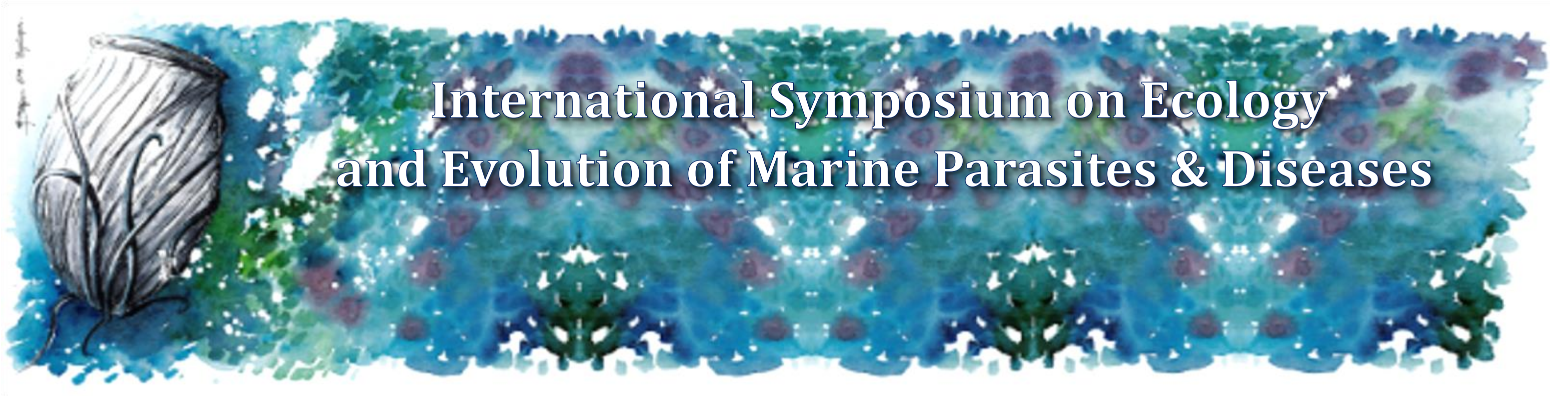

International Symposium on Ecology and Evolution of Marine Parasites & Diseases

BOOK OF ABSTRACTS

Espace Encan
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15th-18th of November 2022

AUTHORS:
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Presentation of the symposium

The **“International symposium on ecology and evolution of marine parasites and diseases”** is a unique meeting combining marine ecology and parasitology. Considering the need to integrate parasitology in ecosystem studies and global change scenarios, this symposium provides a great opportunity to present the latest research findings regarding marines parasites, to gather international experts from various disciplines and to identify next research priorities in this area, both at the European and international levels.

The symposium included seven sessions on parasites affecting marine organisms: parasite adaptation and evolution, biogeopgraphy and macroecology, parasite detection, disease impact and management, epidemiology, environmental parasitology. A workshop focusing on micro-parasites of bivalves was also organised on the last day and was open to interested participants.

The scientific committee :

- Dr. Isabelle Arzul, IFREMER, France
- Dr. David W. Thieltges, Royal Netherlands Institute for Sea Research, The Netherlands
- Dr. Mathias Wegner, Alfred Wegener Institute, Germany
- Pr. Xavier de Montaudouin, University of Bordeaux, France

The organizing committee:

IFREMER, Adaptation and health of marine invertabrates Unit (ASIM), La Tremblade, France
- Isabelle Arzul, Isabelle.Arzul@ifremer.fr
- Lydie Canier,Lydie.Canier@ifremer.fr
- Véronique Betto, Veronique.Betto@ifremer.fr

The Sponsors:

This event has received funding from Ifremer, the Aquitaine Region, the Communauté d'Agglomération de La Rochelle, UMR EPOC/University of Bordeaux, and the European Union Reference Laboratory for Molluscs Diseases.

Website : https://marineparasites.sciencesconf.org/
Online participation: https://app.imagina.com/marine-parasitology-symposium
Twitter account: ISEEMPD 2022 !

Summary and take home messages

The symposium gathered more than 123 participants during three days. Of these 123 participants, 29 followed the presentations remotely and 94 were present in La Rochelle.

These 123 participants came from 22 different countries, 47 of which were from France and about 20 participants from outside Europe. We note the participation of 9 scientists from the United States and 4 scientists from South Korea. The participants were very diversified not only in terms of geographical origin, study models but also disciplines. Moreover, it is interesting to note that 4 participants came from the professional world (marine bivalve hatcheries) and almost half of the participants were young researchers (PhD and post-doctoral students).

The symposium was intended to be waste-free: no program or information was distributed in paper version, they were available online on the Imagina application that participants were invited to download. Participants were also invited to use their own water bottle.

The symposium was structured around 7 different sessions over 3 days and a workshop on the 4th day. Initially 74 abstracts were submitted, of which 53 were for an oral presentation and 21 for a poster presentation. The scientific committee (Isabelle Arzul, Mathias Wegner, David Thieltges and Xavier de Montaudouin) reviewed all the abstracts. All the abstracts received were retained but some submitted for an oral presentation were proposed for a poster presentation in order to stay within the scheduled time slots. The scientific committee had previously identified plenary speakers for each session of the program. These speakers were contacted and invited, with their registration and travel expenses covered by the symposium.

Thus, the **programme** (Appendix A) included 7 plenary presentations of 40 minutes (30 minutes of presentation and 10 minutes of discussion); 37 oral presentations of 20 minutes (15 minutes of presentation and 5 minutes of discussion); 37 posters presented during the coffee breaks, lunches and a special "poster" session at the end of the first day. A workshop focusing on micro-parasites of bivalves was organised on the last day and included 5 presentations.

The plenary presentations were very inspiring and provoked rich discussions. The place given to posters during the symposium and the format of the presentations (15 minutes of presentation followed by 5 minutes of questions) were appreciated by the participants. Finally, the duration of the coffee and lunch breaks (40 minutes and 1h30) allowed participants to continue the exchanges initiated during the sessions and to discuss projects and collaboration. It is also worth noting that the food and service were highly praised.

The discussion at the end of the presentations led to the following conclusions:

- If we consider the number of publications on parasites compared to publications on other species, there is a significant gap between the diversity that exists within parasites and the way it is reported in the literature. This observation should encourage us to publish more on parasites and especially on non-model and less studied species;

- Parasitology is not considered as a functional trait in ecology whereas the impact of parasites is determining at all scales of study and should be taken into account in a systematic way in ecological studies;

- Parasites by definition develop long-lasting interactions with their hosts. Many single and multi-cellular organisms can thus be considered as parasites. If the presentations concerned a large diversity of models, species, habitats, life cycles... one can note the absence of presentation on viruses and very few presentations on bacteria. However, these microorganisms have their place in many other conferences/symposiums;

- The discussions highlighted certain gaps or black boxes. The research teams have more easily funding to approach models that are simpler to study because they are more easily manipulated in the laboratory and more easily detected. However, a large number of species or parasitic stages remain little or not known. This is for example the case of miracidium stages in trematodes;

- The evolutionary relationships between free-living and parasitic species are also not well studied;

- Similarly, there are few links between teams working on parasites in freshwater and in the marine environment. However, we note that some presentations concerned freshwater parasites;

- The development and the use of new sequencing techniques allow to highlight the existence of new species. Nevertheless, these DNA detections are rarely associated with the morphological and biological characterization necessary to interpret these sequence data. Observational data remain essential to give meaning to the results of these new molecular approaches;

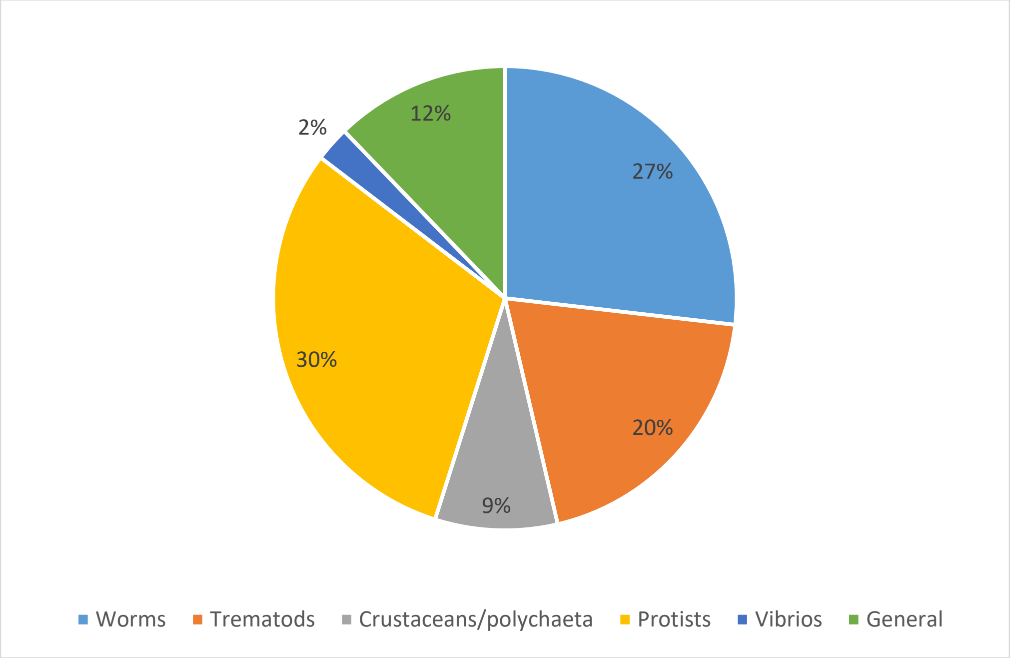
- Whatever the nature of the data obtained, the quality of the data must be a priority in order to attract researchers working with quantitative data

- Long-term series and studies based on high sampling efforts are essential to shed light on the evolution of host-parasite interactions and the place of parasites in ecosystems.

- The value of sample collections was highlighted. Biobanks collecting biological material collected in studies or surveillance programs are valuable. Nevertheless, this material does not always allow to obtain DNA in sufficient quantity and quality to analyze certain samples such as those embedded in paraffin;

- The impact of climate change on the emergence or evolution of parasites in ecosystems is an important subject but not easy to address. The dedicated session had fewer presentations than other sessions. The adaptive potential of both parasites and hosts is rarely studied and relies rather on short-term experiments. The possibility of developing multi-latitude studies to address this issue was raised;

- It is necessary to create more links between disciplines around parasitology in the marine environment and for this a third edition of the ISEEMPD (International symposium on ecology and evolution of marine parasites and diseases) is envisaged in two or three years. Several teams have expressed interest in hosting and organizing this future meeting.



Repartition of presentations (oral and posters) by parasite model

Participants in the International symposium on ecology and evolution of marine parasites and diseases

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Keynotes
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Session 1: Biogeography and macroecology of marine parasites

Parasitology meets macroecology on its own terms: New ways to tackle long-range patterns and processes of parasite diversity

Juan Antonio Balbuena *† 1

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Macroecology is a relatively new, fast-growing field that emerged from the idea that small-scale local processes alone are not able to fully explain the abundance and distribution of species. The study of macroecological patterns and theory provides an effective framework to explore parasite spatio-temporal distributions and disease dynamics in host populations. For instance, macroecology approaches can be useful to match parasites of an invasive host species across its native and introduced range and/or populations of the introduced host species with populations of native species coexisting in sympatry. Unfortunately, there has been a bias in the field towards vertebrates and vascular plants, whereas parasites have been largely ignored despite their important role in ecosystem functioning. To redress this situation, I find it necessary to to align research in ecological parasitology with recent advances in eco-evolutionary theory and approaches. The aim of this talk is to illustrate how the incorporation of current trends in the field can fruitfully contribute to principles and analyses in parasitology. In particular, I will summarize recent research carried out in our lab showing how functional, phylogenetic and network approaches can provide fresh insights into the organization of parasite communities. In addition, I will demonstrate in the context of invasion biology how bipartite network analysis can help us test the enemy release hypothesis and assess the integration of the invasive species in new ecosystems. Funded by Ministry of Science and Innovation of Spain (PID2019-104908GB-I00)

Keywords: functional diversity, phylogenetic diversity, bipartite networks, invasive species

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[*] Speaker

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Uncovering Long-branched Microsporidian Diversity In The Freshwater Isopod Asellus aquaticus

Annemie Doliwa *† [1], Daniel Grabner [1,2], Lidia Sworobowicz [3], Anna Wysocka [3], Alexander Weigand [4], Michał Grabowski [5], Tomasz Mamos [5], Bernd Sures [1,2]

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The canonical, or long-branched (LB-)Microsporidia are known to infect a broad range of animals and protists. It seems probable that their true diversity is highly underestimated and many host taxa are yet to be identified. For example, it is known that LB-Microsporidia are common parasites to various crustaceans, but only little information is available on infections in aquatic isopods such as *Asellus aquaticus*, a morphospecies widespread in various freshwater habitats throughout Europe and Asia Minor. To obtain a first overview on which LB-Microsporidia are present in this host, we examined 247 specimens belonging to several lineages of *A. aquaticus* that originated from 30 sites across Europe and Asia Minor. Individual specimens were measured and dissected to remove the intestines to avoid contaminations and DNA was extracted from the remaining tissues. To detect infections, we amplified the DNA extracts with LB-Microsporidia-targeted primers. In total, 26.7% of the analyzed specimens were positive for LB-Microsporidia, and larger individuals were infected significantly more often than smaller ones. The mean prevalence differed, although not significantly, between habitat types: The lowest was found in springs (8.7%, n=46), whereas the highest was found in ponds (37.7%, n=53). We found no effect of the host OTU on the prevalence except for one host OTU for which no infections were detected. Notably, 17 microsporidian molecular taxonomic units (MICMOTUs) were identified in total, and phylogenetic analyses indicated they mostly belonged to the microsporidian clade IV and were related to LB-Microsporidia known from amphipods. In terms of geographic distribution of these MICMOTUs, there were no detectable patterns. The present study is the first to our knowledge highlighting *A. aquaticus* as a host to an unknown, wide variety of LB-Microsporidia. Future studies should focus on analyzing more specimens for Microsporidia and their geographic distribution in more detail.

Keywords: Barcoding, Prevalence

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[*] Speaker

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Genetic variability of a trematode sporocyst modelled by intraspecific competition

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For parasites, a host represents their source of life. The same or multiple parasite species may simultaneously infect hosts, creating a dynamic environment where each parasite must compete over host resources. However, these inter- and intraspecific interactions may have detrimental impacts on the parasite and host, impairing parasite fitness or endangering the host through overexploitation of the host as a biological resource. Trematode parasites exhibit a complex life cycle that alternates between stages of asexual proliferation (in the first host) and sexual reproduction (in the final host). Miracidium, a trematode in its free-living stage, infects the first intermediate host (usually a mollusc) and transforms into sporocysts (parasitic stage) that can reach up to 20% of the host biomass. It is currently unknown whether this sporocysts biomass results from a single miracidium, which by intraspecific competition demand the use of host resources, or from co-infection. If co-infection is the rule, the trematode invasion of the host tissues might result in a burden that the host might not be able to bear. Using the trematode parasite *Bucephalus minimus* and its first intermediate host, the edible cockle *Cerastoderma edule*, this study aimed to compare the genetic variability of the COI region of *B. minimus* sporocysts within and among cockles. Cockles were collected from two ecosystems with different *B. minimus* prevalence. To amplify the COI region, DNA of five *B. minimus* sporocysts found infecting different host tissues were extracted from a single cockle and repeated in 4 replicates. Genetic variability was analysed through the comparison of COI haplotypes found. The high genetic variability found across sporocysts infecting different cockles, compared to the no variability within the same host, suggests that infection may have been originated from a single miracidium. These findings highlight a possible competition between individuals of the same species over host resources.

Keywords: Bucephalus minimus, Cerastoderma edule, miracidium, COI, genetic variability

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[*] Speaker

Parasites of coastal birds in the north: not a complete story of Notocotylidae (Digenea)

Anna Gonchar * [1]

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This topic started as a taxonomic one but immediately extended from delimiting and distinguishing species to issues like life cycles, host specificity, transmission pathways and intraspecific diversity. Such developments bring intrigue and conceptual challenges even to what first seems as boring family-level inventory.

So, as part of broader studies of Digenea in the White Sea and around, we have been dealing with the family Notocotylidae for over a decade. This research involved sampling from snails (rediae and cercariae) and birds (maritae) in northern coastal ecosystems and versatile analysis of this material. The analysis relied on morphological descriptions (live observations, whole mounts, SEM, confocal microscopy) - and was supported by sequencing genetic markers (rDNA and mitochondrial genes). We even ran one behavioural experiment. All these studies were performed in a context of life cycles and host identities.

So how did these efforts pay off? For now it is a ”more questions than answers” outcome, but estimation of notocotylid diversity has nevertheless advanced. Within the study region, and confined to the marine or brackish environment, we have faced at least 10 species of Notocotylidae. For some of them, we summarized details of life cycles, hosts and phylogeography, and described fine morphological features. For other, only single elements of the puzzle are known so far.

Notocotylid cercariae are very uniform, but at times they are more likely to be distinguished than maritae. The currently accepted taxonomy appears so far from reflecting the evolutionary relations within the family that revising genera becomes a dreadful task. One viable idea could be to look for patterns in the phylogenetic position of notocotylids' hosts - more likely intermediate, but maybe also final. The modest case of the family Notocotylidae contributes to overall understanding of trematode evolution.

Keywords: Digenea, bird parasites, life cycle

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*Speaker

Variability and distribution of parasites, pathologies and their effect on wild mussels (Mytilus sp) in different environments along a wide latitudinal span in the Northern Atlantic and Arctic Oceans

Denis Benito *† [1], Dragana Paleček , Xabier Lekube [1], Urtzi Izagirre [1], Ionan Marigomez [1], Benat Zaldibar [1], Manu Soto [1]

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Histopathological examination in mussels can provide useful information for the diagnosis of ecosystem health status. The distribution of parasites in mussels can be conditioned by several environmental factors, including mussels collecting sites or the presence/absence of other species necessary to complete the complex life cycle of certain parasites. Thus, these variables could not only govern the parasitic burden of mussels but also the presence of pathologies associated to latitudinal gradient is clearly observed in

Keywords: Mytilus, histopathology, distribution, parasites, confounding factors

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*Speaker

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Rhabdocoel flatworms inhabiting marine invertebrates as models for evolutionary patterns associated with the acquisition of endosymbiosis

Marlies Monnens , Tom Artois , Maarten P. M. Vanhove * [1]

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The transition from a free-living lifestyle toward a permanent association with another, non-related species is a large evolutionary step for any organism, reflected in huge changes in body plan. Also at the genetic level, symbiosis has large effects: for instance, a parasitic lifestyle is often associated with rapid and profound genetic changes. It is however unclear whether such phenomena occur in symbiotic species of all organismal groups alike. To test this, we studied mitogenome evolution in three taxa of endosymbiotic flatworms (Umagillidae, Graffilidae, Pterastericolidae, all belonging to Rhabdocoela) infecting marine invertebrates.

We assembled 43 new rhabdocoel sequences, providing the first mitochondrial genomes of endosymbiotic turbellarian flatworms. Interspecific comparison revealed a high degree of mitogenomic variability between rhabdocoels, but nucleotide diversity patterns were similar between endosymbiotic and free-living species. We did not find conclusive divergence rate differences. We report numerous gene order rearrangements: indeed, even among congeners, gene order is not fully conserved. *Atp8*, until recently assumed absent in flatworms, was putatively annotated in several sequences. Selection pressure was tested in a phylogenetic framework and, for several protein-coding genes, is shown to be significantly relaxed in endosymbiotic rhabdocoels as compared to their free-living counterparts. For umagillid flatworms, co-phylogenetic analyses suggest a host switch from sea urchins to sea cucumbers.

