EUROPEAN MARINE BIOLOGY SYMPOSIUM
EMBS 55
Gdańsk I September 19 - 23 2022

Book of abstracts

55th European Marine Biology Symposium

19 – 23 September 2022
Gdańsk, Poland

We would like to thank our sponsors for their generous support.

Main sponsor

MEWO S.A.
Subsea Solutions

Sponsors

University of Gdańsk
Higher education institution

TRIBIO
Environmental Service

NHBS
Wildlife | Ecology | Conservation

HYDRO-BIOS
High Quality Instruments for Sea And Ocean Technology

Genomed S.A.

Marine Biological Association
Promoting marine scientific excellence and representing the marine biological community since 1884

Patronage

Rector of the University of Gdańsk, Prof. Piotr Stepnowski

Polish Scientific Committee on Oceanic Research

Contents

PLENARY PRESENTATIONS

Thematic session: "Main stressors and their impact on ecosystem health"

The impacts, detection, prediction and management of endogenic and exogenic stressors on marine environmental health

Michael Elliott[1,2], Krysia Mazik[1], Anita Franco[3]

[1] Department of Biological and Marine Sciences, University of Hull, Hull, HU6 7RX, UK

Email address: Mike.Elliott@hull.ac.uk

[2] International Estuarine & Coastal Specialists Ltd., Leven, HU17 5LQ, UK

[3] Anita Franco Estuarine and Marine Ecological Consultant, Hull, HU5 3SF, UK

Stressors on marine individuals, populations, communities and ecosystems within a sea area emanate from two sources and may be regarded as pressures; these are defined as the mechanisms of causing change and so which need to be managed to prevent damage to these systems. Firstly, what may be called *endogenic managed pressures*, in which the causes and consequences both originate from inside the sea area being managed – these include, for example, smothering of the seabed by trawling and dredging, and increased nutrients leading to eutrophication. The *exogenic unmanaged pressures* originate from outside the sea area being managed and by definition only their consequences are managed within the area whilst their causes require to be managed by wider measures, even as global levels as with climate heating. These pressures include sea-level rise, ocean acidification, increased warming and the introduction of alien species. The talk indicates the methods for the monitoring, assessment and reporting of these pressures and the tools for predicting the effects as a precursor to marine management. The latter tools include the suite of empirical and deterministic numerical models and indicators and rules-based decision support systems. Finally, the place of these tools in marine management and the implementation of European marine Directives and the OSPAR and HELCOM Regional Seas Conventions will be explained.

Thematic session: “Diversity and physiology of marine organisms. Is there still anything to discover?”

Questions and approaches around climate change and impacts in the ocean: a physiologist’s view

Hans-Otto Pörtner

Alfred-Wegener-Institute, Bremerhaven,
Am Handelshafen 12, 27570, Germany
Email address: hans.poertner@awi.de

Climate change drivers in the ocean entail ocean warming, acidification and loss of oxygen due to warming and enhanced stratification. These drivers individually and together affect ocean life. While some approaches compare the effect size of these individual drivers, other approaches strive to develop an integrative view. Based on principle considerations temperature emerges as a master variable shaping the functioning of all life forms in the ocean. Such functioning depends on the thermal performance curve as a reaction norm characterizing individual species and their lifestages. Overlapping thermal performance curves characterize the temperature range at which species can co-exist at ecosystem level. The talk puts each of the drivers into context and puts an emphasis on how ocean oxygen plays a role in the thermal tolerance and performance of marine animal species.

Thematic session: “Marine molecular ecology – new tools and new findings”

On genetic diversity: new insights from population genomics of marine organisms

Joe Hoffman

Department of Animal Behaviour, University of Bielefeld,
Postfach 100131, 33501 Bielefeld, Germany
Email address: joseph.hoffman@uni-bielefeld.de

Knowledge of the mechanisms shaping the genetic diversity of marine organisms is essential for understanding metapopulation and community dynamics, for predicting future responses to anthropogenic change, for marine protected area design and fisheries management, and for the development of ecological and evolutionary theory. However, the genomic tools needed to unravel those mechanisms have only recently become available. In this talk, I will touch upon some ways in which population genomic data can be used to investigate the factors, both neutral and selective, that shape the genetic diversity of marine populations. I will draw upon examples from our research on diverse marine organisms, including benthic invertebrates and pinnipeds. I will emphasise the importance of combining an integrative approach with advanced genomic analysis techniques to maximise the insights that can be obtained from population genomic data.

Thematic session: “Marine living resources – environmental significance”

Cyanobacteria – are they really so bad?

Hanna Mazur-Marzec

Division of Marine Biotechnology, Institute
of Oceanography, University of Gdańsk,
Gdynia, al. Marszałka J. Piłsudskiego 46, 81-378, Poland
Email address: hanna.mazur-marzec@ug.edu.pl

Cyanobacteria, the Gram-negative bacteria, are important group of primary producers. However, in many eutrophicated aquatic ecosystems, including the Baltic Sea, their blooms pose one of the most serious environmental problems. High biomass of these microorganisms has deleterious effect on the ecological stability of water bodies. In addition, occurrence of cyanobacteria in coastal areas deteriorates sanitary conditions of beaches. Cyanobacteria are also known as producers of a plethora of bioactive compounds, including potent toxins. In the Division of Marine Biotechnology, University of Gdańsk, high inter and intraspecies metabolic diversity of the Baltic cyanobacteria was documented. It was revealed that the metabolic profile of cyanobacteria is a subpopulation-specific trait. Some of the metabolites can be used as specific chemical markers of high significance in different environmental studies. One example is the reconstruction of thousand-year history of *Nodularia spumigena* blooms in the Baltic Sea and Norwegian Fjords. In more recent work, the pharmaceutical potential of bioactive cyanobacteria compounds have started to attract increasing attention. In these studies, the ribosomal and non-ribosomal peptides were found to be most promising. Significant number of the peptides produced by Baltic cyanobacteria showed potent anticancer and antiviral activity and revealed an effect on key metabolic enzymes. In response to the growing interest in cyanobacteria metabolites, a CyanoMetDB was created. This open access data base includes over 2000 compounds and is widely used by scientific community. The study was supported by NCN grant No 2019/33/B/NZ9/02018.

General session

Climate change and marine biodiversity in North Atlantic – competitive exclusion or coexistence?

Jan Marcin Węsławski

Institute of Oceanology Polish Academy of Sciences, Sopot, ul.
Powstańców Warszawy 55, 81-712, Poland
E-mail address: weslaw@iopan.gda.pl

The fast warming European Arctic experience two parallel and partly independent phenomena: sea temperature rise and increased transport of waters from lower latitudes. Considering short evolutionary history of the Arctic (less than 1 mln years) majority of marine species there are still close relatives to the boreal ancestor species. The endemic taxa are very scarce, most endemism is on the level of twin species or subspecies and metapopulations. Now the boreal cousins are meeting their twins and by definition they compete for the same niche and habitat, what shall drive the cold climate species to recede. However there are numerous examples, that coexistence is more common that competitive exclusion

MAIN STRESSORS AND THEIR IMPACT ON ECOSYSTEM HEALTH

Spatial and seasonal patterns in macrobenthic communities along the north-western Barents Sea and Nansen Basin

È. Jordà Molina[1], A. Sen[1,2], B. A. Bluhm[3], P. E. Renaud[4], M. Włodarska-Kowalczuk[5], J. Legeżyńska[5], B. Oleszczuk[5], H. Reiss[1]

[1]Nord University, Universitetsalléen 11, 8026 Bodø,
E-mail address: eric.jorda-molina@nord.no
[2]University Centre in Svalbard (UNIS), P.O. Box 156 N-9171 Longyearbyen, Norway
[3]UiT The Arctic University of Norway, PO Box 6050 Langnes N-9037 Tromsø, Norway
[4]Akvaplan-niva, Fram Centre, Postbox 6606, Stakkevollan, 9296 Tromsø, Norway
[5]Institute of Oceanology Polish Academy of Sciences (IOPAN), Powstańców Warszawy 55, 81-712 Sopot, Poland

The Barents Sea has been coined 'the Arctic hotspot' for climate change due to the rapidity with which environmental changes are taking place. This transitional domain from Atlantic to Arctic waters is home to highly productive benthic communities. This system strongly fluctuates on a seasonal basis in its sympagic-pelagic-benthic coupling interactions, with potential effects on benthic standing stocks and production. Understanding the underlying spatio-temporal mechanisms by which soft-bottom benthic communities are structured along environmental gradients is necessary to predict future impacts of climate change. In this study, we address this need by examining the macrofauna communities along a transect in the western Barents Sea comprising two hydrographic domains (Arctic vs. Atlantic Water across the Polar Front) and three geomorphological settings (shelf, continental slope and abyssal plain) on a seasonal basis. This includes the polar night period, a time of the year for which data is scarce. Preliminary results show Annelida dominance at most stations, except at the station just above the Polar Front, where Mollusca dominated, and a strong decline in macrofauna abundance and biomass towards the slope and basin. Ordination techniques differentiate the shelf stations from the slope and basin, but so far no strong seasonal differences seem to be found in species composition and diversity. Functional traits of the macrofauna community will be analyzed to study their potential seasonality and spatial variation and constrained ordination analysis will be performed to identify the environmental variables that potentially drive community and functional structure at different times of the year.

Kelps and their associated fauna in rapidly changing glacial fjord environment

M. Ronowicz[1], M. Włodarska-Kowalczuk[1], P. Kukliński[1]

[1]Institute of Oceanology Polish Academy of Sciences, Marine Ecology Department, ul. Powstańców Warszawy 55, Sopot 81-712, Poland
E-mail address: martar@iopan.pl

Kelps are conspicuous brown macroalgae of the order Laminariales. They are important primary producers, food source, their presence increases local species richness and creates hot spots of diversity. Nowadays, underwater light conditions are changing due to progressing deglaciation in the Arctic fjords what may lead to various modifications in these assemblages. The aims of this study were to assess standing stock of kelps, the effect of glacier exposure on macroalgae community composition, biomass and density, and associated fauna diversity, as well as range of phenotypic plasticity in kelp morphology in relation to glacier-derived disturbance. Three sampling sites were located at different distances to glacier fronts in Hornsund (Svalbard). Altogether, 403 kelps were collected, measured and weighted. All kelp-associated fauna were identified to the lowest possible taxonomical level. Reorganization of community composition was observed between the clear and glacially exposed sites. There was a shift in the macroalgal biomass towards shallower depths at glacial sites what might be a consequence of glacial activity and reduced water transparency. The highest number of kelp-associated fauna was observed on a holdfast part of thallus (200 species). Holdfast fauna comprised of mostly three taxa: colonial Bryozoa, Hydrozoa, and Polychaeta. The high sedimentation load did not cause reduction in species richness of kelp holdfast-associated fauna but induced the changes in taxonomic composition between dominant groups. Morphological features of particular kelp species varied between sites, what may indicate that kelps can respond to environment in different ways in order to enhance their survival potential in unfavorable conditions.

Modern climate change impact on foraminifera assemblages of Hornsund (Svalbard)

N. Szymańska[1], M. Łącka[1], M. Zajączkowski[1]

[1]Institute of Oceanology PAN, Department of Paleoceanography, Powstańców Warszawy 55, 81-712 Sopot
E-mail address: natalia@iopan.pl

The process of Atlantification and the melting of glaciers are two large-scale mechanisms related to the modern climate change that are occurring in the Arctic. Both processes are especially pronounced along the western coast of Svalbard, an archipelago located in the Nordic Seas. The influx of warm and saline Atlantic Waters (AW) changes the oceanographical properties of local water masses. As a consequence, the environmental stress on local ecological communities increases. Recent studies have shown that both, primary productivity, and benthic communities of Svalbard fjords can be negatively affected by the ongoing Atlantification and melting of glaciers. However, little has been known about how these processes affect modern foraminifera assemblages. Here we present the change in benthic foraminifera assemblages between year 2002 and 2019 in Hornsund fjord (Svalbard). Foraminifera are highly abundant in Arctic fjords and constitute a significant part of inorganic carbon buried in their sediments. Fjords, despite their small size (less than 1% of the global ocean) have been recently found to be an important part of both climate regulation as well as carbon burial processes. This makes studies on foraminifera assemblages of fjords crucial to fully understand carbon burial in polar regions. Our study shows that the current environmental changes have a negative impact on foraminifera abundance in Hornsund fjord. The species composition also underwent a noticeable change, as more agglutinated and Atlantic-water indicative species were found in the assemblage from the year 2019. The study was founded by National Science Center grants No. 2019/33/B/ST10/00297 and No. 2019/34/H/ST10/00682.

Lifelong exposure to warmer temperatures does not produce higher tolerance to marine heatwaves

T. Repolho[1], B. Pereira[1], M. Court[1], G. Barreto[1], J. Varela[1], E. Otjacques[1,2], D. Jacinto[3], R. Rosa[1], M. Diniz[4], J. R. Paula[1,5]

[1]MARE-Marine and Environmental Sciences Centre, Laboratório Marítimo da Guia, Faculdade de Ciências, Universidade de Lisboa, Av. Nossa Senhora do Cabo, 939, 2750-374 Cascais, Portugal
E-mail address: tfrepolho@fc.ul.pt
[2]Carnegie Institution for Science, Division of Biosphere Sciences and Engineering, Church Laboratory, California Institute of Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA
[3]MARE-Marine and Environmental Sciences Centre, Laboratório de Ciências do Mar, Universidade de Évora, 7521-903 Sines, Portugal
[4]UCIBIO-Applied Molecular Biosciences Unit, NOVA School of Science and Technology, NOVA University of Lisbon, Caparica, Portugal
[5]Swire Institute of Marine Science, School of Biological Sciences, The University of Hong Kong, Pok Fu Lam Road, Hong Kong SAR

The frequency and intensity of marine heatwaves have increased due to rapid climate change. However, the study of the capacity for long-term adaptation to higher temperatures has been stalled by the absence of adequate experimental systems experiencing warming across relevant timescales. Here, we examine sea urchins (*Paracentrotus lividus*) from S. Torpes (Portugal), a unique coastal ecosystem that maintained natural thermal fluctuations but has been warmed by 5°C by a coal power plant for 35 years until December 2020. Sea urchins were collected from S. Torpes and Cabo Raso (control location) 9 months following the shutdown of the powerplant to determine if long-term memory of high-temperature exposure provides an advantage in dealing with marine heatwaves. Sea urchins from both locations were exposed to two laboratory-induced marine heatwaves for 15 days. Following exposure, we evaluated sea urchin oxidative stress biomarkers (HSP70, SOD, catalase, GPx, MDA), protein folding (ubiquitin), and coelomic fluid buffering capacity. Except for coelomic fluid buffering capacity, we observed that sea urchins previously exposed to higher temperatures do not retain an advantage in dealing with new heating events. This indicates that repeated exposure to warmer temperatures does not increase physiological resilience in sea urchins.

Macroalgae Morphofunctional Indicators for Ecological Assessing of Coastal Ecosystems

G. Minicheva[1]

[1]Institute of Marine Biology of the NAS of Ukraine, Department of Morphofunctional Ecology of Aquatic Vegetation; 65048, Ukraine, Odessa, Pushkinska St. 37
E-mail address: minicheva@ukr.net

In accordance with the requirements of the Marine Strategy (MSFD, 2008/56/EC), Macroalgae are classified as Biological Quality Elements, on the basis of which it is possible to assess the Ecological Status Class (ESC) of marine ecosystems. The success of using macroalgae as a sensitive ESC assessment tool depends from important methodological position related with the correct choice of functional indicators to be use as Ecological Evaluation Indexes (EEI). The morphofunctional indicators proposed for use, based on the specific surface of algae populations (S/W_p), make it possible to calculate the coefficients of ecological activity, which for seaweeds of the World ocean can range from 1 to 1000 m^2.kg-1 (Minicheva, 1998). The main advantage of morphofunctional indicators as an EEI is the ability to move from a subjective expert judgment on whether a species belongs to the certain Ecological Status Group (Orfanidis, Panayitidis, Ugland, 2011) to accurate quantification ecological labelling (Minicheva, 2013). The Black Sea Commission has approved the method for assessing the macrophytobenthos of the Black Sea using a set of morphofunctional indicators for monitoring according to the MSFD standards (Minicheva, Afanasyev, Kurakin, 2015). At present, this complex of indicators is used to assess and identify trends in ESC changes for the Black Sea coasts of Ukraine, Georgia, Bulgaria, russia federation, as well as the Baltic coast of Lithuania. The use of morphofunctional indicators in the assessing of ESC is the tool for expanding the functional approach in the implementation of MSFD standards to the national coasts of Europe.

Investigation of marine litter in the deep-seafloor: The case of the Eratosthenes Seamount in the Eastern Mediterranean Sea

M. Rousou[1], M. Magagnini[2], L. Vasiliades[1], K. Antoniadis[1], D. Deriu[2], C. Correale[3], D. Capo[3], I. Thassitis[1], N. Michalidis[1]

[1]Department of Fisheries and Marine Research, Ministry of Agriculture, Rural Development and Environment, Republic of Cyprus, P.O. Box 28548, 2080, Nicosia, Cyprus,
E-mail address: mrousou@dfmr.moa.gov.cy
[2]EcoTechSystems, Via Caduti del Lavoro, 27, 60131 Ancona, Italia, magagnini@ecots.it
[3]Lighthouse S.P.A., via Prati, 1/1, 40069 Zola Predosa, Bologna – Italy

Marine litter has been recognized as a worldwide problem with the Mediterranean Sea being among the most impacted areas of the world. According to a recent study, the average density of marine litter in the Mediterranean deep-seafloor is estimated to be 179 items/km2, with some locations, including the Levantine Sea, the densities being >1000 items/km2. The Eratosthenes seamount is located in the EEZ of the Republic of Cyprus. It is a large, elliptical, sediment-covered, carbonate platform that has a relatively flat summit at 780-790m depth. As part of the "Eratosthenes Project" seafloor marine litter was assessed by ROV at eleven sites at depths ranging from 795-1222m and covering an area of 1ha. All marine litter items were recorded, counted and classified into categories, according to the EU Master List Categories of Litter Items. A total of 115 objects were found and classified into 25 categories while 3 objects were defined as "unidentified debris". Densities ranged from 6-16 items/ha with the average density being 10.45+3.45 items/ha. The most common marine objects were artificial polymer materials accounting for 43% with followed by metallic (30%) and glass materials (17%). Metallic items were found in all the investigated stations while plastic debris was found in 10 stations. When compared to other similar surveys the densities recorded on the Eratosthenes seamount (600-1600 items/km2) can be considered among the highest reported in the Mediterranean Sea. Through the current survey an attempt was made in order to address the gap on the marine litter distribution in the Levantine deep-seafloor.

