels of organization (individual/populations) and complexity (single species/interactions) and test whether: i) short-term temperature fluctuations affect individual performance by investigating their feeding behavior, and ii) medium-term climate change-induced temperature fluctuations affect population dynamics of marine nematodes and their species interactions. Microcosm experiments were performed on two congeneric species, namely *Diplolaimelloides meyli* and *D. oschei*, which co-occur in their natural habitat with asymmetric competitive interactions under constant temperature conditions. The two species were incubated in mono-cultures and in two-species combination under constant and diurnally fluctuating temperature of increased amplitude, and measurements related to individual response to food, reproduction and population growth were performed. Results showed that effects of temperature variations on individual behaviour and on population fitness are species-specific. Inter-specific competition negatively affected both species' fitness regardless of temperature conditions, though the effect was more pronounced under fluctuating temperature. We conclude that changes in amplitude of diurnal temperature fluctuations may be very important determinants of the effects of temperature change on species interactions, potentially affecting also assemblage structure and ecosystem functioning.

O14

Shallow-water surf-zone meiofaunal community responses to ocean warming and acidification

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The changes in the environment caused by an increase in atmospheric CO_2 could potentially change the structure of benthic marine communities, of which meiofauna are an important component. The objective of this research was to determine the impact of future levels of temperature and acidification on the meiofaunal communities found in the shallow waters of surf-zone ecosystems off exposed beaches in

north-central Chile (29 °S). Sediment with meiofauna was exposed in microcosms to four treatments; (1) 15 °C and 500 μatm $p\mathrm{CO}_2$, (2) 15 °C and 1000 μatm $p\mathrm{CO}_2$, (3) 19 °C and 500 μatm $p\mathrm{CO}_2$, and (4) 19 °C and 1000 μatm $p\mathrm{CO}_2$. The higher temperatures and $p\mathrm{CO}_2$ values were chosen to reflect future conditions of warming and acidification. The microcosms were exposed to the treatment conditions for a period of 90 days. With respect to meiofaunal abundance, dominated by nematodes, a 2-way ANOVA indicated that there were significant effects of temperature alone (p. 0.005) and the interaction of temperature and pH (p. 0.006), but not of pH alone (p. 0.079). Post hoc Tukey's tests indicated that at 15 °C the effect of pH was significant (p. 0.012) with lower abundances under conditions of reduced pH. However, at 19 °C there was no significant effect of reduced pH. At present day pH levels there was no significant difference in meiofaunal abundances between temperatures. By contrast, at reduced pH levels meiofaunal abundances were significantly higher at 19 m°C (p. 0.002). Thus, the conclusion of this preliminary analysis is that meiofaunal abundances increase with increases in temperature. In addition, the effects of future reductions in the pH of the oceans on meiofaunal abundances will be less severe, if not positive, with higher temperatures.

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Will the warming influence the size in Arctic meiofauna? Patterns in biomass and production size spectra along the latitudinal gradients (60–80° N)

O15

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Body size is a fundamental biological unit that is closely coupled to key ecological properties and processes. Decline in organisms' body-size has recently been predicted to be "the third universal response to global warming" (alongside changes in phenology and distribution of species) in both aquatic and terrestrial systems. Biomass size spectra (BSS) is an important descriptor of community functioning, especially in terms of productivity and energy flow. The climate induced changes in water temperature and productivity can result in the modification of size structure in benthic communities and thus influence the functioning of the Arctic marine ecosystems. In the present study we want to test the hypothesis that elevated temperatures will induce size reduction in meiofaunal communities in the Arctic. Here we present the biomass and production size spectra of meiofaunal communities based on materials collected in six fjords located along a gradient of changing thermal regimes along the latitudinal gradient: temperate (Raunefjorden (60° N), Ulsfjorden (69° N), Norway), temperate/isolated with exceptionally low water temperatures (Balsfjorden (69° N), northern Norway), 'warm' Atlantic water influenced Arctic (Hornsund (58° N), Kongsfjorden (79° N), west Spitsbergen) and a 'cold' High Arctic site (Rijpfjorden (80° N), north Spitsbergen). In each sample, all metazoan organisms were photographed and measured under stereomicroscope connected to camera. From the Nematodes only a subsample of 200 individuals was taken and measured using semi-automated image analysis method. Each individual was classified into $\log_2$ size classes based on its dry weight [μg]. Biomass and production size spectra were constructed by plotting the total biomass/production in each size class against the $\log_2$-transformed size of a class. Spatial variability of size structure and functioning of meiofaunal communities was related to gradients in temperature and other environmental factors (including food quantity and quality descriptors). As water temperatures are foreseen to change in the course of climate warming, the results of this study can be used to discuss the possible climate change effects on meiofaunal communities structure and function in Arctic coastal waters.

O16

Meiofauna at the natural CO_2 vents off Panarea Island, Mediterranean Sea: a proxy for ocean acidification and CO_2 leakage from subseabed storage sites

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The unprecedented rate of CO_2 increase in the atmosphere forms a threat to our oceans. The direct uptake of CO_2 changes oceans carbonate chemistry and pH, a process termed ocean acidification (OA). On the short term, the best option to mitigate atmospheric CO_2 increase is capture and storage (CCS) in deep geological formations in the seabed. Predicting long-term storage security is of course difficult and therefore different CO_2 leakage scenarios require evaluation. Volcanic submarine CO_2 vents form natural analogues that allow studying the effects of long-term exposure to acidified seawater in a holistic approach. Off Panarea Island, we identified a vent area where gas emission ($> 90\%$ CO_2) occurs in a moderate flow controlled by tides. In the water column this seepage results in an average difference in pH minima of 0.385 between the vent and the reference site. The conditions in the water column are therefore a good proxy for future OA and allowed to study the potential adaptive capacities to high CO_2 conditions of *Posidonia oceanica* seagrass and its sessile and motile epibiont communities. In the sedimentary environment we studied the response of meiofauna to acidified pore water conditions (pH minimum: 5.5) as a proxy for CO_2 leakage. Our results indicate that in the light of future OA, changes in *P. oceanica* meadows will mainly occur on the level of the sessile epibiont community composition, while *P. oceanica* seagrass productivity, net epibiont calcification, meiofauna community composition, abundance and function, and biodiversity remain stable. On the other hand, long-term CO_2 leakage, and more specific its effect on granulometry, reduced meiofaunal density, biomass and biodiversity and changed the meiofauna community structure. Nematode functional diversity shifted towards communities dominated by smaller, faster reproducing species and an altered, simplified food web at the vent sites. The loss of species at the vent area also increased the temporal variability in nematode community characteristics and therefore reduces the resilience to other forms of disturbance.

The role of meiobenthos on ecosystem function

The structure and organisation of marine benthic communities in relation to body size

O17

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Few studies consider meiofauna and macrofauna at the same time, even though both form parts of wider ecological networks, and fewer consider interactions between sample size, body size and spatial clustering. It has been suggested that the elements of the structure of the physical environment have fractal properties. If habitat complexity largely determines species diversity this leads to the prediction (for a single perfect fractal) that all organisms, regardless of size, will perceive the environment as equally complex and should have equivalent diversity and, as we move up the size spectrum, species composition should change in a regular and gradual fashion. This study examines the degree to which infaunal assemblage structure varies with mesh size, sample size and sample dispersion within two different areas of apparently homogeneous sediment, a muddy sand and a coarse intertidal sand, in the Isles of Scilly, UK. In each area samples were extracted using a standard range of 5 mesh sizes (63, 125, 250, 500, 1000 μm), with the sample areas and distances between samples scaled to the mesh size. All metazoans were identified to species level. Diversity and species composition did not show a gradual and even degree of change over the size range at either site. Instead, they showed a dramatic stepwise change between the 250 μm and 500 μm mesh size samples, being relatively constant in the < 500 μm and > 500 μm categories, with diversity higher in the former. Higher proportions of species in the < 500 μm categories showed evidence of spatial clustering than in the > 500 μm categories. This suggests a fractal structure within but not between the < 500 μm and > 500 μm body size categories, which is not apparently driven by changes in sediment structure. The biology of marine metazoan benthos does not scale continuously across the full range of taxa and body size as has been recently suggested, but may do so for individual taxa and restricted size ranges.

O18

An observation on the relationship between meiofauna biodiversity and ecosystem functioning at different spatial scales

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Earth is experiencing a pervasive and uncontrolled loss of species, which has raised concerns about the deterioration of ecosystem functions and services. Studying the diversity−ecosystem function relationship (BEF) in the deep sea is of primary importance in the face of biodiversity loss and for our understanding of how the deep sea functions. Up to now, contrasting results (i.e. exponential, negative or null) concerning the relationships between nematodes biodiversity and ecosystem functioning and efficiency have been reported from different deep-sea environments, and considering large spatial scales (e.g. Oceans; Basins) of investigations. It has been hypothesized that the spatial scales at which ecosystem function and diversity are measured are likely to influence the BEF relationship observed, and that their nature is related to the system analysed and the organisms involved. Here, we investigate the relationship between nematodes structural (i.e., H′; $\log_e$; $ES_{(51)}$; J′) and functional (i.e., MI; TD; body shape) diversity and independent measures of ecosystem functioning (bacterial biomass; nematode predators biomass) and efficiency (meiofaunal biomass to biopolymeric carbon ratio; meiofaunal biomass to bacterial biomass ratio) on two open slope systems in the western Mediterranean sea. BEF relationships were investigated considering a local- (100s meters; i.e., each slope system kept separate during the statistical analysis) and a meso- (100s kilometres; i.e., both slope systems taken together) spatial scale of investigation. At a local spatial scale there was no relationship between species/functional diversity and ecosystem function and efficiency after accounting for the effects of environmental variables. At a meso- spatial scale species and functional diversity were significantly and negatively correlated with ecosystem functioning and covariates explained almost half of the variation. These results would suggest a relation of competition between the organisms or even a functional redundancy rather than functional complementary, that usually governs positive BEF relations. Future studies from other regions/systems need to be taken into account, and based on different taxa to provide further insights into the diversity−ecosystem function.

O19

Meiofaunal colonization processes on organic and inorganic substrata at the Lucky Strike vent field on the Mid-Atlantic Ridge

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Despite the fragmented nature of hydrothermal vent fields, nascent vent sites are rapidly colonized by a pool of regional species. While succession of large hydrothermal fauna is relatively well established, we lack information on the associated meiofauna, in particular, on nematodes and copepods. The aim of the present study is to investigate the colonization process of organic and inorganic substrata by meiofaunal assemblages deployed at the Eiffel Tower hydrothermal edifice on the Lucky Strike vent field (MAR), at varying distances from visible hydrothermal activity. Abundance, biomass and diversity of colonizing meiofaunal organisms were compared with the results from a previous two-year pilot experiment (Cuvelier et al. 2014). In total, 46 copepod species were found in our substratum experiment, representing a four-fold increase in copepod diversity in the LS vent field. Overall, the substrata harboured a very heterogeneous community including not only vent-specific species but also uncommon copepod taxa that have not been described from vent sites. The community composition on the substrata changed gradually from active to inactive microhabitats along the gradient of temperature and fluid input, with an increasing heterogeneity and the appearance of rare and exclusive species with decreasing fluid input. While showing the lowest densities, slates exhibited the highest copepod diversity across the activity gradient. High densities of juveniles and larval forms confirmed that copepod communities can be well established in a variety of microhabitats and are capable of spending their whole life cycle under extreme conditions. For the nematodes, inorganic substrata were preferred near the vents, while organic substrata were rapidly colonized in areas not influenced by vent activity. Nematode females were dominant at almost all sites while numerous females at the ovigerous stage and juveniles were reported near the vent emissions, suggesting that nematode populations were reproducing well after nine months. Our data further suggest that inorganic substrata were preferred in the early succession stages, while organic ones required a longer term in order to be densely colonized. The type of substratum significantly influenced the composition of colonizing nematodes after nine months, while after two years the structure of nematode communities was influenced rather by hydrothermal activity.

Benthic foraminifera encrusting dropstones in the Porcupine Abyssal Plain, NE Atlantic: notes on their diversity and faunal cover

O20

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Benthic foraminifera are a major component of modern deep-sea soft-bottom communities. However, many foraminiferal species live attached, either permanently or temporarily, to hard substrates such as ice-rafted dropstones, which are a common feature of the seafloor at higher latitudes globally. Here, we examined encrusting organisms on 127 dropstones taken from the top of a small abyssal hill (~550 m high) located within the Porcupine Abyssal Plain–Sustained Observatory area (PAP-SO, 4850 m water depth, ∼49°N, 16° 30′W). Dropstones in this area were probably deposited during the last glacial maximum and are found mainly on the hills. A total of 97 attached morphotypes (presumed to be morphospecies) were recognised. About a quarter (21) were metazoans, mostly sponges and bryozoans, while the majority (76) were foraminifera or foraminifera-like protists. Between 0 and 15 morphotypes were present on individual stones. Faunal cover varied greatly from stone to stone, ranging from total absence of attached organisms to 100% coverage. The foraminifera were dominated by a variety of mat- and chain-like formations, isolated domes, anastomosing trails, reticulated networks and simpler branched or unbranched tubular structures, interpreted as monothalamous foraminifera (monothalamids). Most had agglutinated tests but a few were predominately organic. Some could be assigned to the Komokiacea or the genera *Rhizammina* and *Telammina*, while others (e.g. many of the mats and chains) were difficult to place into existing taxa. Polythalamous foraminifera were also fairly common and included calcareous species (mostly *Cibicides* spp.), as well as agglutinated forms such as *Ammodiscus*, *Glomospira* and various trochamminaceans. Comparisons against the sediment-dwelling foraminiferan fauna from the same sites indicated that, with the exception of some polythalamous species, the morphotypes were restricted to the dropstones. Thus dropstones can act as island microhabitats in the deep sea, supporting unique species not present in soft-bottom habitats and thereby enhancing foraminiferan diversity at small (within-hill; centimetres to meters) to intermediate (plain vs hills; meters to kilometres) scales. There is a general similarity between dropstone assemblages and foraminifera encrusting polymetallic nodules in the abyssal Pacific, which also host many mat-like, domed and tubular forms and komokiaceans. However, except for the cosmopolitan genus *Telammina*, there was little overlap at the level of morphotypes.

O21

Light history effect in a benthic foraminifer, *Haynesina germanica*, kleptoplast photoprotection mechanisms and PSII quantum efficiency

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Some benthic foraminifera have the ability to incorporate functional chloroplasts from diatoms (kleptoplasty). Kleptoplastic species are present in Bourgneuf Bay, a large mudflat situated south of the Loire estuary (France) and their spatial and vertical distributions are not yet understood. Our objective was to investigate kleptoplast functionality and photoprotection mechanism in a benthic foraminifera (*Haynesina germanica*) exposed to different light regimes using spectral reflectance, epifluorescence observations, oxygen evolution, pulse amplitude modulated (PAM) fluorometry and pigment analysis to understand the effect of light history in kleptoplast functionality. *H. germanica* was capable of using its kleptoplasts for more than one week and *H. germanica* showed net oxygen production with a compensation point at 24 μmol photon m^{-2} s^{-1} and a production up to 1000 pmol O$_2$ cell^{-1} day^{-1} at 300

μmol photon m^{-2} s^{-1}. *Haynesina germanica* Fv/Fm slowly decreased from 0.65 to 0.55 in 7 days when kept in darkness; however, it quickly decreased to 0.2 under high light (70 μmol photon m^{-2} s^{-1}). Kleptoplast functional time was thus estimated between 11 and 21 days in darkness and between 7 and 8 days at high light. A functional xanthophyll cycle was also observed on fresh specimen of *H. germanica* exposed to different short term light regimes. Diatom pigments were identified using HPLC-UV-DAD: chlorophyll *a* and c, fucoxanthin, diadinoxanthin, diathoxanthin and β-caroten. The ratio Xanthophylls/Chlorophyll *a* was calculated in all light conditions, it strongly increased after 30 min under low (25 μmol photon m^{-2} s^{-1}, 1.81±0.07) and high light regimes (300 μmol photon m^{-2} s^{-1}, 1.93±0.08), whereas the ratio stayed low in the darkness (0.52±0.05) and almost came back to its initial value (0.54±0.03) after a very low light period (30 min at 5 μmol photon m^{-2} s^{-1}, 0.90±0.09). These results emphasize that studies about foraminifera kleptoplasty must take into account previous light history. Additionally, this study showed that kleptoplasts are unlikely to be completely functional over a long time, thus requiring continuous chloroplast resupply from foraminifera food source. Their spatial and vertical distributions might thus be linked to their microalgal preys and to access to light.

Biotic interactions of meiofaunal metacommunities in isolated spring fens (Central Europe): an insight from large scale

O22

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Springs are believed to have the most stable conditions among all freshwater habitats due to a stabilizing effect of groundwater. Their ecological communities are thus suggested to be at equilibrium and largely structured by biotic interactions. In our previous research of the Western Carpathian spring fens we have found very abundant and diverse meiofaunal and macrofaunal assemblages. We have already revealed the main environmental gradients driving the spring fen communities and also identified a part of variation caused by the dispersal limitations of species among these isolated habitats. However, the effect of biotic interactions has not been examined yet. Because of the absence of fish, the main “top-down” control in springs is maintained by macroinvertebrates, especially amphipods, which not only have the direct predatory effect but might be also mechanically disturbing the meiofaunal assemblages. Other predators include leeches, beetles, and many insect larvae (e.g., stoneflies and some dipterans). Evidence of competition between meiofaunal species, which may lead to a local exclusion of the species with lower competitive abilities, has been reported from marine and freshwater environment and is likely to influence the meiofaunal assemblages in the spring fens as well. In this study, we aim to test the effect of selected macrofaunal predators on harpacticoids and ostracods in the spring fens and consider the role of interspecific competition in meiofauna. The target question here is if these processes can be also traced on large scale, despite the fact that they perform on the scale of microhabitats.

O23

Meiofauna, a competitive co-habitant or an essential macrofauna sidekick in the French Guiana intertidal mudflats

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The great abundance of meiofauna in benthic habitats has attracted many attempts to disclose their ecological functions, which are not only as food for some small predators (e.g. shrimp, crab larvae, fish juveniles), but also as consumers of primary production. However, their contribution to the trophic network is usually underestimated due to technical difficulties associated with the small size of meiofauna. This study was conducted on the Guiana mudbank, which is considered the most morphodynamic muddy area in the world. It was highlighted as an important feeding zone for many shore birds and coastal fish along Amazonian coast. Nevertheless, there were very few studies on the associated benthic meiofauna assemblages in this region. Our aims are therefore i) to gain insight into the structure and function of the meiofaunal community, which can play a key role in the intertidal mudflat ecosystem, and ii) to investigate the meiofauna and macrofauna interactions. Both abiotic and biotic parameters along a gradient of mud consolidation during wet and dry season were taken into account. The main factors influencing meiofaunal structure were determined with the aid of multivariable analysis, whilst dual stable isotope analysis (C^{13}, N^{15}) were used to evaluate the trophic positions of main meiofauna and macrofauna taxa. With this study, for the first time, the role of meiofauna in a soft bottom food web and its relationship with the upper trophic compartment – macrofauna in the intertidal muddy habitat – have been revealed. In addition, the results of our work are crucial in the context of missing knowledge about the function of benthic ecosystem in highly dynamic Guiana mudflats, which will be subsequently valuable for top predator (bird and fish) conservation aspects.

O24

Meiofauna at the bottom and top of a stream food web

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Running-waters are dynamic ecosystems fuelled both by autochthonous primary production and by the microbial decomposition of land-borne organic matter. In temperate regions, the relative importance of these trophic pathways changes at the pace of the seasons, with massive inputs of plant litter accumulating in streams when the first cold weather arrives in autumn. Meiofauna are a ubiquitous component of stream benthos and are thought to play an important role in the stream food web as trophic intermediaries between microbes and macrofauna. We collected the benthic invertebrates dwelling the sediment, and the biofilms coating macrophytes

and plant litter in a headwater stream in spring and autumn. We measured the carbon and nitrogen stable isotopic signatures of basal resources and invertebrates. Land-borne fine particulate organic matter (FPOM) found in the interstices of sediment and embedded in litter packs was an important resource for the whole food web, even in spring. Although macrophytes harbored the most abundant and diverse assemblages, no invertebrate was found to use macrophytes directly. Instead, they use the FPOM and algae coating their foliage. Meiofauna occupied all ‘trophic levels’ of the stream food web: Chironomid larvae and harpacticoid copepods used litter, deposit-feeding nematodes used FPOM, whereas mites and large nematodes were preying upon a wide range of meio- and macrobenthic invertebrates. Parasitic mermithid nematodes even stood as the “top predators” in this food web, parasitizing large predatory trichopters like *Rhyacophila* spp. Overall, meiofauna showed a narrow range in their carbon signatures, suggesting they had greater affinities with the FPOM trophic pathway than macrofauna which were able to derive energy from a wider range of resources. Our results stress that meiofauna play a central role for the inclusion of FPOM in stream energy flows. Also, it seems that the trophic role of meiofauna might be more complex than initially thought, with the presence of typical permanent or temporary meiofaunal taxa at several ‘trophic levels’ of the stream food web.

Who feeds on whom? First insights into the food web in mosses

O25

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Moss can be found both in aquatic and terrestrial environments and grows on all kinds of substrates like soil, stones or wood. It serves as structurally complex habitat and also as food source for a wide range of meiofaunal organisms such as nematodes, tardigrades, rotifers and crustaceans, all of which are very important organisms in the food web. This extreme habitat makes high demands on the meiofaunal community because biotic and abiotic factors are permanently changing. Limnic meiofauna has been generally understudied, and in semi-aquatic habitats, like moss, largely overlooked. Moss is a potential food resource for meiofauna, containing fine particular organic matter and algae, the question arises if the animals inhabiting moss are feeding on the moss itself or if they use other food sources. The organisms contributing to the high meiofauna abundance and diversity in moss represent a wide range of feeding strategies that allows exploitation of the diverse microbial resources found in this environment. Especially free-living nematodes are a diverse and abundant taxon among the meiofauna. Here we present the distribution of meiofauna organisms in mosses including data of the feeding types of nematodes and first insights into the food web relationships between the organisms (e.g. stable isotope analysis, predator–prey interaction).

O26 Meiofaunal community compositions and their food sources around hydrothermal vents in three seamounts in NW Pacific – copepods like 'hot' food, but nematodes do not?

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In contrast to specific large benthic invertebrates in chemosynthetic ecosystems around deep-sea hydrothermal vents, meiofaunal communities in such habitats have only recently been included in studies of those environments. This is especially true in the Northwest Pacific Ocean, even though there are many seamounts with active vents in their calderas. We studied the variations in meiofaunal composition and their nutrition sources around hydrothermal vents on chimney-like structures (chimneys) and in the adjacent non-vent fields in the calderas of three neighboring seamounts (Bayonnaise Knoll, Myojin Knoll, and Myojin-sho Caldera), in Izu-Ogasawara Arc, NW Pacific. A typical meiofaunal composition (nematodes as the most abundant taxon; harpacticoid copepods as the second) was observed in the sediments on sea-floor in the non-vent (control) fields, and even in the sediment at the base of chimneys. On the surfaces of chimneys, *Stygiopontius* (Dirivultidae, Siphonostomatoida), a typical vent copepod group, was predominant. Genetic analyses on *Stygiopontius* collected from Bayonnaise Knoll and Myojin-sho Caldera showed they are sharing the same or almost identical mitochondrial COI sequences, suggesting they belong to the same species, even though they are separated from each other at 30 km scale. Stable carbon and nitrogen stable isotopic ratios and radiocarbon abundances of meiofauna revealed the dirivultid copepods around hydrothermal vents utilized mainly chemolithoautotrophic microbes ('hot' food). The other copepods (mainly harpacticoids) at the same habitats rely on them to a certain degree. Nematodes, however, showed no preference to chemolithoautotrophic products even on the chimneys.

O27 Nematodes stimulate the growth of a mixed diatom biofilm

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In intertidal sediments, nematodes are usually the most abundant and diverse metazoans, reaching densities up to several million ind/m^2. Despite their abundance, there still is considerable debate as to whether and how they affect the production, activity and community structure of microphytobenthos (MPB) and bacteria, for instance through grazing impacts, bioturbation and excretion of nutrient rich compounds. The aim of this study was to examine the influence of nematodes on the growth of a mixed-species diatom biofilm in an intertidal system. During a 15-day experiment, a diatom assemblage composed of four different species (*Naviculaarenaria*, *N. phyllepta*, *Seminavis* sp. and *Amphora* sp.) and a natural mixed nematode community were incubated both separately and together. The experiment was carried out in a novel type of microcosm which allows simulation of a tidal regime while excluding immigration and emigration of the organisms at stake. Using PAM fluorometry, the increase in diatom biomass was assessed daily. At the end of the experiment, additional sediment samples were taken to compare the Chl a and EPS content and bacterial community structure between treatments. Results show that nematodes had a positive impact on the increase of microphytobenthic biomass. They also influenced diatom assemblage composition: *Seminavis* sp. growth was stimulated by nematodes, whereas the relative abundance of *Amphora* sp. decreased compared to the control. These results complement earlier though separate results which showed that nematodes either affected bacterial activity, abundance or assemblage structure. While the underlying mechanisms remain unclear, this demonstrates that nematodes are able to affect key players in tidal flat ecology and hence most likely also the ecosystem functions these key players have, such as primary production and sediment stabilization.

Metazoan meiofauna communities from nodule fields of polymetallic nodules (Clarion-Clipperton Zone, Pacific) and their dependence on abiotic parameters at local and regional scale

O28

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Manganese nodule deposits in the Clarion-Clipperton Fracture Zone (CCZ) of the eastern Pacific Ocean are of particular economical interest for the recovery of metals, such as Mn, Ni, Cu and Co. Future commercial mining of polymetallic nodules would cause a severe intrusion into the deep-sea environment and will have significant and long-lasting consequences through direct (seabed disturbance, nodule clearance) and indirect (operational and discharge plumes) impacts. Prior to mining-related exploitation, there is a need to obtain baseline data on the diversity, abundance and distribution of the resident fauna in order to assess and predict potential responses to changing environmental conditions. This region is characterized by heterogeneous environmental conditions (such as differences in surface-productivity, topography and sediment characteristics), and thus comprises a great variety of (micro-) habitats. Differences in standing stocks of the metazoan meiobenthos inhabiting the German and French license area of polymetallic nodules in the CCZ were analyzed both at local scale (between different working areas within the same license area) and at regional scale (between German and French license area separated by 1300 km). Environmental factors in terms of displacement volume of nodules, sediment characteristics and total organic carbon have been investigated. One of the main factors determining the total meiobenthic density at the local scale was the presence or absence of nodules in the sampling site, whereas size and abundance of nodules did not show a material effect on this parameter. Within the same license area, differences in community composition between working areas, regardless of nodule abundance were hardly discernible. It was shown as well, that at local scale, the presence of nodules affected positively meiobenthic diversity (at least in terms of the number of major taxa found), but in contrast influenced negatively total meiobenthic density. At a regional scale, meiofaunal density as well as composition of major groups from German and French license areas differed significantly, probably mostly due to the east-west gradient of surface bio-productivity.

O29

Recovery of biodiversity in copepods after anthropogenic disturbance in the Clarion-Clipperton Fracture Zone

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The polymetallic nodule fields in the northeastern central pacific (CCZ) are rich in commercially important metals, like nickel, copper and cobalt. This area is most likely to be mined in the future for industrial exploitation. Deep sea mining will have significant and long lasting impacts on the ecosystem in the deep sea and their fauna i.e. seabed disturbance, nodule clearance, operational and discharge plumes. Prior to mining related exploitation, we need to assess the possibility of recovery of the ecosystem after anthropogenic disturbance events in a wide time frame. In order to analyze the meiofaunal recovery potential, we compared the biodiversity of copepods in anthropogenic disturbed areas and untouched areas. The recovery which already took place was measured first in α-diversity and second in β-diversity. Sampling took place in eight different tracks on the seafloor varying in age from one day, eight months, three years, 20 years and 37 years, to see the different level of recovery after a certain timespan.

O30

Meiofauna in abyssal polymetallic nodule fields: seasonal variability and recovery following anthropogenic disturbance

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The growing demand for metals and recent developments in technology have stimulated the interest in mining polymetallic nodules in the deep sea. The largest, and hence commercially most attractive, nodule fields lie in the deep Pacific Ocean, between 4000 and 6000 m water depth. Baseline surveys are required to fully characterize the ecosystem, whereas disturbance tests are necessary to evaluate the impact on and recovery of the environment. Baseline biological and environmental studies were conducted in the Belgian concession area in the Clarion-Clipperton Fracture Zone (CCFZ). Seasonal variability (March vs. September 2015) in meiofauna communities was assessed and related to the environmental context. In addition, two man-made tracks, an 8-months old dredge track and a 1-day old epibenthic sledge track, were targeted. ROV push cores were taken inside and outside these tracks to determine recovery of the meiofauna (in terms of abundance, composition and diversity). Strikingly, meiofauna was observed in samples from the 1-day old track. For both tracks, meiofaunal densities and taxon richness were higher outside compared to inside the track. Nematodes, which dominated the meiofauna in all samples, were identified down to genus level. These meiofaunal data from the tracks were evaluated in light of the available environmental data.

