Presentation abstracts in sequence of schedule

Marine Research Days 2024 Kalmar, November 26 – 28 2024

Day 1 November 26 2024

Wind drift, turbulent dispersion and algal blooms in the Baltic Sea

Inga Monika Koszalka

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Algal blooms pose a major environmental problem for the Baltic Sea's marine ecosystem and its human stakeholders. Algal mats limit access to oxygen in the surface waters, downgrade aesthetic values of the sea and water quality and affect coastal industries. As the algal blooms are expected to intensify under the climate change and warming of sea waters, it is important to develop reliable hazard and hazard impact forecasting services. This is a tantalizing task however, owing to the complexity of physical and biological processes involved in algae growth and too sparse data to constrain marine ecosystem models. I will present results from a project aiming to develop a forecast framework for algal blooms in the Baltic Sea and associated ecosystem and societal impacts. The framework makes use of Lagrangian (drifting) trajectory simulations. Drifter observations are used to evaluate the ocean model that is in turn used to force numerical trajectory simulations. I will also show implementation of an algae model of low complexity on trajectories. The project focuses on consequences of algae blooms for the water quality on Gotland, in particular for the desalination plats producing drinking water from the sea water complementing the municipal water supply. The interaction with the stakeholders led to formulation of new scientific questions regarding the hazard impacts, which manifested during the extreme weather event Hans Storm in summer 2023.

Summer nutrient and chlorophyll gradients in the Stockholm archipelago (Baltic Sea) – observations and predictions from river and point source nutrient loadings

Jakob Walve, DEEP, Stockholm University

Abstract Eutrophication of coastal waters is usually driven by excessive anthropogenic loading of nitrogen (N) or phosphorus (P), or both these elements. However, the nutrient concentrations in the coastal water, and the eutrophication effects such as phytoplankton biomass, vary between areas and in time, due to differences in water exchange with the open sea and differences in nutrient turnover processes, such as nutrient losses to or release from sediments. For Swedish coastal waters the indicators for N and P status assessment according to the EU Water Framework directive (WFD), are based on deviations from reference values, representing unpolluted, background conditions. These reference values are predicted from (modeled) background nutrient loading concentrations in fresh water inflow, a fixed background open sea endpoint concentration, and a conservative nutrient mixing model for the coastal water salinity gradient. Thus, this model accounts for natural inputs of nutrients, and gives reference nutrient concentration as a linear function of salinity. In this study we evaluate summer nutrient and chlorophyll data from the surface water of 10 coastal gradients (July-

August 2004-2019, in total 30 occasions) in the Stockholm archipelago area of the NW Baltic proper, in relation to the loading of nutrients to these gradients, in order to: 1. Validate the WFD mixing model, separately for N and P, 2. Estimate the nutrient contribution from point sources and potential gain of reducing these point source loadings, 3. To validate the phytoplankton chlorophyll a (chl-a) indicator against the nutrient loading pressure and to use the chl-a to nutrient relationships to predict potential improvements from reduced nutrient loading. Surface water total N (TN) concentrations were linearly correlated to salinity in the majority of the coastal gradients. Moreover, TN concentrations generally were well predicted from the salinity and the weighted TN loading concentration preceding the sampling, although in most areas with some underestimation, indicating additional N input from other sources. This was particularly evident in one shallow area with low water turnover rate, where TN gain processes contribute substantially, such N2-fixation or sediments N release. Point sources were important contributors to the observed TN in several of the gradients. As for TN, total P (TP) was also mainly linearly correlated to salinity. However, for most gradients, the weighted TP loading substantially underestimate the observed TP concentration, i.e. other P sources must contribute. Partly, transport of P from the outer coastal area into the coastal gradients may be underestimated, but P inputs from sediments must also be an important P source. In only one of the gradients, point sources were an important contributor to the observed TP concentrations. The results show that the simple WFD mixing model worked fairly well for predicting summer TN, although it may be difficult to adapt to complex gradients with loading from several different sources to different sub-areas. However, the model consistently underestimates the actual summer TP concentration, implying that also natural (WFD reference) TP concentrations are underestimated. Chl-a was well correlated to both TN and TP concentrations. Since the anthropogenic contribution is larger for N than for P, reduction of N loading has the greatest potential to improve conditions in the coastal gradients.

