VLIZ Science Symposium
on Belgian Marine Biodiversity

Wednesday, 23 May 2018

Oostende, Belgium

PROGRAMME

09:15 – 09:45   Welcome coffee

09:45 – 10:00   Introduction
Dr. Michiel Vandegehuchte, Flanders Marine Institute - VLIZ

10:00 – 10:30   How unknown is the world's biodiversity? Free-living flatworms as an example
Prof. dr. Tom Artois, Hasselt University

10:30 – 10:45   BeRMS, ERMS and WoRMS: Community tools to facilitate our knowledge of marine biodiversity
Simon Claus, Flanders Marine Institute - VLIZ

10:45 – 11:00   Morpho-molecular studies of toxic and non-toxic dinoflagellates and their resting stages (cysts) and their implications for biodiversity assessments
Dr. Kenneth Mertens, Ifremer (France)

11:00 – 11:30   Coffee break

11:30 – 12:00   The effects of biological diversity on marine ecosystem functions
Prof. dr. Frederik De Laender, Namur University

12:00 – 12:15   Identifying marine biodiversity by DNA barcoding and DNA chips
Prof. dr. Marc Kochzius, Vrije Universiteit Brussel

12:15 – 12:35   Pitch presentations

Biological characteristics modulating the sensitivity of calcification to ocean acidification: Comparative approach in echinoderms
Sarah Di Giglio, Université Libre de Bruxelles

Biodiversity monitoring of the soft-sediment fauna
Dr. Annelies De Backer, Institute for Agricultural and Fisheries Research - ILVO

Documenting the SS Kilmore, 10 years after Zintzen *et al.*
Koenraad Van Schuylenbergh, GUE-BE vzw

DNA barcoding of benthic species from the Belgian part of the North Sea for diversity impact assessments
Dr. Sofie Derycke , Institute for Agricultural and Fisheries Research – ILVO

12:35 – 13:40   Lunch break

13:40 – 15:30   Discussions: break-out sessions

15:30 – 16:00   Summary & epilogue
Dr. Michiel Vandegehuchte, Flanders Marine Institute - VLIZ

ABSTRACT

HOW UNKNOWN IS THE WORLD'S BIODIVERSITY? FREE-LIVING FLATWORMS AS AN EXAMPLE

Artois Tom

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Even at the start of the 21st century, the actual biodiversity of the world's marine ecosystems is still largely unknown. Not surprisingly, especially the smallest creatures are much understudied. Among the least known taxonomical groups are the microturbellarians, small free-living flatworms that inhabit sandy beaches or live epiphytically on algae. With a rough conservative estimation of about 15.000 species still to be described, an enormous task still lays ahead for classical morphology-based taxonomy. And not only is the relative number of species already described limited, but on top of that most of them are described from a few marine ecoregions only, mostly from the Western and Northern Europe, and the Mediterranean. The major part of the world's coasts and deep sea habitats never were investigated. This lack of knowledge greatly hampers further research regarding biogeography, ecology or even phylogeny. In recent years we have tried to shed light on several questions regarding the evolution and ecology of these animals, including the origin of a symbiotic life style, the history of major habitat shifts and the "Everything small is everywhere"-hypothesis, research that is still ongoing. These studies were only possible because of a big taxonomical effort and trustable databases, and the results will briefly be presented.

ABSTRACT

BeRMS, ERMS and WoRMS: Community tools to facilitate our knowledge of marine biodiversity

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The World Register of Marine Species (WoRMS) celebrated its 10th anniversary in 2017. Over the past ten years, the content of WoRMS has grown steadily, currently containing more than 242,000 accepted marine species names. WoRMS is therefore unique: there is no comparable global database for marine species, which is driven by a large, global expert community, supported by a Data Management Team and can rely on a permanent host institute, dedicated to keeping WoRMS online. The system has seen several user applications, including facilitating local and regional marine species data management and data analysis, but also answering big scientific questions for example about the estimated number exiting marine species, providing a metric for how much we do and do not know about life in the oceans.

One of the unique features of WoRMS is that it is containing and integrating over 100 global, 12 regional and 4 thematic species databases integrated within a common taxonomy. This allows regional, thematic or ecological expert groups to focus on specific contents of the database, providing additional information and creating community ownership of a specific subcomponent of WoRMS.

A regional example of WoRMS is BeRMS, the Belgian Register of Marine Species. Published in 2010, this register enabled to provide an inventory of all marine species encountered within the Belgian Exclusive Economic Zone, including the intertidal zone.

Now, a major update of the Belgian Census has started. A major literature review, datamining activities of marine biogeographic databases such as the European Biogeographic Information System (EurOBIS) and additional species surveys are planned in order to complete this register, allowing to provide a nearly complete assessment of the Belgian marine biodiversity.