Slow recovery of abyssal meiofauna 37 years after sediment disturbance (polymetallic nodule field CCZ, Northeastern Pacific)

O31

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Sediment samples were taken during cruise SO239 with the ROV dive No. 11 (station 157) by means of push cores (16 in total per dive with an inner diameter of 74 mm) in the 37-year-old mining track after the experimental dredging performed by the OMCO company in 1978. Samples were taken both inside and outside the track. The upper 5 cm were sliced per cm. The aim of these experiments was to investigate resilience and recovery of the micro- and meiofauna after mining disturbance, in relation to the environmental changes following the mining. This track had previously been studied by us in 2004 during the French cruise NODINAUT. The nematodes studied represented 78 genera from 28 families. The most abundant genus in 2015 both in the track and the reference area was *Thalassomonhystera* following *Acantholaimus* (Table 2). The main distinctions between the track and the reference area in nematode community structure was caused by the abundance of *Enchonema* (7.8% and 3.0%, respectively), *Microlaimus* (1.3% and 4.0%, respectively), *Halalaimus* (1.6% and 3.7%, respectively), and *Syringolaimus* (2.4% and 0.2%, respectively). The Principal Coordinates ordination plot shows that samples from the track and from the reference area are grouped separately indicating sufficient distinction between these two areas. The diversity indices for the nematode community inhabiting the track were lower than for the nematode community from the reference area. The rarefaction curve also indicates that nematode diversity (expressed as the expected number of genera found in a sample of certain number of randomly chosen nematode individuals) was lower in the track as compared with the reference site. In addition, there were no notable differences in nematode diversity in 2015 as compared with 2004 in both reference and impacted areas: nematode diversity in the track in 2015 was still as low as in 2004 (in comparison with the reference area). All this indicates a very slow recovery rate of benthic meiofauna communities after sediment alteration in the abyss. Implications for conservation and deep-sea mining will be discussed.

O32

Deep-sea habitats targeted for mining: state of knowledge of the nematode fauna and their potential as indicators of anthropogenic impacts

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The deep-sea realm comprises some of the least-known habitats on Earth, and holds large areas of concentrated material reserves such as polymetallic sulphides, manganese nodules, cobalt-rich ferromanganese crusts, methane hydrates and rare earth elements. Rare metals are used in electronics, and since terrestrial supplies are diminishing, deep-sea mineral resources are likely to be mined in the near future. Prior to the commencement of commercial mining, environmental studies must be conducted to evaluate potential impacts to the biological assemblages inhabiting these areas. Nematodes are potentially the best indicators of impacts in abyssal ecosystems, because of their important functional role, their predominance in terms of density, diversity and biomass as well as their sensitivity. This study reviews the state of knowledge of nematodes from deep-sea habitats targeted for mining, identifies the major knowledge gaps, and recent advances in the investigation of deep-sea nematodes with regard to anthropogenic exploitation impacts. Four deep-sea ecosystems are considered: seamounts (cobalt-rich ferromanganese crusts), hydrothermal vents (polymetallic sulphides), cold seeps (methane hydrates) and sediments associated to polymetallic nodules. Nematodes represent an important component of these ecosystems. Nematode biodiversity is particularly high in some areas such as the Clarion-Cliperton Fracture Zone, while in other ecosystems (e.g. hydrothermal vent) low diversity is associated with highly distinct nematode communities. However, species ranges in these ecosystems remain largely unknown. High specialization and slow biological processes in the deep-sea make rare species of nematodes sensitive to disturbances and much more vulnerable than their relatives in shallow sediments. However, some nematode species can be favoured by stresses induced by exploitation activity, suggesting the use of these species as indicator of impacts in the deep sea. The development of tools for biomonitoring of these exploited environments, represent thus both a scientific challenge and an important need for our society.

Recovery of the saltmarsh meiofauna community following the Deepwater Horizon oil spill

O33

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To quantify the response to and recovery from the 2010 *Deepwater Horizon* (BP) oil spill in the Gulf of Mexico, benthic microalgae and meiofauna were sampled in Louisiana, USA salt marshes. Reference, moderately and heavily oiled marshes were examined. Intertidal marsh plants, including *Spartina alterniflora*, suffered near 100% mortality in heavily oiled marshes. Benthic algae were analyzed using High Pressure Liquid Chromatography to quantify algal biomass and photosynthetic pigment composition. The abundance, diversity and composition of benthic microalgae and meiofauna were significantly reduced or altered in oiled (especially heavily oiled) marshes in the earliest samples taken, 11 mo after oiling. Microalgal biomass and meiofaunal abundances, however, increased thereafter at all oiled sites, and the composition of photosynthetic pigments and meiofaunal taxa at oiled sites increasing resembled reference sites over time. Microalgal biomass recovered after about two years, and the density of total meiofauna as well as meiofauna community composition in oiled sites became equivalent to reference sites in about 3 years. Most of the taxa found in high abundance (e.g., nematodes, copepods, and juvenile polychaetes with larval dispersal) recovered in about three years even in heavily oiled marshes. The rate and intensity of recovery by meiofauna was similar to the recovery of *S. alterniflora* which acts as a foundation species for the saltmarsh benthic community. However as of 2015, the meiofauna community had not yet fully recovered. Taxa including the tube-dwelling polychaete *Manayunkia aestuarina*, amphipods, tanaids and kinorhynchs were decimated by oiling, and were still much lower in abundance in oiled compared to reference sites after 5 years. These slowly recovering taxa are either tube dwellers (that without dispersing larvae are generally slow to colonize new habitats) and/or have specific requirements (e.g., organic matter composition) related to factors that affect sediment quality that were slow to recover after oiling. Progress toward recovery of these groups will continue to be monitored in future collections.

O34

Persistent impacts to the deep soft-bottom benthos four years after the Deepwater Horizon event

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In September–October 2010, three to four months after the Deepwater Horizon blowout was capped, a zone of moderate and severe impacts to deep-sea soft-bottom benthos was identified that extended over an area of 172 km^2. The impact was a loss of -53.7% of macrofauna family diversity and -38.3% of meiofauna major taxa diversity in the most severely impacted zone. The area was resampled in May–June 2011 and May–June 2014 to determine if the identified effects were persisting. The sampling design compared 19 stations in the impact zone to 13 stations in the reference zone that were sampled in all years. While there are some signs of recovery in 2011 and 2014 in terms of abundance, there is evidence of persistent, statistically significant impacts to both macrobenthic and meiobenthic diversity because the relative losses of biodiversity are largely the same as in 2010. A loss in diversity has been shown to correlate with a loss of deep-sea ecosystem services because these fauna serve vital functional roles in the deep-sea (including: biomass production, sediment bioturbation and stabilization, organic matter decomposition and nutrient regeneration, and secondary production and energy flow to higher trophic levels). The persistence of significant biodiversity losses four years after the wellhead was capped indicates that full recovery of ecosystem services has yet to occur.

O35

Nematode assemblages in the Gulf of Mexico continental shelf collected during a two-year survey

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Nematode assemblages along the northern continental shelf of the Gulf of Mexico were examined to better understand the structure of the meiobenthic community in the area, particularly in the aftermath of the Deepwater Horizon oil spill. Meiofauna were collected at 36–187 m depths on the northern Gulf of Mexico (GOM) continental shelf in 2013–2014 on the NOAA ships *Pisces* and *Gordon Gunter*. Thirty-seven sediment samples were collected with a multicorer and were analyzed for trace metals and nematode diversity. The data were analyzed with Primer® 6 software. Over 3800 nematodes were identified from 152 genera and 32 families. Cluster analysis revealed distinct nematode assemblages in the eastern study areas (Florida/Alabama) versus western areas (Louisiana/Mississippi) that correlated with the two known sediment profiles in the eastern and western Gulf shelf, with higher levels of silt

and aluminosilicate compounds in the west due to the outflow of the Mississippi River. Further, significant (SIMPROF) temporal changes were revealed by the cluster analysis, as the 2014 eastern nematode assemblages grouped together but separately from the 2013 eastern nematode cluster, though the collection methods were identical. Conversely, all of the 2013–2014 nematode assemblages from the Louisiana/Mississippi sites grouped as one significant cluster. Nematode densities at each site correlated positively with high levels of Aluminum, near the Mississippi River outflow, and negatively with Calcium and Strontium which are elevated in Florida. Nematode density did not correlate with water depth. The most abundant genera identified in the study were *Sabatieria*, *Dorylaimopsis*, *Pselionema*, *Tricoma* and *Halalaimus*. This study will be useful in understanding the abiotic factors that influence the meiobenthic community and will facilitate future assessments of natural and man-made disturbances.

Taxonomy, systematics and evolution of meiobenthos

How small animals provide clues to large-scale questions

O36

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Recent years of progress in molecular phylogenetics have changed the comprehension of ‘the tree of life’, reaching a consensus on three major animal lineages – Deuterostomia (including vertebrates), Ecdysozoa (including Arthropods) and Spiralia (many worm like groups). However, the vast majority of model animals is of macroscopic size and belongs to the two former lineages, neglecting the huge diversity in Spiralia. Within the third group, Spiralia, several of the understudied, small taxa have shuffled between subgroups, their phylogenetic resolution being critical for reconstructing the evolution of central animal shapes and features such as size, brain and segmentation. In a recent phylogenomic study we assessed the interrelationships among the meiofaunal and macrofaunal members of Spiralia using 402 orthologs mined from genome and transcriptome assemblies of 90 taxa. The meiofaunal ‘problematica’ *Lobatocerebrum* and *Diurodrilus* are found to be deeply nested members of Annelida, and unequivocal support is found for the lastly described phylum Micrognathozoa as the sister group of Rotifera. With several meiofaunal lineages branching off early in the diversification of Spiralia, the concept emerges of a microscopic, acoelomate, unsegmented, direct-developing ancestor of Spiralia. Though this evolutionary scenario is still debatable, it already leads to further questions on e.g., the complexity and functionality of the early spiralian brain and nervous system – possibly composed of very few cells. New detailed studies of the neuromuscular systems in the meiofaunal groups Micrognathozoa, Gnathostomulida, and Gastrotricha as well as miniaturized Annelida uncover a comparably low structural complexity of the brain, composed of relatively few cells. Yet, subdivisions do occur, if not structurally, then in functionality – as indicated by expression patterns of neurotransmitters and neural genes. Moreover, the multiple new data reveals a substantial structural variation even among closely related species, questioning the often-claimed evolutionary conservatism of the animal nervous system.

O37

Open questions on the evolution of the inner anatomy of Gastrotricha illustrated with the case study of the early branching *Diuronotus aspetos*

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Gastrotricha is a cosmopolitan group of meiofaunal animals, which diversity, evolution, and morphology are still only partially known. This group consists of three clades: the mostly marine Macrodasyida, the Multitubulatina (containing only the marine genus *Neodasys*), and the small-sized, mostly freshwater Paucitubulatina. The relationship between these three clades is still discussed, and the phylogeny of Macrodasyida is still unresolved. However, the phylogeny of Paucitubulatina shows some degrees of resolution. We here present the inner anatomy, studied with confocal laser scanning microscopy and immunohistochemistry, of a deep branch of Paucitubulatina, *Diuronotus aspetos* (Muselliferidae), described in 2005. Our detailed reconstructions show a wealth of details on the muscular and nervous systems of *Diuronotus aspetos*, allowing for a comparison with various previously studied Gastrotricha and new homology assessment. Despite its larger size compared to other Paucitubulatina, the musculature does not appear more complex. A substantial rearrangement of the longitudinal musculature and a repetition of dorso-ventral muscles are discussed in comparison to other Gastrotricha. The pharynx of *D. aspetos* is described in details, revealing the presence of an unknown complex of pharyngeal canals, and of pharyngeal sensory cilia unique for Paucitubulatina — but common in other gastrotrich clades. Furthermore, the nervous system is described in details showing intriguing similarities with *Xenotrichula* (Paucitubulatina) and Multitubulatina, leading to suggestions of an evolutionary simplification of the serotonergic nervous system within Macrodasyida. An interesting feature of *D. aspetos* is the presence of a nerve ring anterior of the brain. This so far undescribed structure seems to have gone overlooked in other Gastrotricha (own unpublished studies), often adjacent to the brain neuropile, and might give new insights on the origin of the ventral brain commissure found in most Gastrotricha. The present study hereby adds up detailed and crucial information on the still scarcely morphologically investigated Paucitubulatina, in addition to facilitating a better understanding of the diversity and evolution of different organs systems in Gastrotricha.

Morphological abnormalities observed in free-living nematodes from the Black Sea

O38

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In this study, we aim to summarize our long-term (1988–2015) data about the abnormalities detected in the development of the vital chemoreceptor organs (amphids) in more than 40 nematode species from the Black Sea. Amphid abnormalities are characterized by a wide spectrum of appearances. Accordingly, they may have non-standard number of elements of a species-specific form (1 or 3–5 elements instead of 2); one element of amphid may be underdeveloped or may not have a species-specific form; the topography of amphids in relation to the front edge of the head and to the axis symmetry of the body may be disturbed. Anthropogenic impact on the Black Sea ecosystem is steadily increasing. Its negative effect is revealed in the extinction of species, community perturbations, serious physiological changes in organisms, resulting in different pathological phenomena. It is obvious that the occurrence of specific abnormalities in the vital organs of some nematode species is a result of chromosomal mutagenesis. Repeatability and the wide distribution of species with these types of abnormalities in different regions of the basin are shown. The issues indicated in the present study require future research: 1. What is the specific cause of the amphid abnormalities in nematodes? 2. Are these abnormalities of chemoreceptor organs in nematodes unique for the Black Sea? 3. Do these abnormalities of amphids offer an advantage or a disadvantage compared to the "normal" organs for organisms inhabiting polluted ecosystems or living under the impact of climate change? At present it might only be assumed that we observe the process of either atavism or modern morpho-physiological adaptations to the changing environment.

A symbiotic partnership between diatoms and rhabdocoel flatworms

O39

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Symbiotic associations between microalgae and marine invertebrates are not uncommon, but are rare and understudied in flatworms. Rhabdocoels, such as *Pogaina* and *Baicalellia*, are widespread and locally abundant taxa of meiofaunal flatworms. Microalgal symbionts have previously only been recorded in *Pogaina* and were tentatively suggested to be diatoms. However, the identity of the symbionts and the nature of the partnership have yet to be characterized with either ultrastructural or molecular data. Although diatom symbionts also occur in foraminiferans and dinoflagellates, they are only known in metazoans from the obligate association between the acoel *Convoluta convoluta* and the diatom *Licmophora.* Here, we reveal two new rhabdocoel-diatom associations from the northeastern Pacific coast. Molecular data show that *Pogaina paranygulgus* and *Baicalellia* n. sp. host diatom symbionts within the Naviculales that are closely related to *Gyrosigma* and *Navicula*, respectively. *Pogaina* and *Baicallelia* are closely related, but not sister taxa, suggesting either secondary losses or independent acquisitions of symbiotic diatoms in marine rhabdocoels has occurred. We present details on the ultrastructure, the specificity and the nutritional interactions of these associations and discuss them in a broader context of microalgal symbiosis in meiofauna. Both rhabdocoels and diatoms can reach high densities in interstitial habitats. As such, this study contributes to our understanding of the ecological and evolutionary importance of symbiotic interactions between microalgal and meiofaunal communities.

O40

Phylogenetic and genomic insights on the origins of meiofaunal Spiralia

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Despite the clear advances they have offered in the study of metazoan evolutionary history, molecular phylogenetic and genomic datasets available to date do not adequately represent a number of morphologically unique meiofaunal higher lineages. Chief among these are the recently described animal groups such as Micrognathozoa, as well as the two interstitial "Problematica" *Diurodrilus* and *Lobatocerebrum.* These genera show a certain resemblance to Annelida in their cuticle and gut; however, both lack primary annelid characters such as segmentation and chaetae. This and their ciliated epidermis have led some to propose relationships with other microscopic spiralians, namely Platyhelminthes, Gastrotricha, and in the case of *Diurodrilus*, with Micrognathozoa lineages that are grouped by some analyses into "Platyzoa", a clade whose status remains uncertain. We recently assessed the interrelationships among these meiofaunal and the macrofaunal members of Spiralia using 402 orthologs mined from genome and transcriptome assemblies of 90 taxa. Under all analyses, *Lobatocerebrum* and *Diurodrilus* were found to be deeply nested members of Annelida, and unequivocal support was recovered for Micrognathozoa as the sister group of Rotifera. Bayesian analyses using site-heterogeneous substitution models also place Gnathifera and a clade of Gastrotricha and Platyhelminthes as independent branches at the base of Spiralia, thus separating the two major groups commonly used to model the development of complex protostome morphologies (annelids and arthropods). To confirm this position, and to clarify its evolutionary implications, we have further undertaken to assemble and annotate draft genomes for two representative members of Gnathifera, a gnathostomulid and a micrognathozoan, using whole genome amplification to generate fragment and mate-pair Illumina libraries from single individuals. We present our efforts to generate reference assemblies from these uneven-coverage data, and discuss the degree to which their annotation (e.g. for developmental transcription factors) may inform ancestral state reconstruction efforts. Finally, in light of the mounting evidence that microscopic, acoelomate, direct-developing animals compose some of the deepest branches within not only Spiralia but also Bilateria as a whole, we critically review the concept of one or more origins of large-bodied, morphologically complex bilaterian clades from an originally meiofaunal condition.

Meiofaunal cryptic species challenge species delimitation: the case of the *Monocelis lineata* (Platyhelminthes: Proseriata) species complex

O41

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Given the pending biodiversity crisis, species delimitation is a critically important task in conservation biology, but its efficacy based on single lines of evidence has been questioned as it may not accurately reflect species limits and relationships. Hence, the use of multiple lines of evidence has been portrayed as a means to overcome identification issues, arising from gene/species tree discordance, morphological convergence, or recent adaptive radiations. Among meiofaunal organisms, the marine microturbellarians (Platyhelminthes) are a group whose contribution to marine biodiversity has yet to be fully assessed. Among them, the Monocelididae Monocelidinae (Proseriata) represents a taxon in which the paucity of diagnostic morphological characters is particularly felt. Here, the integrative taxonomic approach has been used to address the study of the taxonomically challenging *Monocelis lineata* species complex. Eighteen populations, which encompass most of the geographic range of the complex, were studied using morphology, karyology, crossbreeding experiments and molecular analysis (18S and 28S sequencing). These different markers provided evidence of four (karyology) to eight (morphology) discrete entities, whereas crossings showed various degrees of intersterility among the tested populations. Molecular species delimitation revealed a different number of candidate species, spanning from five (ABGD and K/Θ methods) to 11 (GMYC method). The Atlantic populations were particularly taxonomically controversial, spanning from one (ABGD) to six (GMYC) candidate species. The incongruence among the different molecular species delimitation methods may thus reflect the multifaceted evolutionary history of *M. lineata s.l.* and hamper the full taxonomic resolution of the complex. However, it should be pointed that the recent divergence time may account for this discrepancy in the number of entities obtained by the species delimitation methods, which tend to be less accurate in detecting species boundaries when divergence times are low. Indeed, our results dated the basal node of all of the analysed entities to approximately 800,000 years ago. Nonetheless, two candidate species were consistently validated by all of the markers and have been formally described: *Monocelis algicola* and *M. exquisita.* The latter species appear to have

a particularly restricted distribution, and the possibility that meiofaunal taxa may be of conservation concern should be considered.

O42

Integrative taxonomy and phylogeography of *Dactylopodola typhle* (Gastrotricha): evidence for a species complex?

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Marine species of the phylum Gastrotricha are a component of the interstitial meiofauna. Like other taxa of this community, they do not possess free swimming larvae or other dispersal stages. In different studies focusing on the emergence of the meiobenthos, gastrotrichs were never found among the near-bottom plankton. So far, gastrotrichs in the water column are only reported once from a high energy intertidal beach. Furthermore, gastrotrichs possess features and behaviors that avoid uncontrolled sweeping off, e.g. batteries of duo-gland adhesive tubes or gluing of fertilized eggs to sand grains. A certain distribution via coastal-parallel sediment transport probably occurs, however, long distance dispersal across the open water should hence be minimized. We aim to learn how such a fundamental biological property affects the genetic–geographic population structure (phylogeography) and speciation processes in interstitial animals. Mitochondrial sequence data (COI) give evidence of large genetic distances between geographic populations of the morphospecies *Dactylopodola typhle* (several sites of the North Sea, Channel, Atlantic and Mediterranean). Phylogenetic and phylogeographic analyses indeed show a strong structuring of this "species" into four distinct COI-lineages. The phylogenetic analysis of a more conserved nuclear marker (short fragment of 18S), however, supports three of these lineages as separate entities. The four mitochondrial lineages correspond to distinct geographic/ecological regions: (a) central North Sea, (b) Channel to Bay of Biscay, (c) Balearic Basin, and (d) Tyrrhenian Sea. Several morphometric values from microscopically documented adult specimens were analyzed and particularly the total body length shows significant differences between the three nuclear clades. Based on our results the species status of *Dactylopodola weilli*, currently categorized as *species inquirenda*, is confirmed. Further taxonomic consequences resulting from our findings are challenging and will be discussed. Concluding, our initial genetic analysis hints to the existence of a species complex consisting of different cryptic genetic species within *D. typhle* plus further highly similar taxa such as *D. weilli* and *D. mesotyphle.*

Can disjunct distributions in kinorhynchs be explained by introduction events? The biogeographical story of *Echinoderes ohtsukai*

O43

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The dispersal ability of kinorhynchs 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 appears to extend over vast geographical areas. Combining molecular phylogenetic data with biogeographical investigations can test this paradox by discerning cryptic species with restricted distributions from species with potentially large geographical distributions. In this communication, we provide the first evidence for a disjunct geographical distribution in the kinorhynch species *Echinoderes ohtsukai* that is consistent with the introduction of an invasive species. Although we collected *E. ohtsukai* from the northeastern Pacific Ocean (British Columbia), this species was originally described from Japan. We demonstrate that specimens of *E. ohtsukai* collected from Japan and British Columbia have identical DNA sequences for the mitochondrial Cytochrome c Oxidase subunit 1 (COI) gene (barcode region). These results are most consistent with a recent introduction of this species into one of the habitats on the opposite side of the Pacific Ocean through human-mediated dispersal. The coast of British Columbia has historically had a high level of maritime traffic connecting to the coast of Japan, and we suspect that related aquacultural activities could have played a major role in transporting kinorhynchs from one coast of the Pacific Ocean to the other. These results will certainly affect the way we currently interpret the distribution of kinorhynch species and other meiofaunal groups, opening new debate and research lines.

European invasion of an Asian phylotype from a cryptic species of benthic foraminifera (*Ammonia tepida*): identifying and dating the event

O44

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Ammonia tepida is one of the morphospecies routinely recognised among European intertidal benthic foraminifers. However, the molecular identification, based on rDNA genes (partial small and large subunits (SSU and LSU)), of specimens sharing this morphotype has shown that there are at least three different phylotypes corresponding to separate species (e.g. Hayward et al. 2004, Mar. Micropal. 50: 237–271). Two of these phylotypes seem to be autochthonous in Europe, whereas the third one was identified in Europe as well as Eastern Asia. Similar disjunct distributions have been interpreted as an introduction of the Asian species in Europe, probably through anthropic means. Preliminary morphometric studies have shown that specimens of *Ammonia tepida* can be discriminated between two morphotypes, one with small pores and one with large pores. The first molecular identifications of these morphotypes indicate that the group with large pores is the allochthonous phylotype, whereas the group with small pores is one of the two autochthonous phylotypes. This morphological distinction will allow us to track down-core both phylotypes and to date replacements observed in recent sediment archives. Our aim is therefore to study the putative silent invasion of the allochthonous species in Europe. The main objectives are to map in more detail the distribution of the three phylotypes in Europe, to characterize their ecological preferences, to date the replacement of autochthonous phylotypes by the allochthonous one at different sites, and to study which vector(s) were responsible for the introduction of this new phylotype.

O45

Genome divergence in meiofaunal populations separated by the Panama Isthmus

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Although meiofauna species traditionally have been considered to have cosmopolitan distributions, recent studies provided the evidence that *Ototyphlonemertes* species (Nemertea, Hoplonemertea, Monostilifera, Ototyphlonemertidae) have a biogeography, with ecological and geological barriers that prevent gene flows among populations. These soft-bodied animals have no fossil records; therefore, considering a well-known geological event, like the rise of the Isthmus of Panama, is a critical opportunity to time-calibrate molecular phylogenies. Most population genetics studies on meiofauna taxa have focused so far on only partial, single, or few nuclear and mitochondrial genes. In this preliminary and pioneering work, specimens of *Ototyphlonemertes* collected from either side of the Isthmus of Panama are used to expand the set of nuclear and mitochondrial loci useful for examining recently diverged groups, by using a population genomics approach. Shotgun sequencing of selected geminate species on the Pacific and Caribbean sides of Panama has revealed distinct variation in the mitochondrial genomes and several nuclear loci, including microsatellites and specific single-copy orthologs. We are in the process of obtaining similar results from other meiofauna taxa, belonging to the phyla Annelida, Nematoda, Gastrotricha, Platyhelminthes, Mollusca, etc. Differences among these nuclear and mitochondrial loci are crucial in (i) determine the rate of divergence between taxa; (ii) test the impact of vicariance on genetic divergence in different taxa that differ for biological traits (e.g., reproduction modality, development, size, evolutionary origin, etc). Moreover, (iii) recently developed mitochondrial metagenomics bioinformatics pipelines, as well as metagenomic targeting of these selected nuclear markers, will be used on pooled meiofauna samples throughout locations that differ for ecological conditions and/or geographic locations. This data will be useful in examining the diversity, allele frequency, variation, and phylogeographic structure of populations throughout ecosystems, and will contribute to fundamental knowledge of ecosystem interactions and how communities respond to environmental change.

The nemertean marine mesopsammic genus *Ototyphlonemertes* is everywhere but its species are not

O46

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Many meiofauna species are thought to have broad distributions unaffected by distance and other common barriers to dispersion. However, recent morphological and/or molecular studies of meiofauna suggest patterns of diversity and distribution that differ among taxa while also conflicting within the same group. We assessed the patterns of geographic distribution in genetic species of a marine meiofauna animal model: *Ototyphlonemertes*, a globally distributed genus of mesopsammic Nemertea. Specimens were collected from several sites around Europe, Northern and Central America, South America, Pacific Islands and Asia. We sequenced regions of two mitochondrial and two nuclear genes. By using single-gene, concatenated, and multi-locus approaches as well as different DNA-taxonomy methods we assessed the diversity and the spatial structures of haplotypes, and tested the correlation between genetic diversity and geographic distance and the spatial structures of haplotypes. The results show (i) the importance of using several genes to uncover diversity and highlight phylogeographic relationships among species, and (ii) independent genetic evolutionary entities have narrower distributions than putative morphological species. Moreover, (iii) a Mantel test supports a positive correlation between genetic and geographical distance. Additionally, samples from the Caribbean and Pacific shores of the Panama Isthmus enable us to estimate lineage divergence times calibrated by the vicariant effect of the geological closure of the seaway across the Isthmus. Thus, we propose that distance, geological and ecological conditions – commonly invoked for larger organisms – also are barriers to the dispersion of and gene flow in marine meiofauna.

O47

Resolving the *Lourinia armata* complex with remarks on the monophyletic status of Louriniidae (Copepoda, Harpacticoida)

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Detailed examination and comparisons of several specimens collected from different localities along sandy beaches of Turkish coasts proved that *Lourinia armata* is a species complex. It has been documented that there are at least two species of *Lourinia* inhabiting in the Turkish coasts, the first being *L. armata* sensu lato and the other is *Lourinia* sp. nov. It has been also demonstrated that the microcharacters such as spinular ornamentations can be very important in distinguishing species of Louriniidae. The family Louriniidae is a poorly known and enigmatic taxon with an unclear phylogenetic relationship with other harpactioid taxa. Only two genera and two species have been described so far. Taxonomic history of the family and its taxa has been complicated and problematic. There is still confusion about the taxonomy of the family Louriniidae, mainly due to the deficient descriptions of certain species such as the type species *L. armata*. The recent inclusion of monotypic genus *Archeolourinia* to Louriniidae dramatically contributed to the confusion of the family. As it stands, the family Louriniidae is clearly polyphyletic since *Archeolourinia shermani* does not belong to family Louriniidae but Canthocamptidae. The problem of polyphyly can easily be solved by transferring *A. shermani* to the Canthocamptidae. But, the exact phylogenetic position of the Louriniidae still remains problematic since none of the diagnostic character supports the monophyly of the family. The most important characteristic that can possibly be used to define Louriniidae is the reduction of maxilliped. But the reduction of maxilliped is shared between Louriniidae and Darcythompsoniidae indicating the sister group relationship between them. In addition to the several other similarities, the examination of the setal pattern between the male antennule revealed new characteristics supporting the sister group relationship between Louriniidae and Darcythompsoniidae.