FORALIEN project: Developing novel methods to identify alien species of benthic foraminifera to assess their impact on native biodiversity of the Swedish west coast

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The FORALIEN project (Marie Skłodowska-Curie Actions) addresses the knowledge gap on non-indigenous species (NIS) of benthic foraminifera in Swedish coastal waters to enhance environmental assessment tools. Foraminifera, single-celled eukaryotes with fossilizable hard shells, are reliable indicators of various pollutants, though, quantitative data on species and their environmental drivers remain limited. Recent metabarcoding analyses reveal that foraminifera contain more genetic species than identified morphospecies, showing diverse environmental needs and the potential to hide NIS. Hence, an efficient taxonomy is needed to detect NIS early and manage large biomonitoring datasets. As NIS can threaten native diversity and ecosystem functioning, their identification is crucial, but the impact of hidden NIS is poorly defined and data on invasive nonpathogenic microorganisms remain scarce, despite their prevalence in ballast water and sediments. For instance, few foraminiferal NIS have been reported in Europe, leaving their distribution, ecological needs, and impact on native biodiversity largely unknown. Foraminifera also offer a unique chance to date NIS arrival time using fossils in sediment records, although few studies to date have used sediment cores for this purpose. Swedish harbors are under-researched concerning foraminifera distribution, despite well-known issues such as of pollution and habitat destruction. FORALIEN will obtain modern and fossil data from Swedish west coast harbors and aims to (1) develop novel methods such as digital PCR and machine learning for faster identification of foraminiferal NIS; (2) analyze NIS spatio-temporal distribution to create a NIS impact index; and (3) identify NIS ecological requirements for better integration into monitoring surveys. These findings will enhance our understanding of foraminiferal NIS ecology and provide standardized methods to detect their arrival, define their impact and forecast future invasions.

Who likes it dark and cold? Marine Carbon Fixation during the polar night.

Carolin Regina Löscher   University of Southern Denmark

The Arctic Ocean is characterized by strong seasonal variation in light and temperature, modulated by the cyclic progression and retreat of its ice cover. Anthropogenic climate change is a massive threat to the Arctic Ocean, with warming being a key threat leading, for instance, to changes in global ocean circulation and sea level rise. The light period in spring and summer has traditionally been recognized as the period of high biological productivity in Arctic open and coastal waters, driving pelagic food webs. But is that all? In this presentation, I will present our latest results on dark and cold primary production carried out by a certain consortium of marine microbes in the Arctic Ocean. This process and the respective microbes might be highly relevant and their response to climate change could determine Arctic ecology to great extent.

Accessing picophytoplankton associated phages- what's their impact in the Baltic Sea Ecosystem

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Picophytoplankton, small yet significant contributors to net primary production, form the foundation of marine food webs. In the Baltic Sea, they can account for up to 80% of total phytoplankton biomass. Their distribution and growth are shaped by a complex interplay of biotic and abiotic factors, with viral activity playing a crucial regulatory role. Marine surface waters can contain up to 10^7 viruses per milliliter, and viral infections significantly impact microbial populations by inducing mortality, driving global carbon and nutrient cycling through the conversion of biomass to dissolved organic matter (DOM). Understanding the identity of phages, along with virus-associated mortality, is essential for revealing the ecological and evolutionary dynamics of picophytoplankton. The picophytoplankton community in the Baltic Sea exhibits a diverse range of ecotypes, characterized by distinct seasonal patterns, distribution, and genomic traits, which differ from those in typical marine and freshwater ecosystems. This study comprises of a representative set of brackish-water picophytoplankton ecotypes from the Kalmar Algae Collection (KAC) to isolate novel phage isolates and investigate host-phage interactions in the Baltic Sea. Results show that virus-induced mortality varies significantly over time and between different picophytoplankton ecotypes. Host-range assays with phage isolates further reveal varying susceptibilities among strains, indicating highly specific phage-host dynamics. These findings underscore the essential role of phages in controlling picophytoplankton populations and shaping the microbial ecology of the Baltic Sea.