Coexistence of ichthyoneuston and microplastic in the coastal waters of the northwest Black Sea

A. Snigirova[1,2], R. Migas[1], S. Khutornoi[1], A. Vinogradov[1], S. Snigirov[2]

[1]Institute of marine biology of the NAS of Ukraine, Pushkinskaya, 37, 65048, Odessa
E-mail address: snigireva.a@gmail.com
[2]Odessa National I.I. Mechnikov University, Dvorianska St., 2, Odessa, 65082, Ukraine

The ability of the planktonic and neustonic organisms to feed on microplastic and transfer it through the food web has been studied extensively. In the Northwest Black Sea there is no information about the interrelation between the ichthyoneuston (IN) and microplastic (MP). Our research demonstrates the spatial distribution of MP and IN in the Odessa coastal region (46°26'28.5; 30°46'21.7) in July – September 2020-2021. Two surface horizons were sampled (neuston, 0-5 cm, and hyponeuston, 5-20 cm). The MP was found in all samples, whereas IN was met only at 50 %. In total 5 species of fish were registered, the most abundant taxa was European anchovy (191 ind. m-3 in neuston and 73 ind. m-3 in hyponeuston). The IN was represented by eggs, only 2 larvae were met. The IN diversity was a bit higher compared to previous years, however, to obtain reliable data other seasons should be included.MP was presented with fibers (75 %) and fragments (25 %). The most abundant were black and red fibres and black fragments. The average density of MP in neuston was several times higher than in hyponeuston (264 part. m-3 and 90,3 part. м-3, consequently). The studies represent lower densities of the MP compared to IN in the neuston; and higher ratios of MP:IN in hyponeuston. Taking into account that the IN is the temporary component of the neustonic community, whereas MP is constant, we may consider that comparable density of MP:IN favor their interrelation, negative effect, and transport through the food web.

Response of coastal benthic communities to climate change in the northwestern Black Sea

A. Varigin[1]

[1]Institute of Marine Biology, National Academy of Science of Ukraine, 37, Pushkinska St., 65048, Odessa, Ukraine
E-mail address: sealife_1@email.ua

Coastal benthic communities of the relatively shallow northwestern Black Sea are historically adapted to certain temperature conditions. Recently, due to global climate change, this region has been experiencing a warming trend. For example, the complete freezing of the waters of the Odessa Bay was recorded ten years ago in 2012. Since then, winters have become warmer, and in summer sea water temperatures reach 30 °C. These climatic changes have accelerated the process of adaptation of heat-loving alien species to the Black Sea habitat conditions. The native benthic species in this region are bivalve mollusks, which act as ecosystem engineers in coastal communities. Several decades ago two invasive heat-loving species appeared in the Black Sea: the gastropod mollusk *Rapana thomasiana* Crosse, 1861 and the bivalve mollusk *Arcuatula senhousia* (Benson, 1842). The first of them is a predator, which has had a significant impact on the population structure of native bivalve mollusks, in particular, mussels *Mytilus galloprovincialis* Lamarck, 1819. Another invader appeared in this region about twenty years ago. It has all the characteristics of an opportunist species, which allows it to quickly capture new habitats, displacing local representatives of bivalves. This is facilitated by the ability of the invader to cover the settlements of native bivalves with a continuous carpet, limiting their possibility to feed and breathe. Thus, in case of successful adaptation of *A. senhousia* in the Black Sea, this species can have a significant impact on the development of native bivalves *Mytilus galloprovincialis* and *Mytilaster lineatus* (Gmelin, 1791).

Microplastic ingestion in three commercial fishes from the Eastern Mediterranean Sea

A. Kostoula[1], E. Moschou-Kounopoioti[2], N. Milatou[1], P. Megalofonou[1,2]

[1]Department of Biology, National and Kapodistrian University of Athens, Panepistimiopolis, Ilissia, 15784 Athens, Greece
E-mail address: katherinekost98@gmail.com
[2]Interinstitutional postgraduate program NKUA-HCMR Oceanography and Management of Marine Environment, National and Kapodistrian University of Athens, Panepistimiopolis, Ilissia, 15784 Athens, Greece

Throughout the last 10 years, a significant amount of research has been carried out addressing the impact of plastics on the marine environment. This study assesses microplastic ingestion in three commercial fishes (*Sparus aurata*, *Dicentrarchus labrax*, and *Boops boops*), wild and farmed, from the Greek seas and lagoons. A total of 60 individuals caught at different areas (Messolonghi lagoon, Rhodes island, and Cyclades islands) were analyzed. Microplastics were found in 45.8% of all individuals examined. The average number of items per individual was ~~of~~ 1.06 ± 1.1 in *Boops boops*, 2.5 ± 1.9 in wild and 2.3 ± 1.7 in farmed *Sparus aurata*, 4.1 ± 1.2 in wild and 3.6 ± 0.7 in farmed *Dicentrarchus labrax*. Microplastic ingestion ranged from 0 to 9 items per individual. The largest number of microplastic items per fish was observed in *Dicentrarchus labrax*. The type of microplstics detected was either in the form of fiber or fragment, while their color and size varied. No significant differences were found in the mean size of the microplastics between wild and farmed fish. Black was the dominant color of microplastics in all three species. The other common colors were red and blue while yellow was very rare.

Health hazard in the Baltic sea: the effect of perfluorotetradecanoic acid on the Baltic blue mussels *Mytilus trossulus*

K. Smolarz[1], J. Obszarski[1], J. Świeżak[1], **A. Lepretre**[1], A. Hallmann[2]

[1]Department of Pharmaceutical Biochemistry, Medical University of Gdańsk, Poland
Email address: augustin.lepretre@hotmail.com
[2]Department of Marine Ecosystem Functioning, University of Gdańsk, Gdynia, Poland

Per/Poli-fluoroalkylated substances (PFAS) are relatively new chemicals, widely used in daily products like clothing, paints or food packages. Their main sources in marine ecosystems include waste waters from anthropogenic areas. Most PFAS are not soluble in water, thus can be transported with sea currents for long distances. Many PFAS are characterized by specific physio-chemical properties allowing them not only to be present in the marine ecosystems, but also to accumulate and biomagnify in food webs. Some were also proven to be toxic to marine fauna.One of PFAS found in environment (and marine biota) is PFTeDA (perfluorotetradecanoic acid). Despite the fact that it's common, not much known about its effect on marine biota. Yet, studies on mammals showed that PFTeDA exerted negative effects on fertility. The main purpose of this study was to examine impact of PFTeDA on benthic mussels – Mytilus trossulus sampled from the Gulf of Gdańsk. Performed exposure lasted seven days, PFTeDA was used at concentrations 30 ng/L and 300 ng /L. As PFTeDA is insoluble in water we used methanol as a solvent. Therefore, apart from control (C), and two doses (30 and 300) we also had methanol control (MC), all in three replicates. In order to assess the effect of PFTeDA on the model species, multibiomarker approach was used. Specific markers included general health (the presence of progressive and regressive changes), reproduction, detoxification mechanisms, and oxidative stress. The results showed no significant differences in the enzymatic activities. However, the histological analyses highlighted elevated number of regressive changes in the gills and the gonads, digestive system and mantle. The observed pathologies included digestive tubules atrophy, local inflammations and the presence of brown cells. Also, reproductive effects such as gonadal atresia were found. These histological changes were more important the higher PFTeDA concentrations.

Recovery of *Chara aculeolata* Kütz. meadows in the Tendrivska Bay (Black Sea)

D.D. Koroliesova[1,2], G. G. Minicheva [1], D.O. Cherniakov [2]

[1]Institute of Marine Biology of the NAS of Ukraine, 65048, Ukraine, Odesa, Pushkinska St. 37
E-mail address: chernyakova.darya@gmail.com
[2]Black Sea Biosphere Reserve NAS of Ukraine, 75600, Ukraine, Gola Pristan, Lermontova St. 1

The results of the aquatic complexes monitoring showed that since the late 1980s there had been significant changes in the structural-functional organization of the bottom vegetation in Tendrivska Bay. Degradation of the *Ch.aculeolata monocenosis* became the most significant. Between 1990 and 1995, the growing area decreased from 45 to 21 km2, simultaneously, the development of epiphytes, Chlorophyta and Rhodophyta species was registered. The phytocenosis of perennial *Ch.aculeolata* with relatively low ecological activity (Specific Surface of Population S/Wp-11.94 m2kg-1) was replaced by species with 2-4 times higher S/Wp. The Ecological Status Class (ESC) of the northwest Black Sea coastal complexes in this period was "Poor" or "Bad according to the WFD and MSFD standards, based on indicators of macrophyte's ecological activity. The decrease of anthropogenic pressure in the late 1990s led to the improvement of the regional ESC. However, the recovery of *Ch.aculeolata* meadows did not occur. *Zostera noltii* phytocenose occurs the area previously occupied by *Chara monocenosis*. In 2021 meadows of *Ch.aculeolata* in the shallows along the Tendrivska Spit were found. Their area was 36 km2, consisted with the values of 1990. The recovery of the *Ch.aculeolata* population correlates with results of the assessment of ESC long-term dynamics, which demonstrate the shift from the category of "Good" to "High", occurred 6 or 7 years ago for most of the region. Thus, the recovery of sensitive species with low ecological activity became possible with the improvement of the region ESC.

DIVERSITY AND PHYSIOLOGY OF MARINE ORGANISMS. IS THERE STILL ANYTHING TO DISCOVER?

Shell mineralogy and chemical composition in Arctic bivalves

A. Iglikowska[1], J. Przytarska[2], E. Humphreys-Williams[3], J. Najorka[3], M. Chełchowski[2], A. Sowa[2], H. Hop[4], M. Włodarska-Kowalczuk[2], P. Kukliński[2]

[1]Laboratory of Biosystematics and Ecology of Aquatic Invertebrates, Department of Genetics and Biosystematics, Faculty of Biology, University of Gdańsk, Wita Stwosza 59, 80-308 Gdańsk, Poland
E-mail address: anna.iglikowska@ug.edu.pl
[2]Marine Ecology Department, Institute of Oceanology Polish Academy of Sciences, Powstańców Warszawy 55, 81-712 Sopot, Poland
[3]Imaging and Analysis Centre, The Natural History Museum, Cromwell Road, London SW7 5BD, UK
[4]Norwegian Polar Institute, Fram Centre, 9296 Tromsø, Norway

Assessment of environmental drivers and natural variability of shell chemical composition are inevitable to understand the future of marine calcifiers functioning under climate change and acidification scenarios. This study provided new data on shell mineralogy in 23 Arctic bivalve species, and the majority (91%) of examined species had entirely aragonitic shells, while certain species had traces of calcite. Furthermore, the concentrations of elements (Al, Ba, Ca, Fe, K, Mg, Mn, Na, P, S, Sr and Zn) were measured in 542 shells representing 25 Arctic bivalve species. Statistically significant differences in shell chemical composition were found among species irrespective of the sampling location. Most species (97%) differed significantly in levels of elements typically bound (K, Na, P and S) or related (Mg, Sr) to organic tissue synthesized as a result of biologically mediated processes. Extrinsic factors, such as temperature and metals concentrations in seawater and sediments, contributed less to uptake of elements. These findings strongly suggest that shell chemical composition is not a passive reflection of environmental metal concentrations. Therefore, this aspect should be considered when planning palaeo-reconstruction of past environmental settings based on analysis of the shell chemical composition.

Phylogenetic analyses of members of the deep-sea inhabiting family Neotanaidae (Peracarida) and some close shallow-water relatives reveal possible colonisation pathways

E. Palacios Theil[1], M. Błażewicz[1]

[1]University of Łodź, Department of Invertebrate Zoology and Hydrobiology, ul. Banacha 12/16, 90-237 Łodź,
E-mail address: emma.palaciostheil@biol.uni.lodz.pl

The depth distributions of marine benthic invertebrates show patterns with two main transition zones: one between shelf and slope fauna, and another between slope and abyssal fauna from 2000 to 3000 m. These patterns appear to result mainly from the limitations imposed on distribution by the decreasing temperature and the increasing pressure to which animals are exposed with the increase in depth. At the same time, 28 biogeographic provinces have been proposed for the lower bathyal and abyssal benthos based on temperature, salinity, and the influx of particulate organic matter. Nevertheless, a number of neotanaid species appear to challenge these vertical and horizontal distribution patterns. Their collection records include wide depth ranges, across the two depth transition zones, some encompassing from the mesobenthos into the hadal zone. In addition, some neotanaid species have been reported from several biogeographic provinces, even from different oceans, despite their (alleged) limited dispersal abilities. Rather than single species, they might represent in fact cryptic species complexes in need of further research. However, there were no genetic sequences available for undertaking such a study so far. Here we present the first phylogenetic analyses focusing on the relationships among neotanaid taxa, as well as their association to some of their shallow-water closest relatives, based on newly obtained fragments for COI, 16s and H3 genes. This allows us to contribute to the knowledge on deep-sea biodiversity, the processes of colonisation of such marine environments and the adaptation of marine life at depth.

Nematode communities of the coastal zone area near the Zmeinyy Island (Black Sea)

I. Kulakova[1]

[1]Department of Ecology of Marginal Communities, Institute of Marine Biology NAS of Ukraine, Pushkinskaya str., 37, Odessa 65048, Ukraine
E-mail address: irakulakoff@gmail.com

Communities of nematodes were studied in the coastal zone area near the Zmeinyy Island (Black Sea, Ukraine). In total of 47 species from 5 orders, 14 families and 31 genera were registered. Species: *Axonolaimus setosus*, *Terschellingia pontica*, *Paracanthonchus caecus*, *Neochromadora poecilosomoides*, *Sabatieria pulchra* and *Sabatieria abyssalis* are the key species in this area. A comparative characteristic of nematodes depending on the type of substrate is given. The percentage of nematodes in the total abundance of meiobenthos in fouling on the traverse was only 16%, while on silty bottoms it reached 60.8%. In fouling, 4 species of nematodes were recorded, while on silty bottom – 36 species. The maximum density of nematodes in fouling reached only 8000 ind. · m–2 (average density – 2031 ± 592.6 ind. · m–2, average biomass – 0.49 ± 0.14 mg · m–2). On silty bottoms, the density of nematodes reached 666524 ind. · m–2 (average density – 130071 ± 57446.7 ind. · m–2, average biomass – 29.11 ± 13.9 mg · m–2). In fouling on the traverse, "omnivores predators" (2B) play the main role, accounting for 50% of the total nematode population. On silty bottoms, the proportion of "non-selective deposit feeders" (1B) increases, reaching 47%. These studies can lay the foundation for further monitoring of changes in biodiversity in the spatial and temporal scale, since. an increase or decrease in the species diversity of nematodes will make it possible to judge the state of meiobenthos communities in the coastal zone of the Zmeinyy Island.

GENERAL SESSION

Estimating Cetacean Population Trends from Static Acoustic Monitoring Data using Paired Year Ratio Assessment (PYRA)

E. P.M. Grist[1,2], T. J. McKinley[3], S. Das[2,4], T. Tregenza[5], A. Jeffries[6], N. Tregenza[1]

[1]Chelonia Ltd., Mousehole, Cornwall, UK
E-mail address: ericgrist@gmail.com
[2]College of Engineering, Mathematics and Physical Sciences, University of Exeter, Exeter, UK
[3]College of Medicine and Health, University of Exeter, Exeter EX2 5DW, UK
[4]Institute for Data Science and Artificial Intelligence, University of Exeter, Exeter EX4 4QE, UK
[5]Centre for Ecology & Conservation, School of Biosciences, University of Exeter, Penryn, UK
[6]Harbor Porpoise Project, PO Box 608, Anacortes, WA 98221,USA

The cetacean conservationist is often faced with evaluating population trends from abundancy data that are either sparse or recorded at different times within different years. This means that the presence of seasonal or diel patterns in the data together with unplanned gaps are frequently a source of difficulty. While sophisticated statistical approaches such as generalized additive modelling (GAM) may assist, they do so at the cost of demanding additional complexity and are easily misinterpreted by non-expert statisticians. We aim to provide a simple and transparent non-parametric trend evaluation approach based on year on-year comparisons of observations whenever they are possible. Our methodology is developed to address the problem of estimating population trends from incomplete data. Such data are typical of those obtained by static acoustic monitoring of cetaceans at logger sites particularly those near the species range margins. We refer to our approach as Paired Year Ratio Averaging (PYRA). We compare its performance with trend estimation using GAM and nonparametric randomisation tests requiring a greater level of skill and experience for proper application.

The LifeWatch Species Information Backbone: connecting information on taxonomy, biogeography, ecology, genetics and literature

S. Dekeyzer[1], L. Vandepitte[1], WoRMS Data Management Team[1], EurOBIS Data Management Team[1], Marine Regions Data Management Team[1], L. Schepers[1]

[1]Flanders Marine Institute (VLIZ), InnovOcean Site, Wandelaarkaai 7, 8400 Oostende, Belgium
E-mail address: stefanie.dekeyzer@vliz.be

The Flanders Marine Institute (VLIZ) is responsible for setting up the LifeWatch Species Information Backbone (LW-SIBb), as a central part of the European LifeWatch Infrastructure. The LW-SIBb (virtually) brings together different databases and systems, within five major components: (1) taxonomy [regional, national, global and thematic databases], (2) biogeography [databases dealing with species occurrences], (3) ecology, [species-specific traits], (4) genetics and (5) literature. Major components of the LW-SIBb are a.o. the World Register of Marine Species (WoRMS), the European node of the Ocean Biodiversity Information System (EurOBIS) and the Marine Regions gazetteer. These systems have a strong link and collaboration agreements with several international initiatives and ESFRIs. The expertise of the LW-SIBb data management teams was incorporated into the Ocean Teacher Global Academy training course "Ocean Data Management" of the IODE program of UNESCO. The LW-SIBb offers a wide variety of tools, functionalities and data services enabling the users to have free and easy access to data and information from a variety of resources, to standardize and quality control their own data, and to cross-check and link with other data available. This presentation will showcase how the LW-SIBb was used by scientific and industrial users, policy makers and civil society. Furthermore, in 2021 several components of the LW-SIBb were featured in two chapters of the Second World Ocean Assessment (WOA II). This global exercise, where hundreds of marine scientists evaluate trends and identify knowledge in gaps in the world ocean, will be repeated for a third time, again relying on the LW-SIBb.