ABSTRACT

MORPHO-MOLECULAR STUDIES OF TOXIC AND NON-TOXIC DINOFLAGELLATES AND THEIR RESTING STAGES (CYSTS) AND THEIR IMPLICATIONS FOR BIODIVERSITY ASSESSMENTS

Mertens Kenneth

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Dinoflagellates are a large group of microalgae (about 2000 species) that live in diverse environments and have a wide range of feeding strategies. Dinoflagellates can produce resting stages during the sexual part of their life cycle, which can preserve in the sediments for millions of years. Several dinoflagellates are harmful in that they produce toxins that can accumulate in the food chain. The identification of dinoflagellates to species level is done using a combination of morphological, specifically microscopic, and molecular techniques, such as single-cell PCR. Here several examples will be given of species identification within different groups of dinoflagellates, highlighting the complexity of identification of dinoflagellates to species level. The implications for biodiversity assessments, such as based on metabarcoding, will be discussed.

ABSTRACT

THE EFFECTS OF BIOLOGICAL DIVERSITY ON MARINE ECOSYSTEM FUNCTIONS

De Laender Frederik

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The biological diversity found back in natural systems is an important determinant of the functioning of ecosystems and their stability in changing environments. However, biodiversity can be defined at various hierarchical levels, going from the within-species to the community and landscape level. In addition, biodiversity at a fixed hierarchical level can affect ecosystem functions and their stability through various mechanisms. I will illustrate this using a theoretical framework, and translate this framework to a simple trait-based model for competitive communities. Next, I will turn to practical examples of how trait diversity at various hierarchical levels can affect marine ecosystem functions and discuss some challenges for future research, including the up-scaling to complex multi-trophic systems ('food webs'). Lastly, I will present a new collaborative research project that will start end 2018, where we plan to study the effect of intraspecific trait diversity on the resistance of species diversity and ecosystem productivity to multiple stressors.

ABSTRACT

IDENTIFYING MARINE BIODIVERSITY BY DNA BARCODING AND DNA CHIPS

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Species identification is a key problem throughout the life cycle of marine invertebrates and fishes: from eggs and larvae to adults in ecological research, but also more applied in fisheries research and control, as well as processed seafood products in consumer protection. The application of molecular genetic tools is a powerful method to assign specimens that cannot be identified by morphological character to certain species and also has the potential to be automated, allowing identifying species with highest precision and in large sample sizes. In DNA barcoding a fragment of the mitochondrial cytochrome oxidase subunit I (COI) gene is sequenced and compared with a reference database in order to identify the species. DNA microarrays use a different approach: the DNA of the specimen to be identified is not sequenced, but applied to a DNA chip and hybridises to species-specific probes, which is detected. This has the potential for a high-throughput technology that can analyse even mixed samples, such as plankton hauls or environmental DNA.

ABSTRACT

BIOLOGICAL CHARACTERISTICS MODULATING THE SENSITIVITY OF CALCIFICATION TO OCEAN ACIDIFICATION: COMPARATIVE APPROACH IN ECHINODERMS

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The increase of the atmospheric carbon dioxide concentration, due to human activities, induces changes in ocean chemistry, namely a decrease in carbonate concentration and an increase in proton concentration. These two phenomena are called Ocean Acidification (OA). In Metazoa, different physiological processes, including calcification, can be affected by this acidification. However, the magnitude of the OA impact differs according to taxa or even within taxa. Several hypotheses about the mechanisms behind these differences were proposed: (1) contrasted acid-base physiologies, (2) differences in variability of the original habitats, (3) differences in the quality or quantity of available foods. For instance, in echinoderms, a taxon provided with a well-developed high-magnesium calcite skeleton, the calcification process is affected by OA but at different degrees according to the considered species. The goal of the present study is to assess the importance of different biological characteristics which could modulate the sensitivity of calcification to OA in Metazoa. A comparative approach using different postmetamorphic echinoderms with contrasted acid-base physiologies and food sources and originating from contrasted habitats (variable or stable) is developed. Studied organisms principally come from long term OA experiments and natural CO_2 vents. The significance of the considered factor is determined by comparing the effects of OA on the skeleton of echinoderms with contrasted characteristics for this factor. The effects on the skeleton is studied at the morphological, mechanical and calcification gene expression levels.

ABSTRACT

BIODIVERSITY MONITORING OF THE SOFT-SEDIMENT FAUNA

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In the last ten years, around 3900 Van Veen grabs and over 1000 beam trawl samples have been collected by ILVO in the Belgian part of the North Sea (BPNS), mainly for impact assessments of human activities such as aggregate dredging, dredged material disposal and offshore wind farms. The main focus of the monitoring programmes is on soft-sediment fauna i.e. macrobenthos, epibenthos and demersal fish. However, for targeted projects also zooplankton, microbial and pelagic fish samples have been collected. Spatial coverage has increased over the years, and together with increased quality checks and better identification tools, this resulted in the discovery of several species new for the BPNS e.g. for zooplankton 9 new species were recorded and published, for macrobenthos approximately 25 new species have been recorded. This certainly is an underestimation, since for monitoring purposes, it is chosen not to identify certain groups to species level e.g. Nemertea, Oligochaeta, Hydrozoa.