Recent Changes in Limiting Nutrients in the Gulf of Bothnia

Karolina Eriksson Umeå Universitet

Assessment of eutrophication in the Gulf of Bothnia is difficult because of the lack of knowledge about nutrient dynamics and the contradicting outcomes by different environmental status indicators. In this study we synthesized available monitoring data from Sweden and Finland to elucidate the spatial and temporal variations in limiting nutrient and to detect signals of eutrophication. The results showed that the Bothnian Bay at large is phosphorus-limited, while the offshore Bothnian Sea is nitrogen-limited. In both the Bothnian Bay and the Bothnian Sea, the DIN:DIP ratio has decreased during the past 10 years, mainly due to increasing phosphorous concentrations, likely originating from the Baltic proper. Once the DIN:DIP ratio becomes lower than ~16-20, blooms of filamentous cyanobacteria such as Aphanizomenon starts to appear, as we now can observe in the Bothnian Sea, which risk decreasing the oxygen levels in the bottom waters. In the Bothnian Bay the DIN:DIP ratio is still well above 20, but the decreasing trend is worrying. Once oxygen becomes depleted, there is a risk of release of phosphorous from the bottoms in both the Bothnian Sea and the Bothnian Bay, which in turn accelerates eutrophication with increased primary production, cyanobacterial blooms and inefficient energy transfer in the food web. We should therefore take action to reduce emissions of nitrogen and phosphorus to our vulnerable but valuable sea.

Unveiling the contribution of particle-associated non-cyanobacterial diazotrophs to N2 fixation in the upper mesopelagic North Pacific Gyre

Christian F. Reeder, Alba Filella, Anna Voznyuk, Arthur Coët, Reece James, Tully Rohrer, Angelicque E. White, Léo Berline, Olivier Grosso, Gert van Dijken, Kevin R. Arrigo, Matthew M. Mills, Kendra A. Turk-Kubo, Mar Benavides

Dinitrogen (N2) fixation is a key process supplying reactive nitrogen in marine ecosystems. Although cyanobacteria have traditionally been considered the primary contributors to N2 fixation in the ocean, recent studies have highlighted the potential role of non-cyanobacterial diazotrophs (NCDs) in this process. Devoid of a photosynthetic apparatus, NCDs have been shown to fix N2 when associated with organic particles, presumably providing them with carbon and energy to support this expensive process. Marine particles have a wide range of sizes and sinking dynamics, which may affect particle-associated N2 fixation and diazotroph communities. Here we investigate the community composition and N2 fixation activity of NCDs in the upper mesopelagic zone of the North Pacific Gyre in association with different particle types (suspended, slow and fast sinking particles). While all particle types showed a high relative abundance of NCD groups such as Marinobacter, Oceanobacter and Pseudomonas, our findings reveal a higher diversity of NCDs in fast sinking particles as compared to suspended particles. Gammaproteobacteria associated with suspended and slow sinking particles had the highest N2 fixation rates (10-60 fmol N cell^{-1} d^{-1} and 13-67 fmol N cell^{-1} d^{-1}, respectively), while other non-identified ‘putative’ NCDs fixed more N2 when associated to fast-sinking particles (121 ± 22.02 fmol N cell^{-1} d^{-1}), suggesting that the particle sinking speed constrains NCD communities and their associated N2 fixation activity. The particle-associated N2 fixation rates measured here are comparable to cyanobacterial single-cell N2 fixation, suggesting that particle-associated NCDs are equally important contributors to pelagic N2 fixation.

Single-cell and bulk rate measurements of nitrogen fixation in the Gulf of Bothnia

Olofsson Malin, et al., SLU

Nitrogen fixation, the process in which dissolved dinitrogen gas is turned into bioavailable forms by diazotrophic activities, is an important process in nitrogen low environments. Until now this process has been overlooked in the Gulf of Bothnia, and therefore never measured. We conducted incubation experiments onboard UMF monitoring ships during August 2022 and 2023 to quantify nitrogen fixation rates along transects of variable environmental factors (e.g., nitrogen and salinity). Rates showed large variation both between stations and years but the highest rates were comparable to the rates detected in the Baltic Proper. We also used secondary ion mass spectrometry (SIMS) to address single cell uptake in filamentous cyanobacteria. Results of these two cruises will be presented and discussed.

Day 2 November 27, 2024

The indispensable holistic perspective of the Arctic Ocean

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The relatively small, but extremely resource-rich Arctic Ocean is under considerable pressure from a resource-hungry world. Our scientific approach is often characterized by national, sectorial approaches. However, the Arctic Ocean cannot be understood, let alone managed, without an all-encompassing, pan-Arctic perspective. In natural science, first steps have been taken to achieve such a holistic understanding of the contemporary Arctic Ocean, but to support a sustainable and wisely managed Arctic Ocean in the future, the integrative work has to be carefully and wholeheartedly expanded. Suggestions, such as the integration of national investigations and the education of a future generation of scientists, can improve the indispensable understanding of the entire Arctic, resulting in an adequate comprehension and management.