Will most suitable spawning grounds for coastal fishes be impacted by climate change? A larval drift modelling approach

V. Silve[1], H. Cabral[1], M. Huret[2], H. Drouineau[1]

[1]INRAE, UR EABX (Ecosystemes Aquatiques et Changements Globaux), 50 avenue de Verdun, 33612 Cestas, France
E-mail address: violette.silve@inrae.fr
[2]Ifremer, STH/LBH; ZI de la Pointe du Diable, CS 10070, 70 29280 Plouzané, France

For many fishes, the larval drift ensures a passive transport by currents between spawning areas and coastal nurseries, but also potential dispersal towards new habitats. As such, species have developed strategies to enhance the recruitment success, including the selection of appropriate spawning grounds. Two main strategies are possible: either the location of spawning areas is stable over years, corresponding to sites with good reproduction success in average, or fishes use environmental cues to select the most appropriate spawning sites each year. However, increased temperature due to climate change may lead to changes in hydrodynamics, shorter larval drifts, and earlier egg laying. As such, the most suitable strategies may change. Hydrodynamic models coupled with individual based models are often used and have proved to be relevant tools to study larval drift. However, these complex models require many parameters, many of which are uncertain, making a comprehensive sensitivity analysis a crucial first step. This study focused on five commercially important fish species (with contrasted spawning strategies and larval ecology) present all over Western Europe, from the Iberian coast to the North Sea. We began by assessing the relative influence of extrinsic and intrinsic parameters and their uncertainty on results of larval drift. Then, the model was used to evaluate if the location of the most favourable spawning areas (allowing higher rates of larvae reaching coastal nurseries) was stable over time, and if differences could be found in "warm" or "cold" year archetypes.

Key ecological processes in hard-bottom shallow benthic assemblages in the high-Arctic — a long-term multipurpose underwater experiment

B. Moreno[1], A. Sowa[1], K. Reginia[1], P. Bałazy[1], M. Chełchowski[1], D. K.A. Barnes[2], A. Iglikowska[3], P. Kukliński[1]

[1]Marine Ecology Department, Institute of Oceanology Polish Academy of Sciences. Powstancow Warszawy 55, Sopot, 81-712, Poland.
E-mail address: bmoreno@iopan.pl
[2]British Antarctic Survey. High Cross, Madingley Road, Cambridge, CB3 0ET, United Kingdom.
[3]Laboratory of Biosystematics and Ecology of Aquatic Invertebrates, University of Gdańsk. Wita Stwosza 59, Gdańsk, 80-308, Poland.

Polar benthic communities in the shallow subtidal are sensitive indicators of environmental changes in the marine realm. Thus, long-term underwater monitoring of benthic organisms is important for assessing the impact of a changing climate on the state of aquatic ecosystems. We describe the design and protocol for monitoring installations at two depths (6m, 12m) and two stations in Isfjorden (Svalbard). Each installation consists of a metal frame with 4 columns x 3 rows (replicas) of HIPS (High Impact Polystyrene) settlement plates facing up and down. Temperature and light intensity data-loggers were attached to each installation. The panels were systematically reviewed or recovered from the experiment over different time frames to assess the dynamics of key ecological processes, yielding photographic and physical samples, respectively. The primary aims of the study are to (1) reveal multi-annual variations of the colonisation of benthic assemblages; (2) measure the growth rate of coral algae along with carbonate chemistry; (3) describe the succession and spatial competition (interference) between zoobenthos species, all in the context of environmental variability and change. Preliminary results indicate that coral algae (*Lithothamnion spp*.) were the dominant spatial competitor on the top panels. On the bottom panels, cheilostome bryozoans were the most speciose 1-yr recruits followed by serpulids, however, the latter were the most abundant, yielding >40% area cover on average. This study will provide important information on the impact of environmental factors on the ecology of key contributors to polar shallow carbonate factories and help us quantify current consequences of environmental change.

Fish productivity and community changes in the Norwegian and Barents Sea with Climate Warming

C. Gordó-Vilaseca[1], F. Stephenson[2], M. Coll[3], C. Lavin[1], M. Costello[1]

[1]Faculty of Biosciences and Aquaculture, Nord University, Bodø 8049, Norway
E-mail address: francesc.g.vilaseca@nord.no
[2]School of Science, University of Waikato, New Zealand
[3]Department of Marine Renewal Resources, Institute of Marine Science (ICM-CSIC), & Ecopath International Initiative (EII), Barcelona, Spain.

Range shifts of marine species are one of the most common responses to climate warming. In the Arctic, one of the oceanic regions warming fastest on earth, these shifts lead to a borealisation of the food web in recent years. However how the effects of these changes on biodiversity remain unclear, and very few studies exist that look at fish community changes in the arctic. We used standardised scientific research trawl surveys from the North Sea to the Arctic Ocean collected from 1995 to 2020 and including 184 fish species. We investigated how changes in the fish community affected the overall fish productivity in the area, and identified the winners and losers from the increase in water temperature observed in the last decades. Our results suggest an overall increase in species richness and fish biomass parallel to the increase in SBT in the area, with several species increasing their biomass over time, and some species declining.

Epiphytic algae of seagrasses in the northwestern part of the Black Sea

K. Kalashnik[1]

[1]Institute of Marine Biology of the NAS of Ukraine, Pushkinska Street 37, 65048, Odesa, Ukraine
E-mail address: kalashnik.eka@gmail.com

Seagrass communities are among the most valuable ecosystems in the biosphere – they are highly productive, affect the structural complexity of habitats, increase biodiversity, and play an important role in the global carbon and nutrient cycles (Nordlund et al., 2018). Epiphytic algae are the most numerous and diverse group of organisms on seagrass leaves. They make a significant contribution to primary production and are also indicators of the state of water bodies (Borowitzka et al., 2006, Balata et al., 2007). In the Black Sea, the most extensive seagrass meadows are located in its northwestern part (NWBS), on the territory of Ukraine (Berov et al., 2021), which creates in these places unique coastal habitats with high biological value. At present, information on seagrass epiphytes in the NWBS is fragmentary, which does not provide a comprehensive picture of this important ecological grouping, which is a permanent component of underwater meadow communities. As a result of many years of research on the microepiphyton of different types of marine macrophytes, it was found that the diversity, quantity and allocation of epiphytic algae on the basiphyte depend on environmental conditions: water temperature, the ecological state of the water body (Kalashnik, 2018). The dominant species in the seagrass microepiphyton of the NWBS are *Achnanthes brevipes* C.A.Agardh, *Cocconeis scutellum* Ehrenberg, *Diploneis bombus* (Ehrenberg) Cleve (Kalashnik, 2019). Multicellular dominant epiphytes are *Acrochaetium secundatum* (Lyngbye) Nägeli, *Hydrolithon farinosum* (J.V.Lamouroux) Penrose & Y.M.Chamberlain, *Ceramium diaphanum* (Lightfoot) Roth, *Ulva clathrata* (Roth) C.Agardh, *Chondria capillaris* (Hudson) M.J.Wynne, *Lophosiphonia obscura* (C.Agardh) Falkenberg (Zinova, 1967).

Is the night only a period for sleeping?: benthic feeding activity during the Arctic polar night.

L. Morales Luna Hadrys[1], A. Romero Ramirez[2], P. Kuklinski[1], M. Chelchowski[1], Monika Kędra[1], P. Balazy[1]

[1]Institute of Oceanology, Polish Academy of Sciences
E-mail address: lmlhadrys@iopan.pl
[2]Laboratoire EPOC-UMR5805, Université de Bordeaux

There is still a general misconception towards the understanding of the polar night as a period of winter dormancy when the primary production stops, resources are limited and the biological processes slow down. Due to logistics constraints, studying benthic marine communities in harsh winter conditions is challenging and not an easy task, therefore remote imaging methods have become an useful approach. In this study, underwater photographs taken 30 minutes apart were analysed to monitor the filter feeding behaviour of a barnacle community, *Semibalanus balanoides*, in a fjord near Tromso, Norway, year round, from July 2019 to July 2020. Almost 2200 images were analysed with special focus on winter time (November 15th 2019 to January 15th 2020) providing insight into understanding filter feeders behaviour during the polar night in the higher latitudes. A community with nineteen barnacles and their feeding behaviour was analysed with AviExplore software. Two barnacles were actively feeding during 80% of the time, four other remained active 50% of the time, and thirteen remained closed over 85% of the analysed period. Even though, not all barnacles were active during this period, other invertebrates were constantly present, which may directly have affected the barnacle feeding behaviour, and which presence can allow to speculate about an organic matter resuspension cycle.

Fifteen years of the World Register of Marine Species (WoRMS): where are we, and what will the next decade bring?

L. Vandepitte[1], W. Decock[1], S. Dekeyzer[1], B. Vanhoorne[1], K. Bouirig[1], D. Bakeev[1], T. Horton[2], A. Kroh[3]

[1]Flanders Marine Institute, Wandelaarkaai 7, 8400 Oostende, Belgium
E-mail address: leen.vandepitte@vliz.be
[2]National Oceanography Centre, European Way, Southampton, SO14 3ZH, UK
[3]Naturhistorisches Museum Wien, Burgring 7, 1010 Vienna, Austria

In 2022, the World Register of Marine Species (WoRMS) celebrates its fifteenth anniversary. Over the past 15 years, the content of WoRMS has grown tremendously, as well as its network of volunteer experts and its connection to regional and global initiatives. Last year, WoRMS has been endorsed as a UN Ocean Decade project under the title ‘Above and Beyond - Completing the World Register of Marine Species’. During the full span of the Ocean Decade, WoRMS will continue its endeavors to be able to provide a full taxonomic overview of all marine life, thereby not only supporting scientists, but everyone who makes use of species names, including policy makers, industry and the public at large. Although already fairly complete, taxonomic gaps still need to be addressed in space and time. New challenges in the field of taxonomy - such as temporary names - need to be explored, thereby looking for the best suitable solution for all WoRMS users. Other high-level objectives for WoRMS within the Decade include serving as a data rescue platform for other taxonomy databases, encouraging continued documentation of species traits which are of critical importance for ecological marine research and to provide improved support and links with and between other global databases and infrastructures that use a marine taxonomic backbone. As an Ocean Decade Project, WoRMS has been linked to the endorsed Action Programme Marine Life 2030: A Global Integrated Marine Biodiversity Information Management and Forecasting System for Sustainable Development and Conservation, with which close collaboration will happen.

Depth-dependent variation in resource utilization of fjord benthic communities

M. J. Silberberger[1], K. Koziorowska-Makuch[1], H. Reiss[2], M. Kędra[1]

[1]Institute of Oceanology Polish Academy of Sciences, Powstańców Warszawy 55, 81-712 Sopot, Poland
E-mail address: marcs@iopan.pl
[2]Faculty of Biosciences and Aquaculture, Nord University, Bodø, Norway

Macrobenthic community composition in fjords differs among biogeographic regions and further among different depth zones within fjords. We used stable isotopes (SI) of carbon and nitrogen (δ13C and δ15N) to study depth-dependent differentiation of macrobenthic food-web structure and resource utilization in the European fjords. In summer 2021, benthic fauna and organic matter (OM) mixtures (surface sediment and suspended OM) were collected from 2 depth zones (100-150 m vs 200-250 m) in 1 Arctic, 2 sub-Arctic, and 1 temperate fjord located along a latitudinal gradient (59-78°N). Within each fjord, the OM quantity in sediment and bottom water was typically larger at deep than at shallow stations, except for the bottom water of one sub-Arctic fjord where extremely high OM concentrations were found at the shallow station possibly due to the close proximity of a strong tidal current. In contrast, the isotopic composition of the OM pools varied almost exclusively among biogeographic regions, while depth had only a small and non-consistent effect on SI ratios of sediment or bottom water. Benthic community composition differed strongly between fjords depending on biogeographic region and local environmental conditions. Suspension feeder, however, were virtually absent from the fauna that was collected at deep stations. The absence of suspension feeders from deep habitats across all biogeographic zones suggests that deep communities rely predominantly on sedimentary OM (food bank) and that deep communities are likely more resilient toward climate change related changes in the timing of primary production and vertical carbon export than shallow communities.

The European Ocean Biodiversity Information System (EurOBIS): your gateway to quality controlled marine biodiversity data

R. Perez-Perez[1], L. Vandepitte[1], J. Beja[1], B. Vanhoorne[1], F. Leclercq[1], L. Tyberghein[1]

[1]Flanders Marine Institute (VLIZ), Wandelaarkaai 7, 8400 Oostende
E-mail address: info@eurobis.org

Large scale marine biodiversity research is fundamental to ocean health. However, marine biodiversity data are often scattered and can be hard to find, access or integrate, turning holistic high-quality research into a challenge.The European Ocean Biodiversity Information System – EurOBIS –, established in 2004, aims at helping to fill this gap in scientific knowledge, by integrating largely scattered marine biodiversity data and making them easily findable and efficiently accessible online. EurOBIS brings together marine and brackish biodiversity data collected within European waters or by European researchers and institutes outside Europe, with a focus on taxonomy and spatio-temporal distribution. However, EurOBIS is not limited to presence/absence data, but is also capable of holding a wide variety of occurrence-related information such as biological quantifications and descriptors (e.g. abundance, biomass, biometrics, life stage, sex), environmental and habitat data or sampling related information. All data undergo openly available and thorough quality control procedures to ensure only high-quality data are offered by EurOBIS. Since 2009, EMODnet Biology uses EurOBIS as its backbone, making the data available through a data portal that offers specific filters and functionalities. In 2014, EurOBIS became part of the LifeWatch Species Information Backbone, where users can run the EurOBIS quality checks on their own data. The EurOBIS database structure and services keep evolving. Soon, new data types such as imagery data and DNA derived data will be available and accessible. Moreover, the implementation of fitness-for-use labels will allow users to query the EurOBIS database based on their area of interest.

Microsporidium *Hepatospora eriocheir* - an emerging pathogen of aquatic invader Chinese mitten crab in the Baltic Sea

M. Stachnik[1], M. Normant-Saremba[2]

[1]National Veterinary Research Institute, Department of Fish Diseases, Al. Partyzantów 57, 24-100 Puławy, Poland
E-mail address: magdalena.stachnik@piwet.pulawy.pl
[2]University of Gdańsk, Faculty of Oceanography and Geography, Institute of Oceanography, Department of Experimental Ecology of Marine Organisms, Al. M. Piłsudskiego 46, 81-378 Gdynia, Poland

Emerging diseases can be defined as infectious diseases that recently expanded their geographic or host range, or prevalence. The role of biological invasions in the emergence of diseases is still under debate. Many invasive species lose their pathogens during the invasive process, other taxa introduced novel parasites into colonised areas. Here, we describe first record of a microsporidian parasite *Hepatospora eriocheir* infection in invasive Chinese mitten crabs (*Eriochier sinensis*) from Vistula lagoon, a brackish waterbody on the Baltic Sea. The microsporidia are a diverse parasite phylum infecting hosts from all major taxa in all environments, ranging from the beneficial insects and aquatic animals, to important parasites of humans. *Hepatospora eriocheir* was first identified in 2007 in the cultured *E.sinensis* from China, as a serious pathogen, causing of hepatopancreatic necrosis disease with a high mortality rate. In Europe this parasite was described in 2011 in Chinese mitten crabs from the River Thames, as morphologically similar to the microsporidium in native Asian populations. Our present study describes a microsporidium infecting non-native Chinese mitten crabs from the Baltic Sea. Phylogenetic analysis based on DNA coding conserved regions of microsporidian small subunit ribosomal revealed that the parasites had almost 100% sequence identity to that of *H. eriocheir* from UK and China. This supports the theory that they were introduced with the invader crab during its first invasions to Europe and Baltic Sea in the early 1900s.

Factors influencing sediment reworking rates in coastal zones of the southern Baltic Sea

M. Szczepanek[1], E. Michaud[2], M. J. Silberberger[1], K. Koziorowska-Makuch[1] Z. Borawska[1], M. Kędra[1]

[1]Institute of Oceanology Polish Academy of Sciences, Powstańców Warszawy 55, 81-712 Sopot, Poland
E-mail address: slominska@iopan.pl
[2]Univ Brest, CNRS, IRD, Ifremer, LEMAR, Rue Dumont d'Urville, F-29280, Plouzane, France

In recent years, various experimental studies have focused on the role of bioturbation in biogeochemical processes. Simultaneously, useful ecological indicators are being developed to estimate the potential bioturbation rate based on functional characteristics and abundance of macrofauna. Nevertheless, there is still a need to broaden the knowledge about actual sediment reworking rates in different marine environments. In this study we assessed sediment reworking rates in five coastal areas of the southern Baltic Sea, affected by different levels of riverine influence and anthropogenic pressure. Ex-situ experiments with luminophore addition on sediment cores containing natural benthic assemblages were conducted. A bioturbation model was applied to assess the rates of two types of sediment reworking i.e., one to quantify the proportion of sediment particles transported from the surface to deep sediments, the other to quantify the proportion of sediment being homogenously mixed at the surface of sediment. Additionally, a wide set of environmental variables together with benthic community characteristics and biological traits was used to explain the variability in sediment reworking. Clear regional patterns of sediment reworking were detected, related to sediment type, quantity and quality of sedimentary organic matter. The intensity of sediment reworking was correlated with benthic biomass, however, at each location different functional groups dominated the assemblage: gallery-building polychaetes in sandy locations, mostly subsurface-dwelling bivalves in sandy-muds, and intensely irrigating chironomids and surficial ostracods in a lagoon. Our study adds knowledge about the actual sediment reworking rates in temperate, non-tidal coastal zones, its relation to environmental gradients and seasonal dependencies.