This large degree of undiscovered (mito)genomic plasticity in rhabdocoels indicates this phenomenon is widespread in flatworms as a whole and not exclusive to the better-studied neodermatans. Our study multiplied the mitogenomic and other genetic resources available for this understudied assemblage of marine helminths, and provides the basis to further study molecular evolutionary changes that accompany the transition to a parasitic lifestyle.

Keywords: echinoderms, endoparasites, Graffilidae, molluscs, Pterastericolidae, Umagillidae

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*Speaker

Living in periwinkles: Large scale distribution and abundance of the ciliate Protophrya ovicola

Andreas Waser * [1], Lotte Geerlings [2], Boukje Heidstra [2], Roger Butlin [3], Sean Stankowski [4], Kerstin Johannesson [5], Pieternella Luttikhuizen [2], April Blakeslee [6], David Thieltges [2]

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Some groups of ciliates specialized to live in or on other organisms. Quantitative data on their spatial distribution, frequency of occurrence as well as the range of organisms inhabited are often not well known. In order to investigate the distribution and prevalence of the presumably parasitic ciliate *Protophrya ovicola* inhabiting periwinkles, we conducted a field sampling in autumn 2017 at 20 locations from seven regions (France, the Netherlands, Sweden and the United Kingdom) along the shorelines North East Atlantic. In addition, we present a comprehensive data set of *P. ovicola* found in the rough periwinkle *Littorina saxatilis* from the North West Atlantic. We found *P. ovicola* in all seven regions and in four species of periwinkles investigated. Our results indicate a wide spatial distribution of the ciliate within the North East Atlantic and a wide range of *Littorina* species being inhabited. Although highest frequency of occurrence and abundance were observed in females of *L. saxatilis*, where *P. ovicola* inhabits the brood pouch of the live-bearing snail, also the mantle cavities of males of *L. saxatilis* and of females and males of the other three species were inhabited by the ciliate. The ciliate inhabits *L. saxatilis* with a higher prevalence in the North East Atlantic than in the North West Atlantic. Given the broad distribution and relatively high frequency of occurrence of *P. ovicola*, further research into the potential effects on inhabited snails is warranted.

Keywords: ciliophpora, gastropods, marine, intertidal

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[*] Speaker

The geographic distribution of Marteilia pararefringens along the Norwegian coast

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Norway represents the northernmost extant of any known *Marteilia* species. *Marteilia pararefringens* was first discovered in an oyster lagoon on the Norwegian west coast in 2016 where it showed varying levels of infection in the local mussel *Mytilus edulis* population. The discovery was puzzling as no known infections of any *Marteilia* sp. have been detected in neither mussels nor oysters along the Norwegian coast since the active surveillance program for bonamiosis and marteiliosis was instated in 1995.

Seemingly isolated to the unique heliothermic environment found in the lagoons, an extended survey was undertaken along the southern and western Norwegian coast to elucidate the distribution of this parasite. Sampling sites were chosen based on three criteria: (1) part of former networks of oyster growers, (2) not part of an oyster network but actively used in oyster/mussel rearing, or (3) not used in any aquaculture, but with a similar heliothermic profile. A total of 26 sampling sites were included in the study. 48 mussels per site were sampled for PCR and histology.

The results indicate that the parasite has a greater distribution along the Norwegian coast than was previously realised. Since its original discovery in 2016, we have found the parasite in an additional four sites, three of which were connected to the original discovery by direct movement of animals and equipment and/or by being geographically close by. The fourth site share no connection with the original discovery and are geographically far apart. It is unlikely that the parasite has spread to this site through direct movement of material from the original site. On-going work focus on the presence of potential intermediate hosts (planktonic copepods) and analyses of potential spreading mechanisms. Genetic analyses are necessary to study whether the affected sites inhabit *M. pararefringens* with the same origin.

Keywords: Marteiliosis, marteilia pararefringens, Norway, oyster lagoon, mytilus edulis, mussel

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*Speaker

EEPOD - Evolution And Ecological Interactions Of Subtidal Gastropods And Their Digenean Parasites – A Project Overview

Hildur Magnúsdóttir *† [1], Árni Kristmundsson [1], Snæbjörn Pálsson [2], Zophonías O. Jónsson [2], Erla Björk Örnólfsdóttir [2]

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[2] Faculty of Life and Environmental Sciences, University of Iceland – Sturlugata 7, 102 Reykjavík, Iceland

Coevolution of parasites and their hosts is an important driver of biodiversity and evolutionary ecosystem dynamics. Despite their importance across the biosphere, research and conservation of parasite biodiversity is sparse, particularly in aquatic systems. This has resulted in a lack of knowledge on how to prevent and deal with ecological chain reactions wherein species of parasites go extinct due to the loss of a single host species, as a result of habitat destruction and climate change for example.

Digenetic trematodes are among the most ubiquitous and numerous parasitic worms and have at least a 200-million-year evolutionary relationship with gastropods. In marine ecosystems, digeneans depend on gastropods at least as one of their intermediate hosts; among them the large, long-lived whelk from the Buccinoidea superfamily (order Neogastropoda). Digenean diversity in buccinid gastropods in the Northern Hemisphere has been studied to some degree, particularly in *Buccinum* and *Neptunea*, while this information on other genera such as *Voluptosis* and *Colus* is virtually lacking in current literature.

In the project introduced here, co-evolution and diversity of a range of North Atlantic and North Pacific Buccinoidea species and their digenean parasites will be addressed based on a combination of host phenotypic and genotypic data as well as parasite community composition, parasite prevalence, and host-parasite co-phylogeny.

To begin with, *Buccinum undatum* L., 1758, the type species of the *Buccinum* genus, will be used as a model system for the development and validation of mollusc-relevant ecological parasitology and evolutionary ecology techniques. The focus of the project will then be expanded to encompass other species from the Buccinoidea superfamily with the objective of establishing the ecological and evolutionary relationship between digenean parasites and their buccinid hosts.

Keywords: Cophylogeny, Coevolution, Digenea, Biodiversity, Intermediate host, Population Ecol-

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*Speaker

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ogy, Buccinoidea, Ecological parasitology

Ecology And Effects Of Digenean Infections In The Common Whelk Buccinum Undatum – A Case Study From Breiafjörur, Iceland

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Parasite community composition and prevalence in the host is determined to a great extent by the population connectivity and life-history strategies of the host species. In the bay of Breiafjörur, West Iceland, *Buccinum undatum*, the type species of the *Buccinum* genus (superfamily Buccinoidea) serves as an ecologically important predator, prey and parasite host in this biodiverse area. The complexity of food webs in the bay, as well as the topography of the habitat, creates an intricate system of drivers of local adaptation and polymorphism in *B. undatum*, a species typified by variable life-history traits and morphology across the North Atlantic.

In the current study, *B. undatum* in Breiafjörur was used as a model system for the relationship of digenean prevalence to buccinid host life-history traits, body condition, shell morphology and population genetics, as well as environmental variables in the bay. The study was based on two datasets collected by 1) monthly sampling of whelk in 5 areas in a N-S transect of Breiafjörur for a 1 $\frac{1}{2}$ year in 2007-2008 with N $\approx$ 10,000 individuals; 2) a single sampling effort at 59 sites along the coastline of Breiafjörur in 2007. Parasite prevalence was determined based on gross clinical signs. Environmental variables considered were latitude, longitude, depth and substrate type. Host life-history traits taken into account were sex, sexual maturity, shell height and age. Shell morphology was based on traditional morphometrics of shell and aperture, and population genetic information consisted of data on microsatellite, mtDNA and SNP variation. Body condition was estimated based on the ratio of digestive gland weight to eviscerated weight of the snail.

Results from the study will be discussed in the context of how digeneans in *B. undatum* affect the host species and to what extent the fine-scaled population ecology of the gastropod host is reflected in the geographic prevalence of digenean infections in the area.

Keywords: Parasite prevalence, Parasite ecology, Digenea, Buccinoidea, Population ecology, Environmental variables

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*Speaker

With a pinch of salt: the fish gill, a surface of exchange for parasites

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Large-scale patterns of species diversity suggest that stability facilitates speciation. Conversely, fluctuating environments are expected to counteract speciation in host-parasite systems. Monogenea (Platyhelminthes, Neodermata) is a group of obligate flatworm ectoparasites living mostly on the gills and skin of fishes. Monogenean gill parasites are exposed to the aquatic environment which can be highly variable in oxygen and salinity levels. In addition, they are directly exposed to the environment of the fish gill, a continuously adapting organ, due to its physiological functions.
While lates perches (Actinopterygii, Latidae) host various monogenean flatworms in the marine and estuarine environments of the Indo-Pacific region, only a single species, *Dolicirroplectanum lacustre* (Monogenea, Diplectanidae), infects the gills of African freshwater lates perches.

These contrasting patterns of speciation on an intercontinental scale across various aquatic habitats provide the ideal study system to investigate the influence of environmental variability on host-parasite speciation.

Thus far, we have investigated the population-level diversification of *D. lacustre* across several African lakes, where high levels of phenotypic plasticity have been revealed.
In order to compare the level of diversification in the parasites with that of the host, we have started the delineation of host units in African basins through morphometrics and geomorphometrics. With the aim to relate the levels of diversification to the stability in the environment of the fish gill, we will quantify the level of gill stress. Fluctuating asymmetry will be investigated using 3D CT scans, and using qPCR, ratios between mitochondrial and nuclear markers will be determined from gill tissue. We will contrast the resulting patterns of diversification in *D. lacustre* with the divergence of its marine congener *Dolicirroplectanum penangi* and the diplectanid *Laticola latesi* coinfecting Indo-Pacific latid *Lates calcarifer*.

Keywords: Monogenea, Host parasite interaction, Gills, Phenotypic plasticity

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*Speaker

Molecular identification of trematode cercariae concurrently found in Manila clam Ruditapes philippinarum on the west coast of Korea

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In Northwest Pacific, at least three different species of trematode cercariae (i.e., *Cercaria tapidis*, *C. pectinata,* and *Parvatrema duboisi*) have been known to infect Manila clam *Ruditapes philippinarum* inhabiting fine sediments in the shallow to intertidal zones. According to the latest study, 5.4% of the clam population in the tidal flat on the west coast of Korea are infected by the trematode cercariae, and 32.4% of the infected clams fail to reproduce in the peak of spawning season. Despite this alarming status, species of the trematode cercariae found in the clam population in Korea have only been tentatively identified through morphological observation. Accordingly, this study aimed to identify these three cercariae species and reveal phylogenetic relationships using molecular analysis. Phylogenetic analysis of ribosomal DNA (rDNA) gene sequences from *C. tapidis*, *C. pectinata*, and *P. duboisi* indicated that only *P. duboisi* in the family Gymnophallidae is currently an accepted species. On the other hand, *C. tapidis* was not comparable to any sequence registered in NCBI, and *C. pectinata* showed 99.9% similarity to the sequence of *Bacciger bacciger*, previously reported from the wedge clam *Donax trunculus* in France. Therefore, we suggest *C. pectinata* be synonymized with *B. bacciger* in the family Baccigeridae. Given that *C. tapidis* have not been observed elsewhere in Europe and America,

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this species is believed to be endemic in Northwest Pacific region.

Keywords: Trematode cercaria, Manila clam, Ruditapes philippinarum, Molecular phylogeny

Spatio-temporal variation of Perkinsus olseni infection in Manila clam Ruditapes philippinarum distributed along the coast of Korea

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Manila clam *Ruditapes philippinarum* is a dominant benthic animal occurring on sandy-mud tidal flats on the west and south coast of Korea, and this clam inherently harbors a high level of *P. olseni*. We investigated patterns in *P. olseni* infection intensity along a 400 km latitudinal gradient on the west and south coast to test whether the infection level varies spatially and seasonally. In 2019, the adult clams were collected from 17 sites on the west coast and 7 sites on the south coast in spring (May) and fall (September). Histology and gill RFTM assay revealed that the infection prevalence of the clams from the west coast was 89.1%, with the mean intensity of 2.1×106 ± 3.2×106 cells/g gill tissue. On the south coast, the infection prevalence was higher with 94.5%, with the mean intensity of 3.1×106 ± 3.8×106 cells/g gill tissue, indicating that the level of infection varies spatially. The overall mean infection intensity was higher in fall (2.5×106 ± 2.8×106 cells) than in spring (2.3×106 ± 3.2×106 cells). In addition, the discrepancy of the infection intensity between the west and south coast was more remarkable in spring than fall, as the infection intensity was 1.7×106 ± 2.1×106 (west coast) and 3.7×106 ± 4.6×106 cells/g gill tissue (south coast) in spring, while the intensity was 2.4×106 ± 2.6×106 (west coast) and 2.5×106 ± 3.0×106 cells/g gill tissue (south coast) in fall. These results imply that the higher

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sea surface temperature on the south coast may play a role in the elevated level of *P. olseni* infection, while this effect is masked in fall due possibly to post-spawning stress of the clam.

Keywords: Perkinsus olseni, Manila clam, Ruditapes philippinarum, spatio, temporal variation, South Korea

First study on Gyrodactylus (Monogenea: Gyrodactylidae) in Morocco, with description of a new species on cyprinids (Actinopterygii: Cyprinidae)

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Monogenean flatworms are mainly parasitic in lower aquatic vertebrates including fish, anurans and chelonians. *Gyrodactylus* is one of the 23 genera of Gyrodactylidae, with 19 viviparous genera and four oviparous genera. With only 40 species described, the total number of *Gyrodactylus* species described from African freshwater fish still remains low. As a result, the known species represent only a fraction of the expected species richness of *Gyrodactylus* in Africa. Only three *Gyrodactylus* species have been described from small African cyprinids, all belonging to *Enteromius*, namely; *G. ivindoensis* Price & Gery 1968 from *Enteromius* cf. *holotaenia* in Gabon, *G. kyogae* from *E. neumayeri* and *E. perince* Paperna, 1973 in Uganda and *G. paludinosus* from *E. paludinosus* in South Africa. No single study has documented members of *Gyrodactylus* in Morocco. The current study focuses on parasites belonging to *Gyrodactylus* isolated from *Luciobarbus pallaryi* and *Luciobarbus ksibi.* A total of 738 cyprinid specimens were collected and examined for infection with *Gyrodactylus.* 26 *Gyrodactylus* individuals were isolated from these hosts. 12 were morphologically characterized, infecting *Luciobarbus pallaryi* having (11 parasite specimens) and *Luciobarbus ksibi* (a single parasite specimen). The low number of specimens of *Gyrodactylus* recorded may be an underestimation due to the fact that only the gills were examined. Morphological and morphometric observations suggest a species new to science. It differs from *G. kyogae*, *G. ivindoensis* and *G. paludinosus* by having a larger hamulus which has long roots, a larger ventral bar with antelateral processes, and a male copulatory organ having one principal spine and six smaller spines. In view of the importance of the cyprinid-monogenean system in studying the aquatic biodiversity and biogeography of North Africa, the present study is a substantial contribution to the parasite species inventory of these fishes.

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Keywords: Gyrodactylus, phenotypic plasticity, new species, Luciobarbus, Cyprinidae

Amphipods as key reservoirs of micro-eukaryotic parasites, a spatial and temporal analysis

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Amphipods represent a common and ecologically relevant constituent of the macrobenthic community in coastal ecosystems around Europe; as such, they bear great potential as hosts for a significant number of parasites in the aquatic environment. However, the symbiotic community associated with taxa within this crustacean order remains largely unexplored, just like its possible role as reservoirs for pathogens of commercially relevant shellfish species. In this study, the populations of amphipod genera *Orchestia*, *Gammarus* and *Echinogammarus,* which are amongst the most common and widely distributed in the North-East Atlantic, were histopathologically, ultrastructurally and molecularly investigated for the presence of protist parasites. In total, 1,832 individuals were collected between April 2016 and September 2017 from different coastal locations around South-West England, including Weymouth's seashore and the Dart, Tamar, and Camel estuaries. Our results show that amphipods hosted a considerable number of micro-eukaryotic parasites from lineages as diverse as Ciliophora, Apicomplexa, Microsporidia, Endomyxa, Syndiniales, Oomycetes, or Filasterea. While the most prevalent, ciliates and gregarines, emerged mostly as ecto- and endo-comensals, symbionts belonging to the other protist lineages appeared to be manifestly parasitic. As some of these organisms belong in well known lineages of pathogens, not only their phylogenetic position but also the tissues they target and infection dynamics were investigated to infer possible life-cycles. The prevalence-based PCA of the infections caused by these organisms showed a marked temporal variability, with microsporidian and paramyxid infections occurring predominantly during summer, and haplosporidian, syndinian, and filasterean parasitizations taking place in spring. The spatio-temporal analyses (PCA, NMDS) comparing the different coastal locations studied, indicated a higher parasitic load in estuaries than in more exposed seashore habitats regardless of the season. In summary, our results show that amphipods constitute an overlooked reservoir for known and novel protist parasites, as well as a hotspot for the detection of hidden environmental diversity of parasite-rich protist clades.

Keywords: Protist, Symbiosis, Microscopy, Ultrastructure, Phylogeny, Spatio, temporal variability, Rhizarian, Alveolate, Stramenopiles, Opisthokonts

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*Speaker

The Persian Gulf: a hotspot for trematode diversity?

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Background and aims: Climate change is fundamentally altering the ocean ecosystems, resulting in decreased ocean productivity, altered food web dynamics, reduced abundance of keystone species, shifting species distributions, and a greater incidence of diseases. The Persian Gulf is considered one of the most anthropogenically impacted regions known for its strong seasonal fluctuations of environmental conditions. Despite this, the Gulf supports a diverse and endemic fauna. The intertidal horn snail *Pirenella cingulata* (Gmelin, 1791) (Cerithioidea) is one of the most abundant and important keystone species in the coastal ecosystem that is known for its wide range of tolerance to both, temperature and salinity. However, our knowledge on the diversity of the horn snail's parasite fauna is very scarce. Therefore, we carried out a comprehensive survey assessing its trematode diversity along the coast off Iran.
Methods: Larval trematodes recovered were examined from nine locations along the cost of Iran and genetically characterised with multiple genetic markers which were further used to infer species identities and conduct family-wide phylogenies.

Results: Diverse trematode fauna of a total of 30 species were recovered from *P. cingulata* off Iran. Matching sequence data led to the elucidation of four life-cycles. Higher overall prevalence of infection was detected along the northern coast which is characterised with lower temperature and salinity ranges.

Conclusions: Here, we provide the first comprehensive characterisation of the digenean diversity in the horn snail *P. cingulata* and expand on trematode life-cycle knowledge by elucidating their first intermediate host. Our study highlights the importance of molecular systematics in the assessment of larval trematode diversity and their life-cycle elucidations and comprises an important baseline to build a framework to model host–parasite dynamics over time.
This study was supported by "Studienstiftung des deutschen Volkes" and the NRF Korea (# 2021H1D3A2A02081767)

Keywords: Trematoda, Perian Gulf, Pirenella cingulata, Cerithioidea

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Nasitrema spp. infections: a common culprit in finless porpoise standings in the Western Pacific

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Background and aims: The narrow-ridged finless porpoise, *Neophocaena asiaeorientalis sunameri*, is an endangered species in the Western Pacific. Stranded animals are reported year-round along the western coast of Korea. To date, underlying causes for the narrow-ridged finless porpoise strandings have not been definitively identified. With the exception of the accidental bycatch in fisheries, infections with the trematodes of the genus *Nasitrema*, parasitising in the cranial sinuses and auditory tubes of cetaceans, are known as common cause for the strandings. Here we report on the *Nassitrema*-associated infections in 62 narrow-ridged finless porpoises found stranded along the coast of Korea between 2016 and 2019.
Methods: Species recovered were morphologically and molecularly characterised. Phylogenetic analyses were carried out based on the 28S rDNA and mt *nad*3 sequence data.