Revised prokaryotic carbon demand and new depth specific morphological features in the Central Arctic Ocean

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The Arctic region is warming four times faster than the global average, potentially influencing prokaryotic carbon cycling in the Arctic Ocean. Estimating the role of prokaryotes is crucial for modeling the distribution of assimilated carbon between remineralized CO2 and biomass fueling the marine food web. No data on prokaryotic growth efficiency are currently available from the Central Arctic Ocean (CAO). Natural morphological features of Arctic prokaryotes also remain undocumented, limiting our understanding of their ecology and evolution. During the Swedish contribution to the Synoptic Arctic Survey expedition in August-September 2021, prokaryotic growth efficiency in the epipelagic zone was 2% (SE ± 0.5%), i.e., four times lower than the northernmost estimate previously used for carbon demand estimates. The thymidine conversion factor, empirically determined at 0.46 (SE ± 0.09) cells [mol 3H-thymidine]-1 , was also lower than previously used values. These revised estimates resulted in five times higher prokaryotic carbon demand for the CAO compared to 30-year-old estimates. The prokaryotic community composition suggested the predominance of Pelagibacteriaceae and Flavobacteriaceae in the surface layers (10-45 m). Morphological analysis of cells showed that extracellular polymeric substances, stalks and pili were twice as abundant at surface layer as compared to deeper layers (274-507 m). In contrast, cells at deeper layers showed a three times higher occurrence of interaction with spherical structures. This indicates depth specific morphological adaptations of prokaryotic cells, likely aiding nutrient acquisition and cell-cell interactions, even at sub-zero temperatures. The metabolic and morphological insights will advance our understanding of prokaryotic life history in the CAO and can be used to improve carbon models.

Mangrove restoration elevates local carbon storage but changes centennial-scale carbon burial dynamics

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Mangrove forests are some of the most effective carbon sinks on Earth, but they are globally threatened. Understanding the effects of active restoration efforts on mangrove blue carbon dynamics has therefore become a conservation priority. Here, we investigated mangrove carbon storage over time in and around the Xuan Thuy National Park in the Red River delta, northern Vietnam, comparing old-growth forests, areas of artificial restoration, and areas of natural spontaneous regeneration. The amount of carbon in the old-growth forest sediments has been higher than the restored or regenerated areas since the 1960s. Stable isotope signatures indicate the stored carbon has been consistently dominated by marine plants and algae for at least the past 120 years. However, since the 1960s in the restored mangrove area, there was a shift in the carbon source, to a dominance of mangrove-derived organic matter. This suggests that restoration activities may change the carbon cycling of mangrove forests, creating a ‘closed’ system of autochthonous carbon fixation and storage, and reduced interaction with marine-derived carbon. Mangrove restoration therefore holds potential for promoting blue carbon storage, but this may coincide with a loss in external linkages – which may have cascading impacts on wider ecosystem functioning.

SwedCoast-BlueCarb project: mapping eelgrass extent and health

Dr Samantha Lavender (Pixalytics Ltd) and Dr Susanne Kratzer (Stockholm University)

In support of broader activities to protect eelgrass beds, stop ongoing losses and facilitate recovery, satellite Earth Observation (EO) based research is being carried out on populations around the Swedish coast. The SwedCoast-BlueCarb project, funded by the Swedish and UK Space Agencies, aims to use a combination of EO and in situ data (for validation) to assess the possible effects of mitigation efforts against climate change in the designated test areas that include contrasting conditions found around Kalmar and on the Swedish West Coast. Initial project activities aimed at finding relevant projects sites and setting up collaborations within academia and monitoring programs. Laboratory-based activities have focused on understanding the absorption and reflectance spectra of submerged vegetation. Initial EO work has focused on consistently processing

satellite datasets, and ongoing work is developing a machine-learning model based on surface reflectance that can concurrently derive the optical properties and submerged vegetation. This approach includes applying Copernicus Sentinel-2 satellite data to map the eelgrass extent with associated uncertainties where the populations exist at a detectable depth. Also, the aim is to understand the water's optical status, which can impact light availability and health, with the coarser spatial resolution (300 m versus 20m for Sentinel-2) marine-focused Copernicus Sentinel-3 mission providing supporting information. A WorldView-2 image (Kalmar Sound) shows the potential improvements with higher spatial resolution (2 m) commercial satellites. Ultimately, an automated processing system will systematically provide products openly online within a GIS-style portal, supporting local authorities and conservationists with the required information to conserve existing populations and potentially support replanting activities. The progress, including the portal, will be showcased during the presentation.