MARINE MOLECULAR ECOLOGY – NEW TOOLS AND NEW FINDINGS

From genus to genome: searching for environmental DNA responses to environmental changes

J. Pawłowska[1], M. Greco[1], N. L. Nguyen[1], J. Pawłowski[1]

[1]Institute of Oceanology, Polish Academy of Sciences, Powstańców Warszawy 55, 81-712, Sopot, Poland
E-mail address: pawlowska@iopan.pl

Recently, the assessment of past climate impacts on marine biodiversity was based exclusively on taxa preserved in the fossil record. However, most marine species do not leave any fossilized remains, so their morphological identification is impossible. Recent advances in environmental genomics have the potential to change this situation radically. The demonstration that DNA can be preserved in marine sediments across geological timescales opened new avenues for using sedimentary ancient DNA (sedaDNA) to reconstruct past climatic and environmental changes. Herein, we discuss the potential of sedaDNA as an indicator of major environmental drivers of planktonic and benthic biodiversity changes in the Nordic Seas. SedaDNA records provide a broader and more complete view of biodiversity by detecting non-fossilized, small-sized, and juvenile taxa. This allows the identification of new potential indicators, e.g., AW inflow, sea-ice conditions, and productivity, which are the major drivers of modern climate and environmental changes. Furthermore, our results suggest that molecular analysis at finer levels can provide valuable information about the occurrence of different genotypes over time. These genotype-level changes can be related to environmental conditions, implying that the genotypes have different ecological preferences and could potentially be used as paleoceanographic proxies. The advantage of paleogenomics in providing complementary insight into biodiversity changes beyond what is shown by fossil records is indisputable. The ancient DNA approach may provide a powerful means to reconstruct paleoenvironments more comprehensively and understand past climatic and environmental changes. The study was funded by the National Science Centre grants no. 2018/31/B/ST10/01616 and 2019/34/H/ST10/00682.

AFISsys – an autonomous instrument for the preservation of water samples for microbial metatranscriptome analysis

J. von Borries[1], S. Charvet[2], L. Riemann[3], J. Alneberg[4], A. F. Andersson[4], U. Fischer[1], M. Labrenz[2]

[1]Hydro-Bios Apparatebau GmbH, Altenholz, Germany
E-mail address: j.borries@hydrobios.de
[2]IOW - Leibniz Institute for Baltic Sea Research, Warnemuende, Germany
[3]University of Copenhagen, Department of Biology, Marine Biological, Section, Copenhagen, Denmark
[4]KTH - Royal Institute of Technology, Science for Life Laboratory, Stockholm, Sweden

Microbial communities are the main drivers of biogeochemical cycling of multiple elements sustaining life in the ocean. The rapidity of their response to stressors and abrupt environmental changes implies that even fast and infrequent events can affect local transformations of organic matter and nutrients. Modern molecular techniques allow for monitoring of microbial activities in the environment through the analysis of genes and expressed genes (messenger RNA) contained in natural microbial assemblages. However, gene transcript turnover in cells can be as short as 30 seconds and stability varies greatly between transcripts. Traditional sampling of in situ communities involves an inevitable delay (hours) between the collection of seawater and the extraction of its RNA, leaving the bacterial communities a sufficient amount of time to alter their gene expression. To address these challenges we designed an autonomous in situ fixation multi-sampler (AFISsys) for reliable sampling of microbial metatranscriptomes at frequent intervals, for refined temporal- and spatial-resolution. To advance the development of such a sampling tool, we examined the minimal seawater volume necessary for adequate coverage of community gene expression, the suitability of phenol/ethanol fixation for long-term preservation of transcripts, and the field eligibility of the instrument itself, in our case in brackish systems. AFISsys is able to collect, fix, and store water samples independently off-shore at high temporal resolution. It can conserve sensitive mRNA directly in the environment for up to a week. Thus, it constitutes an invaluable tool for the integration of molecular functional analyses in environmental monitoring in brackish waters and in aquatic environments in general.

Biodiversity of benthic fauna along natural disturbance gradient in a glacier-influenced Arctic fjord based on morphological and eDNA metabarcoding survey

M. Mazurkiewicz[1], J. Pawłowska[1], I.B. Angeles[2], K. Grzelak[1], K. Deja[1], J. Pawłowski[1], M. Włodarska-Kowalczuk[1]

[1]Department of Ecology, Institute of Oceanology Polish Academy of Sciences, Sopot, Poland
E-mail address: mikolaj@iopan.pl
[2]Department of Genetics and Evolution, University of Geneva, Geneva, Switzerland

Organisms living on a bottom of Arctic fjords are exposed to various stressors that shape their taxonomic structure and functioning. The activity of glaciers along with advection of sea water masses from shelves form variety of environmental gradients that influence marine biota. This study compares the effects of disturbance from glaciers on biodiversity of benthic fauna using morphological and eDNA metabarcoding based methods. Materials were collected at 6 stations along the environmental gradient of decreasing impact of a glacier in Hornsund (Svalbard fjord) and included samples for macrofauna and meiofauna (nematodes) and sediments for eDNA. Three genetic markers were used for the PCR amplification of eDNA: mitochondrial COI, nuclear 18S VIV2 (eukaryotes) and nuclear18S 37f (foraminifera) and were sequenced using the Illumina MiSeq system. Raw sequence data were analysed through SLIM pipeline and ASVs were determined with dada2. A pattern of decrease in taxonomical richness was observed along the fjord towards the glaciers for all analysed groups of organisms/ eDNA markers, with particularly high correlation between morphologically identified macrofauna and eDNA assessed with COI. The analysis of beta diversity showed similar nMDS ordination patterns among samples in the case of morphologically analysed macrofauna and eDNA evaluated with the use of the V1V2 marker and the 37f marker. Our results show that eDNA metabarcoding-based methods may be successfully used for impact assessments of Arctic benthic fauna and may provide comparable results with time-consuming/labour- intense traditional taxonomical surveys.

Diversity of benthic foraminifera from Coastal Svalbard

N.L. Nguyen[1], J. Pawłowska[1], I. Barrenechea Angeles[2], M. Zajaczkowski[1], J. Pawłowski[1]

[1]Institute of Oceanology Polish Academy of Sciences
E-mail address: loinguyen@iopan.pl
[2]Department of Earth Sciences, University of Geneva

Benthic foraminifera represents the main component of meiofauna in the Svalbard Archipelago. Several studies analyzed the distribution and diversity of Svalbard foraminifera, which are based exclusively on the morphological identification of specimens sorted from sediment samples. Here, we present the first assessment of Svalbard foraminifera diversity based on DNA metabarcoding. We analyzed sieved and unsieved sediment samples collected at 15 stations situated in three fjords and two open marine areas in front of tidewater glaciers. More than half of the ASVs (51.7%) could not be assigned to any group in the reference database, suggesting the high genetic novelty of foraminifera in the Svalbard coastal area. The sieved and unsieved samples resolved comparable communities, sharing 1023 ASVs, comprising over 97% of reads. Our analyses show that the foraminiferal assemblage differs between five localities, with communities distinctly separated between fjord and open-sea stations. Each locality was characterized by a specific assemblage, with only a small overlap in the case of open sea areas. Our study demonstrates a clear pattern of the influence of water masses on the structure of foraminiferal communities. This high diversity and specificity of Svalbard foraminifera associated with water mass distribution indicate that the foraminiferal metabarcoding data can be a very useful tool for inferring present and past environmental conditions in the Arctic. The research was financially supported by the Norwegian Financial Mechanism for 2014-2021, project no 2019/34/H/ST10/00682. We express our thanks to the captain and crew of the R/V Oceania.

Environmental DNA methylation of *Lymnaea stagnalis* varies with age and is hypermethylated compared to tissue DNA

B. Zhao[1], P. M. van Bodegom[1], K. Trimbos[1]

[1]Leiden University, Institute of Environmental Sciences, Department of Environmental Biology, Einsteinweg 2, 2333 CC Leiden, Netherlands
E-mail address: b.zhao@cml.leidenuniv.nl

Environmental DNA (eDNA) approaches contributing to species identifications are quickly becoming the new norm in biomonitoring and ecosystem assessments. Yet, information such as age and health state of the population, which is vital to species biomonitoring, has not been accessible from eDNA. DNA methylation has the potential to provide such information on the state of a population. Here, we measured the methylation of eDNA along with tissue DNA (tDNA) of *Lymnaea stagnalis* at four life stages. We demonstrate that eDNA methylation varies with age and allows distinguishing among age classes. Moreover, eDNA was globally hypermethylated in comparison to tDNA. This difference was age-specific and connected to a limited number of eDNA sites. This differential methylation pattern suggests that eDNA release with age is partially regulated through DNA methylation. Our findings help to understand mechanisms involved in eDNA release and shows the potential of eDNA methylation analysis to assess age classes. Such age class assessments will encourage future eDNA studies to assess fundamental processes of population dynamics and functioning in ecology, biodiversity conservation and impact assessments.

Unravelling hidden predator-prey interactions among sea urchin juveniles and micropredators by prey DNA amplification

A. Sutera[1], C. Bonaviri[2], F. Di Trapani[2], B. Hereu[3], V. Macic[4], **R. De Michele**[1]

[1]Italian National Research Council (CNR), Institute of Biosciences and Bioresources (IBBR), Corso Calatafimi 414, 90129, Palermo, Italy
E-mail address: roberto.demichele@ibbr.cnr.it
[2]University of Palermo, Department of Earth and Sea Sciences, via Archirafi 22, 90123, Palermo, Italy
[3]University of Barcelona, Departmento of Ecology, Diagonal 643, 08028 Barcelona, Spain
[4]University of Montenegro, Institute of Marine Biology, Kotor, Montenegro

Rocky reefs can shift from forest to barren, an impoverished state dominated by encrusting algae. Sea urchins, abundant in barrens, are usually held responsible for the maintenance of this state. Processes occurring at the immediate post-settling stage could represent an important level of control of urchin populations. Among the causes of mortality of early settlers, predation is likely to be the most important and microfauna is known to be abundant in algal forests. Despite the potential role of sea urchins micropredators in the dynamic of Mediterrenean rocky reefs, their identity and impact are still largely unknown. The small size of both urchins juveniles and micropredators make field predatory observations and gut content analysis practically unfeasible. Here, we describe a strategy to identify potential micropredators of the juveniles of the Mediterranean sea urchin *Paracentrotus lividus* and *Arbacia lixula*, by amplification of sample DNA with specific urchin primers. We collected 470 potential micropredators, belonging to different taxonomic groups, by SCUBA diving in Spain during urchin juveniles settlement burst. Samples were identified by both visual inspection and by molecular assignment of COI region sequencing. Samples were then amplified with primers annealing in different loci of urchin genome. Successful amplification was indicative of the presence of urchin DNA in the original sample, suggesting recent predation events. Sequencing of amplification products confirmed the match with urchin DNA. Our findings present novel potential micropredators of urchin juveniles and confirm that micropredation by invertebrates represent an important level of control of sea urchin populations in algae forest.

MARINE LIVING RESOURCES – ENVIRONMENTAL SIGNIFICANCE

Responses of coastal fishery resources to rapid environmental changes

H. Peltonen[1], **B. Weigel**[2],

[1]Finnish Environment Institute (SYKE), Latokartanonkaari 11, 00790 Helsinki, Finland
[2]Research Centre for Ecological Change, Organismal and Evolutionary Biology Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, P.O. Box 65, Helsinki FI-00014, Finland
E-mail address: benjamin.weigel@helsinki.fit

Coastal systems experience strong impacts of ongoing environmental change, affecting fish communities and subsequently fishery yields. In the Baltic Sea, the combined effects of climate induced changes and eutrophication-related pressures constitute major threats to its living resources. While much work has been devoted to uncovering environmental impacts on the commercially most valuable fish stocks, only little is known about community wide responses of fished species and how environmental change may affect their yield. Here, we use a joint species distribution modelling framework to disentangle environmental impacts on species-specific fishery yields of 16 fished species along the coast of Finland over four decades. We show that environmental covariates substantially contributed to variations in fishery yields and are likely to have strong impacts on fished resources also in the future. Salinity and near-bottom oxygen concentration emerged as the strongest environmental drivers of yields at the community level, while temperature was particularly important for cod (*Gadus morhua*) and sprat (*Sprattus sprattus*) yields. We found shore density to be an important predictor for fisheries resources especially for freshwater fish. Our results suggest that the changes in environmental conditions during the past four decades had a positive effect on the yields of freshwater and warm-affinity species, while yields of marine cold-affinity species have been mainly negatively affected by contracting favorable habitats, becoming warmer and less saline.

Importance of Arctic kelp forest in environmental conditions modification

P. Kukliński[1], K. Kosek[1]

[1]Institute of Oceanology, Polish Academy of Sciences, ul. Powstańców Warszawy 55, Sopot 81-712, Poland
E-mail address: kuki@iopan.pl

Kelp forests are often compared with their functionality and importance to terrestrial rain forest. In the Arctic their abundance and complexity, in comparison to poverty of life on land, is shockingly rich. Worldwide kelp forests provide not only a substrate for many sessile and motile organisms, enhancing the local biodiversity but also play an important role in carbon sinking and CO2 sequestration. Kelp forests modify wave energy and turbidity. Yet knowledge about all these above aspects is often intuitive rather than numerically quantified– especially in the Arctic. With this study we quantify importance of the kelp forest in environmental conditions modification. The study is conducted in Svalbard Archipelago (Isfjorden). Number of data loggers were installed on the bottom at two locations with kelp forest and two without it (acting as control sites). At each site loggers were installed at five depths 7, 10, 15, 20 25 m. Loggers are measuring parameters such as water temperature, salinity, light intensity, water level (tide), turbidity, chlorophyll levels, pH, O2 as well as currents strength and directions. Although the study is in progress the data obtained so far indicate large pH and oxygen modification on the seasonal scale. Current strength is hugely modified. The study no doubt confirms great impact on surrounding environment.

Selection of priority location for artificial reefs in the north-west Black Sea

Y.V. Sokolov[1]

[1]Institute of Marine Biology of the National Academy of Sciences of Ukraine, 37 Pushkinska St., Odessa, Ukraine.
E-mail address: sokolovev87@gmail.com

The Northwest Black Sea Shelf (NWBS) is a watershed expanse of more than six paleo-rivers. These geomorphological forms of the seafloor relief on the shelf of the NWBS cause extended phytal zones with infralittoral and circalittoral (Minicheva, Sokolov, 2021). At the same time, the runoff of the Danube, Dniester, Dnieper, and South Bug rivers creates zones with vertical thermo-gallium structure in the NWBS, especially in the area of paleo-river valleys, which leads to hypoxic conditions in the bottom layer. One of the possible measures to improve the ecological status class in these areas is the creation of artificial reefs with a conservation function (Zaitsev, 2006; Bolshakov, 1970).Determination of priority placement of artificial reefs of environmental or socio-economic direction was carried out on the basis of geoinformation analysis of international geodatabases (Copernicus Marine Environment Monitoring Service, EMODnet).The algorithm of reef location and typology of its hydro-ecological conditions included:- determination of the facies forms of the seafloor relief, based on the calculation of the «Bathymetric Position Index» (Lundblad, Wright et al., 2006);-Zoning of vertical and latitudinal distribution patterns based on the distribution of PAR, seafloor environmental zones, current velocity and direction, mixing layer thickness, water temperature and salinity, bottom substrate structure, chlorophyll a concentration, oxygen and nutrients concentration. Thus, priority areas for placement of artificial reefs of nature protection (with sanitary mariculture) or socio-economic (useful biological raw materials and recreation) directions were identified and their typology was carried out in the marine water areas of the NWBS.

Salmon (*Salmo salar*) in southern Baltic Sea - condition, diet and presence of Anisakidae nematodes

K. Nadolna-Ałtyn[1], J. Pawlak[1], M. Podolska[1], A. M. Lejk[1]

[1]National Marine Fisheries Research Institute, Gdynia, Poland
E-mail address: knadolna@mir.gdynia.pl

Salmon (*Salmo salar*) belongs to the most important fish species in the Baltic Sea due to the ecological and economic points of view. ICES grouped salmon Baltic rivers into 6 Assessment Units based on management objectives, biological and genetic characteristics of the river stocks contained in a unit. Southern Baltic is a feeding area where mixture of the stocks was reported. Poor status of some stocks led to a fishing ban of salmon in the southern Baltic since 2022. The aim of our studies was to analyse the condition of salmon sampled in Polish marine waters between 2006-2020. Additionally the diet composition and presence of Anisakidae nematodes in 120 samples collected in 2020 were analysed. Generalized Linear Models show statistically significant decline in salmon condition between 2006 - 2020. Presence of Anisakidae nematodes was detected in 13% of analysed livers. The main components of the diet were sprat (*Sprattus sprattus*), three-spined stickleback (*Gasterosteus aculeatus*) and invertebrate Mysis mixta. Diet and presence of the parasites may affect the condition of the salmon. Food components are not only source of nutrients, but also way how fish become infected. (Funding: EU Multiannual Programme for Fisheries Data Collection; own research fund of National Marine Fisheries Research Institute: DOT21 ParaSalmon and DOT22ParaSalmon).

POSTERS

Diel vertical distribution of zooplankton biomass in the open southern Adriatic (Mediterranean Sea)

M. Batistić[1], R. Garić[1], M. Hure[1]

[1]University of Dubrovnik, Institute for Marine and Coastal Research, Dubrovnik, Croatia
E-mail address: mirna.batistic@unidu.hr

Zooplankton play an important role in the trophic dynamics of the deep open southern Adriatic. Detailed vertical and temporal distribution of zooplankton biomass were evaluated during the all seasons (2021/2022) at eight layers from 0 to 1200m depth during the day and the night using open-closing Nansen net (250 µm mesh size) hauls at the open southern Adriatic station. Average zooplankton biomass ranged from 7.25 to 58.51 mgm^{-3} by day and 15.34 -77.47 mgm^{-3} by night and was differed by seasons and sampling layers. During the night, maximal values were in epipelagic layer while during the day maximal values were below 200 m, except in April. Zooplankton biomass was 1.5 to 3.0 times higher at night than during the day. These differences might be in connection with larger and faster zooplankton species which came to the surface in swarms during the night while during the day they were deeper and dispersed throughout the water column and net was not so effective to catch them.