Results: Two species, *N. spathulatum* and *N. sunameri* were recovered in 34 narrow-ridged finless porpoises (overall prevalence = 54.8%). Co-infections were found in 14 of the examined individuals. The phylogenetic frameworks: (i) supported the sister-species relationships between the two *Nasitrema* spp., and (ii) led to the re-identification of six published isolates and re-evaluation of the host-parasite associations of a number of brachicladiids from diverse intermediate and definitive hosts.

Conclusions: Our study provides: (i) the first molecular data for *N. spathulatum* and *N. sunameri*; (ii) the first record of a member of the Brachycladiidae in the East Asian finless porpoise, and (iii) the first record of *Nasitrema* spp. in Korean waters. Our study calls for cautionary approach and highlights the importance of the integrative approach taking into consideration diverse lines of evidence in building a taxonomic hypothesis.
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Keywords: Narrow, ridged finless porpoise, Neophocaena asiaeorientalis sunameri, Nasitrema spp., strandings, Western Pacific

Session 2: Linking parasite detection, disease monitoring and ecology & evolution

Diversity and host range of emerging parasitic protists: the case of the Perkinsea (Alveolata)

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The intensification of global change during this past century deeply disturbed parasitic interaction between hosts and pathogens as reflected in the emergence of new diseases across broad geographic areas. Perkinsozoa is a microeukaryotic parasitic phylum that play a significant ecological role in marine and freshwater environments by infecting key compartment of trophic food webs. Yet, they are a real threat for biodiversity and human activities because most of described parasites are characterised as generalist (broad host range), invasive, pathogenic (leading to mortality event) and having a high phenotypic plasticity potential. In marine environment, three groups were described: the Perkinsidae, the Parviluciferaceae and the Xcellidae infecting respectively molluscs, dinoflagellates and fishes. Conversely only one group were identified in freshwater environment: the Severe Perkinsea Infectious agent, infecting amphibians. In this talk I will discuss across few examples on how molecular methodologies have allowed the discovery of the diversity and the host range of Perkinsea groups in aquatic environments at global and population scales.

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Assessment of the environmental distribution of the protozoan parasite Perkinsus olseni by next-generation sequencing, qPCR and histopathology allows the identification of alternative bivalve hosts

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Perkinsus olseni is a protozoan parasite that infects a wide variety of molluscs worldwide, causing economic losses in the aquaculture sector. Consequently, Perkinsosis has been catalogued by the World Organization for Animal Health (O.I.E.) as a notifiable disease, and international measures have been established to control it (O.I.E., 2019). In the present study, we analysed the spatial and temporal distribution of transmissible stages of *Perkinsus olseni* in an endemic area of the parasite from 2016 to 2018. The pathogen was detected using high-throughput sequencing of the 18S rRNA gene and a specific real-time PCR assay (qPCR) in samples of water, sediment and several bivalve species. Histopathological assays were also conducted on bivalve samples. *P. olseni* was not detected in environmental samples by qPCR; however, eDNA sequencing revealed its presence in both the water and sediment at all sampled points, showing a seasonal pathogen prevalence. As expected, the parasite was detected in clams, but a few cases were also found in mussels and cockles. The presence of the parasite was confirmed in *Cerastoderma edule* by histology and qPCR using RNA to evaluate the presence of proliferative life stages of the parasite. Therefore, this is the first time that *P. olseni* has been found in *C. edule* but with low abundance and infection intensity levels.

Keywords: P. olseni, DNA metabarcoding, eDNA, Real, time PCR assay, Illumina, Bivalves

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Paramyxid parasites infecting a range of decapod crustaceans

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Paramyxids are protist parasites infecting marine invertebrates and causing significant mortalities in their hosts, for example *Marteilia refringens* which has led to mass mortalities in oysters. Paramyxids are a less studied group, and while we have some knowledge of their life cycles, we are lacking detailed information on transmission and host diversity. Several studies have been carried out on amphipods infected with *Paramarteilia orchestiae*, and *P. canceri*, the focus of this study, has been reported from multiple decapod species including brown crab, spider crab and velvet crab. *P. canceri* systemically invades the organs of its host and here, and in previous studies, it has been identified infecting oocytes and spermatocysts, suggesting the possibility for vertical transmission. We investigated *Paramarteilia* species in a range of commercial decapod crustacean species, including velvet crab, spider crab, brown crab, and lobster. Here we present our results for velvet crabs and spider crabs. We examined 30 individual spider crabs following a mortality event, molecularly identifying *P. canceri* in one of these (prevalence of 3%). Our main focus, however, was on velvet crab due to ongoing reported declines in their populations and for this species we carried out two years of seasonal sampling. We confirmed infection by the same species, *P. canceri*, with an average prevalence of approximately 50%. Seasonal infection rates in velvet crab were significantly higher in spring with a similar trend in winter when compared to summer and autumn. Infection rates did not vary significantly with size or between male and female crabs. Our results provide valuable information on this less familiar group of parasites and on the potential for *P. canceri* to negatively affect the health of its crustacean host populations. Findings from this study will inform consideration of parasites within regular monitoring for an ecosystem-based management approach for crustacean fisheries.

Keywords: histology, fisheries, crustaceans

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Molecular approaches as an innovative tool to investigate monogenean host-specificity, using the Sparidae-Lamellodiscus host-parasite system

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From their skin surface to their gastrointestinal tract, teleost fish are parasitized by a large diversity of macro- and microorganisms. Monogeneans (Platyhelminthes) are highly diverse ectoparasites, widely distributed and are often abundant on the fish skin and gills. They have a direct life-cycle and are generally highly host-specific. The establishment of host specificity seems to be regulated at multiple levels during the monogeneans' life cycle. Monogenean eggs hatch into ciliated larvae (oncomiracidia) that are attracted to chemical cues emitted by fish skin. When reaching the host, the larvae lose their ciliature, some of them remain on the skin but most mature ones migrate to the fish gills to develop in adults. Our aim is to investigate the different selection filters that occur at each developmental stage on fish skin and gills. This project focused on a teleost-parasite interaction in the Mediterranean Sea, between Sparidae and their specific monogenean gill ectoparasites from the *Lamellodiscus* genus, where the pattern of host specificity is well-known. To investigate how monogenean host specificity establishes during the infection, oncomiracidia must be characterized, which is nearly impossible using morphological identification methods. We therefore applied a new metabarcoding protocol based on partial 18S rRNA gene and restriction enzymes, to assess parasite diversity on skin and gills of several sparid host species. A high diversity of both expected and unexpected *Lamellodiscus* species was found on each host species, on skin and gills. These results highlighted the strong potential of molecular techniques to investigate how host specificity establishes in monogeneans. The monogeneans' life cycle appeared to be more complex than initially described. The establishment of the adult in fish gills is regulated at multiple levels, from larval host recognition to their capacity to survive and attach permanently to fish gills.

Keywords: Monogenean, Teleost, Metabarcoding, Specificity, Diversity, Host, parasites interactions

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Dynamics of Vibrio aestuarianus in cockles in wild beds of Hauts de France

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Since 2012, significant mortalities of cockles, *Cerastoderma edule*, have been reported in several French wild beds, including wild beds of Hauts de France. During these abnormal mortalities, bacteria belonging to the *Vibrio aestuarianus* species were isolated from dying animals. It was shown that these bacteria isolated in cockles constituted a new subspecies: *Vibrio aestuarianus* subsp. *cardii*. In order to better understand the dynamic of this subspecies and its role in cockle mortality, a monthly monitoring of two age class of two different wild beds (one in bay de Somme and another in bay d'Authie) were performed between 2019 and 2021. It was shown that the bacterium was present in these two beds and affected the different cohorts of cockles (spat/juvenile and adult). This bacterium seemed to develop preferentially during spring and summer but remained present in cockles in winter at low level. *V. aestuarianus cardii* was also found in the sediment and mussels in the vicinity of the cockles only in spring and summer when this bacterium was present in abundance in cockles. The phylogenetic proximity of the different isolates (sediment, cockles and mussels) suggested that during spring and summer, cockles excreted the bacterium in large quantities in the environment and it could be after accumulated in the sediment and/or mussels. It was also shown that *V. aestuarianus cardii* populations were diverse both in terms of genome and virulence. Strains virulent to cockles in experimental pathology were found throughout the year regardless of location and isolation matrix. These strains coexisted in cockle populations with non-virulent strains. More studies will be necessary to understand the characteristics and specificity of virulent isolates and the causes of their development in cockles at certain period.

Keywords: Vibrio aestuarianus cardii, cockles, mortality, diseases monitoring

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*Speaker

Parasitic turbellarians: from invertebrate to vertebrate hosts

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Platyhelminthes provide a high diversity of evolutionary shifts towards a symbiotic way of life. Rhabdocoel flatworms show the highest ecological diversity with multiple origins of an obligate endosymbiotic lifestyle. Although less attention is given to the mostly free living relatives of neodermatans, the endosymbiotic and parasitic lifestyle of turbellarians can give us important insights on the evolution of parasitism in one of the most successful parasitic groups in the animal kingdom.
In the current study, specimens of parasitic rhabdocoels found on gills or skin of different gobiid and coral reef fish hosts in the US and Australia, respectively, were collected. Examination of serial sections and stained whole mounts was followed by whole-genome sequencing.

Infection parameters ranged from 1 to 8 per host individual, with a mean prevalence of 83% (US population). Morphological characterisation suggests the presence of two species of *Paravortex*, representatives of which are typically found in the gut or gills of bivalves. Species of *Paravortex* can be distinguished by the difference in the overall size and position of the embryotic sac with respect to the internal organs. We provide the first molecular data of parasitic turbellarians from vertebrate hosts and elucidate mitogenome level evolution and gene order rearrangements within these rhabdocoels.
Subsequent genome wide comparative analyses will help to reveal common signatures of a symbiotic and parasitic lifestyle across Platyhelminthes. Potentially, studies on free living sister taxa of those flatworms which have adopted a symbiotic lifestyle to various extents could exemplify pathways which may have been adopted by early neodermatans during their evolution.

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Using eDNA-based approach to investigate parasite life cycle: the example of Haplosporidium costale

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The haplosporidian parasite *Haplosporidium costale* also called SSO (Sea Side Organism) was initially reported in Northern America in *Crassostrea virginica.* It was recently reported in France in Pacific oysters *Magallana* (*Crassostrea*) *gigas* showing light mortality. A real time PCR assay was subsequently developed and validated in order to test the presence of *H. costale* in oysters. This parasite, previously considered exotic in Europe was detected in archived samples collected since 2008 either in the context of mortality or field studies. Considering the little information available on this parasite, the new developed PCR assay was used in order to investigate the seasonal development of the parasite in natural oyster populations and its environmental distribution.

Every 3 months over one year, oysters (from natural beds), water, sediment, demersal and macrofauna present around oyster beds were collected in three French coastal zones: Arcachon Bassin, Marennes Oléron Bay and Bourgneuf Bay. Water was filtered in order to sort nano (1-20μm), micro (20-200μm) and meso plankton (> 200 μm).

Real Time PCR allowed the detection of *Haplosporidium costale* DNA in oysters whatever the sampling date and site. However, detection frequency fluctuated between 7 and 67% and the seasonal dynamics was different between sites. Except in two oysters, only late amplification was observed suggesting very low detection level. In contrast to oysters, only one mussel and one cockle among the 575 tested bivalves showed positive PCR results. Over more than 500 demersal samples, two annelid glycera were found positive by PCR. Finally, parasite DNA was detected in some sediment and nanoplancton samples.

This study confirms the presence of the parasite *Haplosporidium costale* in France. Highest detection frequencies were observed in oysters whatever the sampling site and date. Although detection frequencies were high, apparent infection intensities were very low. In contrast to oysters, other bivalve species do not seem to be involved in the parasite cycle. The detection of parasite DNA in two annelid glycera, and some nanoplancton and sediment samples would require further investigation to clarify the interactions between these compartments and *H. costale.*

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Keywords: Haplosporidium costale, eDNA, oyster, Magallana (Crassostrea gigas)

Haplosporidians in European bivalves

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We investigated haplosporidians associated with commonly cultured and fished bivalves from the UK and Ireland, with additional samples from Norway and Spain: the mussels *Mytilis edulis/M. galloprovincialis*, European flat oyster *Ostrea edulis*, Pacific oyster *Crassostrea gigas*, and the common cockle *Cerastoderma edule.* A large proportion of the cockle samples were PCR-positive for a previously published *Minchinia mercenariae*-like lineage, which we describe as a new species: *M. cerastodermae* n. sp. We detected 18S rRNA gene sequence types (18S-types) from *Haplosporidium nelsoni* and *H. costale* in farmed and locally feral *Crassostrea gigas* from a site in southern UK, the recently described *Minchinia mytili* 18S-type associated with mussels, the previously recorded but so far undescribed 'Haplo E', the crustacean-infecting *H. orchestiae*, and sequences corresponding or closely related to *M. tapetis, Bonamia ostreae, H. pinnae, H. pickfordii, H. edule, H. diporeiae,* and relatives of *Urosporidium.* We detected other 18S-types corresponding to previously detected environmental samples, in particular environmental 'lineage D'. In addition we detected eleven novel lineages not previously detected associated with any host species or in environmental samples. Phylogenetic analyses show the relationships of these lineages to known haplosporidians, and to previously detected environmental sequences, providing additional ecological information about the parasites represented by these sequence types. We highlight the implications of increased awareness of parasite molecular diversity for diagnostic assays and surveillance.

Keywords: Haplosporidia, eDNA, host association, Minchinia, Haplosporidium, bivalves, diagnostics

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De novo transcriptome assembly and analysis of the Flat Oyster pathogenic protozoa Bonamia ostreae.

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The flat oyster *Ostrea edulis* is an oyster species native to Europe. It has *declined* to functional extinction in many areas of the NE Atlantic since several decades. Factors explaining this decline include over exploitation of natural populations and diseases like bonamiosis, regulated at the EU and world scales and caused by the intracellular protozoan parasite *Bonamia ostreae.* To date very few sequences information is available for this Haplosporidian species. We present here the first transcriptome of *B. ostreae.* Because this protozoa is not yet cultivable, it remains extremely challenging to obtain high quality *-omic* data. Thanks to a specific parasite isolation protocol and a dedicated bioinformatic pipeline we were able to obtain a high-quality transcriptome for an intracellular marine micro-eukaryote, which will be very helpful to better understand its biology and to consider the development of new relevant diagnostic tools.

Keywords: Bonamia ostreae, RNAseq, Ostrea edulis, parasite, oyster

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Detection and epidemiology of the flat oyster parasite Bonamia ostreae in Lake Grevelingen, the Netherlands

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The oyster parasite *Bonamia ostreae* has been detected in native flat oyster (*Ostrea edulis*) populations of Lake Grevelingen, the Netherlands in 1988 and has established itself in the area over the last three decades. At the time of introduction the population of *O. edulis* was already in decline due to several other causes. However, despite the additional infection pressure of the parasite the flat oyster population seems to withstand and more recently even seems to thrive. There are indications that the flat oyster population in Lake Grevelingen gradually acquired a certain reduced susceptibility for the parasite.

Previous research showed that *B. ostreae* could be detected in flat oysters throughout the year with a peak in prevalence observed in early spring, followed by a rapid decrease in prevalence coinciding with spawning of the oysters. *Bonamia ostreae* could be detected in all weight classes, but the results suggest that the disease especially affected oysters of larger size.

With the recent interest in native oyster restoration programmes in general and the Netherlands in specific our current work focuses on the suitability of Lake Grevelingen oysters as "tolerant" parents for oyster population restoration purposes. Therefore non-destructive sampling methods have been set up and compared with standard sampling methods and more recently, methods for eDNA detection of *B. ostreae.*

Keywords: Ostrea edulis, oyster, parasite, Bonamia ostreae, detection

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[*] Speaker

Potential new species of pseudaliid lungworm (Metastrongyloidea) from two stranded orcas (Orcinus orca) characterised by ITS-2 and COI sequences

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Knowledge about parasite species of orcas, their prevalence, and impact on health is scarce. Only two records of lungworm infections in orcas exist from male neonatal orcas stranded in Germany and Norway. They were identified as pseudaliid nematodes (Halocercus sp.; Metastrongyloidea) which are specific to the respiratory tract of toothed whales, can cause respiratory distress, secondary bacterial infections and bronchopneumonia, and are a common cause of mortality in cetaceans. While prey intermediate hosts were reported in metastrongyloids of marine mammals, there is evidence of direct infections with Halocercus sp. in orcas. Because morphological identification to species level remained impossible due to the fragile structure and ambiguous features, DNA isolations and subsequent sequencing of the ITS-2 (rDNA) and COI (mtDNA) were performed to characterise orca lungworms. COI and ITS-2 sequences of seal and porpoise lungworms were derived to elucidate phylogenetic relationships within Metastrongyloidea. The ITS-2 sequence from orca lungworms was 93% and 72% identical to Halocercus delphinii from common dolphin and Halocercus invaginatus from harbour porpoise, respectively. The COI sequence from orca lungworms showed 85% sequence identity to H. delphinii and 86% identity to H. invaginatus. Nucleotide data from the two analysed loci show sufficient genetic distance to indicate that orca lungworms may comprise a new pseudaliid species. Maximum likelihood (ML) phylogenetic analyses of both ITS-2 and COI loci supported the monophyly of Halocercus with a well-supported clade value of 99 for ITS-2 and 89 for COI analyses. H. invaginatus was resolved as a sister group to the other Halocercus species. The analyses also showed a paraphyletic nature of Pseudaliidae with Parafilaroides gymurus (Filaroiididae) clustering within the clade. Bayesian inference (BI) analyses resolved similar trees as the ML analyses.

The genetic distances between ITS-2 and COI sequences show the fast rate at which mitochondrial DNA accumulates substitutions and the results underline the value of molecular tools for differentiating closely related parasites. Understanding parasite pathogenicity and life history is important to assess health effects on vagile and threatened marine wildlife for conservation purposes.

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Keywords: cetaceans, lungworms, orca, Pseudaliidae, new species, molecular techniques

High-Throughput Sequencing of Environmental DNA as a Tool for Monitoring Eukaryotic Communities and Potential Pathogens in a Coastal Upwelling Ecosystem

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The marine environment includes diverse microeukaryotic organisms that play important functional roles in the ecosystem. With molecular approaches, eukaryotic taxonomy has been improved, complementing classical analysis. In this study, DNA metabarcoding was performed to describe putative pathogenic eukaryotic microorganisms in sediment and marine water fractions collected in Galicia (NW Spain) from 2016 to 2018. The composition of eukaryotic communities was distinct between sediment and water fractions. Protists were the most diverse group, with the clade TSAR (Stramenopiles, Alveolata, Rhizaria, and Telonemida) as the primary representative organisms in the environment. Harmful algae and invasive species were frequently detected. Potential pathogens, invasive pathogenic organisms as well as the causative agents of harmful phytoplanktonic blooms were identified in this marine ecosystem. Most of the identified pathogens have a crucial impact on the aquacultural sector or affect to relevant species in the marine ecosystem, such as diatoms. Moreover, pathogens with medical and veterinary importance worldwide were also found, as well as pathogens that affect diatoms. The evaluation of the health of a marine ecosystem that directly affects the aquacultural sector with a zoonotic concern was performed with the metabarcoding assay.