Perfoliate pondweed meadows in northern coastal areas – reservoirs of potentially pathogenic bacteria with complex organic carbon metabolism

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The perfoliate pondweed, Potamogeton perfoliatus, is a very common macrophyte in freshwater and subarctic coastal areas. This species builds extensive meadows that play a role as a filter removing nutrients traversing from land to sea and maintain essential ecosystem functions. Here, we investigated the function of perfoliate pondweed as a filter of potentially pathogenic bacteria by combining culture-dependent and 16S rRNA metabarcoding approaches. Our results suggest no significant nutrient reduction in the meadow region but the enrichment of potentially pathogenic bacteria, such as Vibrio, Aeromonas and Serratia taxa, particularly attached to macrophyte leaves. The bacterial community composition differed between seawater and macrophyte habitats, with higher relative abundances of Cyanobacteriia attached to macrophytes, without affecting alphadiversity. The metabolic pathways of bacteria for aromatic and polymer compound degradation were enriched in the macrophytes, attributed to members of the genera Pseudorhodobacter, Novosphingobium, and Erythrobacter. Macrophyte-attached bacteria might, therefore, have an ecosystem function as degraders of complex terrestrial compounds when passing from land to sea. Further, the macrophyte meadows may be relevant for human diseases, as they harbor potentially pathogenic bacteria. Keywords: Potamogeton perfoliatus, 16S rRNA Metabarcoding, Epiphytes, Metabolic Pathways, Potential pathogens.

Impact of ship traffic: Mixing, Spreading of Pollution from Scrubbers and Heavy Fuel Oil Pollution

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In recent publications the environmental impact of ship mixing was investigated through combined field measurements and modelling. The results highlight the importance of addressing ship-induced turbulence in marine environmental management. Ship traffic can lead to physical, biological and chemicals changes like enhanced nutrient loads, spreading of pollution and effects on plankton communities. Many ships still operates on heavy fuel oil and uses scrubbers to clean the fumes and release the pollution to the water. Running on heavy fuel also leads to great impact on the marine environment when accidents happen, which was recently the case in Hanö bay, South East Sweden

Long-term environmental changes in the northern Baltic Sea – Impact on food web efficiency and quality

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Climate change causes large environmental changes in many marine ecosystems which can alter the overall food web production. However, there is a large knowledge gap about long-term changes in food web efficiency and food web quality in sub-arctic marine ecosystems such as the northern Baltic Sea. We analysed the fatty acid composition of archived herring samples in the Gulf of Bothnia to evaluate the nutritional quality of herring from 1995-2020. Long-term data on heterotrophic bacterial production and primary production was extracted from the Swedish national marine monitoring program (i.e., the SharkWeb database). Herring biomass production was also evaluated. We then calculated the food web efficiency as the ratio between herring production and the sum of bacterial and primary production. Food web quality measured in terms of omega-3 and omega-6 polyunsaturated fatty acid (PUFA) (i.e., ω3 and ω6 PUFA) content in Bothnian Bay herring has decreased over time, likely due to the long-term decrease in salinity, and dissolved organic carbon. In contrast, omega-3 and omega-6 PUFA content in Bothnian Sea herring did not show any long-term change and variations and did not relate to the environmental changes. During 2001-2009, herring production and bacterial production in the Bothnian Sea was stable. However, primary production has significantly increased. As a result, food web efficiency in the Bothnian Sea has significantly reduced from 2001-2009 likely due to increased primary production which was not efficiently transferred to the upper trophic levels. Our results indicated that climate change-induced environmental changes likely have a negative impact on food web quality in the Bothnian Bay and

food web efficiency in the Bothnian Sea. Keywords: Food web efficiency, food web quality, Fatty acids, Baltic Sea, Herring.