Interannual change in macrobenthic assemblage structure in the Antarctic intertidal (Admiralty Bay, King George Island)

M. Chełchowski[1], P. Bałazy[1], P. Kukliński[1]

[1]Institute of Oceanology Polish Academy of Sciences, Powstańców Warszawy 55, 81-712 Sopot, Poland
E-mail address: chelchowski@iopan.pl

The Antarctic Peninsula is undergoing rapid change due to global warming, including air and water temperature increases. Fauna inhabiting the intertidal zone is particularly exposed to warming impacts, as they are subjected to high variations in both terrestrial and marine environmental settings. This study aimed to assess interannual variations of the intertidal macrofaunal biodiversity, tidal height-related assemblage structural patterns, and their response to variability in environmental parameters on King George Island. Samples were taken during two summer seasons (2011 and 2019) in the vicinity of the Arctowski Polish Antarctic Station at three transects. At each transect samples were collected at low, medium and high tide levels using a 50 x 50 cm frame with 3 replicates per tide level. Water temperature loggers were installed on each of the sampling locations, recording temperature every 5 minutes. Macrofauna was more diverse in 2019, where the average number of species was 24 ± 3 species 0.25 m-2, while in 2011: 19 ± 2 species 0.25 m-2. Conversely to species richness, the higher mean abundance occurred in 2011: 843 ± 373 individuals 0.25 m-2 whereas in 2019: 633 ± 241 ind. 0.25 m-2. There was a significant decrease in the number of species and abundance with increasing tidal height. Our investigation documented highly diverse and abundant fauna in the Antarctic intertidal zone. Taking into consideration further changes predicted for the coastal waters of the Antarctic Peninsula abrupt changes of intertidal macrofauna can be foreseen in the future.

Anarthruridae – a new light on the least known family of Tanaidacea (Crustacea: Peracarida)

W. Cybula[1]

[1]University of Łódź, Department of Invertebrate Zoology and Hydrobiology, Banacha Street 12/16, 90-237 Łódź
E-mail address: wiktoria.cybula@edu.uni.lodz.pl

Tanaidacea is an order of crustaceans classified to Peracarida. They live in virtually all marine benthic habitats. Most of tanaidaceans are small and their body length does not exceed a few millimeters long. More than 1,300 species of Tanaidacea are currently known, but their diversity is highly underestimated. The family Anarthruridae is the less known family of deep-water Tanaidacea. It is distinguished from other tanaidomorphs by cheliped is attached to cephalothorax via pseudocoxa, grossly reduced mouth parts, and reduced exopod in uropods. The family is represented by 29 species from 16 genera (four monotypic). In this work, we summarize the current knowledge on Anarthruridae based on literature data. In addition, we present new data that we obtained from the study of 177 benthic samples collected during several international explorations of different areas of the northwestern Pacific (Sea of Okhotsk, Kuril-Kamchatsky Ditch), Central Pacific, WAntarctica, WAtlantic, Iceland and Mediterranean Sea.

Spring-summer changes in the structure of coastal benthic habitats in the Gulf of Gdansk

M. Gintowt[1], N. Miernik[2], I. Orzechowska[2], M. Miernik[3], L. Kotwicki[1]

[1]Institute of Oceanology of Polish Academy of Sciences
E-mail address: mgintowt@iopan.pl
[2]University of Gdańsk, Institute of Oceanography
[3]Jan Kochanowski University of Kielce, Institute of Biology

The Gulf of Gdańsk is a unique reservoir in the southern part of the Baltic Sea. Specific hydrological and geomorphological conditions influence the development of diversified and relatively rich plant and animal communities, multi-species underwater meadows shape the richness of benthic and pelagic fauna assemblages. A wide range of habitat types are found in this area, from the dominant sandy substrate, through coastal reed beds and regenerating *Zostera marina* underwater meadows, to stony reefs at the foot of the Orlowo cliff, known as oases of biodiversity. The anthropogenic pressure, almost invisible in spring, increases significantly in summer due to the increased number of tourists on the beaches around the Gulf of Gdansk. In spite of the positive changes in the pollution of the waters of this basin, the presence of bathers in the coastal waters itself strongly influences the benthic communities that are found there. It is important to investigate the extent of human-induced changes in these communities, so comparison of results obtained in summer with those obtained in spring is crucial in assessing changes in the environment. Comparison of the obtained results with previous surveys carried out in the coastal area (30 years ago) will be crucial in determining the present condition of zoobenthic habitats under anthropogenic pressure and understanding the direction of ongoing changes.

New species of genus *Stenotanais* Bird & Holdich, 1984 (Crustacea, Tanaidacea) from deep sea

K. Głuchowska[1]

[1]University of Lodz, Department of Invertebrate Zoology and Hydrobiology, Stefana Banacha 12/16, 90-237 Łódź, Poland
E-mail address: kamila.gluchowska@edu.uni.lodz.pl

Tanaidacea are small marine crustaceans living in a large variety of benthic habitats. Family Akanthophoreidae with 10 genera is one of 15 tanaidacean deep-sea families. In our research we are focusing on one akanthophoreid genus — *Stenotanais*, currently represented by four species: *S. arenasi* Larsen, 2011, *S. crassiseta* Bird & Holdich, 1984, *S. hamicauda* Bird & Holdich, 1984 and *S. macrodactylus* Larsen, 2005. Material for our research was collected from depths in wide range: from about 800 to over 5700 m in NE and NW Pacific and the Atlantic during seven deep-sea international expeditions in years 1996–2017. From the analysis of 176 individuals, we distinguished seven morpho-species and analysed their zoogeographical distribution. Each morphospecies was illustrated and dissected for studying morphological details. By analyzing the character of the uropods, we conclude that the genus should be split into two genera. Genetic analyses based on mitochondrial genes COI, 16S and 18S, and the nuclear gene for Histone 3, has confirmed our hypothesis about polyphyletic character of the genus. In result of our work, we describe seven new species, erect one new genus, and present first genetic markers (COI, 16S, 18S and H3) for *Stenotanais*.

Spatio-temporal patterns of macrofauna communities distribution: environmental drivers in the temperate coastal zone

M. Grabowska[1], M. Szczepanek[1], M. J. Silberberger[1], M. Kędra[1]

[1]Institute of Oceanology Polish Academy of Sciences, Powstańców Warszawy 55, 81-712 Sopot, Poland
E-mail address: mgrabowska@iopan.pl

Although the general role of benthic macrofauna in the coastal zone is well acknowledged, detailed knowledge about the spatio-temporal variation in community structure and species composition is crucial for better understanding of ecosystem functioning. Here we identify spatio-temporal patterns in macrobenthic communities and relate them to seasonally changing environmental drivers. For this we have examined assemblages of soft bottom macrofauna along with environmental samples, such as salinity, temperature, grain size, and water and sediment chemistry (e.g. organic matter properties, phytopigments, nutrients) collected during eight sampling campaigns between October 2018 and April 2021 from four coastal environments of various levels of anthropopressure within the Southern Baltic Sea (coastal lagoon, semi-enclosed bay, riverine prodelta, open coast). The gastropod Peringia ulvae and the bivalve Limecola balthica, alternately dominated community biomass and abundance for most parts of the studied area. However, despite the significant role of dominant species, the second and third most dominant species distinguished the different study region. Using multivariate analyses, we identified dominant spatial structure and a weaker seasonal variation in the benthic communities that were best explained by the quantity (total organic carbon amount) and quality (phaeophytin concentration) of the organic matter pools in the sediment. According to our results, seasonal variation in benthic communities is site-specific with no general pattern driving their contribution to ecosystem functioning. Moreover, similarities in community composition of prodelta and open coast with rather contrasting environment and exposure to anthropogenic influence suggest that benthos might be more resistant to changing environmental conditions than expected.

Identifying polar paleoproductivity indicators combining sedaDNA and fossil data

M. Greco[1], J. Pawlowska[1], D. Devendra[1], M. Łącka[1], M. Zajączkowski[1], J. Pawlowski[1]

[1]Institute of Oceanology, Polish Academy of Sciences, 81-712, Sopot, Poland
E-mail address: mgreco@iopan.pl

The Arctic Ocean is experiencing unprecedented transformations due to ongoing warming. The drastic reduction in sea ice extent, duration and concentration has triggered a steady increase in primary production as a consequence of the progressively longer phytoplankton-growing season and increased open-water habitat for phytoplankton growth. Productivity fluctuations of this kind can alter the food web structure and lead to major ecosystem-level changes thus affecting the efficiency of the biological pump and carbon sequestration. By documenting past changes in the biological production of organic matter, ocean paleoproductivity studies provide insights into the causes of such fluctuations, helping make accurate predictions on their consequences for biogeochemical cycles in the Arctic Ocean and its climate. Traditionally these studies have been based on the analyses of microfossil species, like foraminifera, as indicators of productivity levels. With the recent development of sedaDNA (sedimentary ancient DNA) applications on sediment marine archives, paleoproductivity assessments can now be extended to species that do not leave any skeleton behind. Here, we present a new approach that bridges microfossil and sedaDNA data to identify new molecular indicators of past productivity levels. We tested our method on material collected close to the Greenland Ice Sheet, in the Fram Strait. We isolated more the 700 fossil-to-molecular variant associations derived from foraminifera census data and molecular reads, finally identifying 22 foraminiferal potential paleoproductivity indicators. Our results show that if implemented in sedaDNA investigations, this approach could be used to reconstruct fluctuations of other ocean variables.

Population characteristics of *Ampullaceana balthica* (Linnaeus,1758) from southern Baltic Sea

J. Hegele-Drywa[1], K. Seremak[1], W. Sulima[1]

[1]Department of Experimental Ecology of Marine Organisms, Faculty of Oceanography and Geography, Institute of Oceanography, University of Gdańsk, Gdynia, Poland
E-mail address: joanna.hegele-drywa@ug.edu.pl

Wandering snail *Ampullaceana balthica* is a species of air-breathing freshwater snail, tolerating slightly saline waters. Although this species is quite widespread in the Baltic Sea, there is not much information about the population structure and characteristics of its individuals. Such data is crucial in the context of being host of parasitic trematode Fasciola hepatica which infects livers of various mammals, including humans. In 2018 and 2020 snails were collected from Puck Bay in the southern part of the Baltic Sea to determine population characteristics as well as mantle color polymorphism as a result of predation risk and UVR. Shell length of snails caught in 2018 (n=135) and in 2020 (N=193) ranged from 3,31 to 14,53mm (mean 6,6 ± 2,45mm) in 2018 and from 2,61 to 15,36mm (mean 8,39 ± 3,37mm) in 2020. Average wet weight of caught specimens varied from 0,04 ± 0,05g in 2018 to 0,1 ± 0,1 g in 2020 respectively. The wet weight was statistically significantly ($p < 0.05$) correlated with the shell length. On a basis of mantle pigmentation most individuals > 80% collected in 2020 were exposed to environmental stressors whereas in 2018 it was < 30% respectively. Obtained results showed that *A. balthica* established stable population due to good condition of individuals inhabiting the Puck Bay even exposed to predation risk and UVR as environmental stressors.

Diel vertical distribution of copepod abundances and diversity in the open South Adriatic Sea (NE Mediterranean)

M. Hure[1], M. Batistić[1], R. Garić[1]

[1]Institute for Marine and Coastal Research, University of Dubrovnik, Kneza Damjana Jude 12, 20000, Dubrovnik, Croatia
E-mail address: marijana.hure@unidu.hr

Copepod community structure was investigated on a short time sampling scale during a 24-h cycle at one fixed station in the open Adriatic Sea in June 2020 and February 2021 (from 0 to 300 m) using Nansen opening-closing net (250 µm mesh size). In June, the upper oceanic waters were characterized by vertical gradients of environmental factors while in February oceanic waters showed relatively homogeneous physicochemical conditions. During the winter vertical mixing, the bulk of the copepod population remained in the epipelagic zone (0-100 m) over the entire 24-h cycle, with calanoids remained the dominant group. An increasing trend of copepod standing stocks from midnight to early morning in the surface layer found in June is in agreement with previous records of copepod day-night variations in the Mediterranean Sea. Average Shannon-Wiener diversity index was lower in July (2.21±0.27) than in February (2.54±0.18) with the most pronounced differences in a 200-300 m layer, during the whole sampling period. Day-night differences in diversity and number of taxa of the epipelagic area were more pronounced in June, confirming the higher intensity of diel vertical migration in summer as well as deficiency of calanoids during the most intensive daylight. Although the epipelagic community was composed of numerous weak diel vertical migration species, for the majority of investigated copepod taxa migration patterns differed between the seasons suggesting significant influence of environmental conditions on their vertical positioning.

Diverse transcriptome response to salinity change in Atlantic cod subpopulations

M. Małachowicz[1], A. Krasnov[2], R. Wenne[1]

[1]Institute of Oceanology Polish Academy of Sciences, Genetics and Marine Biotechnology Department, Powstańców Warszawy 55, 81-712 Sopot, Poland
E-mail address: mwarzecha@iopan.pl
[2]Nofima - Norwegian Institute of Food, Fisheries and Aquaculture Reaserch, Department of Fish Health, Osloveien 1, NO-1433, As, Norway

Adaptation of populations to environmental variation related to global climate change is a significant aspect of marine ecology and fisheries management. Reduction in salinity of coastal waters is predicted in such areas as the Baltic Sea due to reduced inflow of oceanic water and increased rainfalls. Cod is one of the most significant teleost fish species in the North Atlantic with high ecological and economical value. Population of cod in the Baltic Sea has been traditionally divided into two subpopulations: western existing in higher, and eastern in lower salinity waters. To explore differences between cod subpopulations in adaptation patterns to altered salinity, we conducted exposure experiment and gene expression was analyzed in gill using oligonucleotide microarray. The transcriptome study revealed complexity of salinity adaptation in both cod subpopulations from the Baltic Sea, that involves multiple pathways of the immune system, cell growth and death, signal transduction, ion and lipid metabolism, cytoskeleton, and extracellular matrix. Our results indicate that gene expression was subpopulation-dependent and salinity-dependent, because the number of specific genes was higher than shared genes between localizations and treatments. Shared genes showed mainly different regulation patterns between subpopulations and treatments. This study provides the first overall insights into the pathways and functional categories involved in response of two Baltic cod subpopulations to salinity fluctuations.

Standing stock and functioning of benthic megafauna in warming Arctic

M. Mazurkiewicz[1], K. Meyer-Kaiser[2], A. K. Sweetman[3], P. E. Renaud[4,5], M. Włodarska-Kowalczuk[1]

[1]Institute of Oceanology Polish Academy of Sciences, Sopot, Poland
E-mail address: mikolaj@iopan.pl
[2]Woods Hole Oceanographic Institution, Woods Hole, USA
[3]The Lyell Centre for Earth and Marine Science and Technology, Heriot-Watt University, Edinburgh, UK
[4]Akvaplan-niva, Fram Centre for Climate and the Environment, Tromsø, Norway
[5]: University Centre in Svalbard, Longyearbyen, Norway

Benthic megafaunal organisms are regarded as important actors in benthic habitats, playing a significant role in carbon cycling processes. They can occupy various trophic positions as both primary consumers and food for large predators, and they play important roles in mineral recycling. Moreover, many of these organisms enhance functioning of the ecosystem indirectly through bioturbation and bioirrigation. In this study, we quantify the spatial variability in standing stocks and the functioning of benthic megafauna in coastal waters off Svalbard. Significantly higher standing stock, secondary production, respiration and carbon demand were found in locations assigned as ‘cold’ (as defined by water temperature, prevailing water masses and ice-cover) than in ‘warm’ areas. All above characteristics of megafaunal communities were negatively related with near bottom temperature. The cold locations were dominated by Echinodermata, while Crustacea prevailed in the warm locations. However, the direct impact of temperature alone is not possible to assess. Many indirect effects may be relevant, such as temperature-driven changes in ice cover, ice-algae production and pelagic primary production, or increasing predation from northward expanding carnivores. The study demonstrates that climate change may have negative impacts on the functioning of Arctic megafauna through changes in community structure and reduction of megafaunal biomass and carbon demand.

Contagious cancer in the Baltic clam *Macoma balthica* – recent findings

K. Smolarz[1], A. Hallmann[2], A. Michnowska[1]

[1]Department of Marine Ecosystems Functioning, Institute of Oceanography, University of Gdańsk, Gdynia, Poland
E-mail address: katarzyna.smolarz@ug.edu.pl
[2]Department of Pharmaceutical Biochemistry, Medical University of Gdańsk, Dębinki 1, 80-211 Gdańsk; Poland

Recent studies reported the occurrence of horizontal transmission of cancer cells in several marine molluscs such as *Mya arenaria*, *Cerastoderma edule*, *Mytilus trossulus,* and *Polititapes aureus*, and the disease was found to be of potentially contagious aetiology. As identification of cancer aetiology is an important step in studying cancer epidemiology in wildlife, our purpose here is to present the molecular (based on mitochondrial COI and nuclear EF1α) evidence indicating that neoplasia occurring in the Baltic clam *Macoma balthica* population from the Gulf of Gdańsk (Poland) belongs to the contagious type of cancer termed bivalves transmissible neoplasia (BTN). Due to the fact, that the physiological and biochemical aspects of BTN are unknown, we also present the results of a comparative study done in two clams populations, those with cancer and a healthy one. Data include the measurement of selected biochemical markers such as free amino-acids content, cellular respiration profile, corticosteroids profile and cytometric profile of the cancer cells (phagocytic capacity, cytoplasmic-free Ca^{2+} and reactive oxygen species content). Comparative biochemical studies revealed various differences between healthy and neoplastic hemocytes. Performed functional analyses of mitochondria isolated from healthy and neoplastic clams highlighted altered mitochondrial function of BTN cells when compared to the respiration of normal cells. As significantly increased level of glutamine (Gln) was observed in the BTN-positive clams, an essential role of Gln in energy production in BTN, possibly via glutaminolysis, is speculated. The content of various corticosteroids in healthy and neoplastic *M. balthica* is shown accenting significantly elevated level of cortisol in BTN-positive clams. Also, cytometric studies using SYBR Green allowed differentiating the population of haemocytes collected from BTN-positive clams into healthy and neoplastic. Yet, the assessed phagocytic capacity of haemocytes was similar in both cell groups. Elevated levels of cytoplasmic-free Ca^{2+} and increased oxidative activity of haemocytes isolated from BTN-positive clams were found.