Keywords: DNA metabarcoding, eukaryote, high, throughput sequencing, eDNA, environment, pathogens

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Peaking prevalence in pinnipeds: cestode Diphyllobothrium spp. infections of harbor and grey seals over more than two decades

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Diphyllobothrium spp. (Diphyllobothriidae) cestodes infect the intestinal tract of pinnipeds in the North and Baltic Sea and can cause intestinal obstructions and inflammation as well as nutritional deprivation. Their multi-stage heterogeneous trophic transmission includes crustaceans and fish as intermediate and transport hosts. By infecting accidental human hosts, *Diphyllobothrium* spp. have become an important emerging foodborne zoonosis. Unfortunately, there are great knowledge gaps on species identification, taxonomy and health effects of marine mammal cestodes. The present study investigates *Diphyllobothrium* spp. prevalence in harbor (n=1,408) and grey seals (n=163) collected within the stranding network along the coast of Schleswig-Holstein, Germany between 1996 and 2020. Cestode prevalence was at 3% in harbor seals between 1996 and 2014. Between 1996 and 2006 only one individual (n=60, prevalence 2%) was infected, however, cestodes occurred more frequently between 2007 and 2014 (prevalence 6%). Between 2015 and 2020, cestode infections in harbor seals showed an overall prevalence of 17%. Infections occurred significantly more often in pups and yearlings than in perennials. No sex-related differences were observed. In grey seals, cestode prevalence was rare (1%) until 2016 but increased to 20% from 2017 to 2020. When comparing *Diphyllobothrium* spp. prevalence of both host species from 1996-2014 (3%) and 2015-2020 (16%), our data shows a striking increase of cestode infections. Changes in environmental conditions, shifting abundances of intermediate hosts as well as anthropogenic stressors could be responsible for this. The results show the value of long-term data sets for monitoring ecosystem changes and highlight the use of parasites as indicators for host ecology. Prospective studies should aim to unambiguously identify the species infecting seals as well as elucidate their life history and pathogenic potential for definitive and accidental hosts.

Keywords: cestode, Diphyllobothrium, emerging diseases, zoonosis

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Developing a molecular detection tool for the digenean trematode parasites infecting the common cockle Cerastoderma edule

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Parasites are major regulation factors of marine populations *e.g.*, affecting host reproduction, fitness or predator-prey interactions, and can even lead to mass mortalities of host populations. Pathogenic species need to be monitored even more so when they can impact a key species of economical value such as the common cockle *Cerastoderma edule.* But effective control requires full understanding of host-parasite dynamics. Optical methods of species detection and identification have their limits. Some congeneric species are difficult to differ from one another, other species are cryptic at early development stages making it difficult to study the temporal variability of their infection dynamics. Our study aims to resolve these challenges by developing a molecular tool for the detection and identification of the different trematode species infecting the common cockle as first or second intermediate host in Europe following an environmental DNA approach. To this end, we developed species-specific polymerase chain reaction (PCR) assays to detect two digenean trematode parasites infecting the cockle at different stages. Aligning the mtDNA cox1 sequences revealed interspecific variation for which species-specific primers were designed and used for the specific amplification of the parasite species *Bucephalus minimus,* present as sporocycts or cercariae in the cockle and *Gymnophallus minutus,* present as metacercariae. First, the primers were tested by PCR and quantitative PCR (qPCR) on pure DNA samples extracted from sporocysts/cercariae or metacercariae of the target species. To ensure specificity of the primers, PCR assays were done with a mix of DNA encompassing 12 trematode species that can be found infecting the cockle in Europe as well as a mix of DNA excluding the target species. PCR settings were modified to enhance primer specificity when necessary. Assays were then tested on cockle tissue identified as being infected by the target species by the classic morphological technique under a binocular microscope. We are now currently working on a protocol to apply these PCR assays on DNA extracted from tissues of an entire cockle.

Keywords: Trematodes, Cerastoderma edule, Parasite detection, environmental DNA, cox1

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Full rRNA arrays differentiate between Marteilia refringens and Marteilia pararefringens and identify new/verify current variable regions of interest for diagnostic markers

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The separate species status of the paramyxid parasitic protists *Marteilia refringens* and *Marteilia pararefringens* has been a topic of debate for the past two decades. The two parasites were originally classified as distinct species before being synonymised into a single species comprising two 'types': *M. refringens* M-type and O-type. The two types were redesignated as distinct species (*M. refringens* and *M. pararefringens*) in 2018 based on consistent differences in longer regions of ribosomal RNA (rRNA) array sequences, but from only a limited number of samples. Here we generate full rRNA arrays using long-range PCR and next generation sequencing (NGS) from a larger number of *M. refringens* and *M. pararefringens* infections spanning the geographical range of their distribution to (1) reinforce evidence that *M. refringens* and *M. pararefringens* are genetically distinct species, (2) demonstrate consistent differences within the current diagnostic regions and (3) determine whether newly revealed variable regions outside of the current diagnostic regions could be used as complementary informative marker regions. Phylogenetic analysis of full rRNA arrays (18S-ITS1-5.8S-ITS2-28S-IGS) provides maximal support for, and separation of *M. refringens* and *M. pararefringens* across investigated geographical ranges. Phylogenetic analysis of the most variable regions of the array also supported the two separate *Marteilia* species. Robust marker regions that delimit *M. refringens* and *M. pararefringens* as two separate species will allow the two parasites to be studied independently from one another to investigate the host preference, pathogenicity, and lifecycle of each parasite.

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*Speaker

Keywords: Marteilia refringens, Marteilia pararefringens, Ascetosporea, parasite diagnostics, species delimitation

Estimating infection levels of Eelgrass (Zostera marina) by Labyrinthula zosterae in north-central California

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Seagrasses are an important and challenged foundation species found around the globe, with their population health threatened by increased disease risk related to climate change. Seagrass wasting disease, caused by the net-slime mold Labyrinthula zosterae, is currently present at low levels in north-central California. Climate change may cause an increase in disease intensity for a native species of seagrass (Zostera marina, eelgrass) in north-central California due to increases in salinity and temperature. These environmental conditions are favorable for the mold, L. zosterae.

My goal is to determine the levels of disease intensity in four key eelgrass beds in each of Drakes Estero Estuary (DE), Elkhorn Slough Estuary (ES), and Morro Bay Estuary (MB) in comparison to current environmental stressors. To achieve this, I calculate the percent of lesion coverage on selected eelgrass blades collected from the four eelgrass beds at each site.

I expect to see a higher prevalence and intensity of seagrass wasting disease in beds in the urbanized MB estuary compared to the protected DE and ES, due to a higher stress environment for the eelgrass in MB. However, preliminary results showed a higher percentage of lesion coverage in DE and ES, the denser sampled locations. Understanding the current state of seagrass wasting disease in north-central California is valuable knowledge for managing eelgrass beds to limit the impacts of the disease.

Keywords: eelgrass wasting disease, climate change, estuaries, climate dynamics, coastal ecology, technology

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[*] Speaker

Portable pathogens sequencing for near-real time mollusc diseases surveillance

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Pathogen surveillance and diagnostic methods are constantly evolving. Sequencing can provide critical information to diagnose diseases and inform control and mitigation strategies by identifying genetically distinct pathogen variants that may have different host reservoir species or geographic distributions. However, most reference laboratories for marine mollusc diseases lack the resources or expertise for sequencing and data analysis.

We developed an easy to use, high throughput in-field mollusc pathogen sequencing suitcase, using the Oxford Nanopore MinION portable sequencer, and set up collaborative tools for data sharing, visualisation and analysis.

Sequencing suitcases were deployed and used by five different shellfish industry actors including, famers, hatchers and veterinary labs during oyster mortality events. Data obtained allowed us to identify agents potentially responsible for mortalities within few days. MoPSeq-DB web-platform references curated genomic data related to mollusc pathogens, gives users opportunities to interactively visualise data and provides integrated analysis tools. The database currently primary focuses on the virus OsHV-1, but will later be completed with other mollusc pathogens such as the bacterium *Vibrio aestuarianus* or the protozoa *Marteilia refringens*.

This project will provide robust bases to unify every sequence-based work related to mollusc pathogens and will offer unprecedented opportunities to carry out monitoring and diagnosis in near-real time.

Keywords: mollusc disease, in field sequencing, data sharing and visualisation, web, platform

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Unanswered questions in the life cycle of Hematodinium perezi, a parasitic dinoflagellate (Syndinea/Syndiniales) in decapod crustaceans.

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Hematodinium perezi is a syndinid dinoflagellate that infects temperate water decapods around the world. It is highly pathogenic and infects the hemal sinuses where it rapidly proliferates, eventually killing its host. In North America, it is a common pathogen in the American blue crab, *Callinectes sapidus*. A related species, *Hematodinium* sp., from the Norway lobster, *Nephrops norvegicus*, was the first species to be grown in vitro (Appleton & Vickerman 1996). Later, *H. perezi* was also grown in vitro (Li et al. 2011). Although much is known about the ecology of these parasite, there remain several unanswered questions about their life cycles. We will discuss differences in the life cycles of these two parasites and indicate research questions that may elucidate different aspects of their life history stages. For example, there are clear signs of sexual reproduction in *H. perezi*, but it remains to be determined where sexual reproduction occurs and in what life history stage. All members in the class Syndinea produce a macro-dinospore and a micro-dinospore in their development, but the function of these spores remains unknown. Separately they could be gametes or different infectious or dispersal stages. Free-living dinoflagellates in other classes typically produce isogamous dinospores that fuse to produce a planozygote that encysts for meiosis. At present, there is no evidence of a cyst stage in *Hematodinium* spp. and the function of the different spore types remains unresolved. In addition, we conjecture that another stage, the arachnoid sporont, may be mis-identified in *H. perezi* and may serve as a site of gamogony. Features of this stage include cells sequestered in a large, vacuolated "cyst" that then undergoes rapid division to produces sporoblasts. Additional life cycle comparisons will be drawn with other taxa in the infrakingdom Alveolata.

Keywords: Transmission stages, life history, crab, lobster, sporogony, gamogony, merogony

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*Speaker

Parasites may contribute but not drive host speciation in Lake Victoria cichlid fish

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Because of potentially strong eco-evolutionary interactions with their hosts, parasites may initiate or enhance host diversification. The adaptive radiation of cichlid fish in Lake Victoria provides a good system to study the role of parasites at different stages of host speciation. Sympatric species of *Pundamilia* cichlids represent several replicate species pairs that vary in their age and extent of differentiation. This allows to test whether parasites play a role in speciation of their hosts, in their differentiation after speciation, or neither. We analysed macroparasite infection in males of *Pundamilia* at 4 islands in southeastern Lake Victoria, in 2 sampling years. Sympatric host species differed in parasite community composition and in the infection levels of some of these parasite taxa. Most infection differences were consistent between sampling years, indicating temporal consistency in parasite-mediated divergent selection. Infection differentiation increased linearly with genetic differentiation. However, significant infection differences between sympatric species were only found in the oldest, most strongly differentiated *Pundamilia* species pair, inconsistently with parasite-driven speciation.

Next, we identified 5 distinct species of *Cichlidogyrus*, a genus of highly specific gill parasites that has radiated elsewhere in Africa. Similar to the patterns at the level of parasite genera, infection profiles of species of *Cichlidogyrus* differed between sympatric cichlid species only in the oldest and most differentiated pair, again inconsistent with parasite-mediated speciation. Thus, a certain amount of genetic differentiation (driven by other factors) may be needed for

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parasite-mediated divergent selection to act and to lead to significant species differences in infection. This suggests that parasites may contribute to host differentiation *after* speciation, but do not initiate host speciation.

Keywords: parasite-mediated selection, diversification, adaptive radiation, host-parasite interaction, Cichlidae, Monogenea

Changes in parasite community structure may elucidate causes for ecosystem decline in Lake Victoria.

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Human-induced environmental changes may influence the host-parasite interactions and may lead parasites to expand their host range (i.e. spillover to novel host species). Lake Victoria, the youngest of the African Great Lakes, is a biodiversity hotspot that experienced drastic anthropogenic changes since the 1950s: multiple invasions (e.g. Nile perch), eutrophication, overfishing. Such ecosystem perturbations occurred simultaneously and led to a rapid decline of biodiversity (halving haplochromine species in few decades) and to an overall reduction in complexity, with consequences also on human health (e.g. emerging infectious diseases).

Although parasites contribute to maintain ecosystem health, it is often overlooked how parasite community structure changes in response to ecosystem changes. We expect that low host specificity and host switches are favoured in disturbed ecosystems (we already found indications for this pattern in cichlid fish of Lake Victoria). We aim to understand if recent changes in host specificity of monogenean parasites in Lake Victoria resulted from a natural state of the lake or if it has been recently induced by human disturbances. We use historical collections to detect recent changes in the structure of fish parasites in Lake Victoria. To disentangle which perturbation (eutrophication, predator invasion) mainly caused such changes, we use a space-for-time approach in which we model parasite shifts across lakes that share parasite species as well as closely related cichlids but that differ in disturbance.

Since perturbations that have occurred in Lake Victoria are also occurring in other ecosystems, we can use the changes in host ranges of parasites as sentinel, to better monitor and hence conserve ecosystem health elsewhere.

Keywords: Anthropogenic changes. Host specificity. Host parasite interaction. Aquatic ecology. One health.

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Increasing the taxonomic resolution of larval cestode identifications: key to gaining insights into the ecology and management of fish species.

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Background and aims: The identification of marine tapeworm larvae remains problematic given the lack of morphological features available for specific identifications. For instance, larvae of the Tetraphyllidea (*s. l.*) have commonly been referred to as *Scolex pleuronectis, Scolex polymorphus* or simply as "tetraphyllidean plerocercoids" (TP) in numerous host-parasite checklists or parasitological surveys. Here, I present two case studies where increased taxonomic resolution using molecular tools provide ecological insights into host ecology or have fisheries management implications. **Methods:** The first case study consists of a survey of 30 red cod (*Pseudophysis bachus*) in New Zealand waters from which were recovered five morphotypes of *"S. pleuronectis"*. Prior to this survey, no Tetraphyllidea (*s. l.*) larvae had been reported from this species. The second case study consists of a parasitological survey of 501 rock cod (*Patagonotothen ramsayi*) collected from the Patagonian Shelf from which were recovered at least four different morphotypes of TP. Previous surveys have reported high prevalence of TP in rock cod. Molecular characterisation using partial 28S rDNA sequence data was used for specific identifications. **Results:** In red cod, the presence of two species of Onchoproteocephalidea (rough skate *Zearaja nasuta* as definitive host) and three species of Phyllobothriidea (two infecting dogfish *Squalus acanthias* as definitive hosts) was confirmed. In rock cod, molecular characterisation of the 224 TP recovered is currently under way. **Conclusions:** *Red cod* - Red cod have been reported from the diet of deepwater sharks, pinnipeds, cetaceans, seabirds, and snoek. However, I suggest that juvenile red cod might be more common in the diet of mesopredatory elasmobranchs than previously reported. Furthermore, red cod might play a significant role in the transmission of cestodes in coastal waters of New Zealand. *Rock cod* - Since TP (as a single operational taxonomic unit) has been identified as a potential biological tag for stock discrimination of rock cod in the southwest Atlantic, improved taxonomic resolution will increase the discriminatory power of analyses and provide more accurate tools for the management of this important marine commercial resource.

Keywords: Scolex pleronectis, Scolex polymorphus, tetraphyllidean plerocercoid, stock discrimina-

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*Speaker

tion, cestode life cycle, 28S ribosomal DNA

Piridium sociabile - the inconspicuous commonplace parasite

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Piridium sociabile (*P. soc*) is an evolutionary unique marine parasite, found in the foot of the common whelk (*Buccinum undatum*). *P. soc.* was described by Ruth Patten (1936) and originally thought to be an apicomplexan parasite. However, recent research has demonstrated that *P. soc.* is most closely related to the photosynthetic free-living chromerids, which are associated with coral reefs, and furthermore a major link in the evolution of parasitism, i.e., between non-parasitic photosynthetic algae and the parasitic apicomplexans. Prior to this project, the original description from the 1930s, remained the sole knowledge of the biology of *P. soc*, except for few reports of its presence. The aim of the project is to determine the geographical distribution of *P. soc.* around Iceland and detect other potential host species.

575 common whelks were collected around Iceland along with 258 indiviuals of 25 mollusc species. The molluscs were dissected and samples analysed using a stereoscope, microscope and histology. DNA was also extracted and sequenced to evaluate the relations between *P.soc* and Piridium like organisms.

The results showed a great abundance and high prevalence of P. soc. around Iceland along with a surprising number of other host species, which are parasitized by *P. soc.* related organisms. This indicates that P. sociabile is a prevalent parasite of the common whelk and has a relatively wide distribution. Furthermore, as an ancient or ancestral parasitic form, it has likely parasitized common ancestors of gastropod species and co-evolved with these hosts during speciation events.

Keywords: Distribution, evolution, speciation

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*Speaker

Confocal laser scanning microscopy for taxonomic studies: A new approach for the order Trypanorhyncha (Cestoda) from Balinese waters, Indonesia

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During recent years the parasite fauna of *Neotrygon caeruliopunctata*, *Rhinobatos jimbaranensis* and *R. penggali* from Bali, Indonesia was sampled for fish parasites. For taxonomic examination of parasites belonging to the cestode order Trypanorhyncha, Confocal Laser Scanning Microscopy (CLSM) was used, in addition to standardized Light microscopy (LM) and scanning electrode microscopy (SEM).
The parasites from three ray species were stained with Mayer-Schuberg's acetic carmine and mounted in Canada balsam. This allowed examination with LM and also with CLSM. Besides the carmine red stained preparations, benzylalcohol and benzylbenzuolat (BABB) clearing was used to examine the mature segments of the worms with CLSM. Additional samples were prepared for and examined with SEM.

Eleven species of the cestode order Trypanorhyncha were found. Among these, two new species were found. Comparison of the different methods demonstrated better visualization of the bothrial pits and especially the armature patterns of the Trypanorhyncha with CLSM. The internal organs within the mature segments could be clearly visualized by using the BABB clearing.

This study demonstrates the beneficial application of CLSM in taxonomic studies of the Trypanorhyncha. We were able to create detailed three-dimensional images of the relevant characteristic morphological details. In particular, the possibility to rotate the resulting images allowed a more detailed description of the armature patterns and characteristic hooks. Compared to light microscopy (single plane), more than 200 planes were imaged and displayed in a much higher resolution. Another advantage of CLSM was the ability to visualize internal structures as well, while the SEM can only visualize the surface (ultra)structures.

In conclusion, application of the CLSM is a valuable complementation to existing methods but cannot replace them. However, it can be developed into a standard technique for taxonomic studies of the cestode order Trypanorhyncha.

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Keywords: Neotrygon caeruliopunctata, Rhinobatos jimbaranensis, R. penggali, Mayer, Schuberg's acetic carmine

A first study of monogeneans parasitizing the gills of catfishes from Lake Tanganyika

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Lake Tanganyika, the oldest among the East African Great Lakes is shared by four countries: The Democratic Republic of the Congo (DRC), Tanzania, Zambia and Burundi. It is one of the world's most important hotspots for freshwater biodiversity. It has a rich and diverse ichthyofauna, especially of fishes belonging to the Cichlidae. Hence, we also expect a large diversity of fish parasites.

Monogenean are a group of ectoparasitic flatworms parasitizing freshwater and marine fish species. In Lake Tanganyika, monogeneans of representatives of Cichlidae, but also of Latidae and Clupeidae were already studied. The non-cichlids of Lake Tanganyika, with a rate of endemicity of 59%, are represented by 75 species belonging to 11 families. Among these families, five (Bagridae, Claroteidae, Clariidae, Mochokidae and Malapteruridae) belong to the order Siluriformes. The aim of this study is to survey and identify, for the first time, the monogeneans parasitizing these catfishes.

A dissection of 35 individuals of catfishes belonging to two families: Clariidae (one species: *Clarias gariepinus*) and Claroteidae (three species: *Auchenoglanis occidentalis*, *Phyllonemus typhus* and *Chrysichthys brachynema*) allowed morphological identification of four species of monogeneans. Of these, three are new to science; two from *A. occidentalis* (already described and in press), one from *P. typhus* (under description). One known species was found: *Gyrodactylus transvaalensis* from *C. gariepinus*, its type host. *G. transvaalensis* is also known to parasitize *C. anguillaris*. This parasite was recorded in South Africa and Senegal (West Africa). Its presence in Lake Tanganyika (East Africa) shows wide geographic distribution similarly to other species of *Gyrodactylus* infecting African cichlids.