Land-Sea-Air Exchange of Natural Halogenated Compounds in Northern Sweden

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Climate change is expected to increase precipitation in northern Sweden, leading to higher riverine discharge of dissolved organic matter (DOM) (1). We are using halomethoxybenzenes (HMBs) to follow land-river-estuary transfer and exchange with air: brominated anisoles (BAs), produced by marine algae and bacteria, and drosophilin A methyl ether (DAME = 1,2,4,5-tetrachloro-3,6-dimethoxybenzene), a secondary metabolite of terrestrial fungi (3). Studies were conducted in rivers and estuaries of Bothnian Bay (BB) in Västerbotten County (VC), Sweden (2) and at Lake Torneträsk (LT) (68o 22'N, 19o 06'E) and streams in subarctic Sweden (3). Sampling and analytical methods are reported in (2-4).

Concentrations of BAs in water followed the order: estuaries > offshore > VC rivers > LT and streams. Highest concentrations in estuaries can be attributed to local production. DAME concentrations were highest in VC rivers (land runoff) followed by estuaries > offshore > LT and streams. DAME was also found in soil/litter samples from the VC and LT areas (3-5). DAME was positively correlated with DOM in one estuary with a small river, while there was no correlation in an adjacent bay with no river (2). Preliminary estimates of riverine discharge of DAME into BB are in the tens of kg y-1. In contrast, input of BAs to BB by rivers appears minor relative to *in situ* production (2).

Fugacity calculations suggest net evaporation of BAs and DAME from water bodies and DAME from soils (5). Volatilized HMBs disperse through the atmosphere and return via precipitation and rivers, in cycles that connect ecosystems and provide widespread exposure to organisms (6,7). DAME has the potential for toxicity that is characteristic of persistent organic pollutants (POPs) (6). HMBs bioaccumulate (6-9) and may provide indicators of accumulation pathways in the coastal zone.

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Baltic Sea warming and related biogeochemistry changes

Ketzer, M., Stranne, C., Chang, C., Rhamati-Abkenar, M., Hylander, S., Forsman, A., and Dopson, M.

The Baltic Sea is considered a proxy or a “time machine” for the future shallow and coastal marine environments owing to its singular natural conditions, anthropogenic interference, ecosystem deterioration, and implementation of mitigation actions. Many studies have addressed the deterioration of Baltic Sea environment, but some topics are still open for debate. Here we present our latest results about one of these important topics: the effects of Baltic Sea warming on biogeochemistry and their implications for methane cycling. We found that long-term warming causes the thinning of the sulphate reduction zone and increases the chances of methane release on the seafloor. Our findings are based on (1) six years of observations in a bay in the Oskarshamn area, southeastern Sweden, that has been artificially heated (ca. 5°C in relation to control areas) for 50 years, and (2) a recently discovered major seafloor methane ebullition site in the Landsort Deep area, in the central Baltic Sea.

Size-Dependent Accumulation of Persistent Organic Pollutants and Mercury in Juvenile Herring

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The Baltic Sea has historically been plagued with a high input of persistent organic pollutants (POPs) and heavy metals such as mercury. Although recent decades have seen a decrease in the input of POPs and mercury, extensive legacy concentrations of these compounds still exist in the environment with potentially detrimental effects for both the organisms living in the Baltic and those that consume them (i.e. humans). In addition, environmental changes may increase the bioavailability of these contaminants in the future, through, for example, increased land runoff, melting tundras, increased hypoxia, and more eutrophication, all of which may affect the dynamics of contaminants and heavy metals in biota. Baltic herring (Clupea harengus membras), an economically important species due to consumption by humans, have been extensively studied and analyzed for the presence of POPs and heavy metals for decades. Although a long history of contaminant data exits for herring, previous research has entirely focused on adult fish which feeds partly on benthos, and not juvenile young-ofyear (YOY) individuals which feed only from the pelagic food web. In this study, YOY herring were captured from the coastal Baltic Sea throughout the summer at two stations which differ in eutrophication status, and analysed for dioxins, dioxin-like polychlorinated biphenyls (PCBs), and mercury. Results showed that POPs were unexpectedly highest in the smallest individuals and decreased over the growing season as fish grew larger, indicating growth dilution. An opposite trend was however seen in Hg where the lowest levels were seen in the smaller fish and concentrations increased with fish size. Potential reasons for this contrasting pattern as well as ecological implications are discussed. This study is one of the first to investigate contaminant concentrations in juvenile herring and the results will add to the knowledge of Baltic contaminant cycling and to the origins of contaminants in young coastal fishes.