Role of macrofauna in bioturbation and bioirrigation activity in Vistula outflow

N. Miernik[1], H. Kendzierska[1], U. Janas[1]

[1]University of Gdańsk, Institute of Oceanography, al. Marszałka Piłsudskiego 46 81-378 Gdynia, Poland
E-mail address: natalia.miernik@phdstud.ug.edu.pl

Estuaries are highly dynamic and diverse marine environments. A great variety of habitats affects macrofaunal organisms inhabiting those areas. Macrozoobenthos have a key role in the carbon and nutrients circulation by feeding on the organic matter received through river discharges and indirectly through animals' bioturbation and bioirrigation activity. Macrofaunal impact on conditions inside the sediment is limited to the depth of macrofauna occurrence. The aims of this study were estimation of the bioturbation and bioirrigation activity in the Vistula River estuary by calculating Bioturbation and Bioirrigation Potential Indices (BPc and IPc) as well as determination of the depth of macrofauna occurrence. The research was conducted in the Gulf of Gdańsk. Stations were distributed at increasing distances from the Vistula River mouth from depth 14 to 105 m. The highest values of both potential indices were observed at 24 m depth. The greatest contribution to BPc establishment had the tellinid clams Macoma balthica, and to a lesser extent polychaetes. Similar results were acquired in IPc index, but the polychaetes contribution was higher than in the BPc.

Meiofauna communities below the fish farm in the Middle Eastern Adriatic Sea

B. Petani[1], F. Ape[2,3], S. Mirto[2], I. Župan[1], T. Šarić[1], A. Baričević[1], **B. Mustać**[1]

[1]Department of Ecology, Agronomy and Aquaculture, University of Zadar, Trg Kneza Višeslava 9, 23000 Zadar, Croatia
E-mail address: bmustac@unizd.hr
[2]Institute of Anthropic Impacts and Sustainability in marine environment, National Research Council (IAS-CNR), Lungomare Cristoforo Colombo n. 4521 (ex complex Roosevelt), Loc. Addaura, 90149 Palermo, Italy
[3]Institute of Marine Science, National Research Council (ISMAR-CNR), Via Gobetti 101, 40129 Bologna, Italy

The rapid expansion of aquaculture activities has raised growing concerns about the impact on the marine environment. The goal of this study was to determine impact of fish farm situated in the middle Eastern Adriatic Sea on meiofaunal assemblages and biochemical composition of sedimentary organic matter in surrounding area. Sediment samples were taken at the depth of 34 m, at two aquaculture stations, one located at the edge of the cages (ST 1) and the other directly below the cages (ST 2) and at one control station (CTRL ST) at a distance of cca 700 m from the fish farm. We observed that the presence of the cages induced a significant accumulation of proteins, lipids and biopolymeric carbon in the sediments, resulting in increased total meiofaunal abundances but reduction in meiofaunal diversity under the cages. This significant biodiversity decrease was due to a lower abundance or disappearance of rare taxa more sensitive to organic accumulation in the fish farm stations compared to the control site. In fact, the results of this study revealed differences in meiofaunal community structure between aquaculture sediments and control ones. In particular from the outside to the inside of the cages we found a growing dominance of nematodes in comparison with a gradual disappearance of kinorynchs. These findings, confirming previous studies, suggest the reliability of the nematodes/kinorynchs ratio as an indicator for the assessment of anthropogenic organic enrichment in the sediments due to fish farm biodeposition.

Study on the developmental stages of a Pacific neotanaid species (Crustacea: Peracarida) and comparison to the Atlantic species *Neotanais micromopher*

E. Palacios Theil[1], M. Błażewicz[1]

University of Łodź, Department of Invertebrate Zoology and Hydrobiology, ul. Banacha 12/16,
90-237, Łodź
E-mail address: emma.palaciostheil@biol.uni.lodz.pl

Many aspects of the biology of the crustacean deep-sea family Neotanaidae, including life history, behaviour, diet, type of reproduction, or even distribution, are poorly known. The inherent difficulties of studying diversity at larger depths represent further hurdles to add to the regular problems associated with marine research. Hence, much of our knowledge on neotanaids is often implied, obtained from assumptions based on their morphology, indirect observations such as stomach contents, or comparisons with relatively closed taxa. For example, shallow-water members of the family Tanaidae are known to build tubes, whereas neotanaids are suspected not to do so, due to their lack of cement-glands. The development of marine crustaceans is usually studied by observing living specimens in laboratory cultures during their growth and describing the stages that take place as well as their timeline. The collection and culture of living deep-sea neotanaids is nearly impossible with the means accessible for research at this time, therefore their development must be studied by describing the different stages available in preserved samples. Among the 51 neotanaid species currently described, so far only for the Atlantic species *Neotanais micromopher* has the development been studied. We were able to gather enough specimens of a morphologically similar species from the Pacific, for which the development is here described and compared to its Atlantic congener. This, together with future morphological studies of additional species, phylogenetic and biogeographic analyses as part of an integrative approach, will help us understand the processes that shape biodiversity in the deep sea.

Link between environment, chaetognaths and zooplankton community in a high Arctic fjord

W. Patuła[1], A. Weydmann-Zwolicka[2], **M. Ronowicz**[3]

[1]Institute of Oceanology Polish Academy of Sciences, Marine Ecology Department, ul. Powstancow Warszawy 55, Sopot 81-712 Poland, wero9411@interia.pl
[2]University of Gdańsk, Institute of Oceanography, Department of Marine Plankton Research, Al. Marszałka Piłsudskiego 46, Gdynia 81-378, Poland, agata.weydmann@ug.edu.pl
[3]Institute of Oceanology Polish Academy of Sciences, Marine Ecology Department, ul. Powstancow Warszawy 55, Sopot 81-712 Poland, martar@iopan.pl

Phylum Chaetognatha constitutes about 5-30% of zooplankton biomass in the World Ocean. The phylum consists of about 150 known species, and plays a significant role in marine ecosystems, mainly as important predators on copepods. However, still little is known about their abundance and size distribution in the Arctic. The aim of this research was to study occurrence and size structure of chaetognaths in relation to zooplankton community composition and environmental conditions in Isfjorden (Svalbard Archipelago). The samples from ten stations arranged in the pattern of nested triangles were collected in August 2016 from aboard r/v Oceania. Zooplankton samples were taken by vertical hauls with the use of a standard WP2 plankton net from different depth layers (Surface Layer – SL; Intermediate Layer – IL; Deep Layer – DL), designated based on water temperature and salinity. The chaetognaths were identified, measured and categorized into one of the four size classes (<5; 5-10; 10-20; ≥20 mm). Over 70% of the total variation in zooplankton community variability was explained by environmental factors, the occurrence of chaetognaths, and their interactions. Two species of chaetognaths were found in the study area, *Parasagitta elegans* and *Eukrohnia hamata*. *P. elegans* predominated in each depth layer. There were significant differences in chaetognaths size structure between depth layers. Individuals of both species in the largest size class of ≥20 mm occurred almost only in DL, while the smallest ones were noted mainly in the SL. Their distribution could be related to other zooplankton taxa.

Short term variability of benthic nutrient, carbon, and oxygen fluxes in the coastal zone

M. J. Silberberger[1], Z. Borawska, B. Szymczycha[1], M. Szczepanek[1], A. Winogradow[1], M. Kędra[1]

[1]Institute of Oceanology Polish Academy of Sciences, Powstańców Warszawy 55, 81-712 Sopot, Poland
E-mail address: marcs@iopan.pl

Environmental conditions and benthic communities shape fluxes of nutrients, carbon, and oxygen across the sediment-water interface. While previous studies assumed and confirmed temporal variation in these benthic fluxes among seasons, knowledge about short term variability is still missing. We used ex-situ experiments to measure benthic fluxes of nutrients (NO3-, NO2-, NH4+, PO4-, SiO2), dissolved carbon (inorganic and organic), and oxygen in sediment cores that were collected during 5 sampling events in June and July 2020 (bi-weekly sampling interval) from a single coastal location in Puck Bay (southern Baltic Sea, Poland). Benthic fluxes of oxygen, dissolved carbon, SiO2, and NH4+ showed strong temporal trends throughout our study, while NO3-, NO2-, and PO4- fluxes were characterized by a low baseline and random individual sediment cores with extremely high fluxes. Using a multiple factor analysis (MFA), we show that the observed short-term variability in benthic fluxes is more closely tied to the benthic macrofaunal biomass and less to the environment. However, environmental variables play an important role for the abundances of benthic species and are therefore indirectly connected to the observed changes in benthic fluxes. Our study demonstrates high variation in benthic fluxes on short temporal scales and a connection of this variation to benthic communities. This has implications for the current practice of calculating nutrient and carbon loads, which typically extrapolate measured fluxes from individual experiments to account for an entire season and a specific sediment type, but not for the benthic community composition.

Seawater concentration patterns of human pharmaceuticals along the profile from Europe to Arctic - implications for long-distance ocean transport

A. Sokołowski[1], M. Caban[1], I. Beathe Øverjordet[2], D. Walecka[1], E. Chylewska[1], R. Kallenborn[3,4], S. Kwaśniewski[5], M. Creese2[1], T. Nordtug2[1], E. Wielogórska[2], F. Spiralski[1]

[1] University of Gdansk, Gdynia, Poland
E-mail address: adam.sokolowski@ug.edu.pl
[2] SINTEF Ocean, Trondheim, Norway
[3] The University Centre of Svalbard (UNIS), Longyearbyen, Norway
[4] Norwegian University of Life Sciences (NMBU), Ås, Norway
[5] IO PAN, Sopot, Poland

Pharmaceuticals for human use are considered new, emerging pollutants that pose a threat to the environment not only in coastal waters in the vicinity of the source point but also in more remote marine areas due to possible large-scale ocean transport. Though drugs undergo biotic and abiotic transformation (degradation) at sea many may remain in the marine environment for a relatively long time which implies long-range transport and potential for exposure to organisms living in remote areas. This study has been set up to assess transport of selected pharmaceuticals via ocean currents from mid-latitude areas to the European Arctic. Seawater was collected onboard the IO PAN vessel r/y Oceania during the cruise in June and July 2021. Sampling of water was carried out at 10 sites representing five coastal and offshore regions in the transect from the continental Europe along the Scandinavian Peninsula to the Arctic: North Sea, Norwegian Sea near Bergen and near Lofoten, Greenland Sea west of the Bear Island and west of Spitsbergen. At each site 400 dm^3 of sea water was taken from two water depths, surface (2.6 m) and underneath the summer mixed layer (50 m), and pump through the LV-SPE units to absorb pharmaceuticals on the XAD-16 resin. Pharmaceuticals were then eluted from the resin in purpose-built extraction system and their concentrations were measured using the Agilent 1260 Infinity II HPLC coupled with 6470 triple quadrupole MS. All drugs identified showed > LOQ values at least at one site or water depth. Very low concentrations in the seawater were detected for Ibuprofen, Paracetamol and Propranolol. Concentrations of carbamazepine (antiepileptic) and Fluconazole (antifungal) in a surface water layer demonstrated decreasing trends northward indicating their landborne source.

Seal lice genomics as a marker of host population history

L. Sromek[1], K. P. Johnson[2], S. V. Herrera[2], E. Ylinen[3], M. Kunnasranta[3,4], T. Nyman[5]

[1]Deparment of Marine Ecosystems Functioning, University of Gdansk, Gdynia, Poland
E-mail address: ludmilasromek@ug.edu.pl
[2]Illinois Natural History Survey, Prairie Research Institute, University of Illinois, Champaign, Illinois, USA
[3]Department of Environmental and Biological Sciences, University of Eastern Finland, Joensuu, Finland
[4]Natural Resources Institute Finland, Joensuu, Finland
[5]Department of Ecosystem in the Barents Region, Norwegian Institute of Bioeconomy Research, Svanvik, Norway

Genetic analysis of host specific parasites can be used as a unique marker to investigate the evolutionary history of their host and to gain new knowledge about their biology. Here, we studied recent evolutionary histories of seal louse (*Echinophthirius horridus*) populations parasitizing on different seals species and populations from the Arctic Ocean, the Baltic Sea, Lake Saimaa and Lake Ladoga. Our genome-wide analysis indicates that lice of the four recently diverged ringed seal subspecies (*Pusa hispida* spp.), i.e. Arctic, Baltic, Ladoga and Saimaa ringed seals, like their host, form isolated entities. In contrast, the lice of the Baltic gray (*Halichoerus grypus*) and harbor seals (*Phoca vitulina*) constitute a single population, despite a large phylogenetic distance of their hosts. Using a coalescent-based method of demographic inference, we show that the divergence of lice populations is consistent with the history of lake formation, and that their effective population size follows the census size of the seal host populations. Additionally, our analysis reveals ancient gene flow between the lice of the Baltic grey and ringed seals, indicating that in the past Baltic seals lived in closer contact than they do today.

Studies on the pathology of ulcerative dermal necrosis (UDN) in sea trout from Baltic Sea: fish-to-fish experimental transmission

M. Stachnik[1], M. Matras[1], A. Kycko[2], M. Wasiak[2], M. Reichert[1,2]

[1]National Veterinary Research Institute, Department for Fish Diseases, 57 Partyzantow Avenue 24-100 Pulawy, Poland
E-mail address: magdalena.stachnik@piwet.pulawy.pl
[2]National Veterinary Research Institute, Department for Pathology, 57 Partyzantow Avenue 24-100 Pulawy, Poland

Ulcerative dermal necrosis (UDN) is a contagious fish disease which has been observed in European waters from late 19th century. Since then, outbreaks affecting spawning salmonids were reported in many countries, also in Baltic region. UDN is an infectious skin disease of unknown etiology affecting adult, wild, anadromous salmonids migrating from open seas to fresh water during the spawning season. The UDN transmission model in our study was based on the cohabitation experiment of healthy sea trout obtained from a fish farm and spawners returning in November 2021 from the Baltic Sea to the Słupia River. During the course of the experiment, progressive changes of the skin were observed in farm sea trout. Light and electron microscopy examination of skin samples of affected trout confirmed the progressive degeneration of the skin surface. The cells showed degenerative features, lost their tight connections and became necrotic. Unlike normal skin, these cells were not replaced by new cells from the layer below. The intercellular spaces widened which led to shedding of the cells. The round, pale circles were created by necrosis of pigment cells. The association with any structure identified as virus has not yet been confirmed, and in the later stages of the disease, secondary fungal and bacterial infections have become increasingly evident. Healthy farm fish were also placed in a separate tank as a control group. None of the control fish exhibited lesions of UDN.

Acknowledgments: Financial support was from National Science Centre, Kraków, Poland, UMO-2019/33/NZ6/02929

Posidonia oceanica seeds drifted ashore are not doomed: estimating tidal retrieving and the effect of fruits in protecting seed viability

A. Sutera[1], C. Bonaviri[2], P. Spinelli[1], F. Carimi[1], R. De Michele[1]

[1]Italian National Research Council (CNR), Institute of Biosciences and Bioresources (IBBR), Corso Calatafimi 414, 90129, Palermo, Italy
E-mail address: albesute@gmail.com
[2]University of Palermo, Department of Earth and Sea Sciences, via Archirafi 22, 90123, Palermo, Italy

Posidonia oceanica is a seagrass forming large meadows along Mediterranean coasts, providing ecosystems of paramount importance in terms of associated biodiversity, protection from erosion and carbon fixation. *P. oceanica* meadows are currently receding in many parts of the Mediterranean, due to diverse anthropic activities such as pollution, development and vessel anchoring. *P. oceanica* reproduces in late spring/early summer by releasing large quantities of seeds, enclosed in fleshy buoyant fruits that allow seed dispersal. Depending on winds and currents, it is frequent to find large stretches of drifted fruits and naked seeds in beaches facing *P. oceanica* meadows. These fruits, as well as fruits drifted too offshore, are usually regarded as lost in terms of reproduction potential. Considering the size and large amount of energy storage contained in each fruit and seed, the cost of such loss for the plant may be remarkable. Here, we measured the potential of fruit return to water by incoming tides following drifting events, by tagging fruits and seeds and counting them the day after. Furthermore, we quantified the effect of air, sun and heat exposure on the vitality of drifted fruits and naked seed, by exposing them for a period ranging from 1 to 24h and eventually measuring their germination potential. Results show that a notable quota of fruits returns to the sea after drifting events, and that fruits confer significant protection from desiccation and viability loss.

Toxic effect of diclofenac and 4-OH diclofenac in *Mytilus trossulus* mussels

K. Świacka[1], J. Maculewicz[2], J. Świeżak[1], M. Caban[2], K. Smolarz[1]

[1]Department of Marine Ecosystems Functioning, Institute of Oceanography, University of Gdansk, Av. Piłsudskiego 46, 81-378 Gdynia, Poland
E-mail address: klaudia.swiacka@phdstud.ug.edu.pl
[2]Department of Environmental Analysis, Faculty of Chemistry, University of Gdańsk, Wita Stwosza 63, 80-308 Gdańsk, Poland

The continuous increase in production and consumption of pharmaceuticals is becoming a global concern. Pharmaceuticals are detected in various water bodies around the world, with the predominance of the non-steroidal anti-inflammatory drugs (NSAIDs). Diclofenac is considered one of the more toxic NSAIDs and even small concentrations of this drug have had adverse effects on various organisms. In addition, diclofenac is metabolized by organisms, including humans, resulting in the formation of various derivatives which also enter the environment. Its two common metabolites 5-OH and 4-OH diclofenac were detected several times in the aquatic environment. Knowledge on the toxicity of DCF metabolites is very poor, there are only a few papers that have investigated the acute toxicity of diclofenac metabolites to algae and bacteria. However, none of them studied the effects of diclofenac metabolites on invertebrates. Therefore, the present study aimed to evaluate and compare the potential adverse effects of diclofenac and 4-OH diclofenac on *M. trossulus* mussels. For this purpose, biomarker approach, histological examination and energy economy markers were used. In a 7-day experiment, mussels were exposed to diclofenac and 4-OH diclofenac at concentrations of 68 and 20 µg/L, respectively. Both, diclofenac and 4-OH diclofenac affected protein concent in mussels and caused lesions in different tissues. However, their toxicity was not reflected in the biomarker response, where only inhibition of glutathione reductase activity by diclofenac was found.