Keywords: Siluriformes, Biogeography, new species, East Africa

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New insight into adaptation of the eastern oyster, Crassostrea virginica, to the parasite Perkinsus marinus in the Chesapeake Bay, USA

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Perkinsus marinus and *Haplosporidium nelsoni* are major oyster pathogens of the eastern oyster, *Crassostrea virginica.* Both protozoan parasites have historically caused extensive oyster disease and mortality. However, oyster mortality has decreased since the initial outbreaks of each of these parasites. It is unclear how much current oyster mortality can be attributed to *P. marinus* and *H. nelsoni*, and what the relationship is between parasite prevalence and infection intensity and mortality impacts. To provide insight into the contemporary relationships between infection by *H. nelsoni* and *P. marinus* and oyster disease and mortality, five relays of wild oysters were made from Aberdeen Creek, York River, Virginia, to the VIMS beach on the lower York River, and tracked over the year 2021. Oyster mortality was assessed via box counts, and *P. marinus* and *H. nelsoni* prevalence and intensities via standard histopathology as well as by Ray's fluid thioglycolate method for *P. marinus.* Analyses revealed that *P. marinus* was the primary contributor to oyster mortality, causing about 40% mortality over the year, far below historical highs. In parallel with the field study, infection levels and oyster mortality over the years 1989 to 2021 were analyzed in a linear regression model. Results indicated that both oyster mortality and *H. nelsoni* prevalence have steadily decreased since 1989, however *P. marinus* prevalence and infection intensities have remained relatively high. The reduced mortalities despite the *P. marinus* infections provide further evidence for tolerance adaptation to *P. marinus* in the eastern oyster.

Keywords: Oyster, Perkinsus, Chesapeake Bay, disease tolerance

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Coastal microbiomes in riverine ecosystems of the French coastline: the ROME project

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The Ifremer project named ROME (*Reseau de Microbiologie Environmental Integrée)* aims at evaluating the influence of river inputs on the structuration of estuarine microbiomes and the potential emergence of new risks of microbiological origins for human, aquaculture and ecosystem health.

This project started in September 2020 and is currently deployed in 4 estuarine ecosystems that integrate oyster farms: Veys Bay in Normandy, Brest Bay in Brittany, Marennes D'Oleron in New Aquitania, and Thau Lagoon in Occittania.

The virome, bacteriome and protistome are analyzed from common environmental DNA/RNA samples extracted from both, water samples (fortnightly samples) and adult oyster tissues (monthly samples). eDNA metabarcoding for bacteria and protists and eRNA metagenomics for viruses are used by default to describe the biodiversity of microbiological communities, including parasites and pathogens.

River influence in shaping microbial communities is investigated by comparing one station situated at the river mouths in correspondence of waters submitted to anthropogenic impact through river-off and a second station situated in off-shore waters less impacted by terrestrial inputs. Oyster samples are used as integrator of the microbial site biodiversity, but also to study holobiontic associations, including parasitism, across the different sampled sites.

Preliminary data have shown that different microbial community occur across the in-off shore gradients, differently among sites and according to local river inputs. Some taxa of terrestrial origins (e.g. Fungi) might explain this difference. No RNA human viruses have yet been detected at the studied sites, but a high number of unidentified taxa characterized the coastal virome. Interestingly, known bivalve parasite genera were detected by the metabarcoding approach, including genera that have caused important diseases (e.g. *Haplosporidium*). Other

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genera (*Bonamia* and *Marteilia*), also known to be present in France, have not yet been detected on the basis of the first data.
All result from the ROME projects will be evaluated on the basis of a longer dataset which is in course of acquisition.

MoPSeq-DB: a web-platform to share, visualise and analyse sequence data of mollusc pathogens

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Pathogen surveillance and diagnostic methods are constantly evolving. Sequencing can provide critical information to diagnose diseases and inform control and mitigation strategies by identifying genetically distinct pathogen variants that may have different host reservoir species or geographic distributions. However, most reference laboratories for marine mollusc diseases lack the resources or expertise for sequencing and data analysis. We therefore developed a user-friendly web-application, called MoPSeq-DB.
MoPSeq-DB, is an open-source tool based on the Python web-framework Django. It is deployed through a Docker container, on a dedicated server. Genomes as well as their annotations and variations are stored and organised in a folder architecture designed to make files available to users. Annotation and variation files are parsed and summarised in interactive Javascript graphs using Python and Bash scripts. Then, a pre-built phylogenetic tree, based on all genomes included in the database, can also be visualised and handled.

MoPSeq-DB web-platform references curated genomic data related to mollusc pathogens, gives users opportunities to interactively visualise data and provides integrated analysis tools. The database currently primary focuses on the OsHV-1 virus, but will later be completed with other mollusc pathogens such as the bacterium *Vibrio aestuarianus* or the protozoa *Marteilia refringens.*
This project will provide robust bases to unify all sequence-based work related to mollusc pathogens and will offer unprecedented opportunities to carry out monitoring and diagnosis in near-real time. MoPSeq-DB is, to our knowledge, the first comparative genome browser dedicated to mollusc pathogens. It automates commonly used bioinformatics workflows, enabling convenient and fast data exploration, particularly for non-bioinformaticians, in an intuitive and user-friendly way. It has minimal hardware requirements and is easy to install, host, and update. MoPSeq-DB folder structure enforces systematic yet flexible storage of genomic data of mollusc pathogens, including associated metadata. The platform could easily be declined to other pathogens.

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*Speaker

Session 3: Direct and indirect effects of diseases on marine populations and communities

Insights into long-term interactions between host populations and parasites, environmental change and commercial exploitation, from the Chesapeake Bay oyster disease system

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Direct mortality impacts from marine diseases are perhaps the easiest effects to appreciate. An understanding of broader impacts of diseases on host populations and communities is essential, however, if management of key marine resource species despite diseases is to be effective. In Chesapeake Bay region of the USA, long-term, intensive monitoring of diseases in oyster *Crassostrea virginica* populations, using microscopic analyses providing nuanced insights into infection dynamics and host responses, has generated perspective unique for a major marine disease system. Overexploitation by fisheries likely exacerbated impacts of the emergence of introduced *Haplosporidium nelsoni* in the 1950s. Depletion and fragmentation of host populations, along with reductions in longevity and reproduction, hastened the oyster's decline, while contributing to an altered adaptive landscape for endemic parasite *Perkinsus marinus* that led to a change in its phenotype including a virulence increase. This 1980s emergence of hypervirulent *P. marinus* further devastated oyster populations, but also planted the seed of host recovery: a shift in the timing oyster spawning that may be a key to the present re-expansion of oyster populations. Also critical are developing resistance to *H. nelsoni* and resistance and tolerance to *P. marinus*, all apparent in oyster reproductive output and demographics. Current management of oysters in the region seeks to harness developing disease resistance and the corresponding reproductive and demographic improvements through incorporation of harvest sanctuaries that allow resistant oysters to reach greater ages and fecundities, to more fully exert reproductive advantages.

Interestingly, we may ask whether climate change and the great decrease in oyster populations because of overharvesting and diseases are interacting to produce continued challenges. A continued increase in *H. nelsoni* activity has been hypothesized to relate to eutrophication, to which a dramatic loss in oyster filtration capacity in estuarine systems contributes. Is eutrophication, and specifically the shift from historical benthic production to contemporary pelagic production dominated by dinoflagellates, also producing nutritional and other physiological challenges that exacerbate parasitic diseases?

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*Speaker

Keywords: Oyster, Perkinsus, Haplosporidium, aquaculture, Chesapeake Bay, virulence, resistance, tolerance

Characterization of an emerging apicomplexan parasite in the bay scallop Argopecten irradians irradians

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Since 2019, bay scallop populations in New York have been suffering large-scale summer mortalities resulting in over 90% reduction in biomass. These events were associated with heavy infections by an undescribed parasite. The objective of this research was to characterize this parasite and elucidate factors that regulate disease dynamics. Microscopic and molecular investigations showed that the parasite is an undescribed member of the *Apicomplexa*, with its closest relative being a member of the newly established class *Marosporida.* The parasite, dubbed Bay Scallop Marosporida (BSM), infects and disrupts multiple scallop tissues including kidney, adductor muscle, gill, and gonad. Both intracellular and extracellular stages of the parasite were identified, including sporozoite stages that display structural characteristics of the *Apicomplexa* (e.g., micronemes). Field surveys performed in 2020 and 2021 demonstrated a strong seasonal signature in disease prevalence and intensity, with severe cases increasing as summer progresses before slightly decreasing, likely as a result of the mortality of most heavily infected scallops. Field investigations also showed significantly higher mortality rates in scallop habitats characterized by high temperature and low dissolved oxygen during summer. Laboratory investigations underline higher mortalities in most severely infected scallops exposed to ecologically-relevant high temperature, while dissolved oxygen alone appears to have less effect on disease dynamics. Interestingly, both laboratory and field studies showed contrasted disease severity among different scallop stocks. Overall, our results suggest that BSM infection plays a major role in the collapse of bay scallop populations in New York. In this framework, BSM may synergistically interact with stressful environmental conditions to impair the host and lead to mortality.

Keywords: Shellfish, Scallop, Apicomplexa, Temperature, Genomics

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*Speaker

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Getting into fish brains: Infection and gene expression profiling of a behavioral manipulative trematode

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Parasites usually impact on their hosts at different levels, sometimes altering their behavior to enhance transmission. We studied the trematode *Cardiocephaloides longicollis*, whose metacercariae infect the brain of a variety of fish species, including farmed gilthead seabream *Sparus aurata*. We aim to identify and describe the altered behavior of the fish and relate this to concurrent changes in gene expression and protein profiles.
Different aspects of fish behavior, including vertical distribution, escape behavior and school formation, were investigated in different experiments with control and experimentally infected fish, accounting for infection intensity. Brain tissue, cerebrospinal fluid and metacercariae were collected for RNA-seq and protein analyses. Differentially expressed genes were analyzed in early and mature infection using DESeq2.

The majority of *C. longicollis* metacercariae were located in the tectal ventricle, close to the tectum opticum, which encodes visual stimuli, without causing any tissue damage. However, the sole presence of *C. longicollis* metacercariae seemed to impair host anti-predator and escape behavior, as infected fish were caught more frequently than control fish, and group formation was disrupted longer. Differentially expressed genes and proteins were identified when comparing control and infected fish and in early and mature infections. These were identified as components linked to behavioral changes in other organisms, and with infection and immune evasion strategies.

Transcriptomic and proteomic analyses aided elucidation of the physiological basis of infection-induced changes in host behavior, filling an important gap in our understanding of the molecular basis of fish behavioral responses to digenean trematodes.

Acknowledgments: Czech Science Foundation (20-14903Y).

Keywords: behaviour changes, trematode, fish brain, gene expression

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[*] Speaker

Seal louse and heartworm: an ancient team and its impact on pinnipeds

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Marine mammals serve as a livelihood for a variety of parasites, which show unique morphological and functional adaptions to the amphibious and aquatic lifestyle of their hosts. *Echinophthirius* (*E.*) *horridus*, the seal louse (Anoplura; Insecta) and the heartworm *Acanthocheilonema* (*A.*) *spirocauda* (Spirurina; Nematoda) comprise a unique parasite assembly conveyed to the marine environment. They usually have mild health effects but can cause anaemia and alopecia or arteritis, thrombosis and obstruction in severe cases. *E.horridus* is believed to play an obligatory role as vector for heartworm filariae (*A. spirocauda*) of harbour seals (*Phoca vitulina*). In this study we examined the prevalence of *A. spirocauda* and *E. horridus* in harbour seals (n = 655) and grey seals (*Halichoerus grypus*) (n = 112) between 2014 and 2022 using a unique sample set collected within a stranding network along the North and Baltic Sea coast to analyse time trends and life history traits. Infection of harbour seals with the heartworm *A. spirocauda* was found in 11% (n = 70). The prevalence of *A. spirocauda* varied notably over the eight-year-study period, and showed a significant increase from 4% observed in previous decades. Seal lice were found in 4% (n = 26) of harbour and 10% of grey seals (n = 11). Seal lice prevalence remained relatively low, in line with a previous study in the same area, although grey seals were clearly more often infected than harbour seals. Higher seal lice prevalence but no heartworm infections in grey compared to harbour seals reflect host specificity or different immune traits of seal hosts. There were no sex related differences in infection patterns but a higher prevalence in yearling and young–of-the-year seals, which might reflect vertical transmission patterns or decreased immune function in freshly weaned animals. Histological screening of seal lice revealed larval stages in the hemocoel of lice supporting that seal lice serve as intermediate host and vector of *A. spirocauda.* The increased prevalence of the heartworm *A. spirocauda* over the study period may reflect growing seal populations and higher densities on haul-outs, thereby facilitating transmission by lice vectors. The results underline that parasites are useful indicators for host ecology and ecosystem changes in the North and Baltic Sea.

Keywords: Harbour seals, Parasites, Acanthocheilonema spirocauda, Echinophthirius horridus

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Comparison of the efficacy of a selective breeding programme to increase cockle Cerastoderma edule marteiliosis resistance with that of the natural selection in the inner area of Ría de Arousa

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Infection with the protistan *Marteilia cochillia* led to cockle fishery collapse in *Ría de Arousa* (Galicia, NW Spain) in 2012. Since then, every cockle cohort newly-recruited in the inner area of that ria was destroyed by marteiliosis outbreaks. However, marteiliosis prevalence has progressively dropped in the cockles recruited in that area since 2016 and the survival has augmented, as a result of increased resistance to marteiliosis due to natural selection. Independently, the 2nd generation (F2) of a selective breeding programme (SBP) led by J.M. Fuentes (CIMA) to increase cockle marteiliosis resistance also showed increased resistance.

A common garden approach was implemented to compare the efficacy of that SBP to increase cockle marteiliosis resistance with that of the natural selection. Three broodstocks were formed with cockles from three sources, the shellfish bed of *Noia* (*Ría de Muros-Noia*), where no marteiliosis outbreak has been detected, the bed of *Ariño* (inner area of *Ría de Arousa*), where marteiliosis resistance has increased through natural selection, and the survivors of the SBP-F2 cultured in an affected area. Those cockles were conditioned in the hatchery of CIMA in March 2021, various larvae cohorts from each stock were cultured and, in July 2021, spat were transferred to a raft (outdoor nursery). In September 2021, spat batches from each stock were deployed in two beds of *Ría de Arousa* affected by marteiliosis; mortality and marteiliosis prevalence and severity were estimated periodically.

Cumulative mortality surpassed 80% in the naïve stock (Noia) in both beds just two months after deployment due to heavy marteiliosis (prevalence above 70%). However, cumulative mortality increased much more slowly in the other two stocks in the two beds, ranging from 52 to 71% in June 2022, and marteiliosis prevalence was always below 15%. Significant differences in marteiliosis resistance between the "naturally-selected" stock and the F3 of the SPB were not found.

Keywords: Disease resistance, Selective breeding, Natural selection, Marteilia cochillia, Disease

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dynamics

Another look at disease transmission in marine ecosystems

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By some accounts more than half of the parasites on earth use or transit through aquatic ecosystems. Given this, it is surprising how few studies have examined differences in the disease ecology between marine and terrestrial ecosystems. Marine ecosystems have a higher diversity of host phyla, a greater number of clonal organisms, use free-swimming planktonic larvae, and often have large, open populations when compared to terrestrial ecosystems (McCallum et al., 2004; Poulin et al., 2016). Terrestrial systems have a higher diversity of pathogens that use vertical transmission, often have arthropod vectors, and have more parasitoids than marine systems. Pathogen transmission, host and pathogen density dependence, and host susceptibility are notably different between marine and terrestrial systems. Transmission in particular has evolved along very different modes between systems, largely as adaptations to terrestrial existence (e.g., desiccation, multiple life history stages, and vector-borne dispersal). On the other hand, marine systems are often dominated by suspension feeders (filter feeders) operating at low Reynolds numbers in a viscous fluid environment. Suspension feeding may directly affect pathogen transmission, by directly removing pathogens, or by focusing their transmission to a suitable host. In addition, marine hosts frequently experience high consumer pressure, including natural mortality from cannibalism and intensive, industrialized fishing mortality. Consumer pressure may directly affect populations of susceptible and infected hosts, either by removal of susceptible juveniles or by removal of refractory, cannibalistic adults (fishing). These biotic and anthropogenic factors are closely aligned with marine systems; yet, with the exception of suspension feeding (Burge et al. 2016), they have received little theoretical development in terms of their potential effects on disease transmission and ecology.

Keywords: terrestrial ecosystems, marine ecosystems, parasite transmission, suspension feeding, effects of fishing

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*Speaker

Parasite infection of prawns leads to reduced responsiveness and activity

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We investigated prawn responsiveness to a stimulus and subsequent activity for prawns infected with a bopyrid isopod parasite compared to uninfected prawns. Many bopyrid isopod parasites settle in the gill chamber of decapod crustaceans and feed on host haemolymph. The parasites occupy a large area and lead to a bulge in the carapace of their host. Such infections occur at relatively high prevalence in the common prawn *Palaemon serratus* due to the parasite *Bopyrus squillarum.* In this study prawn responsiveness was examined by poking individual prawns with a plastic rod until an escape response was triggered and the number of pokes required before moving was recorded as an indicator of responsiveness. Prawn activity was measured based on the time spent moving following the initiation of a response. Our results show that bopyrid infection affects both prawn responsiveness and activity, with infected prawns being less responsive (requiring more pokes to move), and less active (moving for less time) in comparison to uninfected prawns. These behavioural changes likely impact host defence mechanisms and, as a result, survival of infected prawns. Future studies could examine prawn responsiveness and activity following exposure to natural stimuli, such as predators, to gain additional insight into the effects of parasite infection in this host-parasite system.

Keywords: behaviour, energy, crustacean, shrimp

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*Speaker

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Suspicion of disease-dependent mass mortality of cockles in Arcachon Bay (France)

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The common cockle (*Cerastoderma edule*) is an important bivalve species along the north-east Atlantic coast in terms of ecological and socio-economic issues. In banc d'Arguin (Arcachon Bay, France), cockle biomass has always displayed large interannual fluctuations. However, in 2018, cockles underwent mass mortalities and never recovered. Between autumn 2017 and summer 2018, the adult density dropped from 140 to 20 ind/m^2. Besides, 2018's recruitment didn't sustain and cockles had completely disappeared in winter 2019. Concomitantly, cockle growth started to stagnate in spring 2018. During this period (Autumn 2017 to Autumn 2018) a multi-diseases seasonal monitoring was performed on 2016's and 2017's cohorts. Concerning macroparasites, trematodes were dominant with several species involved. Among these species, the ones using cockles as first intermediate hosts are reputed as deleterious. Their prevalence increased from 3 to 8%. At the same time, adult cockles suffered from several other diseases/parasites like granulomatosis (with a maximum of 33% in adults), disseminated neoplasia (between 3 % in juvenile cockles and a maximum of 20% in adults), *Nematopsis* disease (> 60% in juveniles and adults) and *Rickettsia*-like (more present in winter with more than 40% in juveniles and adults). Infiltration concerned half of investigated cockles. In parallel, the expression of 28 genes involved in stress were analysed and, along with stunt shell growth, suggest that cockle mortality was certainly related more to a relatively slow process (infection) than to rapid events like high predation or sediment movements.