O48

First parasitic Aegisthidae Giesbrecht, 1893 (Copepoda: Harpacticoida) showing extraordinary convergent evolution with Siphonostomatoida and its phylogenetic position within the family

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The abyssal Central pacific nodule province between Clarion and Clipperton fracture zone (CCZ) is an area inquired for mining of polymetallic nodules. Due to the increasing interest in the exploration of deep-sea minerals, investigation on faunal diversity and recolonization of new habitats in this area is highly demanded. Copepods are relatively divers and abundant resulting in extensive ecological adaptations in benthic marine ecosystems. Aegisthidae is one of the most primitive Harpacticoid families. The evolution of the family is directed towards the colonization of the water column from the benthic sediments. Many genera are hyperbenthic, inhabiting the bottom water layer immediately above the deep-sea floor. Also Aegisthidae are common representative of the bathypelagic community. The colonization of the hyperbenthic and open waters was allied with a deep modification of the body-shapes of these animals. During the expedition SO239 we were able to collect a few specimens representing two species, showing remarkable similarity with Siphonostomatoid copepods. The labrum and labium are elongated forming an oral cone that allocates the stylet-like mandibles. Within Copepoda, this oral cone is typical for Siphonostomatoids, who live associated with invertebrates. But a closer analysis of swimming legs, antennule and antenna denoted a relationship with Harpacticoid copepods instead. The analyzed specimens seem to deserve an intermediate position between these orders. Here we test the ordinal status of these ambiguous copepods using three nuclear genes, small- & large- subunits (18S & 28S), Histon3 (H3) and one mitochondrial gene, cytochrome c oxidase subunit I (COI). Phylogenetic relationship of 63 specimens representing eight potential genera of the family Aegisthidae and two species of order Siphonostomatoida was well supported by Maximum likelihood and Bayesian inference analysis. This analysis shows that the specimens unequivocally belong to the Family Aegisthidae, representing a new genus. They form a distinct clade consisting of two new parasitic species clustering as sister-group of the genus *Cerviniopsis*. This is the first record of parasitic Aegisthidae and an extraordinary example of convergent evolution in Copepoda forced by the adaptation to a completely new way of live. Molecular analysis determined the position of another enigmatic genus as a new sister-genus of *Cerviniella*.

Metabarcoding of marine nematodes from a taxonomist's perspective

O49

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Metabarcoding uses DNA extracted from environmental samples and Next Generation Sequencing technologies to produce molecular barcodes (OTUs) of different organisms present in the sample. It is becoming increasingly popular and affordable, and was used in studies of marine meiofauna, including nematodes. Ideally, OTUs should be identified with respective morphospecies before they can be used in comparative studies, which is impossible to achieve due to incompleteness of nematode reference databases. Fortunately, a lot of ecological information can be derived from the data on nematodes grouped into family-level taxonomic categories. If we cannot identify nematode OTUs to species level because reference databases are not complete, can they be classified into families instead? And which one of the many taxonomy assignment tools works best for this task? Recent nematode metabarcoding data originated from two sites off the west coast of Sweden – coarse sand near the island of Hållö and fine mud from the Gullmarn Fjord. The barcoding region was the $5'$ end of the 18S rRNA. 140 nematode OTUs were generated for both sites, but only six can be identified to species level. Five taxonomy assignment methods were used to place these OTUs in nematode families: Megablast, LCAClassifier of GREST, UTAX algorithm of USEARCH, Tree-building & Bootstrapping and Evolutionary Placement Algorithm. Placement success ranged from 25 OTUs for LCAClassifier to 119 out of 140 OTUs for Evolutionary Placement Algorithm. Thus, OTUs can indeed be classified into families, but not all taxonomy-assignment methods can be used for this. The Evolutionary Placement Algorithm was not only able to place the highest number of OTUs into families. Its other benefits include: placement of OTUs into taxa of different level, depending on the resolution of the reference tree; accumulated likelihood scores allow to assign more OTUs; custom created datasets allow to exclude low quality sequences and follow most accepted classification system. Now the nematode OTUs identified to families can tell us more about nematode communities, how diverse they are, which families are species-rich and which are species-poor, what taxa are represented by larger number of barcode reads, making metabarcoding data more useable in ecological research.

O50

Rapid identification of meiofauna species (Copepoda: Harpacticoida) using MALDI-TOF MS

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Second to nematodes, the Harpacticoida are the most abundant meiofauna group found in marine sediments with a typical density of 200,000 to 300,000 individuals per m^2 (Huys and Boxshall, 1991). To date there are more than 50 families containing around 3000 described species. Because of their small size, species identification is taxonomically very challenging and laboriousẆhile DNA Barcoding provides a suitable tool for identification, it is still very time consuming and cost-intensive because single sediment samples can contain over 1000 specimens and demand a species specific primer setup. An alternative to DNA Barcoding might be the analysis of proteome fingerprints using MALDI-TOF MS (**M**atrix-**a**ssisted **l**aser **d**esorption/**i**onization **m**ass **s**pectrometry), which is commonly used for rapid identification of bacterial colonies and over the last years was tested for some metazoans as well (e.g. Laakmann et al., 2013). Now, for the first time, we successfully applied this technique to meiofauna organisms. We are able to discriminate species based one mass spectra that were generated within a very short handling time and without the use of species specific primers or measurement protocols. This enables the rapid identification of microscopic specimens without deeper taxonomical knowledge, based on a prior generated species database. Currently, we are establishing a species database for harpacticoid copepods from the North Sea to test the applicability of this technique in rapid biodiversity assessment.

NeMys – nematodes taxonomic system in context of marine nematodes ecology

O51

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Identifying nematodes species is often a challenging task for ecologists. No taxonomic keys exist for the World fauna and local guides are available only for some regions. The list of all aquatic nematode species published in 1973/74 by Gerlach and Riemann has yet to be updated. New species are often listed only in the personal catalogues of taxonomists, and access to widespread taxonomic literature is difficult sometimes. These difficulties have led some ecologists to identify species incorrectly, thus impeding ecological analyses across regions. Precise taxonomic identification becomes critical to understand the diversity patterns in species composition along depth and longitudes. In the 1990s, the NeMys ("Nematodes and Mysids") online taxonomic database was created by taxonomists of Ghent University to help students and researchers in identification. The database contains an extensive list of marine and some freshwater species together with original species descriptions. The database now contains over 6500 valid species names and has been integrated within the World Register of Marine Species (WoRMS) according to the classification of De Ley & Blaxter (2002), with further amendments by Schmidt-Rhaesa (2014). The ultimate aim is to have a comprehensive list of all marine nematode species, each with a link to its original description, reference to type specimen, type locality and a history of taxonomic changes. The species distribution data is accumulating also by linking with other databases. NeMys is growing now in two directions – both newly described species and existing species described in less accessible publications. The new species description rate remains high for nematodes, with about 500 new species described in each of the last three decades. These species now come from wider geographical areas outside Europe and from remote habitats such as the deep sea. However, NeMys remains a work in progress, and for most families, the lists of species are not yet complete. The gaps come mainly from rare local editions and regional journals. When complete, NeMys will serve not only for species identification, but also as a tool for studies in nematode ecology.

O52

Global-scale distribution of *Microlaimus* de Man, 1880 with updated list of valid species

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Encountered extensively from intertidal zones to the deep sea, the genus *Microlaimus* is one of the most common genera of the marine nematofauna worldwide. Its distribution encompasses estuaries, mangroves, sandy beaches and tidal flats, but also continental margins, canyons and abyssal plains. It is found dwelling across different grain sizes – from mud to coarse sand – and within a broad temperature spectrum, including warm tropical beaches as well as cold deep waters in Antarctica. In addition *Microlaimus* can be among the most abundant genera in a nematode assemblage, and it is not uncommon to find several species of this genus coexisting in the same environment. Supposedly being an epigrowth feeder, *Microlaimus* may graze on fungi, bacteria and unicellular algae. This genus is characterized as being opportunistic, mainly because of the broad range of disturbed and undisturbed habitats it inhabits. This attribute, together with its resilience to different environmental conditions, might enable a fast reaction after 'fresh' food is settled to the sea floor and it could be one explanation for the genus's broad distribution. Based on our distribution results from different environments, as well as on literature data on genus and species distribution, we unveil the *Microlaimus* distribution in different habitats on a global scale. Moreover, we present an updated list of species with reference to their respective habitats. This study thus displays the most complete picture, so far, on the diversity and distribution of *Microlaimus* on a global scale.

O53

Nematode species and assemblages on Northeast Atlantic seamount Great Meteor

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Great Meteor is a giant seamount rising from seabed at about 4500 m to a summit plateau of square 1450 km^2 at average depth 287 m below sea level. Great Meteor is located at ~30°N and at 1600 m from the nearest continental coast. The plateau of the Great Meteor Seamount is an isolated 'sublittoral habitat' covered with biogenic

coarse calcareous sand consisted largely of shells of planctonic foraminiferans and pteropod gastropods. Meiofauna was sampled during the GroMet expedition (RV Poseidon) in 2010. Nematofauna is very rich; it is represented by about 75 species belonging to 51 genera and 32 families. Dominant family is Selachinematidae, followed by Comesomatidae, Desmodoridae, Ceramonematidae, Thoracostomopsidae and Neotonchidae. A peculiar feature of the assemblages is high percentage of predatory families Selachinematidae (mostly *Latronema*). Another peculiar feature is high percentage and diversity of Ceramonematidae. Most Great Meteor species are presented by probably new species belonging to genera common in shallow coarse sediments. Typical deep-sea genera such as *Acantholaimus* and *Manganonema* are also present but their percentage is low.

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Meiofaunal community structures on the plateau of the Great Meteor Seamount (northeastern Atlantic Ocean) with a closer look to Polyarthra and Harpacticoida (Copepoda, Crustacea)

O54

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The Great Meteor Seamount (GMS) is one of the largest seamounts in the subtropical north-eastern Atlantic Ocean, rising from 4200 m up to 270 m below sea surface. The GMS is also one of the best studied seamounts worldwide concerning meiofauna. It is of volcanic origin and typically guyot-shaped. The plateau alone measures 1465 km^2, with a maximum length of 54 km and maximum width of 31 km, whereas the bottom of the GMS is 110 km long and 90 km wide. Due to the isolated location of the GMS (450 nautical miles south of the Azores, 800 nautical miles west of the African coast at 30° 00′ N, 28° 30′ W), it is of special interest for the stepping-stone hypothesis, which also concerns meiobenthic organisms. Several studies have been conducted on the plateau of the GMS but only qualitative material has been available so far. During the expedition P397 GroMet with the German research vessel “Poseidon” in 2010, the whole plateau was finally sampled quantitatively with a uniform device, the Van Veen grab. Now it is possible to investigate the community structure and distribution patterns of all meiofaunal organisms on the plateau of the GMS. More than 20 different taxa have been identified on the plateau so far. The most abundant ones are the Nematoda, Copepoda and Annelida, each with very high abundances. Hence, the meiofauna on major taxon level is very diverse, like for instance benthic Copepoda (Crustacea). Several taxa, e.g., Canuellidae (Polyarthra) and Zosimeidae (Harpacticoida), neither show any dissimilarity within the community structure nor differences within the distribution pattern on the whole plateau. Moreover, most of the species identified on the plateau are new to science, which can be seen as an indication that the plateau is an isolated area for these species. However, certain species can also be found on other seamounts like Seine and Sedlo, leading to the assumption that the GMS is not as isolated as previously suspected.

O55

Kinorhyncha from the Gulf of Mexico, with a report of two new species

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Meiobenthic samples were collected from 2007–2015 along the United States' continental shelf in the Gulf of Mexico from southern Texas to southern Florida. The samples have yielded a large collection of meiobenthic organisms, including kinorhynchs, which have been a subject of intense study throughout the project period. Due to the long-term nature of the study and the considerable amount of sampling stations, we are now able to present the largest and densest collection of kinorhynchs made so far from a larg geographic area. The study provides new insights into kinorhynch distribution patterns and disbursal ranges, and has contributed greatly to our knowledge about kinorhynch taxonomy. Up to this point three new species, *Echinoderes skipperae*, *E. augustae*, and *E. charlotteae* have been described. Additionally, this long term study has provided new taxonomic data for existing species through the study of museum specimens, and has provided a re-description of *E. bookhouti*. This presentation describes two new species of kinorhynchs in the genus *Echinoderes* and shows their distribution along the Gulf continental shelf. Our estimates suggest that the collected material includes about fifteen additional undescribed species and three known ones. For comparison, the total of described kinorhynch species amounts currently to 230, hence, the contribution of new data from the Gulf material is significant.

O56

A taxonomical study of the free-living marine nematodes in the family Comesomatidae and Enchelidiidae from the sublittoral zone of Korea

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To recognize how many species inhabit the Korea waters, a practical list on free-living marine nematode fauna was made by using results from National Investigation on Marine Ecosystem since the last four years. This faunal list put together unrecorded and unknown species from the ecological project and published free-living marine nematode species in Korea. Total of 233 species belonging to seven orders, 31 families and 121 genera were collected from four localities in Korea. Additionally, we described seven new species (*Abelbolla maemulensis* Hong & Lee, 2014, *Cervonema* sp. 1, *Dorylaimopsis* sp. 1, *Dorylaimopsis* sp. 2, *Dorylaimopsis* sp. 3, *Ledovitiabrevis* Hong & Lee, 2014 and *Setosabatieria* sp. 1) and four unrecorded species (*Dorylaimopsis variabilis*, *Laimella filipjevi*, *Setosabatieria hilarula* and *Vasostoma articulatum*). Pictorial keys for determination of valid species in the genera *Abelbolla* Huang & Zhang, 2004, *Cervonema* Wieser, 1954, *Dorylaimopsis* Ditlevsen, 1918, *Laimella* Cobb, 1920, *Ledovitia* Filipjev, 1927, *Setosabatieria* Platt, 1985 and *Vasostoma* Wieser, 1954 are given.

Evolution and biomechanics of the male copulatory organ in Schizorhynchia (Platyhelminthes: Kalyptorhynchia)

O57

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The flatworm clade Schizorhynchia comprises approximately 150 species of predators that use an anterior proboscis to capture prey. Taxonomy in this group has relied heavily on the light-microscopic structure of the proboscis. Recent molecular–phylogenetic studies do not support the current classification. In addition to the proboscis, schizorhynchs possess a rather complex male organ, variously armed with spines or cirri. However, the last comprehensive review of this organ in Schizorhynchia was published in 1956 using only light microscopy. Using our recent molecular phylogeny for guidance, I have investigated the male copulatory organ in several schizorhynch species by confocal-laser-scanning and transmission-electron microscopy. These studies reveal common features, including an outer sheath of longitudinal muscles surrounding the copulatory bulb (conflicting, in at least one case, with the description originally published), copulatory 'hard parts' comprising an eversible cirrus and/or a tubular extension of the ejaculatory duct, muscular connections between the copulatory bulb and hard parts that appear to be capable of cirrus protrusion during copulation (and retraction thereafter), and an epithelial lining of the ejaculatory duct through which pass neck-like extensions of the prostate glands (a feature that was usually missed in earlier light-microscopic studies). These studies have allowed the development of a general biomechanical hypothesis for the function of these organs, and this hypothesis appears to allow selection of species to be added to the molecular phylogeny, which is presently rather weakly-supported at the base of the Schizorhynchia. More broadly across the Platyhelminthes, certain of these traits in the male organ may represent functional constraints on the evolution of the organ. For instance, it appears that the 'conjuncta-duplex' type of male organ (as defined by Karling), which is widely distributed in Platyhelminthes, is simply a functional necessity for protrusion of a cirrus during copulation.

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O58

Phylogeny and distribution patterns of benthic freshwater Cladocera (Crustacea) confirm antiquity of their mode of life

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We study phylogeny and global distribution patterns of two distant groups of specialized, truly benthic Cladocera (Crustacea): *Leydigia* (family Chydoridae) and *Ilyocryptus* (family Ilyocryptidae). Both taxa contain: (1) a core group – centre of diversity – globally distributed through different continents and being common species there and (2) several basal ("primitive") clades of endemics of subtropical territories which could be regarded as relicts *sensu* Korovchinsky (2006). Deep cladogenesis of two groups most probably was associated with fragmentation of a pan-continent Pangaea, while distribution pattern of the 'core' groups appeared due to some subsequent Caenozoic events. We can assume that the common ancestor of each group already had a truly benthic mode of life. It means that the latter is very antique, it appeared at least in middle-earlier Mesozoic.

The study was supported by the Russian Science Foundation (grant 14-14-00778)

O59

Are freshwater Macrodasyida as rare as previously thought? Integrative taxonomy identifies a new taxon of Gastrotricha Macrodasyida

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Macrodasyida are worm-like, hermaphroditic and marine gastrotrichs with about 350 species. Among all known Macrodasyida only *Marinellina flagellata*, *Redudasys fornerise* and *Redudasys* sp. (Kånneby & Wicksten, 2014), were found in fresh waters respectively from an Austrian stream, a Brazilian artificial reservoir and a USA aquifer. Herein we describe a new freshwater taxon of Macrodasyida from different streams in Minas Gerais State, Southeastern Brazil. The external morphology and internal anatomy were investigated using Differential Interference Contrast (DIC), Confocal Laser Scanning Microscopy (CLSM) Scanning Electron Microscopy (SEM), and Transmission Electron Microscopy (TEM). The systematization of the new taxon within Macrodasyida was inferred by 18S rRNA gene, and the relationships with the other freshwater Macrodasyida species were investigated by COI mtDNA. The adult has a body length from 193 to 376 μm and 1+1 anterior adhesive tubes, 2 pairs of posterior adhesive tubes of unequal length, numerous

cephalic cilia arranged into irregular bands, short around the mouth and longer on the anterolateral head margins, 6 pairs of lateral tactile bristles. Pharynx surrounded dorsally, laterally and ventrally by 10–12 longitudinal muscles which are inserted on the mouth rim and lie externally to circular muscles; the pair of main ventrolateral longitudinal muscles is inserted at the level of the anterior adhesive tubes. Intestine circular musculature external to the splanchnic longitudinal one and not surrounding dorsal and ventrolateral somatic longitudinal muscles. Maximum Likelihood and Bayesian Inference analyses yielded topologies congruent with each other and the new taxon nested within the family Redudasyidae, but COI mtDNA analyses showed clear distances between *Redudasys fornerise*, *Redudasys* sp. and the new taxon. Results suggest that Macrodasyida invaded freshwater environment only once and the Neotropical region seems to be a peculiar place for the evolution of the freshwater macrodasyidan clade.

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The use of meiobenthos on the assessment of environmental impacts

The microcosm approach using meiofauna as an imminent tool for ecotoxicological studies

O60

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The usual procedures for ecological risk assessment have been based for decades on simplified approaches. Although these approaches allowed the development of international regulatory tools capable of reducing the adverse effects on ecosystems, they generally suffer from a lack of ecological realism. Within this context, microcosm studies using meiobenthic communities offer a good compromise between the complexity of the ecosystem and the often highly artificial settings of laboratory experiments. The aim of this oral contribution is to highlight the microcosm approach using meiofauna as an impending tool for ecotoxicological studies. To do so, I will present the results from two case studies that have evaluated the impacts of different contaminants on meiofauna. The first experiment was designed to evaluate the effects of Irgarol and Diuron, the most commonly used biocides in antifouling paints, on meiofauna. Results have shown high mortality, changes in community structure and species loss at biocide levels frequently encountered in the field. Such severe effects contrast to other studies that have detected lower impacts. Considering the relatively high tolerance of meiofauna to pollution when compared to other taxa, it is unlikely that the disparities in results are due to a higher sensitivity of these organisms. It is more plausible to expect that severe effects are due to the microcosm approach used, which considers the entire community and its physico-chemical environment, preserving species interactions and different exposure routes. The second experiment had assessed the ecological effects of exposure to sewage-impacted pore water simultaneously at the community level using meiofauna microcosms and at the population level using laboratory fecundity tests with the copepod *Nitocra* sp. The experiment tested the toxicity of pore-water from three sites according to a contamination gradient. Both approaches were efficient in detecting differences in toxicity between the cleaner and most polluted sites. However, only multivariate data from community analysis detected differences in the gradient of contamination. In addition to information about toxicity, the community level microcosm experiments gave indications about sensitive and tolerant species, indirect ecological effects, as

well as raised hypothesis about contamination routes and bioavailability which are currently being tested.

O61

Comparing ecotoxicological methods from single-species bioassays to model ecosystems

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The pollution of sediments with chemical contaminants is a major environmental concern and considerably contributes to the chemical and ecological status of aquatic ecosystems (EU Water Framework Directive, 2000/60/EC). Therefore, a thorough ecotoxicological assessment in sediments can help to identify causes of stress in benthic habitats and to improve ecosystem health. Especially in fine sediments, meiobenthic taxa are more abundant and species-rich than macrozoobenthos, which is commonly used to assess the ecological quality of sediments. Among meiobenthic communities, nematodes are the dominant organism group in freshwater and marine sediments, representing different trophic levels and occupy significant positions in the food web between micro- and macrofauna. This ecologically relevant taxon can be used for ecotoxicological sediment assessment covering diverse organizational/biological levels in single-species toxicity tests to field studies. However, these various tools had rarely been compared in terms of effects of single chemicals. Therefore, in this study,effects of Zinc (Zn) on natural nematode assemblages were assessed (1) in complex sediment microcosms, including all indirect effects, and (2) in acute community toxicity tests in water (20 mg Zn l^{-1}), considering direct toxicity only. Responses of the various freshwater nematode species in both approaches were (3) compared to effects of Zn on the nematode *Caenorhabditis elegans* in a standardized toxicity test (DIN ISO 10872). The acute tests resulting in a sensitivity ranking of free-living freshwater nematode species, from colonizers to persisters, with *C. elegans* representing the median susceptibility of 15 examined species to Zn, whereas the mixed community responded considerably more sensitive than the single-species test. In the microcosms, Zn showed dose-dependent effects on nematode communities, with species composition already responding at 13–19 mg Zn kg^{-1} sediment (dw), while all other community measures (e.g. abundance, NemaSPEAR[%]) were first affected at 87–127 mg Zn kg^{-1}(dw). These findings were underlined by observed bottom-up effects in the microcosms via Zn effects on bacterial biomass. This study confirmed that nematodes provide suitable and coherent ecotoxicological tools and ecological indices (NemaSPEAR[%]-index) for assessing sediment quality.

Investigating inorganic and organic contaminant effects in free-living nematodes: a multifaceted approach combining single-species and community assays

O62

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Since the past few decades, nematodes have been proven to be excellent biological indicators, including contaminant effects. However, research traditionally have focused either on molecular, individual or community assessments, limited to an environmental compartment type, e.g. marine. Our study combines, thus, ecotoxicological investigations over different freshwater and marine nematode species, including single-species (more specific and controllable) and community assays (ecologically more relevant) for a better understanding of the contaminant effects in nematodes' aquatic communities. Single-species tests included a variety of acute and chronic toxicity experiments. Additionally, we investigate the direct effects of either organic (crude and motor diesel oil) and/or inorganic pollutants (heavy metals) in benthic nematodes. Our results indicate that pollutants effects are species specific, including differences in sensitivity among cryptic species. Although mainly freshwater/soil nematodes have been routinely used in toxicity testing (e.g. *Caenorhabditis elegans*), we show that many cultivated marine/estuarine nematode species are reliable test organisms and potential model species. Species sensitivity varies according to the type of pollutant, concentration level and exposure route. Therefore, we have enough evidence to support the recommendation that (eco) toxicity tests should include a variety of experiments, varying in design, exposure routes and test species, for a complete assessment of contaminant effects in the environment.

Considering cohesive sediments for the chemical and ecological status of aquatic ecosystems – new lines of evidence for a Weight-of-Evidence (WoE) approach based on nematodes

O63

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Toxicants accumulated in fine, cohesive sediments impair the functioning of the benthic community that holds fundamental ecosystem services (e.g. nutrient cycling). Moreover, contaminated sediments represent a permanent source of pollutants for the water phase. Thus, polluted cohesive sediments can impede the achievement of a good chemical and ecological status of aquatic ecosystems and should therefore be considered for the quality assessment of water bodies. However, most of the monitoring tools and pollution indicators cannot be applied to cohesive sediments, as they

are based on macro-invertebrates that do not represent the dominant group in these substrates. Therefore, tools were developed to assess the chemical and ecological status of cohesive sediments that are based on the in-situ nematode fauna inhabiting these sediments: (1) Sediment Quality Guidelines (SQGNema), and indices based on these SQGNema (e.g., mean TEC-Q), estimating the toxic potential of chemicals for nematodes at certain sediment concentrations (Brinke et al., in prep), (2) the NemaSPEAR[%]-index evaluating the ecological status by assessing the abundance of Nematode SPEcies At Risk (Höss et al., 2011, Environ Int 37:940-949). Both indicator tools can be used as Lines-of-Evidence (LoE) in a nematode-based Weight-of-Evidence (WoE) approach for sediment quality assessment. In the presented study these new indices were validated by (1) defining a NemaSPEAR[%] threshold value to draw a line between a good and poor ecological status (2) testing this threshold with contaminated field samples and comparing the NemaSPEAR[%]-index with existing SQGs based on macro-invertebrate data, (3) applying the NemaSPEAR[%] to experimental microcosm data of single chemicals and (4) calibrating TEC-Q thresholds for field samples according to the ecological status (NemaSPEAR[%]). The results showed that a NemaSPEAR[%]-threshold of 30% was able to identify sites with polluted sediments, while the NemaSPEAR[%] correlated well with mean TEC-Q values using SQGNema. A microcosm study showed a dose-dependent response of the NemaSPEAR[%]-index to Zn confirming the indicative power of this index for chemical pollution. Finally, a WoE approach combining these two LoEs applied to a large data set allowed prioritization of sites supporting sediment management actions and confirming the value of these nematode-based indices for quality assessments of potentially polluted water bodies.

O64

How useful can free-living marine nematodes be for Ecological Quality Status (EQS) assessment in transitional waters?

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In the scope of the growing awareness of the threat human activities represent to aquatic ecosystems, there has been a development in environmental policies, mainly focused on the ecological quality assessment. Recently, the role of meiobenthos and nematodes as indicators of ecological quality and their integration in impact and monitoring studies has been valued, being essential to understand the distribution patterns of these communities. This work presents a compilation of research studies performed in an estuarine environment with the main objective of enhancing the knowledge regarding the ecological status and functioning of estuarine systems based on the analysis of meiobenthic and free living nematode communities, both from subtidal and intertidal habitats, using the temperate Mondego estuary (Portugal) as a case study. This estuary has been under environmental pressure since the early 1990's due to different anthropogenic stresses. Spatial and temporal biodiversity of the subtidal meiobenthic community, based on taxonomic and functional approaches showed a reflection of the estuarine gradient, with salinity and grain size composition controlling the distribution of the assemblages. Moreover, the application of Biological Traits Analysis showed the role of oxygen concentration in the distribution of the communities, increasing the knowledge of the functional structure and characterization of nematode communities in the estuary. Following the application of mitigation measures in the estuary, the analysis of the intertidal community revealed a similarity between areas that suffered different pressures (being the variations attributed to factors usually related with estuarine communities' distribution), suggesting that the system has recovered from the early situations. The characterization of the meiobenthos and free living marine nematodes in the studied system allowed the recognition of their potential role as ecological quality indicators, expanding our knowledge on their distribution constraints, ecological and functional characterization while identifying critical features that could be used in an accurate classification of transitional systems.

Application of free-living marine nematodes as ecological indicators according to European directives

O65

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Indices that provide information on the ecosystem resilience and functionality have to be implemented according to European Directives (WFD, 2000/60/EC and MSFD 2008/56/EC). The Water Framework Directive has established the concept of Ecological Quality (EcoQ) as a way to assess the state of health of waters. So far, benthic research has evaluated the EcoQ by applying indices based on macrofauna. Although marine nematodes have been successfully used as bioindicators since 1990 and are among the best meiofaunal candidates for the EcoQ assessment, detailed guidelines still need to be developed. For this reason, a series of nematode descriptors and specific EcoQ thresholds were established by a meta-analysis carried out along the Italian coasts in 2011. These results were used to classify the EcoQ of two shallow coastal habitats of the Adriatic Sea. Rivers were found to be the major disturbance factor in the first area (Central Adriatic Sea), since they are important sources of nutrients and pollutants. The riverine influence was related both to local streams and Po plume. Even if the latter might be considered of lesser extent in that area, its impact at a short distance from the coastline was unexpected. Shannon-diversity Index, Maturity Index, and colonizers−persisters classes highlighted an EcoQ from moderate to bad. Life strategy traits were the most informative faunal descriptors in the case of riverine impact due to their close relation with the environmental variables. The second survey, carried out in the Varano lagoon (Southern Adriatic Sea), showed that grain-size, organic matter, Pollution Load Index and salinity were the main environmental factors affecting nematode assemblages. Maturity Index did not always reflect the distribution of pollutants and trace elements. However, the impact of the San Antonino and San Francesco Canals, the two main inputs of wastewaters from the surrounding agricultural areas, was perfectly revealed by the nematode descriptors. According to the suggested EcoQ thresholds, Lake Varano can be classified as having good to poor EcoQ.