Laboratory exposure of the blue mussels *Mytilus trossulus* to ciprofloxacin and their response at cellular and histological levels

J. Świeżak[1], N. Dube[1], A. Czerwionka[2], K. Smolarz[1]

[1]Department of Marine Ecosystems Functioning, Faculty of Oceanography and Geography,
University of Gdańsk, Av. Piłsudskiego 46, 81-378 Gdynia
E-mail address: justyna.swiezak@ug.edu.pl
[2]Faculty of Chemistry, University of Gdańsk, Wita Stwosza 63, 80-308 Gdańsk

Among many pharmaceuticals in the marine environment reported these days, antibiotic compounds are one of the most prevalent. Ciprofloxacin (CIP), is a broad-spectrum antimicrobial agent that belongs to fluoroquinolone family, used worldwide in human and veterinary medicine. After administration, CIP is not fully metabolized, so this drug and/or its metabolites reach wastewater treatment plants fairly unchanged. Because traditional processes used in wastewater treatment are of limited capacity for the removal of many pharmaceuticals, it can lead to release of these active compounds into aquatic ecosystems. Moreover, due to its high stability in the environment, CIP may appear in concentrations ranging from ng/L in coastal areas to µg/L in the vicinity of treated water discharge. Negative effects of antimicrobials on aquatic organisms are reported more and more frequently; apart from microorganisms their impact has been observed on other biota such as copepods, fish, macrophytes, and microalgae. In bivalves, recent studies have shown the presence of ciprofloxacin-resistant bacteria in their tissues but the effects on the functioning of the molluscs are still unknown. Thus, in this study we exposed the blue mussels *Mytilus trossulus* from the Baltic Sea to ciprofloxacin at 100-500 ng/L concentrations in laboratory conditions for 16 days. We investigated the effects of exposure to the drug at the cellular levels of the bivalves' functioning, namely the activities of two major cellular defense enzymes, catalase (CAT) and glutathione S-transferase (GST), and the levels of oxidative stress products (LPO) in their tissues. Additionally, we screened mussels' tissues to assess potential influence of ciprofloxacin on pathogenic processes leading to organ dysfunctions and progressive tissue degradation.

Molecular genetic differentiation of native and invasive populations of Mediterranean mussel, *Mytilus galloprovincialis*

M. Zbawicka[1], A. Poćwierz-Kotus[1], R. Wenne[1]

[1]Institute of Oceanology PAS, Poland
E-mail address: mzbawicka@iopan.pl

Blue mussels of the genus Mytilus are important ecosystem engineers in intertidal and subtidal communities. Because of its broad tolerance of environmental variation, the Mediterranean mussel, *Mytilus galloprovincialis*, has the greatest ability of all blue mussels to colonise new geographic regions. It has spread in the waters of the temperate zone, due to anthropogenic impact. It is classified as one of the 100 most common invasive species in the world. Human interference with the environment is a threat to natural biodiversity on a global scale. This may involve displacement of native taxa by invading their habitat or by hybridization and introgression between invasive and native species. In case of mussels Mytilus these events are difficult to detect due to the similarity of the invasive species and the native taxon.A genetic method (SNP single nucleotide polymorphism) was used to distinguish between native and invasive mussels. *M. galloprovincialis* has been found e.g. in New Zealand, Australia, Chile, Brazil and Argentina. The results of our research show that the local species *Perna perna* is displaced by the invasive mussel *M. galloprovincialis* in Brazilian farms. In Argentina, we found that *M. galloprovincialis* was introduced into the Puerto Madryn presumably by ship traffic. Hybridization with native mussel M. platensis was observed. The obtained results may contribute to the protection of native species, a better understanding of the evolutionary invasion process and also allow an estimation of the rate and extent to which *M. galloprovincialis* is adapting to the new environment in the Southern Hemisphere.

POSTERS (on-line)

Recent state of the macrozoobenthic communities in the Berdyansk Spit sand habitats

O. Antonovskyi[1], O. Degtyarenko[2,3], V. Tkachenko[1], I. Mytiai[2], P. Zabroda[4], A. Strokanova[2], M. Babichev[2]

[1]Pryazovskyi National Nature Park, I. Bogun Street 46, Melitopol, 72309, Ukraine
E-mail address: antonovskii.o@gmail.com
[2]National University of Life and Environmental Sciences of Ukraine, General Rodimcev Street. 19, Kyiv 03041, Ukraine
[3]I.I. Schmalhausen Institute of Zoology of NAS of Ukraine, B. Khmelnitsky Street 15, Kyiv 01054, Ukraine
[4]Institute of Fisheries and Marine Ecology, Consulska Street 8, Berdyansk, Zaporizhzhya Reg., 71118, Ukraine

Berdyansk Spit - accumulative sand spit in the northern part of the Sea of Azov. The spit and adjacent waters together with the mouth of the Berda River belongs to Wetlands of International Importance and are part of the Priazovskyi National Nature Park, The Emerald Network of Europe. During our research (2018–2021), the salinity of the sea and the bay was characterized by increased values: 11.33–13.62‰. Spit psammocontour is characterized by heterogeneity of the qualitative and quantitative fauna composition. We found 31 species of invertebrates from the Berdyansk Bay side: the number and biomass in September reached 16,621org·m-2 and 283.22g·m-2. Biomass was dominated by Bivalvia – *Mytilaster lineatus* (45.7%), *Cerastoderma glaucum* (14.3%); Gastropoda – *Rissoa venusta* (12.33%), *Hydrobia acuta* (6.57%). Twenty species of invertebrates were registered in the open sea side. Biomass was dominated by *Mytilus galloprovincialis* (2,533.08g·m-2), *M. lineatus* (189.31g · m-2), accounting for 99.79%. On the spit tip 31 species of benthic invertebrates found. Their number and biomass in September reached 2,886org·m-2 and 1,527.63g·m-2. Here *M. galloprovincialis* (755.48 g·m-2), *Mya arenaria* (622.16g·m-2), *M. lineatus* (62.4g·m-2), *C. glaucum* (54.93g·m-2) dominated amounting together to 97.86%. Comparatively good condition of studied communities and their high productivity indicates relatively low deterioration of recent aquatic environment in the area. However in March 2022 as a result of war actions the region was profoundly affected by fuel, ammunition combustion products and oxidation of metals. This caused great influence to the marine ecosystem and our results will help to set correct assessing this change.

Covering behavior of sea urchins *Paracentrotus lividus* in relation to their size and habitat characteristics in the Aegean Sea

E. Bardanis[1], P. Megalofonou[1]

[1]Department of Biology, National and Kapodistrian University of Athens, Panepistimiopolis, Ilissia, 15784 Athens, Greece
E-mail address: manolisbrd@gmail.com

In this study, several aspects of the purple sea urchin's (*Paracentrotus lividus*) covering behavior were examined. The primary objective was to investigate in what extent the covering behavior is affected by the size of individuals and habitat characteristics, such as the substrate. Additionally, the items which urchins use were analyzed, trying to understand what affects their type and quantity. Populations of three different coastal areas of the islands Evia, Naxos and Rhodes were examined using non intervening methods. Results indicated that the numbers of urchins covering themselves differ amongst populations from different regions and between different substrates. Urchins found in sandy substrate display covering behavior in higher rates than those found on rocky substrate. *P. lividus* tend to cover themselves more when they are of small size, while the rates of covered individuals are gradually smaller, when diameter size increases, suggesting the importance of covering may change with size. There is a large variety of materials used by the sea urchins to cover their surface which-for better analysis-were divided in six general categories (a) inorganic material, (b) inorganic material of animal origin, (c) terrestrial plant material, (d) garbage, (e) seaweeds, (f) sea sponges. Material selection doesn't seem to differentiate considerably among the three populations or compared to the substrate types and individual size. Although, the sea urchins prefer lighter materials for coverage, we reach the conclusion that the most important factor determining the material frequency is the availability of each type material.

Diversity and structure of macrozoobenthos communities in waterbodies of the Pryazovskyi National Nature Park

O. Degtyarenko[2, 3], O. Antonovskyi[1], V. Tkachenko[1], I. Mytiai[2], V. Linskiy[2], K. Parinov[2]

[1]Pryazovskyi National Nature Park, I. Bogun Street 46, Melitopol, 72309, Ukraine
[2]National University of Life and Environmental Sciences of Ukraine, General Rodimcev Street. 19, Kyiv 03041, Ukraine
E-mail address: oomit99@ukr.net
[3]I.I. Schmalhausen Institute of Zoology of NAS of Ukraine, B. Khmelnitsky Street 15, Kyiv 01054, Ukraine

Pryazovskyi National Nature Park (PNNP) is one of the largest national nature parks in Ukraine with area of 78,126.92 hectares, 80% of the park consists of water bodies, with diverse of habitats for hydrobionts. Aquatic habitats are dominated by locations with salinity above 10 ‰ within the two-kilometer of the Azov Sea coastal zone, Utlyuk and Molochnyi liman with dynamic salinity. During the period 2010–2021, the diversity of identified and inventoried aquatic invertebrates of Pryazovskyi NNP is represented by 236 species from 50 orders belonging to 7 phylum's. In 2020–2021, 137 species of meso- and macroinvertebrates from 40 orders belonging to 7 phylum (Foraminifera, Cnidaria, Ctenophora, Mollusca, Annelida, Arthropoda (subphylum Crustacea), Ectoprocta)) were noted in the park reservoirs according to the results of the current inventory. Among them 95 species of macrozoobenthos invertebrates. In 2020, 71 species were registered in the Azov Sea, 75 in the Utlyuk liman, 22 in the Molochnyi liman, and 14 in the estuarine areas of the Molochnaya, Berda, Velykyi Utlyuk rivers. We have established the heterogeneity of the qualitative and quantitative fauna composition of the psammocontour of the Azov Sea coastal part. From 10 (Atmanay Dam) to 38 species (Fedotova Spit) were registered in different habitats of the Utlyutsky estuary.Since February 2022, the territory of Pryazovskyi NNP has been occupied by Russian troops. The characteristics of biocenoses obtained by us can be used as indicators in the analysis of the consequences of military aggression on marine ecosystems of the Azov Sea Basin.

Recovery of populations of *Donacilla cornea* (Poli, 1791) in the Odesa district (north-western Black Sea)

S. Ye. Dyatlov[1], O.V. Koshelev[1]

[1]Institute of Marine Biology of the NAS of Ukraine Odesa, Ukraine
E-mail address: sergey.dyatlov@gmail.com

Since the 2000s, D. cornea has been found in its former habitats, indicating a slow re-establishment (Micu and Micu, 2006; Mikashavidze, 2009). Within Ukraine, D. cornea was found near the coast of Crimea and Dzharylhach Island (Kopii, 2012; Linetskii et al., 2020). Two locations of D. cornea were found on the seacoast in Odesa: 1) beach "Chernomorka"; abundance of species there was 126.21±0.22 ind-m-2, biomass 58.0 g-m-2 with mean weight of 0.49±0.06 g per individual; 2) “Golden Beach”; the indices of the development of D. cornea there were: abundance (9.9±0.3 ind-m-2), biomass (2.3±0.04 g-m-2), mean weight per individual (0.23±0.03 g). On the beach of Chernomorsk, the developmental indices of D. cornea were: abundance (19.0±0.6 ind-m-2), biomass (11.8±0.6 g-m-2), mean weight per individual (0.73±0.04 g). The largest development of D. cornea was observed on a sandy spit of the Budaksky Liman. The number of mussels there was 3900 ind-m-2, with a biomass of 5873 g-m-2, and an average weight of 1.5±0.07 g per individual. In the 1960s, the abundance of D. cornea in this area were almost in 6 times higher than nowadays (Chepurnov et al. 1967). Partial re-establishment of D. cornea populations in the “shore-sea” contact zone in the region of Odesa district occurred relatively recently.

Features of the phytoplankton in the Khadjibei Estuary (northern coast of the Black Sea) in the modern period (2016 –2021)

O. P. Garkusha[1]

[1]Institute of Marine Biology of the NAS of Ukraine 65048, Pushkinska St. 37 Odessa, Ukraine
E-mail address: olga_garkusha@ukr.net

According to the research in the summer of 2016, in the phytoplankton of the Khadjibei Estuary, an average of 73.98% of abundance and 71.38% of biomass were cyanoprokaryotes. Throughout the estuary, the water "bloom" is noted due to the significant growing of Microcystis aeruginosa (Kutz.) Kutz with a maximum abundance of $244 \cdot 10^{3}$ colonies in liter and biomass 173 g·m^{-3}. As know, Microcystis aeruginosa is a species-agent of water "bloom". It toxicity is due to endotoxin (Ryabushko, 2003). In the Khadjibei Estuary this species called the water "bloom" with the abundance up to $24 \cdot 10^{6}$cells ·l^{-1} (Nesterova et al., 2006). In the North-Western Black Sea, the maximum abundance of species reached in summer up to 15 ·10^{6} cells ·l^{-1} (Nesterova, 2001). However, in May and September 2019–2021 in the Khadjibei Estuary registered water "bloom" caused by another – cyanoprokaryotic alga *Planktothrix agardhii* (Gomont) Anagnostidis α Komarek 1988 (basonium *Oscillatoria agardhii* Gomont). The maximum biomass of which was 452 g ·m^{-3} with the abundance of 360·10 6 cells·l $^{-1}$. *Planktothrix agardhii* is a toxic microalga that produces hepatotoxin (Aune, Berg, 1986; Eriksson et al., 1988). While *M. aeruginosa* was registered at only a few stations in small quantities with a maximum biomass of 0.016 g · m^{-3}. Probably, the species *P. agardhii* displaces *M. aeruginosa*.

First observation of the Peacock blenny, *Salaria pavo* (Actinopterygii: Blenniidae), in the Sukhyi Lyman, Black Sea, Ukraine

S. Khutornoi[1], M. Son[1], **Y. Kvach[1]**

[1]Institute of marine biology of the NAS of Ukraine, Odessa, Ukraine
E-mail address: yuriy.kvach@gmail.com

There are 9 species of blennids (Actinopterygii: Blenniidae) known in the Ukrainian Black Sea waters (Movchan 2011). The peacock blenny, *Salaria pavo* (Risso, 1810), is a rare fish in the North-Western Black Sea, where it is registered only near the Cape Tarkhankut and near the Snake Island (Boltachev & Karpova 2017; Snigirov et al. 2020). The Sukhyi Lyman is a brackish water bay south of the City of Odessa. The fish fauna of this water body consists of up to 58, including of four bleniids: *Aidablennius sphynx*, *Parablennius sanguinolentus*, *Parablennius tentacularis* and *Parablennius zvonimiri* (Khutornoi 2021). In September 2021, During a snorkeling observations of the bottom dwelling fauna, an individual of the peacock blenny was picoted at the depth 0.4 at coordinates 46.332944N, 30.661555E. The fish could be easily identified by the presence of a high leather crest on top of head, which extends from beginning of eyes to beginning of dorsal fin. The individual was identified as a male. It was observed at the mussel bed on the rocky bottoms. This finding could be recorded as the prolongation of the expansion of the Atlanto-Mediterranean blennid to the North-Western Black Sea. First cases of the expansion were recorded in 1998, when two new blenniid species were registered in the Gulf of Odessa: *Aidablennius sphynx* and *Parablennius zvonimiri* (Khutornoi 1998). Later, in 2019, *Coryphoblennius galerita* was found in the same region (Khutornoy & Kvach 2019).

First information on the phenology of the Black Sea population of invasive Asian date mussel *Arcuatula senhousia*

H. Morhun[1,2], R. V. Migas[3], M. O. Son[4]

[1]Institute of Marine Biology of National Academy of Sciences of Ukraine, Department of Water Quality, Pushkinskaya Street 37, 65048, Odesa, Black Sea
[2]University of Lodz, Department of Invertebrate Zoology and Hydrobiology, Banacha 12/16, Łódź, Poland
E-mail address: halynamorhun94@gmail.com
[3]Institute of Marine Biology of National Academy of Sciences of Ukraine, Department of Environment marginal groups, Pushkinskaya Street 37, 65048, Odesa, Black Sea
[4]Institute of Marine Biology of National Academy of Sciences of Ukraine, Department of Water Quality, Pushkinskaya Street 37, 65048, Odesa, Black Sea

The population of non-indigenous *A. senhousia* in the Black Sea estuaries (Sukhyi Liman and Small Adzhalyk Liman) in 2020-2022 was monitored. It included both benthic and planktonic samples. Spawning and larval development began when water temperatures dropped to 5-10 °C in late October and November. During the winter we observed a mass mortality of adults, so that in early spring the population of mollusks was represented mainly by young specimens up to 5 mm in size and very few large specimens of the last year's cohort. This mortality may occur due to both the extreme water temperatures in the region, which have included episodes of coastal freezing, and the food deficits in the winter. Such phenological strategy differs sharply from the life strategies of Mytilidae of native species, as well as from populations of *A. senhousia* known from some other regions around the world with summer gametogenesis and spawning at higher water temperatures in early fall (Srgo et al. 2002; Watson et al. 2021). The phylogenetic analysis of Ukrainian population based on cox1 gene region revealed that specimens joined the “cold”-water clade revealed by Asif & Krug (2012), thus confirming the distribution of this particular lineage in Europe. The presence of two clades (cold- and warm-water) is attributed to the mollusks’ temperature preadaptation (Asif & Krug 2012), and it is believed the water temperature restrains expansion, limiting the distribution along the coast.

Sprat (*Sprattus sprattus*) as a source of infection of piscivores with Anisakidae nematode parasites in the Baltic Sea

K. Nadolna-Ałtyn[1], B. Huwer[2], U. Krumme[3], R. Klinger[4], J. W. Behrens[2]

[1]National Marine Fisheries Research Institute, Gdynia, Poland
E-mail address: knadolna@mir.gdynia.pl
[2]Technical University of Denmark, Kgs. Lyngby, Denmark
[3]Thünen Institute of Baltic Sea Fisheries, Rostock, Germany
[4]University of Hamburg, Hamburg, Germany.