Keywords: Cerastoderma edule, Mortality, Multi disease, Parasite/Host dynamics

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*Speaker

Natural Sampling of Phytoplankton and Parasitoid Abundances in Cala Santanyí

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Harmful algal blooms (HABs) are algal blooms which can have negative impacts on the environment, human activities and human health. In the Mediterranean, HABs which occur during the touristic summer months are usually caused by dinoflagellates, including some which produce toxins. While many studies have looked at the causes of HABs, fewer have looked at how HABs terminate. One possible reason for the termination of HABs is due to parasitoid infections in dinoflagellates. Cala Santanyí is a touristic beach in Mallorca, Spain, which has experienced HAB-causing events annually. As part of a larger project understanding the biological and biophysical mechanisms of parasitoid-dinoflagellate interactions, ongoing observations of the microplankton community (5–100 um), physical parameters and parasitoid abundances are being measured at this cala, as both HAB-causing dinoflagellates and parasitoids have been observed here. The purpose of these ongoing observations is to measure the year-round abundance, composition and prevalence of dinoflagellates and parasitoids in the Cala, and what physical and/or biological factors influence them. These observations will be combined with future microfluidic experiments exploring individual parasitoid-dinoflagellate interactions to develop a model to predict parasitoid infection rates in dinoflagellate communities. Here we present preliminary observations of phytoplankton and parasitoid abundances from data collected from June 2021 to September 2022.

Keywords: Dinoflagellates, HABs, Mediterranean, parasitoids

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*Speaker

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The effect of the parasitic copepod, Sarcotretes scopeli, on its mesopelagic fish host, Benthosema glaciale

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Background and aims

The mesopelagic fish, *Benthosema glaciale* (Reinhardt, 1837), or glacier lantern fish, is one of the most abundant fish species in Europe and plays an important role in the food-web of marine ecosystems. In west Norwegian fjord systems, *B. glaciale* is commonly infected by the parasitic copepod, Sarcotretes scopeli (Jungersen, 1911). The effect of parasitic infections on the biology of *B. glaciale* is almost unknown.

The prevalence of S. scopeli on *B. glacial* populations in different western Norwegian fjord systems will be mapped and for the first time will the parasites effect on the condition of the individual fish be investigated in detail.

Methods

Samples were collected on board of several larger research vessels between 16.02.2021 to 28.09.2021 from four west Norwegian fjord systems. CTD data were routinely registered in parallel with the physical samples.

The effect of infection on gonadosomatic, hepatosomatic and heartsomatic indices, Fulton's condition factor and host growth were studied separately for the host sexes. Furthermore, the site-specificity of *S. scopeli* on host exterior and interior, and the relative parasitic volume in relation to the host were investigated.

Micro-Computer tomography (Micro-CT) was performed to document the *S. scopeli*'s way through the tissue of the host.

Ageing was performed using otoliths infected and uninfected individuals.

Results

Prevalence of *S. scopeli* on the *B. glaciale* in the investigated fjords ranged from 1,76 – 4,76% and was not affected by the dissolved oxygen concentration. *S. scopeli* was primarily observed attached dorsally on the fish exterior, strictly anterior for the dorsal fin.

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*Speaker

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The relative parasitic volume in relation to the host showed that *S. scopeli* greatly reduces the gonadosomatic index for both host sexes and infected fish were found to be in poorer condition than were uninfected ones in all investigated fjords. Surprisingly, infection did not seem to compromise the growth rate.

Conclusion

Overall, the data suggested that *S. scopeli* acts as a parasitic castrator on the host; that reduced oxygen concentration might not affect the host susceptibility to infection; and that the parasitic attachment site is randomly distributed in the host internal, while the parasite has a high affinity for dorsal attachment on the host external.

Keywords: Parasitic crustaceans, parasitic castration, host control, micro_CT

Trematode infection and host population dynamics under global warming: an agent-based model approach

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The transmission pathway of trematodes to their hosts has been widely experimentally explored, including testing critical environmental drivers such as temperature. However, due to its complexity, models examining the details of this mechanism and its impact on host populations are still scarce. Using NetLogo, and based on results from mesocosm experiments, we developed an agent-based model simulating different stages of trematode infections from the first to the second intermediate host under increasing temperature for a common Baltic Sea benthic ecosystem. Periwinkles, mussels and the trematode *Himasthla elongata* represent our individual agents, interacting with each other and their environment. The model allows to investigate the thermal effect on cercarial rate of emergence and activity, as well as cercariae and host survival, and trematode prevalence in the benthic ecosystem. Adjusting the different parameters of the model to projected warming scenarios can provide useful information and visualization of disease transmission and make predictions of infection dynamics in a future warmer Baltic Sea, as well as other temperate oceans.

Keywords: NetLogo, trematode, transmission, host, modelling, Littorina, Mytilus

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*Speaker

Session 4: Parasite and biological invasions

Invasion of the body snatchers: the role of parasite introduction in host distribution and response to salinity in invaded estuaries

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In dynamic systems, organisms are faced with variable forces that may impose selective trade-offs. Salinity is a major physical driver of estuarine diversity, while parasites are a key biotic force shaping host distribution and demography. We tested for trade-offs between low-salinity stress and parasitism in a castrating parasite and host crab, performing field surveys every 6-8wks over 3yrs along salinity gradients to determine factors influencing parasite prevalence, host abundance, infection probability, and taxa diversity. We examined demographic data from _˜12,000 crabs, and analyzed temperature, salinity, and taxa data from 20 seasonal sampling events. Further, a lab experiment investigated signatures of low-salinity stress on host response (time-to-right and gene expression). We found salinity and temperature significantly affected parasite prevalence, with sites < 10 PSU lacking infection, and populations in moderate salinities at warmer temperatures reaching prevalences as high as 60%. An individual's infection probability was driven by salinity, host size, and season, and host abundance was negatively associated with parasite prevalence. Gene expression was plastic to acclimation salinity, but several osmoregulatory and immune-related genes demonstrated source-dependent salinity response. We identified a salinity-associated genetic marker, suggesting possible selection on standing variation. Altogether, our study furthers understanding of how selective trade-offs in naturally dynamic systems can profoundly shape host evolutionary ecology.

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*Speaker

Predation risk effects on parasite transmission from first to second intermediate trematode hosts

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Predators can affect parasite-host interactions when directly preying on hosts or their parasites. However, predators may also have non-consumptive effects on parasite-host interactions when hosts adjust their behaviour or physiology in response to predator presence.

In this study, we examined how chemical cues from a predatory marine crab affect the transmission of a parasitic trematode from its first (periwinkle) to its second (mussel) intermediate hosts.

Laboratory experiments revealed that chemical cues from crabs lead to a three-fold increase in the release of trematode cercariae from periwinkles as a result of increased periwinkle activity. This positive effect on transmission was contrasted by a tenfold reduction in cercarial infection rates in the second intermediate host when we experimentally exposed mussels to cercariae and predator cues. The low infection rates were caused by a substantial reduction in mussel filtration activity in presence of predator cues, preventing cercariae from entering the mussels. To assess the net effect of both processes combined, we conducted a transmission experiment simultaneously housing infected periwinkles and uninfected mussels. Infection levels of mussels in the treatments with crab cues were 7-fold lower than in mussels without crab chemical cues. This suggests that predation risk effects on mussel susceptibility can override the elevated parasite release from first intermediate hosts, with negative net effects on parasite transmission.

These experiments highlight that predation risk effects on parasite transmission can have opposing directions at different steps in the transmission process. Such complex non-consumptive predation risk effects on parasite transmission may constitute an important indirect mechanism affecting prevalence and distribution patterns of parasites across their life cycles.

Keywords: blue mussel, crab predator, parasite, host, system, partitioning predation, risk effects, risk, induced, trematode, trait, mediated indirect effects

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[*] Speaker

Biodiversity of intestinal helminth parasites of seabirds from the North Atlantic

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Parasites play an important role in marine ecosystems, as almost all marine species harbor at least one species of parasite. For instance, seabirds serve as hosts for several groups of parasites. Due to their long lifespan and high mobility across regions and continents, seabirds represent ideal vectors for the dispersal of parasites, particularly those with complex life cycles.Therefor, dispersal by seabirds is critical in regulating parasite occurrence and population dynamics. In this study, we provide information on the biodiversity of helminths parasitizing coastal (European shag, common gull, and sandwich tern) and pelagic birds (razorbill, black-legged kittiwake, northern fulmar, common guillemot and Atlantic puffin). At least 4 individuals per bird species were dissected and their digestive tracts were examined for parasites. The parasites were identified morphologically to the lowest taxonomical level possible followed by molecular identification. Acanthocephalans, cestodes, nematodes and trematodes were found in all seabird species but Atlantic puffins and common guillemots. The largest number of infected individuals (80%) was found in European shags and northern fulmars. The overall prevalence based on all bird specimens investigated was 13% for acanthocephalans, 23% for cestodes, 28% for nematodes, and 21% for trematodes. European shags also had the highest intensity of parasites (> 400 helminths). Seabirds having large dietary breadth and plasticity, such as common gulls, black-legged kittiwakes, and northern fulmars had higher parasite prevalence than specialised feeders such as diving auks. Due to species- specific differences in geographical distribution, behaviour, and diet among the examined seabirds, the results of this study provide valuable information about the parasites that these hosts can spread in their respective habitats.

Keywords: Acanthocephala, cestodes, nematodes, trematodes, identification, seabirds

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Parasites in paradise: The invasion of the shell boring worm Polydora websteri (Polychaeta: Spionidae) in Dutch coastal waters

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The spread of the invasive marine polychaete *Polydora websteri* Hartman in Loosanoff & Engle, 1943, causes significant economic losses for commercial oyster farms around the world and the worm is responsible for the collapse of multiple oyster aquaculture production sites. *P. websteri* bores into shells of bivalves and causes a build-up of mud and detritus in a layer of nacre secreted by the bivalve, forming a "mud blister". One of its commercially important hosts is the Pacific oyster *Magallana gigas* (Thunberg, 1793). Infected oysters served for human consumption look unsightly which strongly reduces the value. During shucking the blisters can also burst, fouling the meat with dirt.

Over the last few years, *P. websteri* has been recorded for the first time at several European locations, including the Dutch Wadden Sea. However, its presence in the Oosterschelde, a former estuary in the south of the Netherlands with an extensive oyster aquacultural production, remained unknown. In addition, no studies exist to date on the impact of infections on European host populations. Here we report the first sightings of *P. websteri* in wild Pacific oysters in the Oosterschelde and determine the impact of infections on the shell strength and condition of its oyster hosts.

The presence of *P. websteri* at three locations in the Oosterschelde was confirmed using primarily morphological characteristics and additional molecular analysis of several specimens. Across locations, the prevalence of infections ranged from 42.1-53.1%, blister prevalence ranged from 3.1-23.3%. Shell strength analysis and condition index calculations were used to determine the impact of worm infections on oysters. No significant impact was observed for either shell strength or condition index compared to healthy, non-infected oysters. Our results represent the first sightings of *P. websteri* in one of the main oyster production locations in Europe,

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*Speaker

however, we propose that the distribution of the species may already be wider than the studied areas. As the infection of oysters with *P. websteri* can have significant economic impacts on the aquaculture industry, it will be important to document the further spread and to eventually develop prevention and mitigation measures for the oyster industry.

Keywords: Parasitism, Magallana gigas, Polydora websteri, Aquaculture

First genome deciphering of a marine gregarine species: insights into the breath of apicomplexan parasites diversity

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Apicomplexa, protozoan parasites of a very large number of metazoan hosts, are mostly known at -omic and functional levels through studies of intracellular species infecting humans and animals (e.g., Plasmodium, Toxoplasma and Cryptosporidium). The early branching Apicomplexa represented by the gregarines (_˜30% of named apicomplexan species) remain very poorly documented, with only one genome deciphered for a terrestrial species (Gregarina niphandrodes) and transcriptomic data for _˜20 other species. The bottlenecks are biological (these species are not cultivable) and algorithmic (lack of reference data). This dearth of knowledge hides a part of the evolutionary history of Apicomplexa and strongly limits environmental and functional studies on gregarines.
We recently deciphered, for the first time for a marine gregarine, the genome of Porospora gigantea, an intestinal parasite of Homarus gammarus. This species shows unique features among gregarines. Its gymnospores represent an outstanding natural source of highly amplified DNA. Its trophozoites are capable of gliding at 60-100 μm per second, the fastest speed currently recorded for an apicomplexan parasite. Not one, but two genomes were assembled that we named A and B. Of similar size and coding capacity (_˜9 Mb _˜5300 genes), they show a 10.8% divergence at the nucleotide level strongly suggesting two non-interfertile species. But their 18S SSU rDNA sequences differ only by one base. Comparative studies, undertaken at deduced proteomes level, revealed that P. gigantea is as distantly related from G. niphandrodes as it is from Cryptosporidium, Toxoplasma or Plasmodium, revealing an unsuspected diversity for this basal group of Apicomplexa. Expert data mining also revealed a partially conserved gliding machinery.

These pioneering data call to the deciphering of many additional gregarine genomes, to broaden our understanding of the genomic diversity and adaptive capacities of Apicomplexa, and provide molecular references to sustain environmental studies.
Boisard, J., et al., *Marine gregarine genomes reveal the breadth of apicomplexan diversity with a partially conserved glideosome machinery.* BMC Genomics, 2022. **23**(1): p. 485.

Keywords: Apicomplexa, gregarines, genomic data, evolution, adaptation

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*Speaker

Parasites of the invasive American blue crab Callinectes sapidus Rathbun, 1896 (Decapoda, Portunidae) in coastal ecosystems of Morocco: a One-Health approach

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Crustaceans are a well-represented group in coastal environments. Their health is often linked to that of humans and together they are linked to the health of the environment. Therefore, such interconnection is the basis of the 'One Health' concept.

Invasive non-native species pose a risk as possible carriers of invasive parasites and/or enhancers for native parasites, which can lead to a loss of native biodiversity and to disease/mortality of indigenous species as well as risks to human health. The American blue crab *Callinectes sapidus* Rathbun, 1896, native to the western Atlantic, has been established in various Moroccan coastal ecosystems with the recent interest for human consumption. As such, it constitutes a good model for understanding biological invasions in the context of the 'One Health' concept.

The main objective of this study is to understand the interactions between the blue crab and its parasites in Morocco and the western Atlantic to assess their effects on native biodiversity, associated marine diseases, and risks to human health. A literature survey revealed several parasites associated with *C. sapidus* both in native and in introduced areas. Preliminary dissections of 13 specimens from Morocco and examination of their organs under a stereomicroscope did not reveal any parasites. Similar dissection and examination of 21 specimens from the western Atlantic revealed seven parasites, including a digenean, a haplosporidean, and a nematode. As the taxonomical range varies from micro- to macroparasites, various morphological and genetic diagnostic methods will be used to monitor the presence of potentially invasive parasite lineages associated to the American blue crab in Morocco and the western Atlantic. Comparison of

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*Speaker

specimens from the western Atlantic coast and Morocco will allow us to test the enemy release hypothesis and to check for parasite spillover or spillback events and the impacts related to the bioinvasion of the American blue crab in Morocco.

Keywords: Alien, Invasive, American blue crab, Parasites, One Health, Morocco, Western Atlantic

Session 5: Parasites in marine food webs and effect on ecosystem functioning

Adding microbiomes to host-parasite interactions: the next step for marine parasitology?

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After shaking the foundations of medical research, the microbiome revolution is now sweeping through ecology and evolution. In this context, interactions between a host and a parasite can no longer be seen as two-player games: they need to be reframed to incorporate the influence of the microbial communities residing within the host and also within the parasite. I will summarise the implications of host-parasite-microbe interactions for marine parasitology. The focus will be on the microbiomes of parasites themselves. I will introduce the Parasite Microbiome Project, an international consortium of researchers aiming to catalyse research on parasite microbiomes through an integrated and comparative approach founded on multi-omics technologies. I will also present recent results of our studies on the microbiomes of trematode species of New Zealand marine animals, addressing questions including: Do helminths with complex life cycles possess a 'core' microbiome, i.e. a set of vertically-transmitted bacteria that is not shared with any host and persists through the life cycle? How much geographic variation does this microbiome show among trematode populations? Does the composition of a trematode's microbiome affect its phenotype, i.e. its development and interactions with the host? Can a parasite's microbiome be manipulated experimentally? Incorporating symbiotic microbes into the theoretical framework through which we study parasitism is necessary for a better understanding of coevolution and disease ecology, and for the search for new therapies. What lurks within has been ignored for too long: it's time to look at microbes within parasites to determine what strings they can pull.

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Are trait-mediated effects of parasites on marine ecosystem engineers density-dependent?

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Parasites can play major roles in biodiversity-mediated processes through the effect they have on ecosystem engineers. First, parasites are drivers of host density and population size structure. Second, they could modify phenotypic traits of ecosystem engineers involved in their functional role. Yet, studies assessing the effects of parasites on ecosystem function while infecting engineer species are incredibly scarce.

In marine soft-bottom environments, bioturbators constitute an archetypal group of ecosystem engineers. These invertebrates host a large diversity of parasites; of which most are trematodes. The effects of trematodes on the physiology of bioturbators have been broadly assessed but there is no consensus on the impacts of these parasites, the latter ranging from very little effects to increase in the host mortality rate. Marine trematodes are usually naturally highly prevalent. In contrast, infection intensities can be highly variable and major dissimilarities in parasite load between hosts could explained the wide range of trematode effects that have been described. In order to better understand whether there is a density tipping point for trematode impacts on marine bioturbators, we have thus performed lab experiments using the Peppery furrow shell *Scrobicularia plana* as a model ecosystem engineer species. Organisms naturally showing diverse parasite abundances were used to assess the impacts of the density of trematodes on *S. plana* physiological condition and bioturbation activities. Additionally, the indirect trait-mediated effects of parasites on ecosystem processes were evaluated by measuring nutrient fluxes at the sediment-water interface.

We evidence a decrease of the condition index of the bivalves with an increase in the abundance of trematode metacercariae. Highly infected bivalves also show reduced ability to transport sediment particles. Although the impact of the parasite load on the influence of *S. plana* on porewater transport and knock-on effects on nutrient cycling remain to be quantified, our preliminary results suggest a negative density-depend effect of trematode parasites on ecosystem

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engineering processes.

Keywords: ecosystem engineers, trait, mediated effects, invertebrates, trematodes

Are corallicolids exclusive parasites of cnidarians and what role do they play in coral health

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Corallicolids are apicomplexan parasites, originally described from numerous reef-building corals found in tropical regions globally. Apicomplexan parasites are known to cause serious diseases in both vertebrate and invertebrate hosts in terrestrial and aquatic environments. However, it remains unclear whether corallicolids are detrimental to coral hosts or have potentially evolved into coral-associated symbionts. Tropical corals rely on symbioses with related protist organisms, such as the Symbiodiniaceae (dinoflagellates), becoming bleached and moribund if the symbiosis is lost. So, it remains possible that the complicated relationship between corals and their single-celled protists could also involve derived apicomplexans, referred to as apicomplexan-related lineages or ARLs.

The apicomplexans are a large and complicated group, and it has been shown using phylogenomic approaches that parasitism has actually evolved on multiple occasions throughout their evolution, and that some have little or no detrimental effects upon their host. However, the corallicolids are phylogenetically placed as sister to a clade of apicomplexans known to predominately cause pathology and disease, so it seems unlikely that they are inert parasites evolving to become symbionts. One difficulty in understanding their relationship with corals is the lack of developmental stages observed that would normally be expected with apicomplexan parasites, suggesting that alternate hosts are involved in the life cycle of these parasites.

Numerous reef-associated organisms have been screened to look for ARLs in the Caribbean (St Kitts) and the Pacific (Malaysia). Preliminary results suggest that fish blood apicomplexans are a sister clade to the corallicolids or even form part of an expanded corallicolid group. This clade appears to share a life cycle with gastropods, at least basally, whereas corallicolids *s.s.* have been observed in bivalves.