O66

Development of a benthic foraminiferal index of environmental quality for the French Mediterranean coast

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Since 2009 the environmental quality of benthic habitats along the French Mediterranean coast has been monitored every three years in the context of the Water Framework Directive. As part of this survey, benthic foraminiferal faunas have systematically been studied at more than 30 sites. Compared to other meiofaunal or macrofaunal groups, benthic foraminifera offer two main advantages: 1) their high densities in the topmost sediment layer, and 2) the preservation of their shells in the sediment column, allowing the reconstruction of the faunal evolution over the last decennia or centuries. A large effort has been performed recently by the FOBIMO (Foraminifera Bio-Monitoring) consortium to standardize the methodology of sampling and sample treatment (Schönfield et al., 2012, Marine Micropaleontology, 94–95, 1–12). The existing biotic indices are largely based on the relative proportions of stress-tolerant and stress-sensitive taxa. In the case of the French Mediterranean coast, there is a large variability of substrate characteristics, with clayey sediments naturally containing much higher proportions of stress-tolerant taxa than sandy sediments. At present, we are further developing a faunal index which takes this factor into account, by applying a correction for sediment grain size characteristics (Barras et al., 2014, Ecological Indicators, 36, 719–743). Simultaneously, we investigate pathways to exploit the historical development as registered by the succession of dead foraminifera in the sediment column in a more formalized way.

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Responses of meiobenthic communities to sedimentary habitat alteration by dredging waste dumping: a southern Baltic example

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Assessment of the sedimentary environment's potential to recover from a disturbance, such as that produced by dumping of dredging waste onto the seafloor, calls for monitoring the responses of that environment's biotic components to the intensity and persistence of the disturbance. In 2011–2015, we followed changes in community structure metrics (abundance, relative abundance) in two shallow areas off the southern Baltic coast, used as dumping grounds for dredging waste from a new harbour facility. The meiobenthic assemblages showed a rapid response (abundance reduction, composition alteration) to the disturbance at its initial phase, followed by an equally rapid recovery when dumping was temporarily suspended. After the dumping operations were resumed, the responses intensified and expanded spatially, although apparent colonizers (mainly benthic copepods in the meiobenthos) tended to appear intermittently in the disturbed areas. Impoverishment of the benthic communities in the altered habitat persisted after termination of dumping, reflecting the severity of habitat alteration.

Short-term coastal zone management elicits some responsive evidences by benthic fauna at Lake Maryut, Alexandria – Egypt Case Study

O68

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One extensive survey was carried out at Lake Maryut, November 2012, a few months after the completion of two upgrading waste water channels, which redirect the discharge of the Western and Eastern waste water plants to El Mex pump station without mixing with the Lake water. The study aimed to examine the short-term effects of these implementations on meiofauna. A total of 105 sediment samples was collected from five different basins that were subjected to management. Data analysis included two response variables (meiofauna and macrofauna) and fourteen prediactor variables. Predictor variables were categorized into five predictor sets. One geological set included data of grain size, total organic matter, total organic carbon and total phosphorus. The physical set included temperature and salinity data; the chemical set consisted of dissolved oxygen concentration and pH. The biological set included data of benthic microalgae and chlrorphyll *a* as food variable; and fish as predator variables. Fish samples were examined, based on their parasite host, and divided into total fish, fish free parasites and fish host parasites. Results revealed that meiofauna abundances were highest in the basin furthest away from dredging effects and the lowest abundances were recorded at the two sites that were under the effects of excavation. Meiofaunal abundance was significantly different among the basins. Total organic matter was the most important factor significantly affecting benthic fauna assemblages, followed by physico-chemical sets. No relationship was detected between meiofauna and the biological set as a whole whereas meiofauna was correlated with Chl *a* as a predictor variable. A lack of interaction among the biological set could be due to the long life span of some toxic compounds that had been discharged into Lake Maryut in spite of the 1998 governmental ban. Surprisingly, the results revealed a close association between meiofauna and fish host parasites, indicating not only that meiofauna played an important role in the trophic web at Lake Maryut but also that Lake Maryut could be regulated via parasite life cycles rather than microbial cycles. The data set was categorized into five different clusters, based on the relationship between meiofauna and predictor variables, indicating that each basin at Lake Maryut is exposed to different synergetic factors that affect the magnitude and pace of the response of benthic fauna to recent management procedures.

O69

Enzymatic activity on sediments and nematode assemblage responses during seagrass beds habitat recovery following the disturbance of the traditional digging activity of bivalve harvesting

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Sediment digging is an anthropogenic activity connected to the exploitation of living resources in estuarine and marine environments. Knowledge of the functional responses of the benthic assemblages to such physical disturbance is an important baseline for the understanding of the ecological processes of habitat recovery and restoration and for the development of tools for the management of harvesting activities. To investigate the effects of digging activity of the bivalves on *Zostera noltii* seagrass beds, a manipulative field experiment was conducted that included the enzymatic activity of sediments and the associated nematode assemblages. Four plots (two undisturbed serving as control and two dug to collect bivalves - treatment) with 18 subplots were randomly located at seagrass beds in the Mira estuary at the SW coast of Portugal. Samples were randomly and unrepeatably collected from three subplots of each plot on five different occasions, before sediment digging (T0) up to six months after disturbance (T5). Microbial activity in sediments was assessed by determining the extracellular enzymatic activity of six hydrolytic enzymes (sulfatase, phosphatase, b-N-acetilglucosaminidase, b-glucosidase, urease, protease) and two oxidoreductases (phenol oxidase and peroxidase). The microbial community status was also assessed through the measurement of dehydrogenase, which reflects microbial respiration. The nematode assemblages composition, biodiversity and trophic composition on different sampling occasions were also analyzed. The fluorometric and biochemical parameters of the *Z. noltii* plants analysed during the experimental period showed a recovery of the seagrass beds, and an increase of the enzymatic activity of the sediments after disturbance was detected. The nematodes assemblages were similar on all sampling occasions. The seagrass beds and the associated nematodes assemblages showed high resilience to the stress caused by the traditional bivalves digging activity. The obtained results allow the development of a management programme for the commercial fishing activity to maintain good environmental status and minimize the secondary environmental effects on marine and estuarine habitats through the establishment of a baseline for the regulation of the harvesting frequency.

Responses of meiobethic assemblages to nutrient enrichment: a benthic mesocosm experiment

O70

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The impacts of eutrophication and the induced hypoxia, in coastal marine sediments from the oligotrophic eastern Mediterranean, on meiofaunal community structure and diversity were investigated during a high nutrient input mesocosm experiment (160 μM NO_3^- and 10 μM PO_4^{3-}). Hypoxic fine-grained silt-clay sediment, collected from the port of Heraklion bay, and coastal sea water were transferred into total 1.6 m^3 mesocoms (water column 4.5 m depth, 1.5 m^3 volume and sediment 85 lt volume). Water, sediment trap and sediment samples were collected frequently during the 58 days long mesocosm experiment. Significant but delayed response was detected among the sediment biochemical variables due to the eutrophic conditions caused by the addition of nutrients in the water column. Meiofaunal assemblages responded to the organic input, as well, with a time lag. An ongoing significant increase in density was observed in all enriched treatments driven mainly by the dominant taxon of nematodes. Substantial shifts were detected in meiofaunal community structure and diversity. Correlations of meiofaunal densities with particulate matter fluxes indicated that meiobenthic assemblages respond to changes in the trophic status of the water column.

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Part III

Poster presentations

Taxonomy, systematics and evolution of meiobenthos

The Greek Taxon Information System in LifeWatchGreece Research Infrastructure: construction of the preliminary checklists of meiobenthic taxa of Greece

P01

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The Greek Taxon Information System (GTIS) is an application developed by the LifeWatchGreece Research Infrastructure (ESFRI) that has resumed efforts to compile a complete checklist of species reported from Greece. In the framework of GTIS, species occurrence data from Greece are initially extracted from different sources, including regional and Global Species Databases, monographs, and scientific literature, and are then validated by taxonomic specialists. In this work we present the preliminary checklists for meiobenthic marine taxa known to occur within the Greek Exclusive Economic Zone (EEZ). The exhaustive literature review revealed that very few studies from this marine sector report meiobenthic taxa to the species level. More specifically, limited information was found for Gastrotricha, Harpacticoida, Nematoda, and Tardigrada and none for most other meiofaunal taxa. The data made available were found scattered in a small number of literature sources and databases, mostly in old publications and grey literature, covering a small geographical range within the Greek EEZ. The preliminary results of the present initiative reflect (a) the locally limited research effort regarding taxonomic studies of meiobenthic organisms, and also (b) highlight regional gaps in the taxonomic expertise on most meiobenthic taxa in the eastern Mediterranean Sea. Preliminary checklists for meiobenthic taxa produced under GTIS will be published in a special collection dedicated to LifeWatchGreece and will be further disseminated through a scratchpad entitled "Species List of Greece (SpeLog)". Taxonomists who validated the preliminary checklists will be authors in the relevant publications and cited as editors for every record in the GTIS database, along with the data managers who produced the initial data files. The long-term aim of GTIS initiative is to stimulate future research on understudied taxa, filling regional gaps, and thus completing the study of the taxonomy for all species present in Greece. The overall GTIS initiative is open to collaboration with taxonomists from the Greek, European and World scientific community who are interested in contributing to this effort.

P02

World Register of marine Cave Species (WoRCS): a tool for investigating meiofaunal diversity in marine and anchialine subterranean systems

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Marine and anchialine caves are biodiversity reservoirs, harbouring disharmonic faunal communities with high endemism. The study of cave communities is important for understanding the evolutionary history of many taxa; however, our knowledge of cave diversity is highly biased in favour of large-bodied animals, particularly crustaceans. Meiofauna represents an important but often neglected component of cave biodiversity, due to lack of time and expertise for targeted collecting, as well as inadequate taxonomic capacity. Consequently, the significance of meiofauna in cave systems may have been overlooked and so seriously obscuring our understanding of macro-ecological and evolutionary patterns in cave environments. The World Register of marine Cave Species (WoRCS), a Thematic Species Database of WoRMS (www.marinespecies.org/worcs), is here presented as a valuable resource to overcome this problem. The aim of WoRCS is to create a comprehensive taxonomic and ecological database of cave species from worldwide marine and anchialine cave systems, including planktonic and benthic meiofaunal species. The cave-related information is managed by the WoRCS thematic editors in collaboration with the taxonomic editors of WoRMS, who manage the taxonomic content. The database is an open source and includes information on biological, ecological, and occurrence data for all species. Occurrence data are linked to the Gazetteer of the Marine and Anchialine Caves of the World, which is part of the Marine Regions information system and includes geographical and geological information for all studied cave localities. Currently, the database includes approximately 600 meiofaunal species belonging to 21 groups. Most recorded species are amongst hard-bodied meiofaunal groups, such as Podocopida (112 species), Harpacticoida (109 species) and Cyclopoida (96 species). In contrast, few data exist for other groups that are comparatively diverse outside caves, such as Nematoda (41 species) or Platyhelminthes (31 species). The potential taxonomic and geographical biases of our dataset are discussed, along with the different number of cave exclusive species recorded in each group. Our database confirms that further research about cave meiofauna is crucial to an accurate assessment of the biodiversity patterns of cave assemblages, providing support for evidence-based conservation.

An introductory guide to NeMys – the World Database of free-living marine nematodes

P03

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NeMys , the online nematode biodiversity information system erected from the filing cabinet at Ghent University (Belgium) in 1998, is now integrated into the World Register of Marine Species (WoRMS) hosted at the Flanders Marine Institute (VLIZ). This transfer was accompanied by the appointment of an international editor community consisting of expert taxonomists who engaged in the online management of the database. NeMys aims at providing the most authoritative list of names of all marine and estuarine free-living nematode species ever published. Furthermore, in its current format, the website provides the up-to-date classification of species according to the classification of De Ley & Blaxter (2002), with further amendments by Schmidt-Rhaesa (2014), and offers 11 identification keys to genus or species level, ecological information and distribution records in a user-friendly interface. As such, NeMys has become an indispensable tool for ecological and taxonomical research and for educational purposes (e.g. university training in identification of marine nematodes, international workshops in the framework of European research programmes). Registered users have full access to the available taxonomical literature, either through PDFs of entire papers, or as snippets of the relevant information from the literature. This easy access to literature is a major advantage, as the original species descriptions are needed to correctly identify nematodes to species level. The poster aims for the attention of both inexperienced and NeMys-acquainted researchers since it demonstrates both a basic introductory guide to NeMys and some of the most recently added or updated features and tools.

P04

Molecular phylogeny of the Polycystidinae *sensu novo* (Kalyptorhynchia, Rhabdocoela, Platyhelminthes)

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In a recent molecular phylogeny of kalyptorhynchs, Tessens et al. (2014) revised many of the traditionally recognised taxa within the group. The Polycystidinae *sensu novo* now comprises one of the most diverse clades consisting of former members of several different subfamilies within the Polycystididae. However, our understanding of the phylogenetic relationships within the Polycystidinae s. n. is plagued by homoplasy and the absence of key taxa. Here we present a more extensive phylogenetic analysis of the Polycystidinae s. n., including 33 species. Our results are mostly congruent with the analysis of Tessens et al. (2014), but the addition of new species of *Duplacrorhynchus, Yaquinaia, Paraustrorhynchus, Austrorhynchus* and *Polycystis* provides new evolutionary insights. For instance, the Polycystidinae s. n. consists of two major clades with former representatives of the Duplacrorhynchinae occupying basal positions within both of them; therefore, we revised the classification of *Duplacrorhynchus*, *Yaquinaia* and *Parachrorhynchus. Austrorhynchus* is monophyletic, while *Paraustrorhynchus* is paraphyletic with respect to *Alcha evelinae.* Our results confirm widespread convergence of key diagnostic characters in the genital system of most members of the Polycystidinae s. n. We address these findings by reinterpreting different structures in the male and female reproductive systems in order to reconcile comparative morphology with molecular phylogeny.

P05

An 18s and 28s-based clock calibration for marine Proseriata (Platyhelminthes)

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Interstitial meiofauna is among the most diverse and species-rich components of marine biodiversity. Ancient vicariance events, followed by evolutionary stasis, were hypothesized to be responsible of the observed patterns; this, however, would imply a surprisingly old phylogenetic age for these species. The modern molecular phylogenetic approach for dating and solving evolutionary divergence between species is based on the molecular clock hypothesis (MCH), which hypotheses a relatively constant rate of molecular evolution. Unfortunately, opportunities for the calibration of the molecular clock are relatively rare, especially in the absence of fossil record. For this purpose, in marine organisms, the so-called geminate species (i.e., pairs of morphologically similar sister species that occur on opposite sides of a geographic

barrier) represent a powerful tool, which allows calibration points for molecular clock. The first attempt to calibrate the molecular clock in taxa belonging to meiofaunal microturbellaria (Platyhelminthes: Proseriata) based on geminate species is presented here. Two species pairs from both sides of the Isthmus of Panama (rise for the last time about 3.1–3.5 million years ago) have been used: *Minona gemella* (Caribbean) and *Minona* cf. *gemella* (Pacific); *Parotoplana* sp. nov. 1 (Caribbean) and *Parotoplana* sp. nov. 2 (Pacific). The mutation rates per million years were estimated for both geminate species pairs on two ribosomal regions, the complete nuclear small subunit rDNA (18S) gene and the partial nuclear large subunit rDNA (28S) gene fragment (spanning variable domains D1–D6). Similar values of mutation rates per million years were found in both species pairs, ranging 0.12–0.16% for 18S and 0.49–0.52% for 28S. The values obtained were used as calibration points at minimum age, in order to estimate the divergence times within the phylogenetic tree of the whole dataset, and tested on three cases of trans-American (not-geminate) species from Pacific Panama and SE Brazil, belonging to the genera *Kata*, *Archimonocelis* and *Duplominona*. They consistently showed higher divergence times (ranging 9.4–17.9 Myr) than geminate, trans-isthmian pairs. These results suggest potential usefulness of our molecular clock calibration, for future research on phylogeography and evolution of Proseriata.

The structure and function of an enigmatic 'dorsal organ' in the kinorhynch *Cateria styx*

P06

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The Kinorhyncha is a group of exclusively meiofaunal animals characterized by a highly conserved body plan including a head, neck and trunk. The trunk is always composed of 11 articulated segments that carry spines, sensorial structures and glands arranged in species-specific patterns. The rare species *Cateria styx* is peculiar among kinorhynchs because it has a bizarre dorsal organ situated between the trunk segments five and six. The dorsal organ was originally discovered by the German scientist Gerlach in 1956 but has never been studied in detail. Here we comprehensively describe the structure of the dorsal organ using a combination of approaches, including light microscopy, confocal laser scanning microscopy, transmission electron microscopy, scanning electron microscopy, and behavioural observations. These data allowed us to propose hypotheses for the function(s) of the dorsal organ within the ecological context of this particular species, adapted to live 50–100 cm depth in the upper littoral zones of sandy brazilian beaches.

P07

Detailed reconstructions of the brain structure and neurotransmitter reactivity in three species of meiofaunal Dinophilidae (Annelida) reveals unexpected high organizational variation

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Neurotransmitters, -hormones, or -modulators are employed by invertebrates and vertebrates and are thereby broadly used in the analysis of nervous systems. Often these functions are covered by neuropeptides, which show similar immunoreactivity patterns in the nervous system among distantly related animals, indicating a common neuropeptidergic function and origin. Yet this specificity has neither been put to a test with a broad range of neuropeptides, nor in meiofaunal annelids having a compact brain and low cell number. We therefore assessed the immunoreactivity of 13 neuropeptidergic antibodies, which we mapped on a detailed reconstruction of the brain and nervous system in three closely related microscopic annelids (*Dinophilus gyrociliatus*, *D. taeniatus* and *Trilobodrilus axi*). Each of the tested antibodies facilitated specific reactivity in at least one of the investigated species, with *D. gyrociliatus* expressing the highest number of neuropeptides (12 out of 13) as well as most neuropeptidergic cells in the brain (210 as compared to 100 and 101 in *D. taeniatus* and *T. axi*, respectively). Most of the tested neuropeptides are present in the same parts of the nervous system (brain, ventral nervous system, peripheral nerves and/or stomatogastric nervous system) in all three species. The distribution of labelled cells within the brain expressed high interspecific variation, consolidated by intraspecific consistency. The small size of the brains containing 650–750 cells made it possible to map each immunoreactive cell on a DAPI template, revealing no overlap of the peptides tested for. This suggests that a nerve cell can be specific to one neuropeptide and possibly to one function – even in a system consisting of few cells. The detailed neural reconstruction revealed high commissural complexity of the compact meiofaunal brain. The tested neurotransmitters are mostly scattered throughout the entire brain, thereby not clearly demarcating compartments or functional regions. Additionally, the surprising finding that the neuropeptidergic patterns vary among closely related species – unlike the conservation of e.g. the serotonergic pattern – probably indicates a more dynamic evolution of the neuromodulatory landscape than previously expected.

Integrative re-description of *Turbanella hyalina* (Gastrotricha: Macrodasyida) as baseline for future phylogeographic studies

P08

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Recently, it could be proved that genetic cryptic species do exist among morphologically defined species of the phylum Gastrotricha. An early study of the genetic distances between three geographically separated Atlantic populations of the species *Xenotrichula intermedia* shed some initial light on the reported cosmopolitan distribution of many meiofaunal species. Later, distinct differences in the muscle arrangement were detected in two other populations of *X. Intermedia.* These distinct morphological differences were interpreted as an indication for the presence of further ‘cryptic species’. A recent molecular taxonomic survey of some species of the genus *Turbanella* unravelled two independent mitochondrial lineages within *Turbanella hyalina*, the first described marine gastrotrich species of the taxon Macrodasyida. This result has been confirmed by further analysis of a slowly evolving nuclear marker. Hence, there are at least two cryptic genetic species within the nominal species *T. hyalina.* Since the original description by Schultze (1853) is incomplete and does not contain, for instance, data of variability of important taxonomic characters, a re-description was overdue. We conducted an integrative description of *T. hyalina* covering light microscopic, SEM (internal and external morphology), and CLSM investigations (muscular system). Furthermore, an analysis of COI gene sequences obtained from specimens of the original type locality was used to identify the corresponding genetic lineage. The results will serve as baseline for all upcoming phylogeographic and integrative taxonomic studies including this species. For instance, a recent morphometric analysis of a Baltic population of *T. hyalina* yielded a lower number of anterior and lateral adhesive tubes compared to the population from the type locality. This discrepancy could already indicate the existence of another cryptic species and will be tested with mitochondrial and nuclear sequence data in the future.

Phylogenetic analysis of *Xenotrichula* (Xenotrichulidae: Gastrotricha) based on morphological data

P09

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Gastrotricha is a taxon of free-living microinvertebrates present in freshwater, estuarine and marine environments. Currently, this taxon includes more than 800 species divided in two orders, Macrodasyida and Chaetonotida. Chaetonotida comprises about 450 species of tenpin-shaped gastrotrichs, often with an ornamemted cuticle and a single pair of posterior adhesive tubes; some are found in marine and brackish waters, but most (ca. 2/3) live in freshwater habitats. Among the marine taxa, the cosmopolitan family Xenotrichulidae is composed of three genera (*Draculiciteria, Xenotrichula* and *Heteroxenotrichula*) containing 27 species. The genus *Xenotrichula* is the most speciose genus and traditionally divided in two morphological subgroups: the *Xenotrichula* subgroup is characterized by the presence of locomotory cilia of similar size, 2–3 pairs of sensorial cephalic tufs, an anterior pharyngeal bulb, intermedia-like scales (type: *X. intermedia*), a small cephalion, and a bidentade hypostomium; the *Velox* subgroup is defined by subterranea-like scales (type: *X. subterranea*) and the presence of long tentacles. This validity of these subgroup divisions has never been formally tested in a phylogenetic framework. Here, we investigate these subgroup relationships using TNT phylogenetic software. A total of 17 species (two as outgroup) were coded for 37 multistate or binary morphological characters; some characters were contingent. Parsimony analysis with implied weighting produced 12 most-parsimonious cladograms. The *Velox* subgroup formed a monophyletic clade defined by the presence of tentacles, subterranea-type scales and "Kammantiger Zacken". The *Xenotrichula* subgroup appeared paraphyletic but contained a monophyletic subclade of two species: *X. lineata* and *X. paralineata*. Character optimization revealed that tentacles and subterranea-type scales are derived within their lineages. Further testing using additional morphological characters (e.g., muscle patterns, ultrastructre) and/or molecular sequence data (CO-1) should lead to better resolution and therefore a better understanding of evolutionary patterns within the genus.

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P10

A morphological and molecular contribution on benthic ostracods with emphasis on the populations of Caribbean mesophotic reefs

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Ostracods are tiny crustaceans enclosed in a bivalve shell that are found worldwide inhabiting many aquatic environments. The taxonomy, distribution and ecology of marine ostracods remain incomplete in the Caribbean, even though they are among the most successful microcrustaceans of marine ecosystems. In an effort to increase our knowledge of the biodiversity, abundance and distribution of benthic ostracods, several sediment samples from mesophotic coral ecosystems (MCEs) of Puerto Rico and US Virgin Islands were collected at different depths (30–102 m) using technical diving. Ostracods were either hand sorted directly from the sediment or after a

Ludox AM-30 colloidal silica resuspension and centrifugation step, used for mass-extraction of meiofauna and macrofauna. The highest densities of ostracods were found in the deepest samples (≥ 67 m) and these were the most abundant and diverse assemblages. The total community of ostracods collected belongs to the subclasses Myodocopa and Podocopa. The Myodocopa was represented with specimens of the families Cylindroleberididae, Sarsiellidae, Cypridinidae and Rutidermatidae; on the other hand, some of the families that represented the Podocopa were Bairdiidae, Macrocyprididae, Pontocyprididae, Cytherellidae and Loxoconchidae. The subclass Podocopa showed the highest number of individuals and species. Using a morphological and molecular barcoding approach (28S rDNA), we provide the first report of the biodiversity of ostracods in the MCEs of NE Caribbean.

Is the mitochondrial Cytochrome Oxidase subunit I, a useful phylogenetic marker in Copepoda?

P11

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The mitochondrial Cytochrome Oxidase subunit I (COI) remains the most representative gene in GenBank for metazoans. Its wide use reflects the availability of useful universal primers across phyla and the fact that COI is the flagstaff of DNA barcoding. DNA barcoding is an important tool to biodiversity studies for the last 20 years, especially if it is integrated in a taxonomic framework, because it provides a complementary and independent data set to morphology for the understanding of evolutionary and genetic relationships within and among species. We are exploring the usefulness of this mitochondrial gene in recovering phylogenetic relationships among higher taxa in Copepoda. The phylogeny of Copepoda at the higher level will be resolved with higher confidence with genome wide data but surprisingly, COI is recovering monophyletic taxa at the Order level. Results corroborate to an extent a recently phylogeny based on partial 28S. We discuss the limitations of a phylogenic approach using single or a few genes for such a highly divergent taxon.

P12

Phylogenetic revision of the taxon *Paralaophontodes* Lang (Copepoda: Harpacticoida: Laophontodinae)

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Lang (1965) established the taxon *Paralaophontodes* Lang, 1965 within Laophontodinae (Copepoda, Harpacticoida, "Ancorabolidae") to relocate *Laophonte echinata* Willey, 1930 into that new genus as *Paralaophontodes echinata* (Willey, 1930). Nowadays the taxon encloses three species, namely *P. echinata*, *P. elegans* Baldari and Cottarelli, 1986, and *P. exopoditus* Mielke, 1981. Bozic (1964) described *Laophontodes robustus* Bozic, 1964 from the Island La Réunion (Indic Ocean), which was later on displaced into *Paralaophontodes* by Lang (1965). However, already Lang (1965) doubted on the distinct specific status of *P. robustus* (Bozic, 1964), pointing to its strong similarity with *P. echinata.* Lastly, Wells and Rao (1987) formally synonymized *P. robustus* with *P. echinata.* On the other hand, three additional species: *Laophontodes armatus* Lang, 1936, *L. hedgpethi* Lang, 1965, and *L. psammophilus* Soyer, 1974 are still placed in the genus *Laophontodes* T. Scott, 1894 despite their strong morphological similarity with *Paralaophontodes* species. Careful comparison reveals, however, that all named species share several apomorphies. A detailed phylogenetic discussion is presented, leading to the conclusion that *Laophontodes armatus*, *L. hedgpethi*, and *L. psammophilus* have to be displaced into *Paralaophontodes.* Moreover, justification for the re-establishment of *P. robustus* is given.

P13

A new species of *Paralaophontodes* Lang (Copepoda: Harpacticoida: Laophontodinae) of Chiloé Island (Chile)

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In the frame of a huge phylogenetic revision of the paraphylum "Ancorabolidae" Sars, 1909 the taxon Laophontodinae Lang, 1944 is object of a recent detailed reconsideration. In that context a new species of the laophontodin taxon *Paralaophontodes* Lang, 1965 collected in the northwest of Chiloé Island (Chile) is described. The new species can doubtlessly be assigned to *Paralaophontodes*, sharing all generic autapomorphies, among others e.g. (i) the presence of characteristic sclerotized processes on the cephalothorax and body somites; (ii) the occurrence of a shock of hair-like setules dorsally on cephalothorax; (iii) maxillipedal syncoxa lacking an apical seta, and the shape of the first swimming leg that is (iv) strongly strengthened and (v) shows a distinctly elongated second segment. Within *Paralaophontodes*, the new species cannot be assigned to any of the known species, due to the complete loss of an endopod at the third swimming leg (P3) in the female. That derived character is shared only by *Paralaophontodes robustus* (Bozic, 1964); however, both species differ

regarding the following features: (i) cephalic lateral extensions strongly triangular in *P. robustus*, but of moderate triangular extension only in *Paralaophontodes* sp. nov.; (ii) pedigerous somites bearing swimming legs 2–5 dorsally with tiny socles in *P. robustus*, while bearing strong sclerotized processes in *Paralaophontodes* sp. nov.; (iii) P1 exopod-2 with 4 bare geniculate setae in *P. robustus* but with 5 geniculate setae in *Paralaophontodes* sp. nov.; (iv) P2 and P3 exopodal segments fused in *P. robustus*, but separated in *Paralaophontodes* sp. nov. Therefore, the erection of a new species to allocate the Chilean specimen is well-justified.