Furthermore, compilation and harmonisation of data from targeted research projects, long-term monitoring and environmental impact monitoring allows to have information on occurrence of alien species, on biodiversity changes over time and on habitat discrimination, and it can serve modelling (both species and habitats). For example, we have updated the occurrence and characteristics of the Belgian benthic habitats. Based on structural characteristic, five communities were identified, each with their own indicator species, sediment properties and spatial distribution. In addition, species-specific biological trait data on life history, morphological and behavioural characteristics was added, and as such we provide for the first time, insights in the functional characteristics of the benthic habitats. In the coarser permeable sands, more free living mobile species were found causing diffusive mixing, whilst the finer sand and mud communities had more sessile, tube building and burrow dwelling species.

With this pitch presentation, we want to stress that monitoring data, collected in the framework of different environmental monitoring projects, yields a wealth of information, that can be used for different research purposes such as an update of species new for the BPNS, species-habitat distribution models and biodiversity over time.

ABSTRACT

DOCUMENTING THE SS KILMORE, 10 YEARS AFTER ZINTZEN *ET AL.*

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Zintzen et al studied the marine life on the SS Kilmore between 2003 and 2005 0, 0. GUE-BE divers now return to the wreck to evaluate her present condition, capture photo and video, build a 3D photogrammetric model 0 and survey the marine life. This presentation invites the scientific community to fine tune our project goals and help us interpret our results.

Global Underwater Explorers (GUE), a global leader in scuba education, conservation and exploration, emerged out of a desire to safely explore and protect the underwater world and to improve the quality of education and research in all things aquatic 0. GUE divers have advanced experience that enables them to safely reach depths and locations that many recreational divers never could. They can assist researchers, as well as launch their own initiatives, like the discovery of the 16th century Swedish warship Mars 0 or a 12,000-year-old human skeleton in the Mexican Hoyo Negro cave system 0.

GUE-BE that unites the Belgian GUE community 0, released a website 0 about its 2017 Project with a short documentary on the Westhinder and a 3D model with centimeter-level detail. The subject of our 2018 Project is the SS Kilmore, which sank in 1906 and now lies at 32 m. GUE-BE volunteers will explore her on five days between May and September 2018, quantify her fauna, create a 3D model, website and documentary about her history, condition and environmental significance, map abandoned fishing gear, and record temperature and visibility.

Although several GUE-BE volunteers are scientifically trained, they are not biologists and have no such aspirations. We therefore reach out to the research community to help us identify the most relevant species and data collection method, and determine the observed animals. By collaborating as citizen scientists, we hope to contribute to initiatives like BeRMS2020 0.

References

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[2] http://www.vliz.be/projects/bewremabi/

[3] Raoult V., et al (2016) "GoPros™ as an underwater photogrammetry tool for citizen science," PeerJ [1] 4:e1960 https://doi.org/10.7717/peerj.1960

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[5] oceandiscovery.org

[6] http://press.nationalgeographic.com/2014/05/15/

[7] http://www.gue-be.be/

[8] http://westhinder.gue-be.be/

[9] http://www.marinespecies.org/berms/

ABSTRACT

DNA BARCODING OF BENTHIC SPECIES FROM THE BELGIAN PART OF THE NORTH SEA FOR DIVERSITY IMPACT ASSESSMENTS

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Species living in or near the seafloor fulfill a variety of ecosystem functions. Understanding how benthic communities respond to human activities is crucial to determine how such activities impact the functioning of the benthic environment. In the Belgian part of the North Sea, ILVO is extensively monitoring different benthic ecosystem components, and explores new ways to characterise the structural and functional benthic diversity. DNA-based approaches such as metabarcoding may complement and speed up the characterisation of changes noted in these communities during impact assessments. Linking sequences to taxonomic data is indispensable when information on ecosystem functioning is the key concern. However, the taxonomic resolution of metabarcoding is still hampered by a lack of reliable reference sequence data to which the metabarcode sequences can be compared. We compiled longterm monitoring data from soft sediment macrobenthic, epibenthic and pelagic fish communities in the Belgian part of the North Sea. For macrobenthos, 334 species belonging to nine phyla have been registered in the past 15 years. The classes Polychaeta, Malacostraca and Bivalvia are the most species rich and include 40%, 37% and 13% of all species, respectively. ILVO aims to barcode as many benthic species as possible to validate and - when proven to be reliable - to implement DNA-based methods for biodiversity impact assessments. To this end, ethanol preserved voucher specimens are morphologically identified, photographed and stored as reference material for DNA sequencing. Partial or whole specimens are subjected to DNA extraction and COI Sanger sequencing. At present, the genetic reference database contains 95 macrobenthic species, representing the aforementioned classes and phyla. In addition, 85 epibenthic species and demersal/benthopelagic fish have been barcoded. Collection and sequencing of additional species is an ongoing effort. Next to DNA barcoding, we also explore new library preparation methods for high throughput sequencing of benthic communities by using different COI primer sets and primer free approaches such as long read 18S rRNA sequencing, on mock communities, ethanol fixatives and field samples. These methods will be compared to morphologically identified samples to assess whether comparable patterns in species and functional diversity patterns in impacted versus non-impacted sediments are found by the different approaches.

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This participants list was assembled on 16 May 2018. Any changes after this date have not been processed.

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