Keywords: Corallicolid, apicomplexan, symbiosis

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[*] Speaker

Trophic interaction between parasitic isopods and their associated fish hosts

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Parasitic isopods of marine fish show various differences in preferences of attachment site and host specificity. Moreover, until now little is known about their feeding strategy (food utilization) especially with respect to their sex and their site of attachment. In order to address these aspects, we conducted bulk stable isotope analyses of carbon and nitrogen in two different host-parasite associations - *Cymothoa sodwana* from largespotted dart (*Trachinotus botla*) (n=11) and *Cinusa tetrodontis* from evil-eye puffer fish (*Amblyrhynchotes honckenii*) (n=32). Different fish tissues (see below) as well as male and female parasites were collected during different sampling campaigns in June and September 2017 at different localities along the Indian Ocean coast of South Africa. As thorax and legs of the parasites exhibit different turnover rates of stable isotopes they were considered separately in order to address short- (thorax) and long-term (legs) changes in parasite's diet. The Bayesian mixing model (MixSIAR) was used to calculate proportions of the isopods diets considering the host muscle, scale/skin, gills and heart (representing a proxy for blood) as food sources. The result showed clear differences between the dietary proportion patterns of males and females of *C. sodwana* as adults (thorax signatures), but similarities in long-term diet (legs). The isopod *C. tetrodontis* from puffer fish showed no differences between males and females in general, however the result pointed on differences between their long- and short-term diets. Thus, our study pointed on higher flexibility regarding the nutrition strategy of males and females of the selected isopod species, which might be attributed to their site of attachment as adults and to the partial free-living mode of life during their development.

Keywords: parasitic isopods, stable isotopes, diet, trophic interactions

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Abiotic and biotic drivers of Anisakidae infestation levels in fish

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Parasites are often considered as a threat for animal or public health only. However, modern ecological vision underlines the need to integrate parasites and their biotic interactions in ecosystem studies. Data on Anisakidae distribution in fish are numerous but often restricted to infestation level descriptions, with few analyses of the driving factors and of the underlying mechanisms. In this work, levels of Anisakidae species in two economically and ecologically important fish species were evaluated, in relation with biological and abiotic drivers. Whiting and jack mackerel were collected during ecosystemic surveys in 2014 and 2021 in the English Channel and the North Sea. For each fish, diet was inferred by coupling stable isotopes and stomach content analyses. Anisakidae infestation levels were estimated in different tissues or organs.
For both fish species, abiotic and biotic factors induced significant differences in infestation levels. For jack mackerel, host length and fishing depth, through their impact on fish diet, were key drivers for *Anisakis* abundances. For whiting, Anisakidae distributions were significantly different between sampling areas and fish length classes, probably due to feeding habits and prey abundances.

Results of the present study confirmed the need to include parasites in an integrated approach based on population interactions to study ecosystem functioning, consistently with the current call for integrated approaches, *e.g.* One Health or Ecosystemic Approach to Fisheries Management. It also highlights that data from non-harvested group of species (such as zooplankton) are requested to understand infestation levels observed in fish. Moreover, such fundamental data may be of use for applied research *e.g.* stock definition or food safety.

Acknowledgements: Travers-Trolet, M., Verin, Y., 2014. CAMANOC cruise, RV Thalassa, https://doi.org/10.17600/14001900; Auber, A., Lazard, C., 2021. IBTS Cruise, RV Thalassa,

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https://doi.org/10.17600/18001237

Keywords: food webs, fish length, geographical distribution, Anisakis, Contracaecum

Genetic diversity of anisakid nematodes: a tool for monitoring the anthropogenic disturbances of marine ecosystems?

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The completion of the heteroxenous life-cycle of anisakid nematodes requires stable trophic webs of the marine ecosystem. As a result, the life-cycle of anisakid nematodes characterized by various degrees of habitat disturbance could be affected by changes in host population size. Indeed, when the population size of the hosts participating in the life-cycle of these parasites is reduced, due to different anthropogenic causes, the population size of their anisakid endoparasites could also be reduced. This would result in a higher probability of genetic drift phenomena in anisakids gene pools. A comparative analysis of the genetic variability values (by a multilocus genotyping approach) and parasitic infection levels with anisakids from Boreal and Austral Regions, was performed. So far, high values of genetic variability and parasitic infection levels have been observed in Antarctic, sub-antarctic as well as in Arctic anisakid populations and species of the genera *Contracaecum*, *Pseudoterranova* and *Anisakis*. Quantifying population density and estimating the genetic variability of anisakid nematodes, whose life-cycle is embedded in marine ecosystem food webs, could be an indirect analysis of the demographic reduction and population bottlenecks (due to anthropogenic causes such as habitat fragmentation, and overexploitation) of those definitive and intermediate/paratenic hosts, which are involved in their life-cycle. Monitoring the demography of anisakid parasites and their genetic diversity would be future tools for monitoring the impact of habitat disturbance on biodiversity, at both species and gene level, over a spatial and temporal scale level.

Keywords: Anisakid nematodes, genetic variability, ecological indicators

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Feeding experiments and stable isotope analyses to unravel parasitic interactions

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Parasitic trophic interactions have been largely excluded in food web studies, but recent research has highlighted their integral role in affecting food web properties. Previous efforts to unravel trophic interactions between parasites and their hosts have used stable isotope analysis of whole tissues (bulk SIA, 13C and 15N), but these studies show a considerably high variability in the isotopic differences between parasites and their resources. Furthermore, this variability, combined with likely effects on the isotopic composition of infected hosts, further confound trophic interactions within food webs. This EU-funded project proposes to develop an innovative integrated approach combining field sampling and laboratory feeding experiments with the simultaneous analysis of bulk SIA and compound-specific stable isotope analysis of amino acids (CSIA-AA). This novel technique allows for the detection of changes in individual amino acids during trophic transfer and for comparison of source *vs* trophic amino acids to identify the trophic level of individual animals. Combining field samplings, laboratory-based feeding experiments with four common coastal parasite-host systems, and the use of bulk SIA and CSIA-AA will allow for determination of isotopic changes caused by dietary shifts or parasitic infections in both hosts and parasites. We aim to make a significant contribution to our understanding of parasitic trophic interactions and their potential to affect the isotopic composition of infected hosts. Acknowledgments: Horizon 2020 - Research and Innovation Framework Programme (MSCA -IF, project number 101027941).

Keywords: stable isotopes, experimental assays, host, parasite interaction, trophic transfer

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Session 6: Environmental Parasitology

Is the world wormier than it used to be? Answers from a new subdiscipline: the historical ecology of parasitism

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Many disease ecologists and conservation biologists believe that the world is wormier than it used to be – that is, that parasites are increasing in abundance through time. This argument is intuitively appealing. Ecologists typically see parasitic infections, through their association with disease, as a negative endpoint, and are accustomed to attributing negative outcomes to human interference in the environment, so it slots neatly into our worldview that habitat destruction, biodiversity loss, and climate change should have the collateral consequence of causing outbreaks of parasites. But surprisingly, the hypothesis that parasites are increasing in abundance through time remains entirely untested for the vast majority of wildlife parasite species. Historical data on parasites are nearly impossible to find, which leaves no baseline against which to compare contemporary parasite burdens. If we want to know whether the world is wormier than it used to be, there is only one major research avenue that will lead to an answer: parasitological examination of specimens preserved in natural history collections. Natural history specimens are "parasite time capsules" that give ecologists the opportunity to test whether infectious disease is on the rise and to identify the driving forces. In this talk, I will discuss the potential of this approach and present some of its recent insights. I anticipate that parasitological examination of natural history specimens will facilitate major advances in a new sub-discipline – the historical ecology of parasitism – and will finally answer the question: is the world wormier than it used to be?

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*Speaker

The potential of marine trematode parasite communities to indicate ecosystem changes

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Marine coastal ecosystems are threatened by growing pressures related to global change. The accurate evaluation of an ecosystem's biodiversity and status is by consequence of increasing importance to assess potentially undergone changes and predict their future trajectory for management and conservancy purposes. Easy to examine biotic indicators sensitive to ecosystem changes are thus continuously sought for. Marine trematode parasite communities were examined as potential indicators of environmental changes. To this end, we examined the trematode community infecting the common cockle Cerastoderma edule which inhabits the intertidal flats of Banc d'Arguin, a sand bank on the French Atlantic coast. Monthly data extending over 16 years and sampled at a single station were compared to field book notes describing the changes of the closely surrounding landscape. In complement to this temporal approach, we sampled cockles and benthic macrofauna at 15 stations presenting different substrate features along the intertidal flat of the bank. Over time, seven out of nine changes of the trematode community structure presented concordances with changes in landscape. We hypothesize this was related to the environment heterogeneous substrate (i.e., temporal succession of oyster parks, bare sands and seagrass) with cascading effects on host populations. However, some changes could not solely be explained by changes in landscape. Our spatial study showed that, while benthic fauna assemblages were strongly differentiated by substrate heterogeneity, trematode communities exhibited intricate infection patterns with a complex interaction between substrate heterogeneity and larval dispersal ability of parasites. Our study suggests the possibility that trematode communities might be potential indicators of subtle changes in the environment. However, it remains unclear which scale of environmental changes trematodes are actually sensitive to.

Keywords: Trematodes, Cerastoderma edule, Temporal and spatial variability, Environmental changes, Biotic Indicator, Substrate heterogeneity.

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[*] Speaker

Using molecular and experimental approaches to uncover how Lamellodiscus monogeneans establish specificity for their sparids (Teleostei) hosts

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Among the many organisms that parasitize teleost fish, monogeneans (Platyhelminthes) are ectoparasites often very abundant on their host skin and gills. Monogeneans have a direct life cycle and are generally highly host specific compared to other parasite groups. The establishment of host specificity mechanisms involves different steps of monogeneans' life cycle. One of these steps takes place when the ciliated larvae (oncomiracidia) hatches and actively searches its host(s) from chemical cues emitted by fish skin. We investigate the selection filter that operates at the fish skin level, where larvae settle before migrating to the gills, focusing on a third player: the fish microbiote. Indeed, bacterial communities are suspected to contribute to these cues and could thus play a significant role in host-parasite specificity mechanisms.
We focused on a well-known association between Sparidae, a family of Mediterranean fishes, and monogeneans of the *Lamellodiscus* genus. These parasites display various patterns of host specificity and species richness for their different fish hosts species.

For various sparid species, we previously demonstrated a link between the composition of *Lamellodiscus*communities (determined from morphology) and the bacterial communities of the gill and skin mucus (using metabarcoding of the 16S ribosomal gene). To go further we then characterized the chemical composition of secondary metabolites in sparids external mucus (liquid chromatography coupled to non-targeted mass spectrometry - LC-MS). We show that there is a specific chemical signature for skin and gill mucus, as well as species specific metabolite profiles. We analysed We analyzed whether these profiles are related to *Lamellodiscus* diversity and bacterial communities composition from external mucus.
To complete these molecular approaches, we seek for a specificity filter unique to each host that could operate on the *Lamellodiscus* larval stage. We assessed *in vitro* the preferences and chemotaxis of oncomiracidiatowards the skin mucus from different sparid species, and characterized the morphology of different *Lamellodiscus* by scanning electron microscopy.

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Keywords: Sparidae, Specificity, Skin mucus, Oncomiracidia, Metabarcoding, Metabolomics, Chemotaxis, Morphology

Metal accumulation by intestinal parasites of seabirds

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Accumulation of chemical contaminants by gastrointestinal helminth parasites has been documented in various taxa. Often, infected hosts have lower contaminant burdens than uninfected conspecifics, which could stem from parasites acting as "contaminant sinks". However, most of the available literature deals with parasites of fish and mammals, while the capacity of parasites to act as "contaminant sinks" has been largely neglected in seabird hosts. This study aimed to explore the diversity of helminths in seabirds from the North Atlantic, and their capacity to bioaccumulate metals. Fresh carcasses (N=39) from six seabird species (4–6 individuals per species) found stranded on the French Atlantic coast were dissected to collect internal tissues (muscle, liver, kidneys) and helminths from the gastrointestinal tract. Helminths were present in 50% of all birds, with prevalence ranging from 0 to 80% depending on host species. The intestinal parasites were sorted by taxonomic group (acanthocephalans, cestodes, nematodes, trematodes) under a binocular lens, and the species were identified morphologically or molecularly (see abstract by Musiol et al.). When several helminths were present within a host (> 20), specimens belonging to the same species were pooled from individual birds, and their element concentrations (As, Cd, Cu, Fe, Mn, Pb, Sb, Sn, and Zn) were determined by ICP-MS. Element concentrations were also determined in host tissues and compared to accumulation rates in the parasites. The results will answer the following questions: 1) if and which helminths have higher metal concentrations than their host, and 2) if infected birds have lower metal concentrations than uninfected birds. Seabirds are one of the most endangered groups of animals. Understanding the interaction between parasites and contaminants in this group is thus critical in the context of climate change which is predicted to alter both contaminant biogeochemical cycles and parasite infection dynamics.

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Keywords: trace metals, seabirds, accumulation, helminth

DYNAMICS OF DIGENEA PARASITES – EDIBLE COCKLE SYSTEMS IN THREE COASTAL ECOSYSTEMS ON THE NORTH-EASTERN ATLANTIC

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Dynamics of four trematode parasites - edible cockle *Cerastoderma edule* systems were compared in three coastal ecosystems along a latitudinal gradient on the North-Eastern Atlantic. Then, we tested the role of environmental drivers in controlling these dynamics.
Trematode parasite load in cockles was monitored monthly for two years in Arcachon Bay (France) and Merja Zerga lagoon (Morocco) for the cockle cohorts of 2005 and 2006 as well as in Oualidia lagoon for the cockle cohorts of 2009 and 2010. On each occasion, the number of metacercariae was assessed by trematode species (thus utilizing the cockle as the second intermediate host). Episodes of significant increases and decreases in infestation intensity of the most dominant and common digenea in the three sites (*Himasthla quissetensis*, *Himasthla interrupta*, *Curtuteria arguinae*, and *Gymnophallus minutus*) were attributed to parasite infection and parasite-dependent mortality events, respectively.

The four Digenea parasites showed different infestation patterns in the three coastal ecosystems. Globally, parasite infestation can occur at any time of the year but the most significant variations in infestation are between 17 and 22○C. Therefore, the most important seasons of increase are poorly defined at Oualidia where temperatures are rarely unfavourable. At Merja Zerga, the period extends from spring to autumn with lower values at the peak of summer temperatures. At Arguin, inhibition is more likely to occur at low temperatures, concentrating infestations in summer and autumn.
Temperature appears to be an important controlling factor, but more in an on/off system about a favourable thermal window (around 17-22○C) than proportionally. Moreover, in almost all cases, the infestation was correlated with time (seasons) and individual biomass of the host.

Keywords: Trematode parasites, Phenology, Cerastoderma edule, Environmental drivers

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Investigation of infestation levels and diversity of Cryptocotyle metacercariae (trematode) isolated from commercial fish species sampled in the English Channel and the North Sea

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Background and aims

Marine fish are often speckled with "black spots" caused by host response to larval trematode infection. These unaesthetic spots and the presence of parasites may lead to important economic loss in fishery and may have impacts on public health. *Cryptocotyle* (Lühe, 1899) is among the trematodes inducing this response. So far, its impact on human health and its distribution among commercially important fish is still unknown. The present investigation describes tool development for the quantification and identification of *Cryptocotyle* infection and reports for the first time, *Cryptocotyle* distribution from commercial fish species of the English Channel and North Sea.

Methods

Tool development was carried out on optimization of digestion, assessment of viability and identification of metacercariae. Then, an epidemiological study was performed on seven fish species collected by bottom trawling during International Bottom Trawl Survey in the English Channel and the North Sea in 2019 and 2020. Infection level was estimated by counting visible black spots. Metacercariae were isolated using chemical digestion and characterised from a morphological point of view and from a molecular perspective with sequencing of *cox1* gene and *ITS* region.

Results

Orbital stirring was found less destructive. Viable and morphologically identified metacercariae were recovered up to 8 days post fish death. *C. lingua* metacercariae were characterized from fish caught off the Channel and from Danish marine waters. In epidemiological investigation,

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[*] Speaker

prevalence, intensity and abundancy show differences between fish species and fishing areas. Whiting and pout were the most infected species. *C. lingua* was mainly identified and some *C. concava* and Bucephalidae were also found.

Conclusion

Optimized protocols for a reliable quantification, detection and identification of *Cryptocotyle* were performed. This allowed the first description and identification of *C. lingua* and *C. concava* metacercariae in the English Channel and North Sea ecosystems.

Keywords: trematode, fish, epidemiological study, aquatic ecosystems, Cryptocotyle

Immune priming against Vibrio tapetis in the Manila clam, Ruditapes philippinarum.

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France has seen a decline in aquaculture of the Manila clam, *Ruditapes philippinarum*, over the past decade years due to in part to mortality events brought on by environmental conditions and diseases. Given the difficulties in treating bivalve diseases through routine approaches, solutions need to be adapted to limit the impact of disease and improve the sustainability of bivalve aquaculture. Recent findings indicate that numerous invertebrate groups previously thought to rely solely on an innate immune system possess a capacity for immune memory, and studies in bivalve species including the Manila clam support the potential for exploiting this capacity to improve its immunity against the pathogen *Vibrio tapetis*, responsible for Brown Ring disease along the Atlantic coast.

The experiment focuses on evaluating the ability of heat-killed (HK) *V. tapetis* and its extracellular products (ECPs) as immune priming agents and improve immunity against live *V. tapetis*. Adult clams were primed with either sterile sea water (SSW), ECPs, of HK-*V. tapetis* via injection into the adductor muscle, and left for one week in standard infection conditions. On day 7, half of the animals from each group (control, ECP, and HK) were injected into the adductor muscle with a dose of virulent live *V. tapetis* (strain CECT4600). Sampling was carried out at 2- and 5-days post-priming and post-challenge. Mortality was recorded in each group over the course of the experiment to evaluate differential survival in immune-primed clams compared to positive controls. Hemolymph samples were analyzed on a cytometer to evaluate immune parameters. Remaining hemolymph was stored for RNAseq analyses. Extrapallial fluids were collected for pathogen quantification, the digestive gland was collected to evaluate potential changes to the gut microbiota community, and mantle samples were taken for RNA and protein analyses, in order to evaluate functional changes in host physiology.

This study offers novel insights on the cellular and molecular modifications associated with immune priming and sets the basis for developing a feasible and easily applicable tool to limit disease in Manila clam hatcheries. The results also provide valuable knowledge for further developing immune priming as a sustainable solution to limit diseases in other commercial bivalve species.

Keywords: Manila clam, Brown Ring disease, immune priming, aquaculture

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[*] Speaker

Truly a hyperparasite, or simply an epibiont on a parasite? The case of Cyclocotyla bellones (Monogenea, Diclidophoridae)

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Cyclocotyla bellones Otto, 1823 (Monogenea, Diclidophoridae) is one of the few monogenean species reported as hyperparasitic: the worms dwell on cymothoid isopods, themselves parasites of the buccal cavity of fishes. We present here observations based on newly collected monogenean specimens from *Ceratothoa parallela* (Otto, 1828), an isopod parasite of *Boops boops* off Algeria and also investigated its diet to address whether *Cy. bellones* is indeed a hyperparasite, i.e., whether it feeds on the isopod. We also compared the body shape of various monogeneans belonging to the same family as *Cy. bellones*, the Diclidophoridae, including *Choricotyle* cf. *chrysophryi* Van Beneden & Hesse, 1863, collected from *Pagellus acarne* off Algeria. No morphological character of the anterior organs suggested any special adaptation in *Cy. bellones* to the perforation of the crustacean cuticle. The wall of the oesophagus and of the intestine of *Cy. bellones* was lined with a dark pigment similar to what is usually observed in haematophagous polyopisthocotyleans, and which is derived from ingested fish blood. We noticed that an anterior elongate stem exists only in diclidophorids dwelling on parasitic isopods and never in those attached to the gills. We hypothesize that the anterior stem of the body of *Cy. bellones* is an anatomical adaptation for the monogenean to feed on the fish while dwelling on the isopod. We thus consider that *Cy. bellones* is an epibiont of the parasitic crustacean, as it uses it merely as an attachment substrate, and is not a true hyperparasite.