An inventory study on meiofauna around Dokdo island, Korea

P14

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Dokdo is an oceanic volcanic island which is located in the southwestern part of the East Sea, 216.8 km far from the mainland of Korea. For pursuing the conservation of biodiversity and a sustainable use of bio-resources around Dokdo, an extensive survey was carried out. Its main aim was to establish a comprehensive inventory system on the basis of providing the species list of biological resources, securing various samples, and discovering unknown organisms. As a result of the one-year survey on marine benthic meiofauna around Dokdo island, eight putative new species were discovered from the fine sand to coarse shell crumbs in the subtidal sediments at 6 to 132 m depth. They consisted of three gastrotrich, two harpacticoid, two poecilostomatoid, and one cyclopoid species, respectively. This presentation provides a comprehensive species list of meiofauna hitherto known from Dokdo island, Korea, with illustrations or photomicrographs of the above-mentioned species as well as photographs showing ecological aspects around the seas of Dokdo island.

P15 Two new ancorabolid species (Copepoda: Harpacticoida: Ancorabolidae) from South Korea

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Members of the predominantly deep-water family Ancorabolidae are among the most morphologically distinct and ornate copepods in the Harpacticoida. During an extensive faunistic survey of Korean marine benthic copepods, two new species of Ancorabolidae were recorded, belonging to the genera *Arthuricornua* Conroy-Dalton, 2001 and *Dendropsyllus* Conroy-Dalton, 2003, respectively. Both sexes of each species were represented in the muddy sediment collected at 100 m depth off the south coast of Korea. *Arthuricornua* n. sp. differs from the type and only species, *A.anendopodia* Conroy-Dalton, 2001, by the presence of three pairs of elongate dorsal processes on the second to fourth pedigerous somites, the absence of the inner seta on the third endopodal segment of legs 2–4 in the female, and the presence of a hyaline membranous extension near the ventral posterior margin of the caudal ramus. *Dendropsyllus* n. sp. is differentiated from its three congeners on the basis of the lateral armature on the antennary endopod (two spines and one seta), the absence of the inner seta on the third endopodal segment of leg 2, and the 1-segmented condition of the endopods of legs 3–4. This contribution presents the first report of the subfamily Ancorabolinae in East Asia. Concise differential diagnoses accompanied by illustrations of both sexes are given as well as remarks on relationships with previously described species. A key to species of *Dendropsyllus* is presented.

P16 A new species of the genus *Sarsamphiascus* Huys, 2009 (Copepoda: Harpacticoida: Miraciidae) from a sublittoral zone of Hawaii

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A new species of *Sarsamphiascus* Huys, 2009 was collected from sandy sediments of Hawaii at 14 m depth. While the new species was morphologically most closely related to *Sarsamphiascus kawamurai* (Ueda & Nagai, 2005), two species were distinguished by the combination of following morphological characteristics: the elongated segments of antennule in the new species, the position of inner seta of P5 exopod in both sexes (more proximal in *S. kawamurai*), the genital double-somite with microspinules on ventrolateral surface (without in *S. kawamurai*), the caudal ramus with few spinules along the distal margin (without in *S. kawamurai*), the terminal caudal setae with ornamentation (naked in *S. kawamurai*).

A new species of *Arenosetella* Wilson, 1932 (Harpacticoida: Ectinosomatidae) from east coast of Korea P17

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A new species of the genus *Arenosetella* Wilson, 1932, belonging to Ectinosomatidae Sars, 1903, is described from the specimens collected from interstitial habitat of sandy beach in Sokcho-si, Gangwon-do, Korea. There are 23 species and subspecies described within the genus *Arenosetella.* This genus has common morphological characters: 1) the third exopodal segments with two outer spines, 2) the exopod of P5 with three setae, 3) the P5 with one surface seta, and 4) the dorsal armature of paired claws, lappets or spiniform processes on anal somite. *Arenosetella* n. sp. has a superficial resemblance with *A. bidenta* Itô, 1972, however it differs from the latter in following characters: 1) rostrum reaching to end of first segment of A1 (reaching to end of third in *A. bidenta*), 2) the dorsal surface of P2−P5 bearing somites with two or three horizontal rows of spinules (with one row of spinules in *A. bidenta*), 3) the dorsal surface of genital double somite with two rows of spinules (with four rows of spinules in *A. bidenta*), 4) the tip of mucroniform processes on anal somite reaching to at least end of caudal rami (reaching to distal half of caudal rami in *A. bidenta*), 5) the caudal rami with two spines near inner distal corner (with one spine in *A. bidenta*), and 6) the P4 basis with outer seta (described "absent?" in *A. bidenta*).

A new genus of Leptastacidae T. Scott, 1982 (Copepoda, Harpacticoida) from the sand beach of Yellow Sea, Korea P18

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For the study of diversity of meiofauna, we collected sediment samples in a sandy beach. The research was conducted at five stations using acrylic corer. Among the nine taxa of meiofauna found (Nematodes, Copepods, Foraminiferans, Polychaetes, Oligochaetes, Ostracods, Cumacean, Amphipods, and Tardigrades), nematodes and copepods were the most abundant. In this study, eight families (Ameiridae, Argestidae, Cletodidae, Cylindropsyllidae, Ectinosomatidae, Leptastacidae, Miraciidae, and Tisbidae) of Harpacticoids were collected. In the family Leptastacidae, we recognized a new species belonging to a new genus, which is closely related to the genera *Paraleptastacus*, *Cerconeotes*, and *Steroxiphos.* This species has unique character in combination with the setal formula of swimming legs. In addition, the new species is distinguished from the congeners by the fused caudal setae IV and V, and the shape of female P5, and caudal ramus shape.

P19

A new genus (Crustacea: Copepoda: Harpacticoida) from Jeju island, Korea

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A new harpacticoid copepod is sampled and described from off Jeju Island, Korea. This species displays a unique set of characters, including clearly demarcated rostrum from the cephalosome, the spinular row on the rostrum, the well developed frill along the posterior margins of each body segment except for cephalosome, long and cylindrical caudal rami, only four segmented female antennule, the paired genital aperture in the female, no sexual dimorphism in the legs P1–P4, the highly reduced P5 and P6 in the male. The above combination of characters differs the present new species from any extant genera within the order Harpacticoida, and therefore a new genus is proposed for the new species. The present new genus shares synapomorphic characters with the members of Rhizothricidae, and provisionally was allocated in the family Rhizothricidae.

P20

A new species of the genus *Echinolaophonte* Nicholls, 1941 (Copepoda: Harpacticoida: Laophontidae) from Jeju Island, Korea

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A new species of *Echinolaophonte musa* sp. nov. is described on the basis of materials collected from the subtidal sandy bottom (30 m depth) at Jeju Island, Korea. The present new species is similar to other species of the genus in having single large recurved process on posterior surface of cephalothorax, paired spines dorsoventrally on each body segments, large and expanded rostrum, 6-segmented antennule, long and slender leg 1 basis as long as enp-1, and 3 setae on leg 5 exopod. However, the new species differs from its congeners as follows: strong projections on cephalothorax, the shape of dorsal projections on each segment excluding anal segment, ratio of length to width in caudal ramus, very short exopod comparing with enp-1, bifid long rostrum, and very small 4th innermost seta on baseoendopod of leg 5. It becomes to be the second member of the East Asia. In addition, the worldwide distribution of the *Echinolaophonte* is provided and discussed.

Two new Asian species of the genus *Scottolana* Huys, 2009 (Copepoda: Harpacticoida: Canuellidae)

P21

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Two new species of Canuellidae belonging to the genus *Scottolana* Huys, 2009 are described from specimens collected from Gusipo Beach (muddy sand) in Korea and from Kata Beach (fine sand) on Phuket Island in Thailand. So far 14 species are currently known in the genus, of which only two species *S. bulbifera* (Chislenko, 1971) from Russia, China, and Korea and *S. geei* Mu and Huys, 2004 from China are recorded in Asia. Those new species, *Scottolana coreana* sp. nov. and *S. huysi* belong to the *longipes*-group represented by the presence of two postgenital segments in female and caudal ramus with hook-like extension on the inner board. *Scottolana coreana* sp. nov. closely resembles the description of *S. geei.* However it is easily distinguished by characters as follows: (1) the ratio of caudal ramus, and length of its setae I and VII, (2) setules on P1 enp-2, (3) ornamentation on inner margin of P1 exp-1, and (4) shape of genital field in both sexes. *Scottolana huysi* sp. nov. is also closely related to *S. geei.* However, it is unique and different from *S. geei* by (1) indistinctly 4-segmented antennule in the female, (2) 5-segmented male antennule, (3) larger genital field in the female, (4) the absence of the anterior surface pore on the female P4 exp-3, and (5) the morphology of caudal seta II, being long and plumose, with a bulbiform base in the female only.

Genus *Hemicytherura* (Ostracoda: Podocopida: Cytheruridae) from Hujung beach, Korean East Coast

P22

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The genus *Hemicytherura* (Podocopida, Cytheruridae) so far has about 110 species distributed worldwide. This number includes Recent and as well as Cretaceous fossil species. The genus is characterized by a prominent asymmetry between valves and strong ornamentation with numerous ridges on the valve surface. Animals are of a comparable small size – usually less than 1mm, and they are commonly found in marine interstitial waters. Five species have been reported from Korea so far: *H. cuneata* Hanai, 1957, *H. kajiyamai* Hanai, 1957, *H.* cf. *clathrate* (Sars, 1866), *H. tricarinata* Hanai, 1957, and *H. yeosuensis* Choe, 1985. Those species were only listed as a part of ecological study and no taxonomic description has been provided. Here we report a presumably new species of the genus *Hemicytherura* collected from interstitial waters of the Hujung beach, Korean East Coast. The species is closely related to *H. cuneate* Hanai, 1957, *H. kajiyamai* Hanai, 1957, and

H. tricarinata Hanai, 1957. The similarity includes ornamentation of the valves and the morphology of appendages. However, our species has a hemipenis which clearly distinguishes it from the above species. Here we provide its taxonomic description and a key to the recent species from East Asia.

P23

Checklist of freshwater Gastrotrichs from South Korea

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Freshwater gastrotrichs are known from various habitats as planktonic and benthic fauna, and approximately 480 species are recorded consisting of two macrodasyid and others chaetonotid in the world. Faunistic studies on freshwater gastrotrichs from Korea, since the first report by Lee and Chang in 2000, have been accomplished. As a result, 16 species of seven genera in three families are currently recorded from South Korea. In this presentation we provide a checklist of freshwater gastrotrichs hitherto known from Korea, with a revised key to the Korean species. We also present illustrations and photomicrographs of some taxonomically significant species belonging to the genera *Chaetonotus*, *Setopus*, and *Neogossea*.

P24

First Record of interstitial polychaete, genus *Pharyngocirrus* (Annelida: Polychaeta: Saccocirridae), from the East Sea, Korea

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Interstitial polychaetes are meiobenthos living in marine sand and gravel habitats. It is composed of eight families that are not closely related to each other. In Korea, any faunistic or taxonomic study on this group has not been performed. Specific figure of Saccocirridae is elongated and slender body with numerous similar segments, small prostomium with two long tentacles, two small brown eyes and pygidium with adhesive structures. Saccocirridae is divided into two genera, *Saccocirrus* and *Pharyngocirrus*. Two genera could be distinguished by both morphological characters and habitats. We collected interstitial polychaete specimens from Oeongchi Beach, Sokcho-si, Gangwon-do, Korea. Our specimens belong to *Pharyngocirrus* Di Domenico, Martínez, Lana and Worsaae, 2014. Twelve species have been described in the genus *Pharyngocirrus*. This genus is characterized by the presence of unilateral gonads, pharyngeal muscular organ and anterior ventral ciliation. Our specimens are believed to be *Pharyngocirrus uchidai* Sasaki, 1981 except for the number of pygidial adhesive papillae.

A new species of *Microcharon* Karaman, 1934 (Isopoda: Asellota: Microparasellidae) from marine interstitial water, Shizuoka, Japan

P25

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A new species of *Microcharon* Karaman, 1934 (Isopoda: Asellota: Microparasellidae) was discovered from Miho-Masaki beach, Shizuoka, Japan and this is the first record of the genus *Microcharon* in East Asia. Most of other known species have been described and known for Mediterranean Basin. The new species, *Microcharon* sp. nov., was distinguished from its congeners by having 1) degraded article 6 of the antennules, 2) antennal flagellum composed of 12, 3) endite of the maxilliped with no hooks on proximomedial margin, 4) distolateral lobe of male pleopod 1 rounded, 5) exopod of male pleopod 3 very elongate, reaching beyond the endopod apex. In this study, the new species was described herein and compared with its most closely related European congeners. In addition, we provided partial sequences of the 18S rDNA which is the first such data for the entire family.

Following the path of Karl Zelinka: have the kinorhynch fauna of Naples changed 100 years later?

P26

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Prof. Karl Zelinka, from the University of Vienna, published a Monograph on the phylum Kinorhyncha in 1928, largely based on materials sampled from Naples and Trieste. Many of his species descriptions still are valid, but the original locality has not been sampled again. We sampled the bay of Naples extensively for kinorhynchs, following the sampling sites of Zelinka and adding several additional localities. A detailed account on the species diversity has been accomplished, recording coincident, new and missing records in order to test the stability of kinorhynch populations after a long period of time.

P27

A new world opens up: deep-sea Kinoryncha from the Polymetallic Nodule fields in the CCZ

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Kinorhyncha is an exclusive meiobenthic phylum of free-living marine ecdysozoan of small size, 0.1–1 mm. Kinorhynchs or mud dragons appear from the intertidal to the deep-sea bottoms all around the world. Despite the great advances in the kinorhynch research during the recent years, most of the 210 described species were recorded at relatively shallow waters whereas the deep-sea kinorhynch fauna is still largely unexplored. This fact reflects just a bias of sampling strategies rather than true distribution. Kinorhynchs at the deep-sea bottoms are not very abundant but, as other abyssal communities, they are characterized by extremely high diversity: to date and summarizing, three new genera and 16 new species, most of them belonging to weird genera, have been identified from 17 sample stations collected from the bathyal to the abyssal zone. Our work is focused on the polymetallic nodule fields along the CCZ region, a deep-sea area mostly unexplored with special environmental conditions, such as the presence of singular habitats formed by the nodules. Therefore, the amount of expected new taxa at the area may be even higher than in other samples collected from soft sediments. The present contribution is the first step of a wider project with a dual aim: 1) to increase our knowledge of deep-sea kinorhynch diversity and particularly in polymetallic nodule fields; 2) to check whether some taxa are associated to a specific environment (nodule vs. sediment); 3) and if so, to predict the potential impact of anthropogenic disturbances (such as seafloor mining activities for nodules). To do this, samples from around 80 stations were studied, all of them collected using a multicorer during the SO205 expedition in 2010, 4095–4405 m depth. According to the known information about the deep-sea, together with the special environmental conditions at the CCZ area and the idea that we only know 20% of the kinorhynch diversity, we expect that the study of the material from the CCZ area give rise to a huge amount of new kinorhynch taxa, some of them probably showing bizarre morphological traits, which lead us to understand better the evolutionary pathways into the group.

A taxonomic evaluation of subtidal meiofauna in Turkey with the description of a new species of *Cephalorhyncha* (Kinorhyncha: Cyclorhagida) from Aegean coast of Turkey P28

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Effective conservation and management of biodiversity and ecosystems depends largely on the taxonomic determination of species composition. Unfortunately, insufficient taxonomic information intercepts our capacity to make informed decisions about conservation and sustainable management of biodiversity and ecosystems. Turkey has numerous sandy beaches distributed along its coastline, but the marine meiofauna has been poorly explored despite the fact that the country has a vast coastline of about 8,300 kilometres. The present state of knowledge on Turkish subtidal meiofauna will be discussed. From a taxonomic perspective, mostly the Copepoda has been studied to a greater extent. Oppositely, the marine and meiobenthic Kinorhyncha has been very poorly explored. Kinorhynchs are found in different habitats, but generally in muddy sediment. The phylum comprises about 222 species within 23 genera. We contribute to the knowledge of kinorhynch biodiversity by describing *Cephalorhynca* sp. nov. from Aegean coast of Turkey. Samples were collected using the Karaman–Chappius method from intertidal zones of two different localities. The new species distinguish from the other species of genus by having flosculi in midventral positions on segment 3–8, by differences in its general spine and sensory spot positions, and in its zoogeographical distribution and habitat. Until now, species of *Cephalorhyncha* are known from the Pacific Ocean only, hence, the record of the genus at the Aegean Coast, makes it new not only for Turkey, but also for Europe and the Mediterranean. The new species of *Cephalorhyncha* represents the fourth kinorhynch species recorded from Turkey, and increases also the number of known *Cephalorhyncha* species to four.

First data on the presence of Mystacocarida (Crustacea) in Turkey with notes on their ecology and distribution P29

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Mystacocarida is a class of tiny crustaceans that live in interstitial water between sand grains of marine beaches, but they are commonly found through many parts of the world. So far, only 10 species distributed in two genera namely *Derocheilocaris* and *Ctenocheilocaris* have been described. Searching the previously published literature revealed no data about the presence of mystacocarid in Turkish Seas. Extensive sampling along the Turkish coasts revealed several mystacocarid populations

identified as *Derocheilocaris* sp. In order to make ecological evaluations, monthly meiobenthic samples were made by Karaman–Chappius method from Alata beach and the results were compared throughout one year period. Temperature, conductivity, salinity, pH and dissolved oxygen measurements were taken by portable analyzers. The analysis of the physical and ecological parameters revealed no significant relationship between the presence of mystacocarids and physicochemical parameters. It is concluded that the mystacocarids demonstrate very patchy distribution along the sandy beaches and a more comprehensive ecological studies must be carried out in order to find relationship between mystacocarids and ecological parameters.

P30

Towards the cosmopolitanism of *Florarctus kwoni* Chang & Rho, 1997 (Tardigrada, Halechiniscidae): a new record from Turkey

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Florarctus kwoni was originally described from Palawan Island, the Philippines and later reported from Moorea, French Polynesia. During examination of interstitial samples of intertidal zones of Turkey, *F. kwoni* was discovered for the second time since its original description. The detailed morphological comparisons have revealed that the Turkish populations of *F. kwoni* are conspecific with other populations of *F. kwoni* reported from distantly related parts of geographical regions. Confirmed disjunct distribution of true interstitial tardigrad species recorded from widely separated parts of the earth is an interesting case and raising questions in need of answers. Possible mechanisms responsible for the distribution of *F. kwoni* in such widely separated parts of the world are discussed. Turkey has numerous sandy beaches distributed along its very long coastline of about 8,300 kilometres, but the marine meiofauna has been poorly understood. Almost nothing is known about the taxonomy of Turkish meiofaunal tardigrads so that this is fifth marine tardigrad species from the country.

A new record of water bears from Turkey, *Megastygarctides setoloso* Morgan & O'Reilly, 1988 (Tardigrada: Arthrotardigrada)

P31

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The tardigrade fauna of Turkey is very poorly known and only few studies were conducted up to now, mostly on terrestrial species (Maucci 1972; 1974; 1978). The results of a single research on marine Tardigrada in Turkey were published by Kharkevych & Sergeeva (2013) and these authors reported only two species: *Dipodarctus subterraneus* (Renaud-Debyser, 1959) and *Tanarctus ramazzottii* Renaud-Mornant, 1975, from deep waters of Bosporus Strait. This is the first record of the very rare Arthrotardigrade *Megastygarctides setoloso* Morgan & O'Reilly, 1988 from Turkey (Black Sea). Up to present, a confirmed locality of this species is Atlantic Ocean (Scotland) (Kaczmarek et al. 2015). Kharkevych (2013) reported *Megastygarctides* conf. *setoloso* Morgan & O'Reilly, 1988 from the Black Sea (Crimean Peninsula) but this locality needs a confirmation. In the present research a few populations of *M. setoloso* were collected by push cores from three stations at a depth of 2–4 m in August 2015. Samplings were done in the framework of a seasonally conducted meiobenthos project supported by TUBITAK (The Scientific and Technological Research Council of Turkey) and MoS (Ministry of Science of Montenegro) (Project Number: 114Y376). Here we present the first comprehensive morphological study (based on imaging in Scanning Electron Microscopy (SEM), Phase Contrast (PCM) and Nomarski Contrast (DIC) Light Microscopies) of this species along with some ecological remarks.

Arthrotardigrades from off the coast of Kii Peninsula, Honshu, Japan

P32

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Most marine representatives of the phylum Tardigrada belong to the order Arthrotardigrada (Class Heterotardigrada). This order is known for its high morphological diversity harbouring approximately 180 species. Reports of this group from the Japanese coast (Northwest Pacific) are limited and restricted to relatively easy accessible water depths (0–40 mbsl). To enrich information of arthrotardigrades in Japanese waters, I have examined sediment samples collected off the coast of

Kii Peninsula, Honshu, Japan from the water depths of 97–88 m, 177–175 m and 169–164 m bsl. The following eleven species (including some undescribed species) some genera (including one undescribed genus), five sub-families and four families were found: *Batillipes* sp. (Batillipedidae), *Coronarctus* sp. (Coronarctidae), an undescribed genus and species (Dipodarctinae, Halechiniscidae), *Parmusa* sp. (Euclavarctinae, Halechiniscidae), *Chrysoarctus* sp. (Halechiniscinae, Halechiniscidae), *Angursa clavifera*, *Raiarctus* spp. and *Tholoarctus* sp. (Styraconyxinae, Halechiniscidae), *Actinarctus* sp. (Tanarctinae, Halechiniscidae) and *Neoarctus* sp. (Neoarctidae). Neoarctidae and *Chrysoarctus* (Halechiniscinae, Halechiniscidae) are reported for the first time from the Pacific. Euclavarctinae (Halechiniscidae) is reported for the first time from the Northwest Pacific. The morphology of the undescribed taxa is discussed.

P33

Marine Tardigrada of the White Sea, North Russia

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Five species of marine tardigrades are recorded in the White Sea, three of them was discovered for the first time. All species were found in the same area in the vicinity of the White Sea Biological Station of MSU (Kandalaksha Bay). *Halobiotus stenostomus* (Eutardigrada) and *Batillipes mirus* (Arthrotardigrada Batillipedidae) were previously registered in upper sublittoral and intertidal zones. Recently three more arthrotardigrade species have been found in sandy intertidal at depth 20–30 cm in sediment. *Batillipes* aff. *rotundiculus* differs from *B. rotundiculus* Rho et al. (Korea) by body length, median cirrus length and length of digits. *Styraconyx qivitoq* (Halechiniscidae, Styraconyxinae) from White Sea differs from *S. qivitoq* Kristensen & Higgins originally described from Greenland by length of some cirri. *Tanarctus* aff. *ramazzoti* (Halechiniscidae, Tanarctinae) differs from *T. ramazzoti* Renaud–Mornant initially found in the Bay of Biscay by length of spines on fourth legs.

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Nematodes associated with foraminifera *Reophax curtus* in the White Sea

P34

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Nematodes were found in living agglutinated foraminifera *Reophax curtus* (shell length is about 1 mm) in silt sediment at depth about 30 m in the White Sea. Nematodes are detected in 201 out of 2337 exposed foraminifera, so the intensity of invasion is about 8.6%. Usually the nematodes are located in the youngest large chamber with residual live cytoplasm. A nematode population within one host foraminifera specimen includes often males, females and juveniles. The number of nematodes may vary from one to six or more individuals. Morphology of males agree with that of the family Camacolaimidae and probably with the genus *Camacolaimus* (comma-like amphid just anterior to the level of cephalic setae, often tooth-like rod in the stoma, elongate glandular posterior widening of the pharynx, two outstretched testes, spicules with knobs bent ventrally, etc.). While males are slim the females are corpulent and spindle-shaped. All the males look similar in appearance whereas females are presented by two distinct morphotypes. Morphotype 1 is characterized by having four cephalic setae, comma-like amphids and paired antidromously reflected ovaries. Morphotype 2 is distinguished by lacking evident anterior sensilla and peculiar paired ovaries, each as a spheric cluster of numerous and relatively small oocytes and a small hemispheric germinal zone. Intestine of both female morphotypes look as partly or entirely devoid of internal lumen and cell borders. Evidently, the nematodes spend considerable part of their life cycle within foram where they feed at the expense of the host.

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A new species of the genus *Parironus* (Nematoda: Enoplida: Ironidae) from Yellow Sea, Korea

P35

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During a survey of the offshore marine ecosystem in Korea, a new species of the genus *Parironus* was found from Yellow Sea, in muddy sediment. The family Ironidae is comprised of two subfamilies, nine genera and 89 species. The genus *Parironus* was first established by Micolestzky in 1930 with type species *Parironus keiensis.* Several key characteristics of *Parironus* include short stoma, three teeth, presence of inner labial papillae, outer labial and cephalic setae, narrow spicules with set-off proximal ends, as well as conical tail with no caudal glands. Five species of *Parironus* have been described to this date, and this is the first record of *Parironus* within coast of Korea. *Parironus* sp. nov. can be distinguished from other taxa within the genus by its three equally sized teeth, smooth spicule without projections, presence of supplementary organ and its short distance with respect to cloacal opening. Emended diagnosis of the genus, as well as a pictorial key for *Parironus* species identification, are constructed.

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Buccal cavity and intestine structures of *Sphaerolaimus balticus* (Nematoda, Monhysterida)

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Sphaerolaimus balticus is a common predatory species in the White Sea intertidal zone. *S. balticus* swallows and ingests entire prey nematodes. TEM and SEM studies reveal some details of its alimentary tract. Buccal cavity is voluminous, barrel-shaped. Major part of the stoma is made up by modified somatic cuticle and thus presents a cheilostome. Anteriormost part of the cheilostome is truncate conical in shape and bears fine longitudinal ribs arranged in six groups, five or six ribs in each group. Evidently, mouth opening and conical part of the cheilostome can be widened by contraction of anterior longitudinal muscles while a prey is being swallowed. The cheilostome ribs can hold a prey while mouth and anterior cheilostome are tightened. Posterior voluminous part of the cheilostome is formed by inner layer of somatic cuticle having spongy texture (shagreen ring). Posterior edge of the broad shagreen ring forms six projections where longitudinal muscles attach. Gymnostome is very narrow. Stegostome is cup-shaped; its cuticle is thick and posteriorly descends to much thinner internal cuticular lining of the pharynx. Internal cuticle of the pharynx triradial internal lumen is thickened considerably in the radii thus forming six longitudinal cuticular ribbons. Intestine consists of five or six epithelial cells on cross section. Apical surface of the cells is complicated by very long and dense microvilli and wide three-layered glycocalyx. The glycocalyx structure looks differently in empty and filled intestines.

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Intestine structure of some White Sea free-living nematode species of various feeding types

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Intestine structures were studied using TEM methods in ten White Sea species including *Bathylaimus arcticus*, *Oxystomina* sp., *Paracanthonchus caecus*, *Halichoanolaimus robustus*, *Desmodora communis*, *Draconema ophicephalum*, *Paramonhystera filamentosa*, *Sphaerolaimus balticus*, *Odontophora deconinki* and *Sabatieria ornata*. Nematode intestine is a simple tube made up by a single layer of epithelial cells. Outer surface of these cells are covered by basal membrane, and apical surface of cells have microvilli, which are immersed in glycocalyx; an extracellular matrix, which may have very different structure. Microvilli and glycocalyx are the most diverse structures in various species. There are some correlations between microvillar layer and glycocalyx structures with feeding types of nematode and (less evident) with taxonomic position of nematode species. Predatory species and non-selective deposit feeders (feeding type 1B of Wieser, 1953) have complicated glycocalix while presumably herbivorous species (feeding type 2A) have glycocalyx as amorphous matrix and/or lamellar layer. Nematodes with intermediate glycocalyx type (lamellar, amorphous with different structures) belong to various feeding types. Generally, the smaller-sized nematodes (*Oxystomina* sp., *Desmodora communis* and *Draconema ophicephalum*) share some similar features: short and thick microvilli and amorphous glycocalyx.

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New species of *Sphaerolaimus* and *Parasphaerolaimus* (Nematoda, Sphaerolaimidae) from the Gulf of Tonkin (The South China Sea)

P38

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Free-living marine nematodes of the family Sphaerolaimidae Filipjev, 1918 (Nematoda: Monhysterida) are broadly distributed and have been found in various habitats. At present, genus *Sphaerolaimus* is represented by a combination of species (total 44) part of which was misidentified and must be transferred to the genus *Parasphaerolaimus*. So, there is a need for a revision of the genus. Examination of material recently collected during the joint Russian-Vietnamese expedition to the Gulf of Tonkin (The South China Sea) conducted in March, 2015 has revealed one new species of *Parasphaerolaimus* and three new species of *Sphaerolaimus*. In present work we describe and illustrate new species with the aid of light and scanning electron microscopy.