Sprat (*Sprattus sprattus*) is a key fish species in the Baltic Sea ecosystem. It is one of the most important fish species in the pelagic food web, where it is a major prey of piscivorous consumers such as cod, salmon and marine mammals. However, sprat may not only be a source of energy and nutrients, but infected fish might also be a source of parasitic infection for their consumers. The aim of the present study was to investigate the current spatial differences in prevalence and abundance of anisakid nematodes in sprat along a wide salinity range. Sprat samples (whole fish) were collected in five different areas along a west-east transect from Kiel Bight to the southern Gotland Basin during surveys in first quarter 2020. Fish were visually inspected for the presence of nematodes following standard ichthyological analyses and digested in artificial gastric juice to reveal the presence of Anisakidae nematodes. Genetic analysis confirmed the presence of three zoonotic parasites: Anisakis simplex, *Pseudoterranova decipiens* and *Contracaecum osculatum*. Sprat might play a major role as transmitter of these nematode parasites in the Baltic Sea. (Funding This work was supported by the European Maritime and Fisheries Fund and The Danish Fisheries Agency (33113-B-20-161)).

Free-living heterotrophic flagellates from coastal sandy sediments of northwest Black Sea

S. Nikonova[1]

[1]Institute of Marine Biology of the NAS of Ukraine, Department of Ecology of Marginal Communities, Pushkinskaya str., 37, Odessa 65048, Ukraine
E-mail address: niconova.svet@gmail.com

The northwestern part of the Black Sea is a shallow shelf zone. Its hydrological and hydrochemical regime is formed under the influence of the river runoff of large rivers (Danube, Dnieper, and Dniester). The species composition and changes in the main integral characteristics (abundance, biomass, size structure) of heterotrophic flagellates from sandy sediments were studied. Samples were taken in the transformation zone of river waters of the Dnieper-Bug Estuary along a salinity gradient from 10‰ to 17‰ in the sublittoral (depth 3 m) and at the water's edge at each site. Most species were found solely at one site, but 7 species were widespread (*Colpodella perforans*, *Bodomorpha reniformis*, *Protaspa tegere*, *Caecitellus parvulus*, *Anisonema acinus*, *Petalalomonas pusilla* and *Rhynchomonas nasuta*). In the least influence of river masses zone the species composition, abundance and biomass of heterotrophic flagellates were higher due to the occurrence of marine species while in the desalinated zone only eurybiont and fresh species are present. The maximum abundance of flagellates reached 7740 ind.·cm-3, biomass – 2800·10-6 mg·cm-3 (average density 1465±624 ind.·cm-3, average biomass 809·10-6±248·10-6 mg·cm-3). At the water's edge, compared with the sublittoral, the community of flagellates is characterized by a depleted species composition, lower abundance and biomass, and the predominance of small-celled flagellates (< 10 μm), which reach 97% of the population. The species composition of heterotrophic flagellates, their abundance, biomass, and size structure were studied for the first time in the northwestern part of the Black Sea.

Mineralogical and geochemical composition of CaCO3 skeletons of benthic invertebrates from the brackish Baltic Sea

A. Piwoni-Piórewicz[1,2], S. Strekopytov[3,a], E. Humphreys-Williams[3], J. Najorka[3], P. Kukliński[1,4]

[1]Institute of Oceanology, Polish Academy of Sciences, Powstańców Warszawy 55, 81-712, Sopot, Poland
E-mail address: anna.piwoni-piorewicz@ug.edu.pl
[2]Institute of Oceanography, University of Gdansk, Al. Marszałka Piłsudskiego 46, 81-378, Gdynia, Poland
[3]Imaging and Analysis Centre, Natural History Museum, Cromwell Road, SW7 5BD, London, United Kingdom
[4]Department of Life Sciences, Natural History Museum, Cromwell Road, SW7 5BD, London, United Kingdom
[a]current address: National Measurement Laboratory, LGC Limited, Queens Road, TW11 0LY, Teddington, United Kingdom

Biomineralization is a fundamental process in the world's oceans, whereby the seawater ions are used by organisms to produce mineralized calcium carbonate structures, namely exoskeletons such as shells, tests or tubes. Biomineralizing invertebrates occur across almost all latitudes, depths, and salinity regimes, representing a variety of anatomies, physiologies and functions. They are key ingredients essential for the sustainability of ecosystems through their contribution to habitat structure, biodiversity, food webs, sedimentation, and carbon cycling. Our understanding how much environmental conditions control the production of skeletons is still inadequate, and in the era of climate change, essential. The Baltic Sea is characterised by brackish conditions with clear surface salinity gradient, what allows to trace the influence of seawater salinity on biomineralization, and to predict the impact of desalinated conditions on calcifying fauna. The study found the invertebrates in the Baltic Sea are able to build skeletons made of calcite, aragonite or mixture of both. The type of carbonate used is species-specific, which is an indication of biological control over the skeleton composition. Yet, the differences in the ratio between calcite and aragonite in bimineralic species are most likely an effect of salinity and its influence on the solubility of calcium carbonate, as well as energetic costs of the organism functioning. The concentrations of elements (Ca, Na, Sr, Mg, Ba, Mn, Cu, Pb, V, Y, U, Cd) in skeletons are likewise under significant influence of the biological control, that in low salinity basin is highly species-specific and may even dominate the environmental impact.

Transgenerational effects of ocean warming and deoxygenation on *Gammarus locusta*

T. Repolho[1], B. Pereira[1], M. Court[1], E. Otjacques[1,2], R. Rosa[1], M. Diniz[3], J.R. Paula[1,4]

[1]MARE-Marine and Environmental Sciences Centre, Laboratório Marítimo da Guia, Faculdade de Ciências, Universidade de Lisboa, Av. Nossa Senhora do Cabo, 939, 2750-374 Cascais, Portugal
E-mail address: tfrepolho@fc.ul.pt
[2]Carnegie Institution for Science, Division of Biosphere Sciences and Engineering, Church Laboratory, California Institute of Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA
[3]UCIBIO-Applied Molecular Biosciences Unit, NOVA School of Science and Technology, NOVA University of Lisbon, Caparica, Portugal
[4]Swire Institute of Marine Science, School of Biological Sciences, The University of Hong Kong, Pok Fu Lam Road, Hong Kong SAR

Elevated temperatures and reduced oxygen availability have been shown to have marked adverse effects on marine biota. Yet, the ability of organisms to rapidly adapt to these stressors has been poorly understood. This study aimed to assess the transgenerational effects of end-of-the-century predicted levels of ocean warming (+ 3ºC) and deoxygenation (90% air sat. O2) on the oxidative stress and hormonal profiles of keystone crustacean, Gammarus locusta. To this end, three generations of gammarids were exposed to present-day and future climate change scenarios, following a full-factorial design. Subsequently, animals were sampled, and HSP, SOD, MDA and ubiquitin were quantified, as well as hormones (GABA, dopamine, acetylcholinesterase and serotonin) and DNA damage. For the first time, these results will untangle the transgenerational effects of ocean deoxygenation and its factorial exposure to ocean warming on an intertidal amphipod.

Macrobenthic invertebrates of the Utlyuk liman: data on spatial distribution for assessing the risks of ecosystem degradation under war actions

V. Tkachenko[1], O. Antonovskyi[1], O. Degtyarenko[2,3], V. Anistratenko[3]

[1]Pryazovskyi National Nature Park, I. Bogun Street 46, Melitopol, 72309, Ukraine
E-mail address: ratovar.2014@gmail.com
[2]National University of Life and Environmental Sciences of Ukraine, General Rodimcev Street. 19, Kyiv 03041, Ukraine
[3]I.I. Schmalhausen Institute of Zoology of NAS of Ukraine, B. Khmelnitsky Street 15, Kyiv 01054, Ukraine

The Utlyuk liman is an 45 km long estuary in the northwestern part of the Sea of Azov. It is a mesohaline, shallow water body with a mixed-type bottom substrate (CW34). According to EUNIS, the habitats of the studied area belong to types A2.2, X03 and have the highest degree of conservation. Material was collected in 2012–2021. Since February 2022, this territory is under Russian occupation. Species abundance and biomass of macrozoobenthic communities vary depending on the types of habitats. The highest species number (37) was found in the habitats of EUNIS: X03; highest biomass values (1,336.01 g m-2) is registered in the habitat A2.2 (N 46.315547°; E 35.297365°). Most common biocenoses in the Utlyuk liman are formed by Bivalvia. Except for 2015, bivalve biocenoses covered all studied areas. We register on average about 15–18 taxa in the biocenoses of bivalves, and maximum 37. The dominant biomass in these groups varies between 70–95%. *Mytilaster lineatus* (Gmelin in Linnaeus, 1791), *Cerastoderma glaucum* (Poiret, 1789), *Abra segmentum* (Récluz, 1843) are usually dominant in the Bivalvia biocenoses in the Utlyukskyi estuary. Gastropoda biocenoses were recorded only in 2015. Dominant species in these communities were Rissoa venusta Philippi, 1844, Theodoxus major Issel, 1865. Biomass of dominants in these biocenoses was 60–70%. Of the 21 taxa inherent in this group, 15 are common. Gastropoda formed biocenoses on all substrate types in the EUNIS habitat: A2.2. Summarizing, the macrozoobenthos of the Utlyuk liman is formed predominantly by Bivalvia biocenoses.

Health state of *Scophthalmus maeoticus* population from the Romanian Black Sea coast

A. Țoțoiu[1], V. Niță[1], E. Bișinicu[1], G. E. Harcotă[1], N. Patriche[2]

[1]National Institute for Marine Research and Development "Grigore Antipa", 300 Mamaia Blvd, 900581, Constanta, Romania
E-mail address: atotoiu@alpha.rmri.ro
[2]Institute of Research and Development for Aquatic Ecology, Fishing and Aquaculture Galați, Portului, Street no. 54 Galați, Romania

The stock evolution of the main commercial fish species depends, first of all, on the activity of industrial fishing, but just as important is the fish population's health state. Pathological investigations performed on turbot populations (30 specimens) between 2016 and 2019, on the Romanian Black Sea coast, highlighted the presence of bacteriosis and parasitosis. The highest frequency bacterial infection was vibrosis, manifested mainly in a chronic form, being localized at the skin level. *Aeromonas hydrophila* and *Pseudomonas fluorescens* showed a lower degree of virulence. The parasites with the greatest impact on the turbot population were *Trichodynia* and *Botryocephalosis*. The etiological agent of trichodynia was *Trichodina domerguei*, the degree of parasitism reaching up to 100 parasites/host. The disease does not pose a major danger to the lives of fish populations in the wild, but can be a gateway for other pathogens through the diseases caused. Following the research, it was found that the turbot was infested with the flatworm *Botriocephalus scorpii*, located in the fish stomach in a very large number, causing severe damage. The high level of diseased fish can also be linked to the stress of environmental factors combined with various types of pollution, including chemical and organic. The permanent destruction of juveniles, feeding habitats and breeding areas by various anthropogenic activities leads to damages in the immune system and favours the easy onset of contamination with various pathogens.

Polyploidy, chromosomal mosaics and different genome types in the chimeric thalli of the cosmopolitan red algae *Porphyra*

E. Varela-Álvarez[1], J. Loureiro[2], P. G. Meirmans[3], M. Castro[2], V. Laizé[1], E. A. Serrão[1]

[1]CCMAR Centro de Ciências do Mar, Universidade do Algarve, Faro, Portugal
E-mail address: evarela@ualg.pt
[2]Department of Life Sciences, Centre for Functional Ecology, University of Coimbra, Coimbra, Portugal
[3]Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, The Netherlands

It is expected that the amount of DNA and genetic variability among cells across the same individual to be relatively constant. However, some species in nature have individuals with genomic heterogeneity having cells with different genome sizes and/or genetic composition (chimeras). In this study, we focused on one of those unusual species, the red algae *Porphyra* known to form part of the marine food products commonly known as 'Nori', where individuals are composed of genetically different cells lines. This is because after meiosis, the four meiotic cells in *Porphyra* are not released as individuals spores, but instead grow together into a single chimeric leafy thallus through consecutive mitotic divisions. We compared ploidy levels, genome sizes and genetic differentiation using flow cytometry, karyotypes and microsatellite markers in the most abundant *Porphyra* species in Europe to verify if the thallus of these species to study their genetic heterogeneity. Our results show multiple ploidy levels with the presence of two different genome types of different sizes (a and b) with separate rounds of genome duplications within the vegetative thalli all distributed along the thallus in sectorial mosaics. We conclude that *Porphyra* species belong to an aneuploid/euploid system, where genome duplications, mixoploidy, chromosomal dynamics and the presence of different genome types in the chimeric thalli, which play a role in shaping the genetic diversity of these taxa. Our results provides new insights on red algae biology and evolution and raise additional questions on what constitutes an individual.

Phytoplankton structural and functional changes in Mamaia Bay (Romanian Black Sea coastal waters) over the last two decades

O. Vlas[1], L. Boicenco[1], L. Lazăr[1], E.-D. Pantea[1], M.-M. Făgăraș[2]

[1]National Institute for Marine Research and Development `Grigore Antipa` (NIMRD), 300 Mamaia Bdv., Constanta 900581, Romania
E-mail address: ovlas@alpha.rmri.ro
[2]`Ovidius` University of Constanța, 124 Mamaia Bvd., Constanța, Romania

The need for a better understanding of the eutrophication impact on coastal ecosystems has been one of the main reasons for exploring the relationships between primary producer communities and nutrient concentration fluctuations. Changes in nutrient concentrations in the environment can also have effects on the phytoplankton species composition, the amount of food available to zooplankton, and the energy transfer to higher trophic levels. The present study aims to understand the factors that control the phytoplankton composition and dynamics in Mamaia Bay to estimate the climate change and anthropogenic pressure impact on coastal ecosystems. In order to observe the phytoplankton's structural and functional changes in the last two decades, we processed and interpreted the data collected from Mamaia Bay between 2000 and 2019. The first step was to combine the sheets in a single excel table and standardize and update each species' scientific names according to WoRMS. Then, the phytoplankton evolution trends were analyzed in relation to physico-chemical parameters (processed by the NIMRD Chemical Oceanography Department), by phytoplankton qualitative and quantitative comparative analysis for the last two decades, also consulting the available literature. The results highlighted that the significant changes in the last 20 years in phytoplankton's community structure were mainly caused by rising temperatures and N/P ratio variations. The increase in diversity and the quantitative phytoplankton decrease in the Romanian Black Sea coastal waters in the last 10 years are clear evidence of the efforts made to limit eutrophication since Romania's accession to the European Union.

Genetic structure of pike (*Esox lucius* Linnaeus, 1758) populations along the Polish coast of the southern Baltic Sea

A. Wąs-Barcz[1], R. Bernaś[2], S. Sakowicz[2], M. Greszkiewicz[3], A. M. Lejk[4], D. P. Fey[5]

[1]National Marine Fisheries Research Institute, Department of Fisheries Resources, Kołłątaja 1, 81-332 Gdynia, Poland
E-mail address: awas@mir.gdynia.pl
[2]Inland Fisheries Institute, Department of Migratory Fish, Rutki 49, 83-330 Żukowo, Poland
[3]National Marine Fisheries Research Institute, Department of Fisheries Oceanography and Marine Ecology, Kołłątaja 1, 81-332 Gdynia, Poland
[4]National Marine Fisheries Research Institute, Department of Logistics and Monitoring, Kołłątaja 1, 81-332 Gdynia, Poland
[5]National Marine Fisheries Research Institute, Department of Fisheries Oceanography and Marine Ecology, Kołłątaja 1, 81-332 Gdynia, Poland

The pike (*Esox lucius*) is a species of eco-evolutionary and socio-economic importance, occurring in a broad range of aqueous environments – from inland freshwater to brackish coastal waters. It was widespread along the entire coast of the Baltic Sea. A drastic decline in the stocks of Baltic pike in the 20th century caused large-scale restocking activities in the area, often with non-native material from more abundant freshwater pike populations. Research into the genetic variation and structure of the species in the Baltic Sea was necessary as part of the key knowledge required for the management and conservation of the species. Appling fourteen microsatellite markers, we analysed the genetic differentiation of 495 Baltic Sea pike sampled along the Polish coastal waters and in Præstø Fjord, in southeastern Zealand Island, Denmark. Using traditional F-statistics and a Bayesian approach implemented in STRUCTURE we confirm the presence of genetic structure within the analyzed region. It was most likely the result of both evolutionary forces and anthropogenic factors. The rivers of Puck Bay showed the greatest discrepancy, while the populations related to the Vistula delta and the Vistula itself formed a strong common cluster. The results of this work indicate a number of negative phenomena related to stocking. Relocation of populations and variability decrease with all consequences were noticed. Our results contribute to current knowledge on the population genetics of Baltic Sea pike in a previously unsampled area, where the species is close to extinction.

Dolphins in the aquatory of the Black Sea Biosphere Reserve (BR "Chernomorsky")

Z. Selyunina[1]

[1]Black Sea Biosphere Reserve, Ukraine, 75600, Kherson region, Gola Pristan, st. Lermontov
E-mail address: scirtopoda@gmail.com

The aquatories of the Black Sea Biosphere Reserve include the Tendrivska and Yagorlytska bays of the Black Sea, kilometer strip of the Black Sea along the island of Tedrivska Spit andsmall part in the Dnieper-Bug Estuary. These water areas are Wetlands. There are 3 species of dolphins: *Delphinus delphis*, *Tursiops truncatus*; *Phocoena phocaena relicta*, Abel, 1905 in regions fauna. All species included in the Red Book of Ukraine, *Ph. phocaena* is categorized as endangered (IUCN). Dolphins can be mostly seen in the sea along the Tendrivska Spit, in the western deep-water part of the Tendrivska Bay, in the mouth of the Dnieper-Bug Estuary*. Ph. phocaena* regularly reach 70 km and further along the Dnieper River. There is a recorded case of these dolphins entering the Ingulets River (120 km from the sea). In our waters, dolphins appear in the late March - early April and stay until October. Their appearance in the waters of the BSBR depends of the timing of migrations and the number of mass species of schooling fish, aggregation of aquatic invertebrates. According to the long-term observations in our region, *D.delphis* dominates among dolphins. The average occurrence of this species is the highest over the past 15 years - 56%, in *T.truncatus* - 25%, *Ph.phocaena* - 19% of the total number of dolphin sightings. Among the remains of dolphins washed ashore in our region, focaena prevails (more than 60%). Long-term monitoring allows identifying the dynamics of the number of species, determining the factors of influence, and predicting trends in the dolphin's populations.

INDEX