Keywords: hyperparasitism / Epibiosis / Cyclocotyla bellones / Cymothoidae / Nutrition / Adaptation

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[*] Speaker

Session 7: Climate change and diseases

Parasites in a warming world: a complex affair

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Global warming is considered a major driver of the emergence of parasitic diseases in aquatic systems. Overall, transmission rates, infection intensities and pathology of many parasites and pathogens are expected to increase with rising temperature. In particular, parasites with complex and temperature-dependent life cycles, such as trematodes, will be sensitive to climate changes. However, the species-specific reactions and responses to these changes are still unknown for most host-parasite taxa, making accurate predictions of the ecosystem-wide consequences of climate change on individual parasites, host populations and entire communities a persistent challenge. Using examples from freshwater and marine habitats, I will highlight the complex, and sometimes unexpected, outcomes of the interplay between parasites and temperature changes. In a set of laboratory, mesocosm and field experiments, we explored how temperature regulates transmission of free-living trematode stages, and can lead to higher infection intensities in hosts. Although these temperature-driven infection dynamics mainly occur in summer, their impacts on host performance and survival can manifest months later during the winter season and often remain undetected. Besides these direct effects of parasite infections, non-consumptive or fear effects have been shown to drastically alter host behaviour even before infections occur and will be further enhanced by warming temperatures. Making a complex situation even more complicated, experimental results have highlighted that parasite infections may also protect hosts against heat stress, suggesting that the interactions between host–parasite systems and their changing environment are much more complex than a simple additive effect of multiple stressors. To further explore the impacts of climate change on these intricate interactions, host-parasite systems from Arctic and Subarctic habitats, where global warming effects are already increasingly evident, can serve as sentinels to build a better mechanistic understanding of climate-disease interactions.

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*Speaker

Amphipod's biochemical response to thermal stress is modulated by trematode infection but not its feeding rate or survival

Dakeishla Diaz-Morales * [1], Maral Khosravi [2], Daniel Grabner [1], Nazmun Nahar [1], Claudia Bommarito [2], Martin Wahl [2], Bernd Sures [1]

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Understanding the thermal limits of marine ectotherms has aided in predicting the effects of global warming. Although parasitism is one of the most common interactions between species in nature, the role of parasites in the thermal tolerance of their hosts is frequently overlooked. This study examined the ability of the trematode *Podocotyle atomon* to modulate the feeding behavior and biochemical condition of *Gammarus locusta* when exposed to temperatures ranging from 2○C to 30○C. The optimal temperature for gammarid survival was 10.1○C, and it remained unaffected by trematode infection. Male gammarids showed higher shredding rates than females, particularly at higher temperatures. Although the difference was statistically insignificant, infected gammarids shredded more in colder temperatures than uninfected ones. The direction of the infection effect on phenoloxidase was affected by both temperature and sex. Specifically, phenoloxidase activity increased at 16 and 18○C, especially for uninfected females at 18○C. Both infected males and uninfected females had increased catalase activity at higher temperatures. An increase in the activity of this enzyme at lower temperatures was found only for infected females. The concentration of lipids was significantly influenced by temperature in a bell-shaped curve as well as by sex, with males having fewer lipids than females. Gammarids' lipid content decreased by 14% as a result of infection. Infected males had significantly less glycogen than uninfected, while infected females showed the opposite trend. The findings show the role of parasites and host sex for maintaining organismal homeostasis under thermal stress and offer important information about the organismal stability of a common amphipod in a warming sea.

Keywords: Climate change, host, parasite interactions, trematode, immunocompetence, gammarid, heat stress

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[*] Speaker

Anthropogenic noise pollution and wildlife diseases

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The global rise of anthropogenic noise has long been ignored, especially in aquatic environments, because humans have limited abilities of detecting underwater sound. In recent years, the impact of noise pollution on wildlife has gained growing awareness in the scientific literature and in wildlife management practices. However, the consequences for marine wildlife diseases have received almost no attention to date. We have set to outline how anthropogenic noise can affect the occurrence and severity of infectious wildlife diseases in aquatic environments. We argue that there is potential for noise impacts at three main stages of pathogen transmission and disease development: 1) pre-infection exposure, 2) infection upon exposure, and 3) severity of post-infection consequences. Each of these stages is illustrated by relevant examples from the literature on anthropogenic noise and aquatic wildlife diseases. We hypothesize major repercussions of noise pollution effects for wildlife for both individuals, populations and communities and, as such, call for intensifying research efforts. We pinpoint a number of important avenues for future studies into noise impacts on wildlife diseases.

Keywords: acoustic climate change, anthropogenic noise, cumulative effects, environmental change

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*Speaker

Annual cycle of cercariae release from intertidal snails in the subarctic White Sea – an experimental study

Kirill Galaktionov * [1], Ivan Levakin , Kirill Nikolaev , Anna Vinogradova , Daniil Fedorov , Vladimir Prokofiev

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Background and aims. Annual dynamics of cercariae release from the infected snails under subarctic climate has the long pause in the cold period. The aim of this study was to estimate experimentally the dependence of the daily cercarial emission on temperature (T) and the time of the spring emission delay (SED), from the point when the temperature becomes optimal to the actual emission onset.

Results. Experiments. I. We estimated the average daily cercarial emission (DCE) for four trematode species from the intertidal snails *Peringia ulvae* (*Cryptocotyle concava* and *Maritrema subdolum*) and *Littorina littorea* (*Cryptocotyle lingua* and *Himasthla elongata*) at the White Sea for T ranging from 8○C to 30○C in increments of 2○C. The dependence of DCE on T was asymmetrical, but was well described by the sum of two Gaussians (R2 = 0.86–0.98). The maximum mean daily T in the White Sea was always below the emission optimum. II. We estimated DCE for *C. concava*, *C. lingua*, *H. elongata* and *M. subdolum.* Snails were collected from under the ice in March (hydrological winter) and kept at "spring" temperature until differences in DCE from Experiment I disappeared. Maximum SED was observed for *H. elongata* (52 days). *Cryptocotyle* spp. and *M. subdolum* showed a short-term spike in emission immediately after the T increase. III. Cages with uninfected blue mussels were set up in the intertidal during the warm season. Every 10 days, we dissected batches of the mussels to determine the abundance gain (AG) of *H. elongata* and *C. parvicaudata* metacercariae. After a brief (10-day) spring spike, AG gain of *C. parvicaudata* correlated with water T (r = 0.79). AG of *H. elongata* matched its T-based DCE, but only with a SED correction.

Conclusions. Under the conditions of a warming climate, one should expect a significant increase in the transmission of common trematode species in the coastal waters of the northern seas due to expansion of the optimal zone for intramolluscan stages development.

Keywords: cercarial emission, intertidal snails, temperature, Subarctic, climate change

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*Speaker

Cockles in Danish Waters – Are They Carrying Potential Pathogens, Not Just Harmful for Themselves But Also for Other Mollusc Species?

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Cockles (*Cerastoderma edule* and *C. glaucum*) have been fished commercially in Danish waters for decades. In Denmark, the European flat oyster (*Ostrea edulis*) in the Limfjorden is affected by *Bonamia ostreae*, a parasite found in the population in this area for the last 9 years, also in connection with mortalities in affected batches. Another notifiable parasite *Marteilia refringens* has not been found. During the last decades, the proportion of Pacific oysters (*Crassostrea gigas*, an invasive species in Denmark) has increased, resulting in commercial fisheries of this species. In other countries with Pacific oyster stocks, disease caused by the bacterium *Vibrio aestuarianus* have resulted in mortalities in affected batches. *Vibrio aestuarianus* can also be pathogenic in cockles as well as the *Marteilia* species *Marteilia cochillia.* The intention was to screen cockles for the mentioned pathogens, and to investigate if e.g. cockles are carrying *Bonamia* parasites and thereby could spread the disease in the Limfjorden.
Molecular methods were used for screening of the cockles samples; a duplex Real Time PCR method for *Bonamia* sp and *Marteilia refringens* (Canier *et al.* 2020) and a Real Time PCR method for *Vibrio aesturianus* (EURL mollusc diseases SOP, 2021).

The screening resulted in findings of *Bonamia*-positive cockles as well as findings of *Vibrio aestuarianus* in certain batches of cockles. It is speculated if cockles can be one of the drivers for the *Bonamia*-infestation in Limfjorden as well as if *Vibrio aestuarianus* can be a potential pathogen becoming important for mortalities in Pacific oysters during future potential warmer summers.

Canier L, Dubreuil C, Noyer M, Serpin D, Chollet B, Garcia C & Arzul I (2020). A new multiplex real-time PCR assay to improve the diagnosis of shellfish regulated parasites of the genus *Marteilia* and *Bonamia*. *Preventive Veterinary Medicine* **183**, 105126 https://doi.org/10.1016/j.prevetmed.2020.105126

Keywords: Cockles, Bonamia ostreae, Vibrio aestuarianus

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*Speaker

The Effects of Climate Change on a Multispecies Community with Invasive Parasites

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Temperature increases and invasive species are two major processes invoking changes to existing multi-species communities. The combined effect of both processes in the dynamics of host and invasive parasite species remains understudied, even though parasites and ectotherm hosts both have temperature-dependent physiological rates. Optimal temperatures may differ between parasites and their hosts, and between recently invaded and native species. In the Wadden Sea, 1-2 new invasive species arrive every year and the water temperature is projected to increase by 1-5 ◦C by the end of the century. Our project aims to determine the impact of temperature increase on: a) The development speed and survival of two invasive parasitic copepods (*Mytilicola intestinalis* and *Mytilicola orientalis*), b) The immunity and survival of two bivalve hosts (native blue mussels *Mytilus edulis* and invasive Pacific oysters *Crassostrea gigas*), and c) The impact of copepod infection on both host species. These aims serve our ultimate goal to understand the dynamics of the whole system and to use this system as a model for host-parasite interactions under climate change in multispecies communities. We will use a combination of pre-existing data, controlled laboratory experiments and eco-epidemiological modelling. The project will run 2022-2026 and the first results are expected in late 2022.

Keywords: Climate Change, Copepoda, Introduced Species, Mytilus edulis, Crassostrea gigas

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*Speaker

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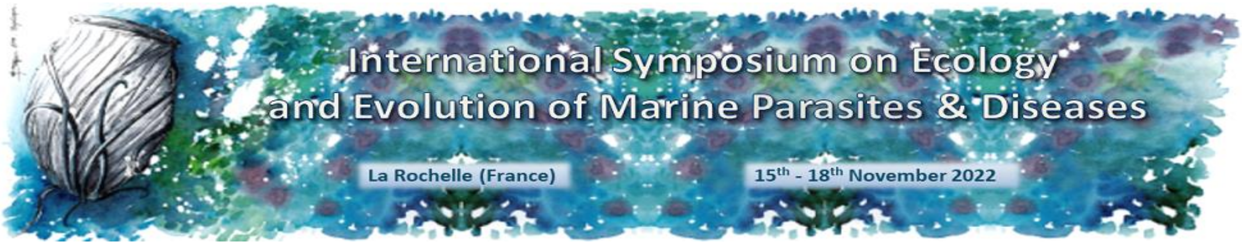
Programme of the Symposium

15th - 18th of November 2022



Tuesday 15th of November

8:30- 9:15: Registration
9:15- 9:30: Welcome address

Session 1: Biogeography and macroecology of marine parasites, *chairman: David Thieltges*

9:30- 10:10:	**Keynote by Juan Antonio Balbuena, Universitat de Valencia, Spain:** Parasitology meets macroecology on its own terms: New ways to tackle long-range patterns and processes of parasite diversity
10:10 - 10:30:	Genetic variability of a trematode sporocyst modelled by intraspecific competition, Correia Simao
10:30 - 11:00:	*Coffee break*
11:00 - 11:20:	Living in periwinkles: Large scale distribution and abundance of the ciliate *Protophrya ovicola*, Waser Andreas
11:20 - 11:40:	Parasites of coastal birds in the north: not a complete story of Notocotylidae (Digenea), Gonchar Anna *- remotely*
11:40 - 12:00:	Rhabdocoel flatworms inhabiting marine invertebrates as models for evolutionary patterns associated with the acquisition of endosymbiosis, Vanhove Maarten
12:00 - 12:20:	Uncovering Long-branched Microsporidian Diversity In The Freshwater Isopod *Asellus aquaticus*, Doliwa Annemie
12:20 - 12:40:	Variability and distribution of parasites, pathologies and their effect on wild mussels (*Mytilus* sp) in different environments along a wide latitudinal span in the Northern Atlantic and Arctic Oceans, Benito Denis *- remotely*
12:40 – 14:00:	***Lunch***

Session 2: Linking parasite detection, disease monitoring and ecology & evolution, *chairman: Ana Born-Torrijos*

14:00 - 14:40:	**Key note by Aurélie Chambouvet, CNRS, France:** Diversity and host range of emerging parasitic protists: the case of the Perkinsea (Alveolata)
14:40 - 15:00:	Molecular approaches as an innovative tool to investigate monogenean host-specificity, using the *Sparidae-Lamellodiscus* host-parasite system, Scheifler Mathilde *- remotely*
15:00 - 15:20:	Haplosporidians in European bivalves, Bass David
15:20 - 15:40:	Assessment of the environmental distribution of the protozoan parasite *Perkinsus olseni* by next-generation sequencing, qPCR and histopathology allows the identification of alternative bivalve hosts, Raquel Ríos-Castro
15:40 – 16:20:	*Coffee break and poster session*
16:20 - 16:40:	Paramyxid parasites infecting a range of decapod crustaceans, Martin Signe
16:40 - 17:00:	Parasitic turbellarians: from invertebrate to vertebrate hosts, Kmentova Nikol
17:00 - 17:20:	Dynamics of *Vibrio aestuarianus* in cockles in wild beds of Hauts de France, Garcia Céline
17:20 - 17:40:	Using eDNA-based approach to investigate parasite life cycle: the example of *Haplosporidium costale*, Arzul Isabelle
17:40 - 19:30	**Poster session & drinks**

Wednesday 16th of November

Session 3: Direct and indirect effects of diseases on marine populations and communities, *chairman: Annika Cornelius*

9:00 - 9:40:	**Key note by Ryan Carnegie, VIMS, U.S.A:** Insights into long-term interactions between host populations and parasites, environmental change and commercial exploitation, from the Chesapeake Bay oyster disease system
9:40 - 10:00:	Another look at disease transmission in marine ecosystems, Shields Jeff
10:00 - 10:20:	Characterization of an emerging apicomplexan parasite in the bay scallop *Argopecten irradians irradians*, Allam Bassem
10:20 - 11:00:	*Coffee break and poster session*
11:00 - 11:20:	Comparison of the efficacy of a selective breeding programme to increase cockle *Cerastoderma edule* marteiliosis resistance with that of the natural selection in the inner area of Ría de Arousa, Villalba Antonio *- remotely*
11:20 - 11:40:	Getting into fish brains: Infection and gene expression profiling of a behavioral manipulative trematode, Born-Torrijos Ana
11:40-12:00:	Seal louse and heartworm: an ancient team and its impact on pinnipeds, Herzog Insa
12:00 – 13:30:	*Lunch*

Session 4: Parasite and biological invasions, *chairman: Annabelle Dairain*

13:30 - 14:10:	**Key note by April Blakeslee, Easy Carolina University, U.S.A:** Invasion of the body snatchers: the role of parasite introduction in host distribution and response to salinity in invaded estuaries
14:10 - 14:30:	First genome deciphering of a marine gregarine species: insights into the breath of apicomplexan parasites diversity, Florent Isabelle
14:30 - 14:50:	Parasites in paradise: The invasion of the shell boring worm *Polydora websteri* (Polychaeta: Spionidae) in Dutch coastal waters, Willems Max
14:50 - 15:10:	Predation risk effects on parasite transmission from first to second intermediate trematode hosts, Cornelius Annika
15:10 - 15:30:	Biodiversity of intestinal helminth parasites of seabirds from the North Atlantic, Musiol Michelle
15:30 – 16:20	*Coffee break and poster session*

Session 7: Climate change and diseases, *chairman: Isabelle Arzul*

16:20 - 17:00:	**Key note by Christian Selbach, Norway:** Parasites in a warming world: a complex affair
17:00– 17:20:	Amphipod's biochemical response to thermal stress is modulated by trematode infection but not its feeding rate or survival, Diaz-Morales Dakeishla
17:20– 17:40:	Annual cycle of cercariae release from intertidal snails in the subarctic White Sea – an experimental study, Galaktionov Kirill *- remotely*
17:40 - 18:00:	Anthropogenic noise pollution and wildlife diseases, Berkhout Boris W.

Social dinner 19h45-22h00

Thursday 17th of November

Session 5: Parasites in marine food webs and effects on ecosystem functioning,

chairman: Xavier De Montaudouin

9:00 - 9:40:	**Key note by Robert Poulin, University of Otago, New Zealand:** Adding microbiomes to host-parasite interactions: the next step for marine parasitology - *remotely*
9:40 - 10:00:	Abiotic and biotic drivers of Anisakidae infestation levels in fish, Gay Mélanie
10:00 - 10:20:	Are corallicolids exclusive parasites of cnidarians and what role do they play in coral health, Freeman Mark
10:20 - 11:00:	***Coffee break and poster session***
11:00 - 11:20:	Are trait-mediated effects of parasites on marine ecosystem engineers density-dependent?, Dairain Annabelle
11:20 - 11:40:	Genetic diversity of anisakid nematodes: a tool for monitoring the anthropogenic disturbances of marine ecosystems? Simonetta Mattiucci - *remotely*
11:40 - 12:00:	Trophic interaction between parasitic isopods and their associated fish hosts, Nachev Milen
12:00 – 13:30:	***Lunch and poster session***

Session 6: Environmental Parasitology, *chairman: Mathias Wegner*

13:30 - 14:10:	**Key note by Chelsea Wood, University of Washington, USA:** Is the world wormier than it used to be? Answers from a new subdiscipline: the historical ecology of parasitism
14:10 - 14:30:	Metal accumulation by intestinal parasites of seabirds, Carravieri Alice
14:30 - 14:50:	Dynamics of Digenea parasites – edible cockles systems in three coastal ecosystems on the north-eastern Atlantic, Bazairi Hocein
14:50 - 15:10:	Immune priming against *Vibrio tapetis* in the Manila clam, *Ruditapes philippinarum*, Smits Morgan
15:10 - 15:30:	Investigation of infestation levels and diversity of *Cryptocotyle metacercariae* (trematode) isolated from commercial fish species sampled in the English Channel and the North Sea, Duflot Maureen
15:30 – 16:20	***Coffee break and poster session***
16:20 - 16:40:	The potential of marine trematode parasite communities to indicate ecosystem changes, Stout Leslie
16:40 - 17:00:	Truly a hyperparasite, or simply an epibiont on a parasite? The case of *Cyclocotyla bellones* (Monogenea, Diclidophoridae), Bouguerche Chahinez
17:00– 17:20:	Using molecular and experimental approaches to uncover how *Lamellodiscus monogeneans* establish specificity for their sparids (Teleostei) hosts, Revault Judith

17:20– 18:00: Meeting conclusion / discussions

Friday 18th of November

Workshop on micro-parasites of marine molluscs

9.00 - 9.15	Introduction to the Workshop, Isabelle Arzul
9:15 - 9:30:	Presentation on the activities of the ASIM Unit (Adaptation and Health of Marine Invertebrates, Ifremer) on micro-parasites of marines molluscs, Isabelle Arzul
9:30 - 10:00:	Disease monitoring and epidemiology through sequencing approaches at ASIM (Ifremer), Germain Chevignon and Maude Jacquot
10:00- 10:30:	***Coffee break***
10:30- 11:00:	Short and long-read sequencing for microparasite characterisation, Chantelle Hooper
11:00 - 11:30:	eDNA, microbes-pathogens, & systems-based studies, David Bass
11:30 - 11:45:	Review on transmissible cancer diseases, Antonio Villalba
11:45 – 12:00	Discussions and workshop conclusion

12:00 End of the Symposium