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Three new species of *Paramesacanthion* (Nematoda: Thoracostomopsidae) from the deep North-Western Pacific

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Free-living marine nematodes of the genus *Paramesacanthion* Wieser, 1953 (Nematoda: Thoracostomopsidae) are broadly distributed and have been found in various habitats. Within the genus we consider sixteen species as valid and two species (*Paramesacanthion brevilabiatum* Schuurmans Stekhoven, 1946 and *Paramesacanthion microsetosum* Allgén, 1932) only descripted from females, as species inquirendae. Of the valid species, four were described from the deep-sea. Examination of material recently collected by the Russian-German deep-sea expedition Sokho Bio (Sea of Okhotsk Biodiversity Studies) to the Kurile Basin of the Sea of Okhotsk on board the R/V *Akademik M.A. Lavrentyev*, conducted in the summer of 2015, has revealed new species of the genus. Here, three new *Paramesacanthion* species are described and illustrated by means of LM, SEM and LSM pictures.

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Meiofauna and geologic features: investigations of meiofauna in the Puerto Rico Trench and Kuril Kamchatka Trench, as well as in the Vema Fracture Zone with focus on harpacticoid copepods

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The deep sea is the biggest ecosystem on earth (Rex, 1981) but still poor studied (Hessler & Sanders, 1967; Tyler, 2003). Based on the physical characteristics, long time it was assumed that the deep sea is a stable and constant environment. However, since the 60s it is known that the deep sea is dynamic (Tyler, 1988). Embedded among continental slopes and abyssal plains are geological structures such as mid-ocean ridges and deep sea trenches. These structures can lead to a unique fauna community (Ramirez-Llorda et al., 2010). Some years ago it was thought that geological structures prevent distribution of deep sea meiofauna (Gage & Tyler, 1991) but recent studies showed that there are no barriers for some species, genera or families (e.g. Gheerardyn & Veit-Köhler, 2009). Two expeditions in the Atlantic and Pacific Ocean brought meiofauna material from depths between 4869 m and 8349 m. Additional to the abyssal plains, the Vema Fracture Zone and the Puerto Rico Trench as well as the upper slope of the Kuril-Kamchatka trench were sampled.

One of the most abundant taxa within the meiofauna is the copepods (Giere, 2009). As model organism, harpacticoid copepods were used for answering questions about community structures, biodiversity and distribution patterns. Herby, two questions are: Does the fracture zone serve as a passage through the Mid-Atlantic Ridge for harpacticoid copepods? Are there differences between trenches and adjacent abyssal plains at the whole meiofauna community level?

References

Gage, J.D. & Tyler, P.A., 1991. Deep-Sea Biology: A Natural History of Organisms at the Deep-Sea Floor. Cambridge University Press, Cambridge, UK.
Gheerardyn, H. & Veit-Köhler, G., 2009. Deep-Sea Res I 56 (10): 1804-1815.
Giere, O., 2009. Meiobenthology: The microscopic motile fauna of aquatic sediments. 2nd edition. Springer, Berlin.
Hessler, R.R., Sanders, H.L., 1967. Deep-Sea Res.: Oceangr. Abstr. 14, 65–78.
Ramirez-Llodra, et al. 2010. Biogeosciences 7, 2851–2899.
Rex, M.A., 1981. Annu. Rev. Ecol. Evol. Syst. 12, 331–353.
Tyler, P.A. (Ed.), 2003. Ecosystems of the deep oceans (Vol. 28). Elsevier.
Tyler, P.A. 1988. Oceanogr. Mar. Biol. 26, 227–258.

Preliminary data on harpacticoid copepods diversity of the Voronin Trench (the Kara Sea)

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The Kara Sea (the Arctic Ocean) is ice-bounded during almost ten months of the year. Because of difficult navigation conditions, the meiofauna of this region, and harpacticoid copepods, in particular, are still unexplored. Some preliminary data on benthic harpacticoids from the Voronin Trench, obtained during the 63th Cruise of the R/V "Akademik Mstislav Keldysh" (September/October 2015, depths 52–335 m), are reported. Mean harpacticoid abundance varied from 20 to 46 ind/10 cm^2 with one exception (76 ind/10 cm^2 on the heterogeneous silty sands on the 240 m, where conditions for meiofauna were favorable). As a whole, copepods consisted from four to 15 percents of all meiobenthic organisms. Ameiridae, Argestidae, Pseudotachidiida, Miraciidae and Ectinosomatidae were the richest families. Comparison with shallow-water data from the other part of the Kara Sea (the Yenisei Gulf, our data) and with deep-sea data from the Laptev Sea (Gorbunov 1946) shows considerable difference in composition. Among the species identified, some are the typically Arctic forms (*Danielssenia spitsbergensis*, *Mucrosenia kendalli*) but most of them are new for Arctic waters (*Cylindronannopus bispinosus*, *Haloschizopera clotensis*, *H. bathyalis*, *Metahuntemannia pseudomagniceps*, *Mesocletodes duosetosus*, *Proameira* cf. *echinipes*, *Nematovorax* cf. *gebkelinae*, *Cletodes* cf. *tuberculatus*).

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The metazoan meiobenthos along a depth gradient in the north-east Kara Sea (from the Taimyr Peninsula to the Voronin Trench)

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Meiofauna of the Kara Sea the (Arctic Ocean) is still poorly studied, as compared with macrofauna. Taxonomic composition and ecological structure of meiobenthic communities of the north-eastern part of the Kara Sea were investigated during the 63th cruise of RV Akademik Mstislav Keldysh (September–October 2015). Sediments were sampled by Niemistö corer at seven stations arranged in one transect (depth range 52–335 m). Transect was located on the shelf adjacent to the Taimyr Peninsula to the southern tip of the Voronin Trench (North-Eastern part of the Kara sea). Meiobenthic total densities increased with depth from Taimyr Peninsula (305 ± 40 ind/10 cm^2) to the north and reached a maximum at a depth of 240 m (1511 ± 267 ind/10 cm^2). However, with further increase of depth, the abundance decreased (378 ± 145 ind/10 cm^2). Taxonomic composition of meiobenthos on the shelf included five to seven taxa, whereas diversity increased to 10 taxa at 240 m and further decreased with increasing depth. Nematodes dominated (80–86%) at all stations except the most shallow (46%), followed by harpacticoids. The peak of abundance and diversity of meiobenthos coincides with the region of maximum hypsometric curve of the sea bottom relief (transition from shelf to slope). The major factors determining the distribution of meiobenthos in the investigated area were the relief, the grain size composition, and near-bottom hydrodynamics.

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Non-calcareous foraminifera in the near-shore sediment of the Pomeranian Bay (southern Baltic Sea): a poorly known component of the Baltic Sea benthic biodiversity

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Non-calcareous Foraminifera are usually meiofaunal-size (0.032–0.500 mm) protists the cells of which, rather than being enclosed in a calcareous shell, are protected either by a layer of agglutinated particles (agglutinated forms) or by an organic wall (soft-walled forms). While the first have good fossilisation potential and are important in palaeoceanography, the other do not fossilise and are thus missing from inventories of fossil foraminiferal assemblages. They belong to the least known taxa, although studies have been conducted or are in progress on their morphological and molecular diversity from the deep-sea to shallow inshore areas (e.g. the Black Sea).

In the Baltic Sea Proper, non-calcareous foraminifers (primarily the agglutinated forms) were reported in the older literature, mostly from the offshore areas, although soft-walled forms were found in abundance in the western part of the sea. In the light of recent analyses of the Baltic Sea biodiversity, these foraminifers can be counted among the least known components of the biota. When monitoring several inshore areas of the Pomeranian Bay, we have come across assemblages of non-calcareous foraminifers. Observations on these assemblages are discussed, as are the different morphotypes found and their responses to seasonally varying input of phytodetritus to the bottom and its accumulation in the sediment.

Meiofauna diversity of the US Great Lakes

P44

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Meiofauna serve important functions in ecosystems and are used as indicators of pollution and disturbances (algal blooms, sedimentation events, and waste fouling) in aquatic systems. They also serve as indicators of invasive species, changing in species/community composition and density as invasive disturbance increases and native organisms are displaced. In the Great Lakes, the role of meiofauna in the trophic food web has been linked to the health and spread of native and non-native species, including the round goby (*Neogobius melanostomus*), mussels *Dreissena rostriformis bugensis* and *Dreissena polymorpha*, and native fish species including bluegill (*Lepomis macrochirus*) and yellow perch (*Perca flavescens*). Previous studies have examined meiobenthic communities within the Great Lakes in order to better understand the effect of invasive species within the lakes, however these studies were limited in scope and/or taxonomic coverage, and did not focus on overall meiofaunal community structure and composition. To address knowledge gaps about meiofauna across the Great Lakes, I propose a research project that will examine meiofaunal communities on a broad and comprehensive-scale through the use of metagenomics, which will show general community structure and percent contribution of meiofaunal groups to benthic communities for all five of the Great Lakes. Taxonomy will be used to ground truth the nematode portion of the metagenomic community analyses, and attempt to match molecular operational taxonomic unit (OTU) richness to morphologically identified nematode species richness. Nematodes have been identified as dominant meiofaunal organisms within Great Lakes meiofauna, and are linked to the presence/absence of other important animals throughout the lakes, such as invasive dreissenids, sport fish, and waterfowl. The inclusion of nematode taxonomy will provide an estimate of precision for metagenomics analyses. By sampling meiofauna throughout all five of the Great Lakes, meiofaunal community comparisons can be made both within and between the lakes. This study will provide a modern baseline for meiofauna in general within in the Great Lakes, and attempt to create a comprehensive species list for nematodes in the lakes. Ideally this study will assist future studies in examining change over time in community composition, diversity, and taxonomy.

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Unrevealed biodiversity of mud dragons (Kinorhyncha) from the Spitsbergen fjords

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Kinorhynchs are poorly known from the Arctic region. Their occurrence in Spitsbergen fjords has been reported in some ecological studies but always at phylum level, with no further identification. Therefore, information on biodiversity of Arctic kinorhynchs is rather limited in comparison to other meiofauna taxa. It is unfortunate, since kinorhynchs of Spitsbergen fjords may account for 10–15% of the total meiofaunal abundance, which makes them the second most important group in the meiofaunal assemblage. In order to contribute to the knowledge about kinorhynchs, their biological diversity and diversity patterns, two West Spitsbergen fjords (Hornsund and Kongsfjorden) were investigated. Sediments were collected along the fjords' axes, at depths ranging from 78–310 m depth. The sediments of the two fjords were homogenous, composed of medium-grained silt. The unusually high abundances (up to 290 ind./10 cm^2) were not reflected in the high diversity of kinorhynchs in the fjords. Up to now, the study has revealed relatively low diversity, with seven species belonging to *Echinoderes* and representatives of *Krakenella.* Specimens representing *Echinoderes* dominated in the community, comprising over 90%. Four *Echinoderes* species (*E .eximus*, *E. peterseni*, *E. aquilonius*, *E angustus*) were originally described in 1988 from Disko Island (West Greenland), while three additional ones are novel. The study will present the distribution of kinorhynchs species in the investigated area and provide an updated list of *Echinoderes* species in the Arctic region.

The response of meiobenthos to environmental changes

Nematode biomass and morphometric attributes as biological indicators of local environmental conditions in Spitsbergen fjords

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Spitsbergen marine ecosystems, located at the border between the North Atlantic and the Arctic Ocean, can be regarded as natural observatories of ecosystem modifications due to changes in environmental drivers influenced by climatic variability. The cross-shelf water-mass exchanges are known to affect the physical and biological systems of the fjords, and make them particularly sensitive to environmental changes. Two high-latitude fjords were chosen for the present study: Hornsund and Kongsfjorden which are located on the west coast of the island of Spitsbergen and differ in terms of hydrographical conditions and food source availability for benthic organisms. We studied the nematode communities of these two glacial fjords with respect to their morphometric attributes and biomass to evaluate whether their differences reflect differences in hydrographical and biogeochemical conditions. Sediments collected from Kongsfjord, which contained organic material of higher quality than sediments from Hornsund, supported nematode communities exhibiting higher biomass and morphological diversity. Wider spectrum of length/width ratio (L/W) and size spectra, with biomass dominance in the higher weight-classes were observed in Kongsfjord. Moreover, high abundance of short and plump nematodes in the Kongsfjord nematode assemblage, characterised by a L/W ratio of < 12, was noted. This morphotype, which is almost absent in the Hornsund fjord, is considered to be an indicator of well-oxygenated sediments with favourable food sources and may further confirm that the organic material in the Kongsfjord sediments is of higher quality. The study will provide evidence that the morphometric characteristics of nematodes are suitable for detecting differences in sediments, particularly with regard to organic matter content.

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Patterns of diversity in marine Gastrotricha from southeastern Brazilian coast is predicted by sediment textures

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For the interstitial microscopic fauna a wide distribution conception is accepted for several phyla because their life history is characterized by few offspring, a short life cycle, absence of dispersal stages, and limited swimming ability. This assumption is being revised since more information has become available on their biogeography and general macro ecological treats. This study analyzed the variability of marine Gastrotricha diversity among benthic habitats and localities along the Brazilian coast through collections and research bibliographic. We assessed the differences in the gastrotrichs diveristy across habitat patches (local, < 106 m^2) and large geographic areas (regional, 106–1010 m^2) and tested the hypothesis that sediment textures, location, tidal zones, and their interactions, are potential explanatory variables that affect the Gastrotricha diversity. We performed spatial autocorrelation analyses for the response variables, explanatory variables, and residuals with simultaneous autoregressive (SAR) models. Richness estimates, species composition and beta diversity were used as response variables of biodiversity. The number of gastrotrichs, macrodasyids, and chaetonotids species was mostly explained by sediment sorting and the highest richness was detected in poorly sorted sediments. Species composition and beta diversity were correlated with tidal zone, location, and average grain size, and the highest turnover of species was expected on islands. The general diversity patterns observed in our study that were explained by sediment textures, tidal zones and localities, are expected to be observed along other marine coastlines in the world and may be correlated with sediment transport and deposition processes.

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The relationship between sediment grain size and the distribution of living benthic foraminifera in Sinop Bay (Black Sea, Turkey)

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In this study, assemblages of living benthic foraminifera collected from Sinop Bay were identified and their relation with the sediment grain size composition was evaluated. Three replicates of push core samples were obtained from a total of eight stations with different depths (2, 3, 4 and 10 m) in summer periods of 2009 and 2015. Examination of rose Bengal-stained foraminifera revealed a total of 26 species belonging to 15 genera, 12 families and five orders for the summer period of 2009, and a total of 16 foraminifera species belonging to 11 genera, six families and four orders for the summer period of 2015. For both periods, the range of the species composition in the study area were associated with six different sediment types and it was observed that the smaller the grain size, the higher the species diversity. Several species belonging to the genera *Nonion* de Montfort, *Cribroelphidium* Cushman & Brönnimann and *Elphidium* de Montfort and the family Hauerinidae occurred at the stations with a smaller grain size structure, whereas the species of *Ammonia* Brünnich and also *Massilina secans* (d'Orbigny, 1826) appeared at the stations with a larger grain size composition. Depending on the fact that the amount of organic material was higher in sediment of the stations during both sampling periods, it was determined that the porosity decreased and it was reflected in the species diversity of the benthic foraminifera.

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Agglutination patterns of benthic foraminifera in relation to mesoscale bathymetric heterogeneity in deep-sea ecosystems: an example from the Porcupine Abyssal Plain, NE Atlantic P49

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Abyssal hills, small topographic features rising above the abyssal seafloor ($<$ 1000 m altitude), have distinct environmental characteristics compared to abyssal plains, notably the presence of coarser-grained sediments. As a result, they are a major source of habitat heterogeneity in the deep sea. The aim of this study was to investigate whether there is a link between abyssal hills and the test characteristics of selected agglutinated benthic foraminiferal species. We analysed 1) the overall morphometry, and 2) the granulometric and chemical (elemental) characteristics of the agglutinated tests of ten common foraminiferal species (*Adercotryma glomerata*, *Ammobaculites agglutinans*, *Cribrostomoides subglobosus*, *Lagenammina* sp.1, *Nodulina dentaliniformis*, *Portatrochammina murrayi*, three *Reophax* sp. and *Recurvoides* sp. 9) at four sites (two on top of abyssal hills and two on the adjacent plain) in the area of the Porcupine Abyssal Plain Sustained Observatory, northeast Atlantic. The foraminiferal test data were compared with the particle size distribution and elemental composition of sediments from the study sites in order to explore possible grain size and mineral selectivity. We found differences in the visual appearance of the tests (i.e. the degree of irregularity in their shape), which was confirmed by morphometric analyses, related to seafloor topography. The agglutinated foraminifera selected different sized particles on hills and plains, reflecting the distinct granulometric characteristics of these settings. These characteristics (incorporation of coarse particles, test morphometry) could provide evidence for the recognition of ancient abyssal hill environments, as well as other palaeoceanographic settings that were characterised by enhanced current flow. Furthermore, analyses of sediment samples from the hill and plain sites using wavelength dispersive X-ray fluorescence (WD-XRF) yielded different elemental profiles from the plains, probably a result of winnowing on the hills, although all samples were carbonate-rich. In contrast, the majority of the agglutinated tests were rich in silica, suggesting a preferential selection for quartz.

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Hills and plains: the influence of topography on deep-sea benthic foraminiferal assemblages

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Benthic foraminifera are an important component of soft-bottom meio- and macrofaunal communities on abyssal plains (3500–6000 m water depth). Although often perceived as vast flat areas, abyssal plains also encompass numerous abyssal hills. These topographic rises, which reach heights up to 1000 m above the seafloor, are believed to be one of the most pervasive landforms on Earth. Major topographic features, for example, seamounts and submarine canyons, are known to have an effect on food availability and sediment characteristics, which are ultimately linked to community composition and biomass. However, the potential influence of relatively small abyssal hills on associated benthic communities is poorly understood. In the case of benthic foraminifera, previous studies have assessed the effect of small-scale (centimetres to meters) seafloor features (e.g. biogenic structures, organic matter patches) but nothing is known about the effects of larger topographic features, such as abyssal hills, which increase habitat complexity at broader scales (mesoscale, i.e. decimetres to kilometres). In order to address this issue we collected samples from four different sites in the area of the Porcupine Abyssal Plain Sustained Observatory (PAPSO; northeast Atlantic, $>$ 4,300 m water depth), two on tops of abyssal hills and two on the adjacent abyssal plain (three replicate samples per site). We test whether (1) benthic foraminiferal abundance and diversity are enhanced on abyssal hills, (2) community composition is different on the hills and the adjacent abyssal plain, and (3) mesoscale environmental heterogeneity is more important in structuring foraminiferal assemblages compared to small-scale patchiness. Preliminary results suggest that benthic foraminiferal density and diversity on the abyssal hills is comparable to that on the neighbouring abyssal plain. However, the assemblages on the hills harbour some species not found on the plains, thereby enhancing foraminiferal diversity at regional scales.

Nematode community structure along the Blanes submarine canyon (NW Mediterranean Sea)

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Submarine canyons are probably among the most dynamic systems along continental margins resulting in high seafloor heterogeneity. Since nematode assemblages are strongly related to changes in seafloor characteristics such as sediment composition and food supply, they are expected to vary significantly along submarine canyons. By studying nematodes in Blanes Canyon (Iberian margin of the NW Mediterranean), we identified the major environmental drivers in the canyon system for the taxonomical and functional nematode diversity. Replicate multicore samples were collected along the axis of Blanes Canyon, from 500 to 2000 m depth. Additional subcores were used to analyze the main sediment characteristics (including grain size, organic content and phytopigments). Nematode densities did not show a clear decreasing pattern with bathymetry, since peaks occurred at 1200 and 1750 m depth. Overall, the community composition was similar from 500 to 1200 m depth, dominated by non-selective deposit feeders. The abundance of selective deposit feeders progressively increased in the deepest stations, especially at 1750 m depth. The highest trophic diversity was detected at 900 m depth. The presence of the mouthless *Astomonema* genus in all samples (except at the deepest ones) is of particular interest its occurrence being restricted to the deepest sediment layers (2–5 cm). Higher and lower values of diversity were found at 500 and 2000 m depth respectively. Differences in nematode communities were mainly explained by proxies for food quantity and quality such as Chl-a, CPE and Chl-a:phaeo, as well as by total carbon and grain size (clay and sand contents).

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Copepod colonization of organic and inorganic substrata at a deep-sea hydrothermal vent site on the Mid-Atlantic ridge

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The few existing studies on vent copepods indicate a low connectivity with the surrounding environments and reveal a high endemism. However, information about the dispersal ability of copepods and the colonization of hydrothermal vents as well as their ecological connectivity is limited. The objective of this study is to understand copepod colonization patterns at a hydrothermal vent site in response to environmental factors such as temperature and fluid flow as well as the presence of different types of substrata. To address this objective, an *in situ* experiment was deployed using both organic (woods, pig bones) and inorganic (slates) substrata along a gradient of hydrothermal activity at the Lucky Strike vent field (Eiffel Tower, Mid-Atlantic Ridge). The substrata were deployed in 2011 during the MoMARSAT cruise and were recovered after two years in 2013. Overall, copepod density showed significant differences between the deployed substrata when combining the individual substrata from different stations. In turn, copepod density showed no significant differences between sites. Highest densities were observed on woods at sites with moderate or low fluid input, whereas bones were the most densely colonized substrata at the two sites with higher hydrothermal influence. Although differences in copepod diversity were not significant, the observed trends revealed overall increasing diversity with decreasing temperature and fluid input. Overall, slates showed highest diversity compared to the organic substrata. Temperature and fluid input had a significant influence on copepod community composition, resulting in higher similarity among stations with relatively high and low fluid inputs, respectively. While vent-specialists such as dirivultids dominated substrata at high vent activity, the experiment demonstrated increasing abundance and dominance of non-vent taxa with decreasing temperature and fluid input. Effects of the substratum type on community composition were not significant, although at sites with moderate or low fluid input, woods exhibited distinctive communities with high densities and relative abundance of the taxon *Nitocrella* sp. In conclusion, copepod colonization and species composition were mainly influenced by hydrothermal fluid input and temperature rather than the type of substratum. The outcome of this study provides fundamental knowledge to better understand copepod colonization at hydrothermal vents.

Study on the meiofauna community and species diversity in the coastal region of Korea

P53

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Diversity and community structure of meiofauna which inhabit in the coastal area of Korea were studied during two season, spring and summer, 2015. Investigation was conducted for a total 68 stations (50 stations in the Yellow Sea and 18 stations in the western part of the South sea) using van Veen grab, and were subsampled with acrylic corer. The community of meiofauna consist of 12 taxa (Nematodes, Copepods, Foraminiferans, Polychaetes, Oligochaetes, Kinorhynchs, Halacaroideans, Bivalves, Ostracods, Cumacean, Amphipods and Isopods). Abundance and biomass of meiofauna showed some pattern as the seasonal and regional differences (Spring > Summer; Yellow Sea > South sea), and nematodes and copepods were dominant group during the study. During this study, eight orders, 24 families, 76 genus, 149 species of nematodes and 20 families, 52 genus, 89 species of the harpacticoids were identified. Species diversity also showed pattern that the Yellow sea was relatively higher than the South sea. Comparing with the previous studies, most of species (142 species of Nematodes; 77 species of Copepods) seem to be new to science in the survey.

Large-scale distribution patterns of nematode fauna within mangrove forests

P54

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The hotspot of tropical marine biodiversity at Indo-West Pacific is a well-recognized macroecological pattern described for a number of coastal plant and animal species, although neither the processes nor the mechanisms responsible for it are well understood. Data comprising mangrove trees and associated macroinvertebrate species corroborate this pattern. Therefore, our aims were: (1) evaluate the relationships between nematode richness and richness of mangrove trees from different biogeographic regions (*i.e.*, Indo-West Pacific and Eastern Pacific/Atlantic-Caribbean regions); (2) assess if local landscape attributes have equal or more importance than biogeographic patterns in structuring nematode richness. To evaluate which factor is more important to determine the distribution pattern of nematode richness a multiple quantile regression was made using 95th percentile. Nematode data were compiled from published research papers, while richness of mangrove trees were based on Ellison et al. (1999) and Ellison (2008) and local attributes of mangrove forests were obtained from Giri et al. (2011) and Hutchison et al. (2014). The most

parsimonious model according to backward step AIC selection includes richness of mangrove trees, total mangrove area, average mangrove patch area, average patch above ground production, mangrove shape index, longitude and latitude as important explanatory variables. Although variability in nematode richness was explained mostly by total mangrove area ($t = 2.038$, $p < 0.05$) as well as by mangrove shape index ($t = -2.48$, $p < 0.01$). Our results contrast with distribution patterns of brachyurans and littorinid gastropods, considered strongly associated to richness of mangrove trees. Nematode genera evolved independently of mangroves and richness in tropical regions is probably more associated to sediment properties than with mangrove trees. We expect differences in community composition between oceanic basins, but not differences in richness of nematode genera. Nematode richness is more associated with local characteristics than with large-scale distribution patterns of mangrove forests. These differences suggest, at least for nematodes, that habitat quality and landscape configuration should be considered when macroecological patterns are investigated.

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Diversity and distribution of the meiofaunal community (free-living marine nematodes) in the tropical mangrove ecosystem of Andaman bay region

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Mangroves are a unique marine environment known to provide several microhabitats. The mangroves of Andaman and Nicobar Islands are well spread over a vast area of 617 km^2, which forms 13% of the total mangrove cover of India (4663 km^2). The mangrove ecosystem supports a diverse fauna, especially the soft substratum, that provides habitat for various infaunal and epifaunal species. Nematodes are among the most abundant meiofaunal communities around the globe found to inhabit such an environment. The present study investigates the diversity and assemblage structure of free-living marine nematodes for a period of one year in four mangrove regions along the South Andaman coast based on the substratum. A total of 49 species from 31 genera was identified with densities ranging between 339 and 452 individuals per 10 cm^2, covering Enoplida, Chromadorida and Monhysterids. Among these three orders, Monhysterids were found to be dominant in which *Sphaerolaimus* and *Daptonema* genera were abundant. Environmental parameters were analysed in order to understand the correlation of nematodes with the parameters and the impact of these factors on their distribution. A strong positive correlation was found between salinity and temperature ($r = 0.82$; $p < 0.0001$). Spatial variations of the nematodes were observed and disparities in salinity were found to influence the nematode population in the mangrove soft substrata of this island. In addition, sedimentary characteristics such as sand, silt and clay also play key roles in structuring the assemblage pattern of nematodes. Studies pertaining to nematode diversity in the Andaman Island group are still scarce. The current study provides baseline information on understanding the diversity of nematodes in the mangrove ecosystem of Andaman Islands. Studies devoted to the ecological interactions need to be initiated to better understand the role of mangroves (vegetation) on structuring the species assemblage of nematodes in this highly productive environment, which could be a key factor for its conservation and management.

Meiofauna of bromeliads from the tropical forest of the Yucatan Peninsula with emphasis on microcrustaceans

P56

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Bromeliad water tanks (Phytotelmata) house a diverse fauna of invertebrate specialists, however the great variety of studies performed in such habitats have been insect-dominated. There has been little research about Phytotelmata associated crustaceans, especially in North and Central America, and the main factors that limit their presence in these habitats. This study is part of recent research efforts aimed to understand the diversity of microcrustaceans in semi-terrestrial habitats and Phytotelmata in the Yucatan Peninsula (PY). Herein we focus on the microcustaceans (Copepoda, Ostracoda and Cladocera) and secondly on other meiobenthic communities associated to four species of Bromeliacea (*Aechmea bracteata*, *Tillandsia dasyliriifolia*, *T. fasciculate* and *Tillandsia* sp. 1) distributed in two natural protected areas of the YP (Calakmul and Sian Ka'an). Bromeliads were sampled in different biotopes (mangroves in estuaries, deciduous lower forest, palustrine vegetation and seasonal evergreen forest) to get a better view about the diversity in phytotelmata in that region. Although 92 species of microcrustaceans have been recorded in Phytotelmata worldwide, the list of taxa is not yet complete as the results of this study have unveiled. Around 25% of the bromeliads analyzed contained copepods; *Phyllognathopus vigueri*, *Epactophanes richardi* and one member of the family Ameiridae are recorded. Copepods were found in samples with higher diversity of other taxa (suggesting the preference of copepods to more complex communities). Ostracoda were the most typical crustacean inhabitants of the bromeliads (50%), with three species commonly found (*Elpidium* cf. *martensi. Callistrocypris* cf. *mckenziei* and *Caaporacandona* sp. 1). Findings of Cladocera include a member of the family Daphniidae (*Simocephalus* sp. 1), and represent the first record of the genus inhabiting phytotelmata. A list of organisms belonging to other taxa is included (Nematoda, Tardigrada, Insecta, Arachnida, and Rotifera–Bdelloidea and Monogononta). The presence of microcrustaceans is correlated with different variables (bromeliad species, presence of other taxa, associated vegetation, substrate, presence of pools, etc.) in order to understand the main factors that drive their success in such environments. This study could serve as the basis to more knowledge about invertebrate communities in bromeliads and the colonization of semi-terrestrial habitats in tropical areas.

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Emergence patterns of harpacticoid copepods in the Wadden Sea (southern North Sea)

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Harpacticoid copepods move actively in the water column for mating or to improve their living conditions. This behavior is regarded as a key component of bentho-pelagic coupling. Emergence and recolonisation from and into the sediment are affected by specific factors like salinity, current velocity or sediment grain size. Since comparative studies that include both the emergence and recolonisation of copepods in the North Sea are still lacking, this investigation was initiated to study the migrating patterns during a full tidal cycle in the intertidal zone of a backbarrier island in the central Wadden Sea. Tidal currents, wave action, precipitation and evaporation have a strong impact on the stability of the traps as well on the sediment surface. Therefore, specific modular emergence and recolonisation traps were developed which can cope with these special requirements. Applying these traps the diversity and abundance of Harpacticoida emerging and recolonizing during nocturnal and diurnal high tides were recorded. In contrast to studies from other ecosystems, no significant difference in emergence rate between nocturnal and diurnal conditions was detected. Comparing to other similar studies the migration patterns in the intertidal zone might be different as individual behaviour is influenced by the strongly fluctuating abiotic environmental conditions.

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The meiofaunal composition of two separate coral reefs of Dahab, Gulf of Aqaba

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Tropical coral reefs are known to be one of the hotspots of biodiversity. In contrast to the constant interest in the macrofauna of these reefs, the meiofauna has not been estimated in the same ratio. Therefore, the composition of meiofaunal organisms of the coral reef flat of Napoleon and the slope of Moray Garden (Dahab) was examined on a major taxonomical level with focus on the Harpacticoida, Copepoda. Differences can be stated within the Harpacticoida, but not for the meiofauna on a major taxonomical level. Furthermore, the biodiversity of the Harpacticoida is significantly higher at Moray Garden compared to Napoleon Reef. At Moray Garden the sediment is more heterogeneous than at Napoleon Reef. This leads to different pore sizes with a positive effect on the colonization of the Harpacticoida. Nevertheless, the interstitial living harpacticoids of both examined reefs show a high diversity, which is comparable to the biodiversity of macrofauna in coral reefs.

Meiobenthic and copepod assemblages associated to subtidal rocks in the marine protected area of Portofino (Italy)

P59

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Rocky-subtidal meiobenthic assemblages are poorly studied, especially in their ecological aspects. A study on meiobenthos and harpacticoid copepods of the Marine Protected Area of Portofino promontory (Ligurian Sea, Italy) was carried out during summer 2009 and winter 2010 in 20 stations. Different depths (5, 10 and 20 m), slope (vertical and inclined) and types of macrobenthic cover were considered in each station. Samples have been collected by a purposely built diver held suction device. A total of 30 meiobenthic taxa were found revealing the species richness of the study area. Nematoda and Copepoda were the dominant taxa, followed by Platyhelminthes. Harpacticoid copepods were present with 22 families and 43 genera, mainly represented by Miracidae (23%), Laophontidae (22%) and Longipediidae (12%). Meiobenthic and copepod assemblages appeared mainly influenced by seasons, and indirectly by the type of macrobenthic substrate cover. In particular, PCA showed a correlation between meiobenthic crustaceans (i.e. Amphipoda, Ostracoda and Copepoda) and cover by Ochrophyta and Chlorophyta, while Platyhelminthes, Gastrotricha and temporary meiobenthic groups such as Ophiuroida resulted more associated to macrobenthic cover by Rhodophyta, Polychaeta, Bryozoa, Ascidiacea and to abiotic substrates. The copepod genus *Ameira* resulted negatively correlated to Ochrophyta and Chlorophyta and the genus *Diathrodes* to Rhodophyta, Polychaeta, Bryozoa and Ascidiacea. Accordingly, meiobenthos tends to colonize mainly areas with a greater spatial complexity, and therefore a higher number of ecological niches mainly represented by clusters of algae of considerable size. These microhabitats host different taxa with different trophic habits and/or different morpho-functional adaptations that allow the settlement of different meiobenthic and copepod assemblages.

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Microscale distribution of marine mites in *Posidonia oceanica* meadows: are they spatially segregated?

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Halacarid mites (Halacaroidea: Halacaridae) are meiobenthic organisms, mostly marine, occurring at all latitudes and depths. Since the description of the family more than 200 years ago, more than 1000 species have been described and currently classified in 64 genera and widespread in a great variety of marine and freshwater habitats. This ecological ubiquity is correlated with a wide range of trophic guilds within the family, which includes carnivorous, herbivorous and scavenger opportunistic species. Although these species are commonly reported sympatrically, all available information comes from broad faunistic surveys, which dismiss the environment variation at a micro-scale. We here investigate the morphological traits on the distribution patterns at a micro-scale of the halacarid species inhabiting *Posidonia oceanica* meadows. Halacarids were extracted from samples collected during four sampling campaigns (from December 2015 to July 2016) at three microhabitats in a *Posidonia oceanica* meadow at Santa Pola (Alicante, Spain). These habitats included *Posidonia* fronds, *Posidonia* root sediments and sediments without *Posidonia*. Temperature, salinity, depth, granulometry, organic matter, and size and dry weight of the fronds were collected along with each sample. The halacarid assemblages at each sample were described in terms of species composition, abundance of individuals and morphological dissimilarities. Different morphological traits of each species were characterized based on bibliography and on anatomical studies combining light and scanning electron microscopy, as well as biometrical analyses. This information was used to test the hypothesis that different habitats might have different species composition with species with different adaptations, explicitly, species with phytophagous-like gnathosome prefer fronds, and smaller species with elongated bodies dominate at the interstices of the sediments (habitat sorting) versus a hypothesis in which the species distribution depends on other factors and occurs everywhere (neutral paradigm).

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Seasonality in abundance of phytal meiofauna from the NW Mediterranean Sea and impact of a benthic HAB (*Ostreopsis* cf. *ovata*)

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A temporal survey of the metazoan meiofauna inhabiting the brown macroalga *Halopteris scoparia* was conducted in 2008 and 2009 in the Bay of Villefranche-sur-Mer (France) where summer blooms of the toxic benthic dinoflagellate *Ostreopsis* cf. *ovata* occur increasingly. Seaweeds *ca.* 5 cm in length were sampled in triplicate at 0.5 m depth at station “les Marinières” (MAR: 43° 42.161′ N–7° 19.191′ E) on 7 and 18 different dates in 2008 and 2009, respectively. Total meiofauna per seaweed ranged from 878 to 39360 individuals over the 2-year period. Organisms belonged to 16 major taxa/groups. Nauplii dominated and were on the average 45.5% of total organisms. They were followed by copepods (22.3%), nematodes (15.5%), polychaetes (5.3%), ostracods (3.6%), gastropods and bivalves (2.3% altogether), halacarid mites (2.1%), turbellarians (1.7%), juveniles of amphipods, isopods and tanaids (1.4% altogether), tardigrades (0.2%), kinorhynches (0.1%), and occasional insects and pycnogonids. Total meiofauna abundance per g of spin dried seaweed varied with time, from *ca.* 1200 to *ca.* 8000 individuals, and was the lowest in winter of both years. The temporal abundance pattern of the total fauna was the result of the abundance distributions of the individual taxa/groups. Each taxon/group did not behave equally however, and appeared to be influenced differently by the toxic summer blooms. For example, while the abundance pattern of the nauplii and the ostracods were out of phase with the temporal distribution of *Ostreopsis* concentrations, that of the tardigrades closely matched the temporal fluctuations of the toxic dinoflagellate. Multivariate statistical analyses involving current environmental variables and *Ostreopsis* concentrations will be presented to highlight the major factors driving the temporal changes observed in the community composition and structure.

A comparative study of nematode assemblages associated with *Sargassum muticum* in its native range in South Korea and as an invasive species in the English Channel

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Canopy forming algae are important habitat providers in coastal ecosystems. Several canopy forming species are invasive and spread to outside their native geographic range. We explored the role these invasive algae play in providing habitat for meiofaunal species. The nematode assemblages living in the intertidal algae *Sargassum muticum* in Europe where it is an invasive species and South Korea within its native range were compared. *Sargassum muticum* is a native species in Southeast Asia and is a successful invasive species in North America and on European coasts. A nested survey design was used with three regions in each country, replicate shores in each region and three patches on each shore. The composition of the nematode assemblages was compared in Korea and England. Patterns of alpha, beta and gamma diversity were described. Significant differences among each spatial scale (patches, shores, regions and countries) were found in nematode assemblages. Despite differences in their assemblage structure at each spatial scale, cosmopolitan species were found and the dominant feeding type (epigrowth feeder) was similar. We briefly speculate on whether the assemblage in the UK was acquired from the existing species pool or whether any nematodes hitched a lift to Europe.

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Harpacticoids in the Western Carpathian (Central Europe) headwater streams: analyses of between and within-site variation

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Meiofauna in running waters has been known to have highly patchy distribution. The spatial variation has been usually explained as a response to environmental variables on different scales. In this study we examined the harpacticoids assemblages on large (regional) and small (within-site) scale. We sampled in three mesohabitats (streamline, pool and moss) in 26 headwater streams across the Western Carpathians (Slovakia and Czech Republic). The total abundance had median of 113 individuals (max 4174 ind.) and 16 species of the family Canthocamptidae were identified. Headwaters were inhabited mainly by common ubiquist species (e.g., *Attheyella wierzejskii*, *Bryocamptus spinulosus*, *B. pygmaeus*, *B. echinatus*). Two non-common species were found frequently in relatively high abundances (*B. typhlops*, *Moraria poppei*) and several rare species were recorded (*B. mrazeki*, *Pilocamptus pilosus* and *Maraenobiotus vejdovskyi*). First, we explored the within-site variation in species composition and richness. Non-metric Multidimensional Scaling (NMDS) did not show any differences in species distribution among mesohabitats. Species composition was rather typical for each stream than for each mesohabitat. Individual-based rarefaction showed significantly higher species richness in pool and comparably lower species richness in moss and streamline. Only *A. crassa* had significantly lower abundances and frequency in moss mesohabitat. A slight affinity for moss mesohabitat was observed for *B. pygmaeus*. An analysis on large scale using distance based Redundancy Analysis (db-RDA) revealed a significant relationship of harpacticoid assemblages to sandy substrate and big stones. Results of a cluster analysis suggested an existence of spatial pattern. Two groups of sites corresponded with geographical areas of the Inner (group 1) and Outer (group 2) Western Carpathians, which differ in bedrock characteristics. Group 1 had higher median total abundance (608 individuals) than group 2 (146 individuals). Common ubiquist species (*A. wierzejskii*, *B. spinulosus* and *B. pygmaeus*) were negatively related to poorly porose flysh bedrock in the Outer Western Carpathian sites. Our study showed significant spatial variation of the harpacticoid headstream assemblages in the area on the large, between site scale rather than between mesobahitats, which may be due to longer environmental gradients.

Harpacticoida (Copepoda) fauna of the Caspian Sea in comparison with faunas of the other seas formed on the base of the Sarmatian basin

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The Sarmatian basin existed 10.5–14 mlllion years ago and included the modern water areas of the Black, Azov, Caspian and Aral Seas. After its breakup 5–7 mlllion years ago, the newly-formed seas/lakes had different history of hydrology and ecosystems development. The present article is concerned with the Harpacticoida fauna of the Caspian Sea. On the basis of the original materials collected in the Southern and Northern Caspian Sea the harpacticoid fauna and the taxocenes structure are described. One third of the species found are new for the region, and three species are new for science. The seasonal and interannual dynamics of harpacticoida from the littoral zone of the Southern Caspian was studied. It is shown that because of the instability of the maritime climate there is no pronounced seasonal periodicity of species complexes in the littoral zone of the investigated coast. A comparative analysis of the faunas of the Aral, Caspian, Black and Mediterranean Seas was performed. All areas are clearly divided into two distinct blocks: the Mediterranean and the Sarmatian, which indicates the relationship between faunas of the fragments of the previously single relict Sarmatian Sea basin. However, the environmental characteristics of the harpacticoid faunas in the seas, fragments of the Sarmatian Sea, vary considerably. The fauna of the Caspian Sea, which keeps the Sarmatian features the most, consists mainly of brackish species, while the marine species are few. The Aral Sea, the water level of which dropped dramatically over the last century, has passed to the hypersaline category. Fauna of the desalinated Azov Sea, which is connected to the Black Sea, is a mixture of freshwater and brackish species, with some inclusions of marine species, which regularly migrate from the Black Sea. The fauna of the Black Sea consists mostly of marine species, about a quarter of which are endemic. Thus, because of the different hydrochemical conditions, the Caspian, Aral, Azov and Black Seas vary considerably in the structure of Harpacticoida fauna currently. However, these water areas are united by a numerous group of brackish species, which probably formed the main part of the Harpacticoida fauna in the Sarmatian basin before.

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New data on the fauna of microcrustaceans (Copepoda, Cladocera) from the High North – Svalbard, Norway

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Most of the Arctic freshwater habitats are small and shallow, often drying out in the summer or freezing solid during winter. However, during summer, there is an extensive development of micro-invertebrates, including microcrustaceans, known to respond to environmental parameters affected by the climate. Svalbard Archipelago is an internationally valuable and environmentally sensitive High Arctic area with considerable amount of small, shallow freshwater habitats. Here we present results from a study run in August 2014 and 2015 with the aim to increase the knowledge on species diversity and distribution in both freshwater and brackish water habitats (meiobenthos, littoral and pelagial). Altogether 20 microcrustacean species were found. Seven species (*Alona werestschagini* Sinev, 1999; *Polyphemus pediculus* Linnaeus, 1761; *Diacyclops abyssicola* Lilljeborg, 1901; *Ameira minuta* Boeck, 1865; *Epactophanes richardi* Mrazek, 1893; *Geeopsis incisipes* Klie, 1913; and *Nitokra spinipes* Boeck, 1865 were new to Svalbard. *Bosmina longispina* Leydig, 1860 – an already known species – was found in 8.7% of the localities and is an example of species which seems to respond positively to a warmer climate by becoming more common. The number of species increased with distance (age) to the glacier. Habitats close to the glacier had no cladocerans and only one or a few copepods were present. Cladoceran species (i.e. daphnids) occurred both in lakes and ponds with increasing distance to the glacier. This study has broadened existing knowledge on Svalbard's biodiversity, and might provide useful information for future Arctic Freshwater Biodiversity Monitoring activities.

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Differences in meiofauna community structure in two contrasting summer conditions in Antarctica (Admiralty Bay, King George Island)

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During a baseline study on the meiobenthic community structure in Admiralty Bay and Bransfield Strait (Antarctica) differences observed between years were astonishing, which triggered us to search for larger climatic and oceanographic features that could explain our findings. Here we explain the possible influence of climate conditions on the meiofauna community. Sampling was carried out on board the

Brazilian Navy Vessel NApOc "Ary Rongel" in Dec/2008 and Dec/2009. At each depth (100, 300, 500, 700 and 1100m) sediment from three box-corer deployments was subsampled for meiofauna and environmental variables. Meiofauna samples (4.9 cm^2, 6 cm high) were washed between sieves (1–0.03 mm) and retained organisms were analyzed. Mean sediment grain size and deviation increased with depth and distance from the shore ($p < 0.05$). In Dec/2008 mean grain size was smaller and phytodetritus biomass was higher than in Dec/2009 ($p < 0.05$). In Dec/2008, meiofauna densities varied from 276 ± 216 ind/10 cm^2 at 700 m to 6682 ± 464 ind/10 cm^2 at 300 m. Densities were lower at 700 and 1100 m than at 100, 300 and 500 m ($p < 0.05$). In Dec/2009, densities varied from 1345 ± 1129 ind/10 cm^2 at 100 m to 2742 ± 1600 ind/10 cm^2 at 700 m ind/10 cm^2, and differences were not significant. Higher meiofauna densities were positively correlated with higher phytodetritus biomass and prokaryotic densities, while negatively correlated with larger grain size and C/N ratio. In 2008, sea-ice covered the bay surface for less than 20 days, the spring was the hottest ever recorded, and by November all snow had melted. In contrast, the winter in 2009 was intense, sea-ice covered the bay for more than 80 days and melting began after December. We believe that, during spring 2008, fresh water runoff from melted snow carried fine sediments and nutrients to the bay that favored intense phytoplankton blooms, while the strong winds registered contributed to the rapid sinking of the phytoplankton. So, larger amount of fresh phytoplankton would trigger rapid meiofauna growth, especially in the shallower samples. In 2009, the ice break and the fresh water runoff were delayed, and the phytoplankton blooms were registered only in early 2010, so less food was available to trigger meiofauna growth.

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Morphological and functional adaptations of nematodes to habitat types

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Sediment grain-size is a key factor in structuring meiofaunal and nematode assemblages. Accordingly, a statistical analysis was carried out on a data set of samples collected in two different scientific cruises in the Maldivian archipelago. We tested possible variations of some morphological and functional characters of marine nematodes (buccal cavity, amphid shape, cuticle ornamentation, tail shape, and life strategy) to variations in sediment grain size and hydrodynamic conditions. In the first survey, possible changes of morphological and functional characters were analysed in fine to very coarse sands. All the characters were significantly different between the sediment types. In particular, medium-coarse sands appeared the most diversified sediments both in taxonomical and morpho-functional diversity. Cuticle ornamentation and life strategy were well diversified also in very coarse sands, while tail shape was especially diversified only in fine sediments. When the same traits were analysed to test the influence of different levels of hydrodynamism, all of them (with the exception of tail shape) were significantly different and more diversified in intermediate energy conditions. In conclusion, medium-coarse sands, and habitats with intermediate energy level appeared to favour not only a great taxonomical diversity, but also a great diversity of morphological and functional adaptations that reflects their great heterogeneity in micro-niches.

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Microdistribution of meiofauna in freshwater ecosystems

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Meiofauna massively inhabit inland waters, from cold seepages to thermal springs, and from stream marshes to deep lake sediments. Surprisingly, freshwater ecologists still poorly consider meiofauna, leading to gaps in basic understanding of the importance of meiofauna in freshwater ecosystems. For instance, detecting distribution patterns is a key pre-requisite for ecologists to identify mechanisms that structure communities. At the scale of meiofauna, sand grains are homes and a few meters of the riverbed are valleys. In this context, we decided to study the distribution of meiofauna at horizontal and vertical 'small' scales (i.e., cm–to–m) in the sandy bed of an artificial mesocosm and a stream. To the best of our knowledge, this study is the first which specifically investigates this question in freshwaters. We hypothesized that meiofauna density, diversity and biomass might be patchy, and chiefly constrained by the distribution of resources hot-spots in the sediment. We also anticipated an effect of inter-specific affinities or competition on the shaping of community distribution. Nematodes generally dominated meiofaunal communities, although gastrotrichs were important contributors in stream superficial sediment. Nematodes and harpacticoid copepods showed clear affinities with resource hotspots in deep sediments. Larvae of chironomids showed a very patchy distribution, without clear causality with resource availability. In the artificial mesocosm, diversity and biomass changed, especially along the vertical scale. Nematode assemblages were dominated by bacterivorous *Eumonhystera* and *Monhystera* species. We found similar distributions of those two species as peaks of abundances were located in the same patches, suggesting that co-existence prevailed over competition for those species. Overall our results highlight variations of meiofauna community structure at small scales, and hence the necessity to take into account small-scale heterogeneity of the environment to better understand the ecology of these fascinating animals.

Effects of the non-indigenous bivalve *Ruditapes philippinarum* on meiofaunal communities of the Tagus estuary P69

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The Manila clam, *Ruditapes philippinarum*, whose native range is in the eastern Pacific, has dispersed worldwide. It has been introduced into several European coastline locations over the last 30 years and it has established wild populations at large areas. Although impacts of this non-indigenous specie have been documented in several invaded systems, there are no studies addressing changes associated to the colonization of portuguese systems. The major goal of this study was to investigate the response of meiofauna assemblages, particularly nematodes, to the occurrence of the Manila clam and density in the Tagus estuary, Portugal. Meiofauna samples were collected at 40 sampling stations distributed along the Tagus estuary gradient within the known occurrence area of *R. philippinarum.* Density, diversity and trophic composition patterns were determined to investigate the effects of i) spatial distribution patterns and abundance of *R. philippinarum* and ii) environmental variables on meiofauna/nematodes communities. The obtained results showed that nematodes are the most abundant meiofaunal taxa in Tagus estuary. Although the nematode community distribution pattern was mainly structured by environmental factors, *R. philippinarum* densities also played an important role. As benthic infauna can profoundly influence nutrients cycling and since food is an important limiting factor for many benthic populations the densities of *R. philippinarum* may be inducing changes in the estuary via food web interactions. In this study we suggest that those changes are probably the result of reduced access of meiofauna to potential food sources and/or increased availability of additional organic matter sources by deposition of feces. This study also shows that the use of meiofaunal communities, particularly nematodes, can be an extremely valuable tool to detect early levels of disturbance in aquatic ecosystems caused by the presence of non-indigenous species.

Meiobenthic distribution and nematode community structure in estuaries of Primorye region (Russia, the Sea of Japan) P70

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Meiofauna from the intertidal zone of estuaries (Razdolnaya, Sukhodol and Avvakumovka) was investigated. Samples represented a cross section of various benthic habitats from near-freshwater to marine, from pure silts to fine-sandy bottoms. River's estuary meiobenthos is characterized by significant fluctuations in the density and taxonomic composition. Eleven taxonomic groups Acarina, Amphipoda, Bivalvia, Chironomidae Gastropoda, Harpacticoida, Nematoda, Oligochaeta, Ostracoda, Polychaeta, Turbellaria were presented. The meiobenthic community comprised everywhere a fauna strongly dominated by nematodes in all stations. The density of the total meiofauna assemblages ranged between 500 ind/m^2 and 242000 ind/m^2 (mean density 46800 ± 5000 ind/m^2); biomass ranged between 1.0 to 11070.0 mkg/m^2 (1089.2 ± 245.9 mkg/m^2). The influence of the different environmental settings of the estuaries of Primorye region on nematode diversity patterns will also be discussed. Sixty-seven species of nematodes were identified and subdivided into (1) species of marine origin, (2) euryhaline species preferring higher salinity biotopes, and (3) euryhaline species preferring low salinity biotopes. The Multi-Dimensional Scaling analysis of data on nematode abundances revealed that samples from the upstream areas were clearly separated from the downstream areas. The downstream areas were mainly composed by the genera *Anoplostoma*, *Paradontophora*, *Sphaerolaimus* and *Terschellingia* and the upstream area by the freshwater nematodes – *Dorylaimus* and *Tobrilus*. Ecological indices were calculated for the description qualitative and quantitative characteristics of nematode communities. Trophic structure of the free-living marine nematodes is not related with salinity changes and depends on sediment type.

The role of meiobenthos on ecosystem function

Structure and taxonomic composition of subtidal macro- and meiobenthic assemblages in the Northeast Sakhalin shelf (the Sea of Okhotsk)

P71

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In this study, the distribution pattern of macro- and meiofauna from ten stations of Chayvo Bay along Sakhalin coast between 52.2 and 53.6 °N was studied in summer period. The stations were situated on soft sediments (predominance of sandy fractions) at water depths of 10 to 29 m. All benthos samples were obtained using a van Veen bottom grab sampler (grab area 0.2 m2). Three replicate samples were taken at each station. We observed changes in the composition, structure and seasonal succession patterns in the benthic community over a period of 3 years. The density of macrobenthos ranged between 85 ind/m^2 and 6627 ind/m^2 (mean density 1423 ind/m^2); biomass ranged between 10.3 to 4269.13 mkg/m^2 (197.5 mkg/m^2). The density of the total meiofauna assemblages ranged between 75.5 x 103 ind/m^2 and 50 x 106 ind/m^2 (mean density 20456 x 102 ind/m^2). Considerable inter-year fluctuations of species abundances as well as species richness, diversity, trophic and size structure were recorded. Patterns observed for quantitative distribution of meiofauna were compared with those from larger-sized benthic fauna. The data showed an increase in total macrobenthos biomass with depth throughout the studying area. Common traits among the main structural/functional benthic changes observed and their causes are discussed.

Co-occurrence of cryptic nematode species: true coexistence or mediated by differential microhabitat preferences?

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Research on 'cryptic species', i.e. species which are morphologically indistinguishable but genetically distinct, has increased exponentially over the past decades. The frequency of uncovering 'cryptic species' complexes with DNA sequence data calls into question estimates of the existing number of species and has implications for our understanding of biodiversity−ecosystem functioning relations. Such cryptic diversity is, for instance, prominent in free-living marine nematodes. At least 10 cryptic lineages have already been discovered in the bacterivore *Litoditis marina* complex (a.k.a. *Rhabditis* or *Pellioditis marina*) associated with decomposing macro-algae in the littoral zone of coastal and estuarine environments. Four of them (Pm I, Pm II, Pm III and Pm IV) apparently co-occur in the field, along the south-western coast of The Netherlands. Coexistence of ecologically highly similar species is at odds with non-neutral ecological theory of competition between closely related species, where real coexistence requires stabilizing mechanisms such as differences in ecological niche. We aim to investigate whether these four species truly co-occur or show temporal and/or spatial niche differentiation in their natural environment. The lack of easily distinguishable morphological characters prohibits classical identification approaches, but we use a rapid qPCR-based detection and relative quantification of the four co-occurring cryptic species. We collect different macroalgae (i.e. *Fucus* spp. and *Ulva* sp.) and separate parts of the algae (i.e. thallus, receptacula and bladders) from the intertidal, at different times, to examine preferences for, and short-term temporal variability in microhabitats. Results demonstrate to what extent the distributions of the four cryptic species overlap spatially and temporally and highlight differences in their microhabitat preferences.

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Meiofaunal communities of the US Arctic shelf and slope: insights from morphological and environmental DNA sequencing approaches

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Rapid change is occurring in the Arctic concurrently with increased human activity, yet our knowledge of the structure and function of high-Arctic sediment communities is still rudimentary. The Beaufort Sea is particularly poorly sampled, and largely unexplored at slope depths, providing little information with which to assess the impacts of petroleum exploration activities now beginning in this area. We are investigating diversity and community structure of meiobenthic communities on the continental shelf and slope of the Chukchi and Beaufort seas across a range of depths (50 to 1000 m) using traditional taxonomic and environmental DNA sequencing approaches. The shallow Chukchi shelf experiences tight benthic-pelagic coupling and influx of nutrient-rich Pacific waters, which sustain areas of elevated benthic productivity. The Beaufort slope is topographically complex and characterized by an east-west gradient in benthic habitat characteristics, with heavy input of terrestrial organic matter particularly in the region of the Mackenzie River delta. Warmer, saltier subsurface Atlantic water masses impact benthic communities at mid-slope depths, likely influencing turnover in community structure observed with depth. Food resources are patchy and seasonally variable across the region. Differences in nematode assemblages were detected across the Beaufort Sea shelf/slope, across depths within the Beaufort Sea, and between the Beaufort and adjacent NE Chukchi Sea, which were apparent using both morphological and environmental sequencing data. Sequencing data also revealed an abundance of protists in sediments which have been mostly ignored in studies of ecosystem dynamics in this region, and may represent an important component of the food web. We also examine associations between meiofaunal and bacterial communities at a subset of locations in the Beaufort Sea to consider potential interactions between these two groups.

Diagnostic PCR reveals diversity in diets of meiofaunal flatworms

P74

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Marine intertidal environments, specifically sandy beaches, are increasingly affected by a number of anthropogenic changes-among them, sea-level rise, increased storm frequency and intensity, and the practice of beach nourishment. Using a historical data-set from the early 1970's for comparison, we have documented changes in the meiofaunal community at a series of beaches along a barrier-island (Bogue Banks, North Carolina) on the East Coast of the United States. However, relating these changes to the above-mentioned anthropogenic effects requires knowledge that we presently do not possess in detail for any outer-beach meiofaunal community: (1) a complete picture of trophic relationships in the meiofaunal community, (2) a rapid way to estimate community composition, and (3) data that could bear on movement of single species into and out of the community over time. We have chosen to address the first-listed area using diagnostic PCR. This technique has the advantage of identifying trophic interactions at the species level. We have shown previously that the technique is effective in identification of specific nematode prey consumed by selected flatworm predators. Here, we report results, obtained using an enlarged set of primers, that reveal predation by flatworms on gastrotrichs, harpacticoids, other flatworms, and on temporary meiofauna-larvae of benthic macro-invertebrates that reside briefly in the meiofauna prior to settlement and metamorphosis. Diagnostic PCR therefore appears to be a promising technique for the elucidation of meiofaunal food webs.

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A worm's life in a hanging drop

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Individuals can be seen as the 'single-cell' components of ecosystems. Understanding the variation of individual traits is a key constraint to resolve population-level effects. However, we still have a very limited knowledge of inter-individual variability in meiofaunal-sized organisms, perhaps because their minute size does not ease extensive records of individual traits. We present here a simple method to reveal variability in life-history traits at the individual-level. The hanging drop method has been derived from microbiology and first used with nematodes by Muschiol & Traunspurger (2007). This cultivation method is based on the use of semi-solid droplets of culture medium with a constant concentration of bacteria, that hang from the lid of plastic culture multi-well plates and in which single nematodes are 'jailed' and can be checked/filmed with a stereomicroscope through the lid of the plate. Nematodes are regularly transferred to fresh drops, allowing for recording fundamental traits such as growth rate, fertility, eggs' hatching times and life span. So far, this method has been used to accurately measure life history traits of model species under standard conditions. We present the results of a life history trait experiment with the free- living nematode *Plectus acuminatus*, which is common in aquatic habitats like sediment or moss in comparison to other free-living nematodes.

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Evaluation of a current Ludox centrifugation method in the deep sea, important caveats

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The extraction of deep-sea meiofauna is now often achieved through Ludox centrifugation techniques. These methods take advantage of the specific gravity differences between the animals and the sediment in which they are found. The differences cause the meiofauna to float while the sediment particles sink, providing a decrease in the amount of time that is required to sort a sample. However, through examination of deep-sea sample collected off the west coast of the United States this technique was found, to the best of our knowledge, to have previously undocumented caveats. First, the extraction efficiency varied between the two individuals performing the extraction. This can lead to the misinterpretation of observed patterns in abundances. Second, the extraction method was significantly less efficient for nematodes belonging to the order Desmoscolecida. The lower extraction efficiency leads the total nematode abundance to be underestimated by a median of 1.3%. Although small, this could have greater consequences when performing comparisons between nematode families.

The importance of meiofauna, an ecosystem services modeling approach

P77

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Disturbed ecosystems provide case studies by which the role and value of benthic meiofauna can be tested. The impact of the Deepwater Horizon oil spill provides such a test case by comparing the pre and post communities. The role and value of the benthic meiofauna are being determined by developing a whole ecosystem model for the northern Gulf of Mexico that incorporates ecosystem services. This is being accomplished by (1) expanding on an existing Northern Gulf of Mexico Ecospace model and incorporating provisioning, recreational, and cultural ecosystem services into the trophic flow ecological modeling framework, (2) gathering and inputting biomass data pre- and post-DWH event into the model, and (3) running simulations with the model to test how ecosystem services have been changed and to test the resilience and potential recovery of offshore environments. Provisioning, recreational, and cultural ecosystem services will be quantified by modeling things like catch, catch value, biodiversity, and recreational fishing effort.

Patterns of diversity of Tanaidacea along Eastern-Atlantic and Mediterranean coast: effect of habitat and latitude

P78

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Tanaidaceans constitute an order of peracarid crustaceans with about 1500 species worldwide distributed around all oceans. The group is a major component of the macro- and meiobenthic diversity of infaunal communities at all depths. However, our knowledge on distribution patterns and ecological preferences of most of its species is fragmentary, in part due to the lack of an integrative investigation on ecological parameters affecting the diversity of the group. In this context, the tanaidacean fauna of the Iberian Peninsula and North-west African coast may show a special relevance, as it might comprise both Mediterranean and Atlantic species, with several taxa widely distributed. The goal of our study is two folded. First, we want to complete the knowledge of the tanaidacean fauna of the Iberian Peninsula (Atlantic and Mediterranean coasts) and the Canary and Balearic Islands by examining new material collected from a range of habitats, including sediments, algae, *Posidonia oceanica* meadows and anchialine caves. Second, we want to integrate this information into a database that includes all the published records for Tanaidaceans along the North-east Atlantic and Western Mediterranean coasts (50°N–14°N; 31°W–7°E). The database contains ca. 1700 records for nearly 70 species and includes information on depth, pH, salinity, temperature, concentration, habitat, locality, date of capture and sampling method. Using this information, we intend to infer the optimal habitat and distribution range for every species, as well as alpha and beta (partitioned as nestedness and turnover) diversity indexes across different regions. These indexes will be then investigated in order to test the effect of latitude and habitat on them.

The use of meiobenthos on the assessment of environmental impacts

Meiofaunal communities of Nisida and the environmental status of the Flegrean area

P79

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Nisida is a volcanic islet of the Flegrean Islands archipelago connected to the mainland by a stone bridge. It lies very close to Cape Posillipo, just north of Napoli. The islet has a circular shape, with a flooded crater forming the bay of Porto Paone. In the 1800s Nisida was the site of a Bourbon prison, then an Italian state penitentiary, and is now a reformatory for juvenile offenders. Since then the access to the island has been limited and this has resulted in a very preserved area. However, in the 1900s Nisida was encroached upon by the unsightly steel industry in Bagnoli affecting the state of health of its marine communities. Recently Meiofauna has acquired an important role as an indicator of the marine ecosystem. We performed a meiofauna survey in Porto Paone, with sampling taking place from June 2014 to December 2015 in four areas, resulting in the division of the bay into four quadrants (North–South; West–East). In each area four samples to cover all kinds of substrate present were collected. To have a comparable parameter of the anthropogenic effect on meiofauna communities we performed sampling also in the nearest area of Bagnoli during the period from November to December 2015. The fauna extraction was performed according to Heip et al. (1985). In Porto Paone, throughout the whole study period we found a diversity resulting in the presence of 24 taxa. A seasonal fluctuation was observed with major diversity reported during the fall with the presence of 20 taxa versus 14 taxa in summer. Comparing the same period (November/December 2015) of sampling in Porto Paone and in Bagnoli we found significant differences in taxa presence, i.e., 20 and 8 taxa respectively. Besides giving an overview of the meiofaunal communities in Porto Paone to fill the gap in the recent literature, this work represents a starting point for monitoring the environmental recovery of the Flegrean marine area.

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Meiofauna Network (MeioNet): a young ‘meiofaunologists’ network for the environmental assessment of the Adriatic coastal areas

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In the framework of the IPA Adriatic project BALMAS (‘*Ballast water management system for Adriatic sea protection*’; www.balmas.eu), we have challenged the idea of an active ‘meiofaunologists’ network, to realize a concerted meiofauna sampling from different Adriatic ports/coastal areas and to put effort on meiobenthic analyses and target taxa identification. Up to now eight Adriatic ports have been sampled: Trieste, Venezia, Ancona, Bari, Koper, Split, Durres and Bar, thanks to the collaboration of the colleagues from the different institutes involved in the project. Due to the high sensitivity to environmental perturbations, to the great abundances, and to the short biological cycles, the meiofauna provide rapid responses to environmental changes. For these peculiarities the meiofauna can be an extremely useful tool for investigating the environmental effects of anthropogenic disturbance and, consequently, for the assessment of the marine ecological status in a given area. Among meiofaunal groups, nematodes and copepods have been identified as key informative taxa. Nematodes have been already allocated among the suitable indicators for the assessment of the ecological quality of marine ecosystems by the Water Framework Directive (WFD, 2000/60/EC). Furthermore, even if meiobenthic animals lack a pelagic larval stage in their life cycle, some researchers have reported that ballast tanks can be a ‘home’ for an assemblage of viable and reproducing meiobenthic organisms (e.g., nematodes). They apparently use cisterns as a regular habitat, which, at the same time, serves as a depository of individuals/species physiologically and ontogenetically ready to colonise suitable sedimentary environments. This has implications for the zoogeography of meiobenthic taxa and for their role as non-indigenous invasive species. The MeioNet objectives will be: (1) to investigate the meiofauna populations (i.e., distribution and diversity) from different ports and environmental conditions; (2) to up-date the genera/species list(s) of target functional groups (e.g., nematodes; copepods) inhabiting impacted coastal areas of the Adriatic Sea; (3) to use the meiofauna, and in particular target taxa such as nematodes and copepods, as suitable tool for the Environmental Quality Assessment (e.g., changes in the structural and functional diversity of meiobenthic populations compared to previous data from literature).

Spatial patterns of meiofaunal assemblage at the Noho site in the Okinawa Trough, NW Pacific: traditional vs. semi-automated methods

P81

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Submarine resources, such as seafloor massive sulfide (SMS) deposits, are expected to become developed in the near future. Mining activities would affect the surrounding seafloor environment and benthic ecosystem. It is necessary to evaluate such mining impacts in order to minimize the adverse effects on the ecosystems. Meiofauna is widely recognized as a useful indicator for assessing the effect of anthropogenic and natural disturbances on deep-sea ecosystems. However, traditional methods of investigating meiofauna, which includes counting and identifying small-sized meiofaunal specimens one by one under a microscope, is labor-intensive and time-consuming. Alternative methods, which can rapidly deal with an abundance of meiofaunal samples, are required when conducting long-term environmental impact assessments. The flow cytometer and microscope (FlowCAM, Fluid Imaging Technologies), originally developed to analyze microplankton semi-automatically, has the potential to resolve this need. We investigated the meiofaunal assemblages at the Noho site in the Sakai hydrothermal vent field, located in the middle of the Okinawa Trough, north-west Pacific Ocean. This site is a target area for the 2016 drilling expedition by the D/V *Chikyu*. The sediment samples were collected during the research cruise of the R/V *Kairei*, KR-15-17 in November 2015, using a push corer on the ROV *KAIKO Mk-IV*. The aim of this study was to collect pre-impact data on the meiofaunal assemblages at this site. In addition, we compared the assemblage data obtained with a semi-automated method with those obtained using traditional methods.

Fixing, storage time and DNA extraction applied to DT-RFLP for ecological and molecular studies of marine nematode assemblages

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The application of molecular methods offers an alternative faster than traditional methods based on morphology. Molecular approaches offer the potential to investigate questions that would be unmanageable using traditional approaches, in those cases where a large number of samples are being studied. It is almost impossible to process all the samples in a short period using traditional methods, especially given the rapid deterioration of marine sediment samples. The dT-RFLP (directed Terminal-Restriction Fragment Length Polymorphism) allows a rapid assessment of biodiversity changes in nematode assemblages. However, after the nematodes have been extracted from benthic sediments, a high content of vegetable detritus remains. This could be a limitation of the DNA extraction process and furthermore, of the dT-RFLP analysis. Therefore, an experimental study was designed to investigate the best fixative, the level of DNA degradation over time and the best DNA extraction method for marine nematodes. Here, three different DNA extraction methods were tested (two commercial kits and one with phenol-chloroform) to investigate the best DNA extraction method for benthic nematodes. The fixation of benthic nematodes was tested using three different storage fixatives (70% ethanol, DESS and freeze drying) to investigate with which one benthic nematodes are better preserved for dT-RFLP analysis. The storage time was investigated using five different time points (0, 2, 4, 8 and 12 months) where in each one the DNA was extracted. This gave an opprtunity to study the level of DNA degradation over time. Benthic nematodes were collected from Mira Estuary (SW, Portugal) and preserved in different fixatives and during different time periods. DNA was extracted and PCR-amplification performed to test the suitability of the extracts for molecular applications. In order to test whether choice of DNA extraction method, storage fixative and storage time have an effect on nematode community composition, dT-RFLP was performed. Real-time PCR (qPCR) was also performed in order to investigate whether previous choices have an effect in benthic nematode quantification. Both the dT-RFLP and qPCR processes showed differences in nematode community following the different methods under investigation. This study demonstrates that dT-RFLP applied to marine nematodes communities facilitates a faster and more efficient approach for ecological and molecular studies.

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The use of marine nematode species in ecotoxicological bioassays

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Within ecotoxicology, different nematode species have been used to assess ecological impacts of contaminants. However, these studies have been conducted mainly with freshwater and terrestrial nematodes and the use of marine nematodes, despite their numerical and ecological importance, remain poorly explored. In this study, we tested the potential of two species of marine nematodes as useful indicators to be employed in ecotoxicological bioassays. *Litoditis marina* lives on macroalgae in the littoral zone of coasts and estuaries around the world and *Diplolaimella diavegatensis* in sediments. Both feed on bacteria and are easily cultivated in laboratory. We have investigated the effects of three sublethal concentrations of sodium dodecyl sulfate (SDS) in the growth, reproductive output and survival of these two nematode species. SDS is the most common chemical compound used in cleaning and personal hygiene products and therefore is frequently found in industrial and domestic sewage. The two species were synchronized and maintained in agar plates. Survival rates were continuously observed for seven days. Growth was estimated by measuring the length of nematodes from egg stage to six days. The reproductive output was considered by the number of eggs and juveniles per female observed in seven days. Survival, growth and reproductive output of both species were significantly affected by all concentrations of SDS compared to control treatments but responses were species specific. Juveniles of *D. diavegatensis*, unexpectedly, showed maximum values for the three parameters at the low and medium concentration of SDS but reduced values at the highest concentration. *L. marina*, on the other hand, showed reduced growth and reproductive output at all concentrations of SDS compared to controls. Survival did not differ between treatments. These results suggest different life-history strategies of the two species in response to this particular pollutant highlighting the importance of detailed analysis of different life-cycle traits as well as considering multiple species in toxicity testing even when these are ecologically similar. Finally, the results of this study confirm the potential of these two marine species as suitable ecotoxicological tools to be used as models in toxicity testing that evaluate ecological effects of contaminants in the marine environment.

Responses of meiofauna and nematode communities to crude oil contamination in a laboratory microcosm experiment

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In this study, we aimed to conduct a laboratory evaluation of the effects of crude oil contamination on the meiofaunal and nematode communities inhabiting an intertidal sandy beach. This objective was accomplished by examining changes in the structure of meiofaunal and nematode assemblages after exposure to different concentrations (0.5%, 1%, 2%, 4%, 8%, 15%, and 20%) of total petroleum hydrocarbons (TPH) in microcosms. The concentrations of TPH in the experimental microcosms did not significantly differ from those in the control microcosms after 60 days. The average density of total meiofauna in the 0.5%, 1%, 2% and 4% experimental microcosms was 157.9 individuals, which was higher than the density in the control microcosm. The average density of total meiofauna in the 8%, 15%, and 20% microcosms was 90.7 individuals, which was lower than the density in the control microcosm. The density of nematodes was similar to that of the total meiofauna. Cluster analysis divided the microcosms into two groups: group 1: control, 0.5%, 1%, 2%, and 4% microcosms; and group 2: 8%, 15%, and 20% microcosms. However, SIMPROF analysis showed no significant difference between the two groups ($p > 0.05$). A total of 2240 nematodes were recorded in this study. *Bolbolaimus* spp. (37.1%) were dominant among the nematodes. Cluster analysis results for nematode communities were similar to those for the meiofaunal communities. The total meiofaunal density, nematode density, and number of *Bolbolaimus* spp. individuals were significantly negatively associated with TPH concentration (Spearman

correlation coefficients, $p < 0.05$). Within the nematode community, epistrate feeders (group 2A: 46%) were the most abundant trophic group. Among the treatment groups, the abundance of group 2A increased in low-concentration microcosms (0.5% and 1%) and decreased in high-concentration microcosms (2%, 4%, 8%, 15%, and 20%), whereas the abundance of nematodes with other feeding types did not differ significantly.

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Effect of the Hebei Spirit oil spill on intertidal meiofaunal communities in Taean, Korea

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On December 7, 2007, the M/V Hebei Spirit was struck by a crane barge on the Yellow Sea approximately five miles off Taean, South Korea. Approximately 10,900 t of crude oil spilled into the sea from the Hebei Spirit. The spilled oil spread rapidly in the water and onto the nearby coast due to strong winter winds and currents. In this study, we studied the effects of an oil spill on meiobenthic communities in sandy intertidal areas of Taean. The distribution patterns of meiofauna were monitored for five years at two contaminated sites (Site 1, 2) and one uncontaminated site (Site 3). The sampling sites showed different patterns of change in density of meiofauna over this period. For the first two years after the accident, the density of meiofauna fluctuated among the sites. Seasonal variations in the density characteristics were observed at two contaminated sites after three years from the oil spill accident. At the end of the 5-year period, the density differences among the sites decreased. In the initial 6 months after the accident, the density of meiofauna was higher at site 1 than at site 2 in which the level of oil pollution was higher. Nematode densities did not decrease in the initial period after the oil spill. However, the species assemblage of nematodes was altered by the oil pollution. An nMDS analysis of nematode species compositions showed that after the accident Immediately samples (January and winter 2008) were separate from other samples in which the level of oil pollution was lower. Because it is difficult to identify the influence of contamination on biological communities, long-term monitoring to assess the recovery of dominant species and community structures could overcome this problem.

Benthic responses to saltmarsh restoration following the Deepwater Horizon oil spill

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Salt marshes are sometimes slow to recover after being impacted by an oil spill. Here, the results of a study designed to enhance restoration of an oiled marsh are described. Replicated (n = 5/treatment) plots in an area of intertidal salt marsh that was heavily oiled in the 2010 Deepwater Horizon (BP) oil spill, but lagging in plant recovery, were treated in 2014 by planting the macrophyte *Spartina alterniflora*, by adding fertilizer, and by planting *S. alterniflora* and adding fertilizer as separate treatments. Control plots and reference marshes were also monitored. Microalgal, meiofaunal, and macroinfaunal responses were examined after 2 and 7 months. Benthic microalgal biomass increased after two months in the presence of *S. alterniflora* and with fertilization. Simultaneously, increases in the total numbers of macroinfauna (due almost exclusively to increases in polychaetes in the genus *Capitella*) occurred in plots where *S. alterniflora* was planted but not in plots with nutrient addition. These results indicate increased density was a facilitatory response (perhaps caused by enhanced larval settlement) associated with the foundation species function of *S. alterniflora* rather than to increases in food associated with higher microalgal biomass. However the facilitation effect was temporary; microalgal biomass and macroinfaunal densities were similar in all treatments after seven months. Meiofauna (using metrics that include copepod, nematode and total meiofauna density and the number of copepod species) did not respond to nutrient addition or to the planting of *S. alterniflora.* Densities and diversities of macrofauna and meiofauna were much lower overall in the restoration sites than in reference sites indicating that restoration was still ongoing at the time of sampling. Amphipods, tanaids, and the meiofaunal polychaete *Manayunkia aestuarina* ‘avoided’ restored plots, while *Capitella* sp. and the copepod species *Nannopus palustris* were much more abundant in treatment plots than reference areas. Previous studies indicate that the macroinfauna of restored salt marshes takes months to years to become equivalent to reference sites, and plots will continue to be monitored to better understand the factors that affect marsh restoration.

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Effects of metal contamination on life-history traits and lipid metabolism of *Caenorhabditis elegans*

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A full life-cycle experiment with the model organism *Caenorhabditis elegans* was conducted to estimate in how far ecotoxicological relevant endpoints (ECx-values), resulting from a standardized bioassay (DIN ISO 10872), could be transferred to effects on population level of this free-living nematode. The hanging drop method in semi-fluid culture medium was used to follow basic life-history traits of *C. elegans* the essential heavy metal Copper (Cu) and in the control medium respectively. Life-cycle parameters like juvenile growth rates, age at sexual maturity, egg-laying rates, total reproduction and lifespan were examined at the individual level, allowing a direct comparison between treated and untreated test organisms. Besides these patterns, the 3D-distribution of lipid droplets in single individual worms was visualized using Raman spectroscopy (Coherent Anti-stokes Raman Scattering; CARS). Using CARS we were able to determine the shape, size and location of lipid droplets in relation with Cu exposure conditions. Using this direct optical approach, we gained insights into the physiological state of individual tissues, and a better understanding of fundamental mechanisms affecting the life-history traits due to a chemical stressor were aimed. Preliminary results illustrated clear dose-dependent effects in terms of the shape and size of lipid droplets in the tissues of investigated treated individuals of *C. elegans*. This approach holds promise for further investigation of meiofauna responses to environmental contamination at an unprecedented level of resolution, from cellular- to single individual-level.

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A test of the Pearson and Rosenberg's macrofauna succession model on free-living marine nematodes impacted by aquaculture activities

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Over the last decades, many studies have investigated the response of macrofauna on organic enrichment, and it has become well established that macrofauna is a useful bio-indicator of pollution since it quickly responds to changes in environmental conditions. Aquaculture, a rapidly increasing industry, has been recognized as a potential source of pollution for the coastal marine environment due to the progressive accumulation of organic matter on the sea bottom, which usually causes significant changes in the physicochemical characteristics of the sediments. Pearson and Rosenberg (1978) describe predictable changes in the structure of benthic assemblages in relation to spatial distance from a pollution source, regarding the species, abundance and biomass composition. While Pearson and Rosenberg's model is frequently used for analyzing macrofauna data and its usefulness has been verified only in macrofaunal assemblages, in this study we aim to test it for the first time on a meiofaunal taxon. Recently, meiofauna communities have been considered as good indicators of environmental conditions as they exhibit several advantages in comparison to macrofauna, e.g., their small size, high abundance, high turnover rates, and lack of larval dispersion. Here, we tested how the species-abundance-biomass curves of nematode assemblages change along gradients of organic enrichment at seven commercial fish farms in the eastern Mediterranean. Our results show that, while the nematode species-abundance-biomass curves do not exactly follow those of the macrofaunal succession model, they do show considerable consistency, with the abundance and biomass curves being always above the species curves and peaking one or two times along the gradient. Furthermore, the ecotone zone appears to be located always at intermediate distance, in the area between 5 and 25 m from the cages.

Abyssal meiofauna communities in the UK-1 exploration area of the Clarion-Clipperton Zone (Northeast Pacific)

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The interest in marine mineral exploitation has been increased rapidly in recent times. The Clarion-Clipperton Zone, located in the northeastern Pacific, holds major deposits of polymetallic nodules, and it therefore is an area prospected for mining. However, how the sediment dwelling fauna in this region will be affected by the environmental impacts of mining activities is still poorly understood and makes a baseline evaluation of the benthic communities a prime concern. Metazoan meiofauna have numerous advantages for investigating the response of living assemblages to disturbances such as nodule uptake or deposition of suspended sediments: they are highly abundant and diverse, widely distributed and display a high sensitivity to environmental changes due to high turnover rates. The objective of the present study was to investigate the baseline conditions of metazoan meiofauna community structure in the UK-1 license area in the eastern part of the Clarion-Clipperton Zone associated with abyssal sediments and polymetallic nodules. Samples were retrieved from 10 randomly located stations at depths ranging from 3900–4400 m using an OSIL Bowers & Connelly mega core. The study is a part of a benthic biological Abyssal Baseline Study (ABYSSLINE) required prior to potential mining of the polymetallic nodules.

P90 Deep-sea meiobenthic communities in the former experimental disturbance test site in the Clarion-Clipperton Fracture Zone (CCFZ, sub-equatorial NE Pacific) nodule field

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In July 1995, an experiment (IOM BIE) aimed at producing disturbance of the seafloor sediment imitating that generated during nodule mining was carried out in the Clarion-Clipperton Fracture Zone (sub-equatorial NE Pacific) by the Interoceanmetal (IOM), a 6-nations consortium with a mission to prepare future nodule development. A 1.5 x 2 km area of the seafloor, at ca. 4300 m depth, was impacted by a series of tows of a device known as the Benthic Disturber. The programme relied on changes in parameters describing the meiobenthic assemblage structure as the major proxies with which to assess the magnitude and intensity of the disturbance. Those proxies included both qualitative (genus-level taxonomic composition of nematodes and harpacticoids) and quantitative (abundance of the total meiobenthos and dominant taxa as well as the relative abundances of the latter). An attempt was also made, by resampling the test site during follow-up cruises undertaken at various time intervals (22 months and 5 years) post-disturbance, to determine the degree of recovery in the disturbed area and its recolonization. The meiobenthos did respond to habitat disturbance, the major response being seen in the reduction of abundance immediately after the disturbance. Effects observed during the follow-up studies involved some degree of recovery, accompanied by alteration in the taxonomic composition of nematode and harpacticoid taxocoenes. It is not known, however, how persistent those effects are, and how the long-term recovery proceeds. These issues are tackled by the Joint Programming Initiative (JPI) Oceans Pilot Action project “Ecological Aspects of Deep-Sea Mining”. The project involved, i.e. a cruise on board RV SONNE (SO 239) in March-April 2015, i.e. twenty years after the original disturbance, during which the IOM BIE site was resampled to yield data on the meiobenthic assemblage structure for comparison with the community status from before and just after the experimental disturbance. The findings of this work in progress are presented.

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Monitoring the impact of human activities in Admiralty Bay, Antarctica: nematode assemblages

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The West Antarctica Peninsula is one of the most vulnerable region to global changes, and also a place with numerous research stations. The Brazilian Antarctic Station “Comandante Ferraz” (CF) is located in Admiralty Bay (King George Island), an Antarctic Specially Managed Area (ASMA1). A joint project (Network 2), done from 2002 to 2006, allowed a preliminary characterization of the influence of sewage and hydrocarbons in the sediment. Slight pollution was observed only in the proximity of CF sewage outfall within a distance of 700 m, and a continuous monitoring program of the marine environment has been established since 2007. In order to compare the periods, nematodes genera were identified in two austral summers, 2004/2005 and 2010, in two and three areas, respectively, in which two points were sampled at 20−30 m depth. The chosen areas were in front of the Brazilian Station (CF1, CF2), under anthropogenic influence, and the reference areas at Botany Point (BP1, BP2) and Ullmann Point (UP1, UP2). Sampling of sediment was done with a mini box corer, in triplicate, and a core of 4.9 cm^2 and 5 to 6 cm height was employed to collect meiofauna (between 500 and 44 μm mesh size). *Aponema*, *Sabatieria*, *Daptonema*, *Molgolaimus*, *Acantholaimus* and *Odontophora*were were the dominant genera in both summers. Similarity analysis revealed no significant differences in genera composition between the points and summers, including CF1 (sewage influence), and CF2 (in front of the oil tanks). Nevertheless, in 2010, diversity was lower in both CF points, nematode density was lower in CF1, where the dominance of this group was higher than at the other points. The differences in nematode community structure found in CF1 suggest that some impact due to human activities in front of the Brazilian Station occurs, although of small magnitude and range.

This study contributes to the monitoring program under the scope of the INCT–APA (National Institute of Science and Technology – Antarctic Environmental Research – CNPqproc. n° 574018/2008-5, FAPERJ no. E-16/170.023/2008)

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Benthic foraminiferal responses to anthropogenic manipulation on a wild oyster reef

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Benthic foraminifera are known to respond quickly to environmental changes. Biological indices are used in marine subtidal areas (Barras et al., 2014) to monitor impacted marine environments (Mojtahid et al., 2006, 2008). Such indices could be useful in transitional marine environments such as estuaries and mudflats where no accurate indices are available. To develop such tools and to improve our knowledge on benthic foraminifera in intertidal environments, we followed the spatial and temporal distribution of benthic foraminifera in Bourgneuf Bay, a coastal bay with a large mudflat situated south of the Loire estuary on French west coast. At this location, wild oyster reefs are present. Partial release of organic and inorganic nutrients through oyster excretion enriches the nutrients flow leading to microphytobenthos bloom around the reef. To show this relation and to understand the relation between the different biological compartments, we analysed the foraminiferal composition of the sediment around the reef before and after an anthropogenic manipulation. In July 2014, the oysters of the reef were removed in order to assess their impact on microphytobenthos and meiofauna. In this study, we showed a strong impact of this anthropogenic manipulation on benthic foraminiferal densities and species composition. These results confirmed the strong and quick responses of benthic foraminifera from intertidal areas to environmental changes and showed that intertidal benthic foraminifera can be used as an index to monitor transitional marine environments.

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First communication about free-living marine nematode communities from San Jorge Gulf, Argentina

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This paper describes a baseline study on nematode biodiversity from different geographic positions on San Jorge Gulf (45–47 °S and 65–67 °W). The purpose of the study was to give the first inventory of the fauna of these habitats, to know the dominant taxa of free-living marine nematodes (61–110 m depth), and to show the diversity inside this gulf. San Jorge Gulf is of strategic interest to Argentina because it sustains economically valuable shrimp fisheries (*Pleoticus mulleri* Spence Bate, 1888) and could become a new offshore oil exploitation area in the near future. So it is urgent to know about its biodiversity. The expedition took place from January 29th to March 4th 2014 on board the Research Vessel CORIOLIS II in the continental margin of the San Jorge Gulf areas, focusing on physical, chemical and biological oceanography. The benthos sampling consisted of 13 Box Corer stations. The meiofauna samples were collected with a cylindrical Plexiglas corer, preserved in 5% formaldehyde in filtered seawater with rose Bengal, sieved through both 500 and 50 um mesh sieves, and separated using the LUDOX TM method. After that, permanent mounts were prepared on glass slides and sealed. The nematodes found were identified up to the lowest taxonomy level possible. The geographical position (GPS), salinity, temperature and granulometry, have been recorded. Sediment analyses were carried out by dry sieving and classified according to the Wentworth scale. The differences in nematode species composition between latitudes and environments were analyzed by multivariate methods. The results indicate the presence of four different communities of nematodes following sediment granulometry. The largest diversity was found in the North–East border of the San Jorge gulf with dominance of fine sands. Relationships between shrimps and meiobenthos are discussed.

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