Are small pelagic fish competing for resources in the central Baltic Sea?

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Small pelagic fish, or forage fish, are the most abundant fish in the pelagic. However, only few species compose the forage fish stocks, making them prone to high fluctuation with consequences for lower trophic levels, such as zooplankton, and higher trophic levels, including predatory fish, marine mammal, and sea birds. Environmental parameters and plankton dynamics are often reported to be the main drivers of fish stock dynamics, whereas interspecific competition is often overlooked. Here, we used DNA metabarcoding, stable isotopes and microscopy to identify the entire resource use and overlap of the three dominating forage fish in the Baltic Sea, the two clupeid species, herring (Clupea harengus) and sprat (Sprattus sprattus), and the three-spined stickleback (Gasterosteus aculeatus). The fish and their zooplankton prey were sampled in the central Baltic Sea in May 2022 and 2023 and October 2022, during the SPRAS and BIAS monitoring surveys, respectively. We found that clupeids shared a similar diet in spring, composed mainly of the copepods Pseudocalanus and Acartia, whereas stickleback favoured different copepods species and the rotifer Synchaeta. Consistently, stickleback had a distinct isotopic niche with lower d13C than the two clupeid species. However, in fall, all fish preyed on different assemblages, mainly composed by various copepod species. This was further supported by the isotopic signatures that differed across all fish species. Our results show that resource competition was overall limited, but sprat and herring had the strongest trophic overlap in spring, when zooplankton biomass is low. Our study suggests that the distinct niche of stickleback have enabled its recent increase, and that the clupeid niche overlap in spring may not fully explain sprat and herring decline. These findings illustrate that an improved understanding of species interactions is key to advice ecosystem management for sustainable fisheries and marine biodiversity protection.

Aquarius – Providing transnational access to integrated research infrastructures

Björn Lindell, Swedish University of Agricultural Sciences

Aquarius is a Horizon Europe funded programme with a duration of 4 years starting in March 2024. The budget is €14.5 Million and it will bring together research infrastructures from 45 organisations spanning 18 nations.

The aim is to provide free & supported access to a comprehensive & diverse suite of 57 integrated research infrastructures to address challenges & explore opportunities for the long-term sustainability of our marine & freshwater ecosystems.

AQUARIUS will

- Provide single-point access to a curated catalogue of 57 diverse marine & freshwater research infrastructure services
- Design, develop, & manage 2 Transnational Access Funding Calls, providing free & supported access for selected projects to the research infrastructure
- Deliver scientific & technical training to apply for & use the research infrastructures

- Ensure advanced data management to make data FAIR (Findable, Accessible, Interoperable, & Reproducible), according to open, global standards
- Maximise impact ensuring that AQUARIUS & the projects it supports deliver to the goals of the Mission ‘Restore our Ocean & Waters by 2030

AQUARIUS will launch two transnational access funding calls for research and innovation project proposals. Proposals must demonstrate how they will integrate multiple infrastructures and contribute to the defined Mission Ocean challenges. Calls are open to scientists from research and academia, from industry, and from citizen science groups, according to the defined eligibility criteria.

- Call 1 – Open: 11 November 2024 – 20 January 2025
- Call 2 – Open: 02 September 2025 – 28 October 2025

SWERVE - Current Achievements and Future Directions

Lovisa Thoursie, Göteborgs universitet

Current Achievements Since its launch in early 2024, SWERVE has made significant progress. The project has successfully established a network of research vessel users, launched its official website (swerve.se) and completed the first ship-time application round. The allocations from this call is set to be announced by the end of 2024 for ship-time scheduled in 2025–2026. In addition, SWERVE has also created a National Marine Technicians Network (NMTN), available to marine technicians across Sweden. Members of this network participated in the first annual training course, held in November, with a focus on CTD systems. Three other activities that SWERVE has begun carry out, that will continue during the upcoming year, is creating a national sensor inventory, the work with data delivery and standardised routine for CTD data management. SWERVE now has a solid base to stand upon, when looking at the progress the project intends to do during the upcoming years. Future Directions Looking ahead, SWERVE intends to build on the work already begun, while also implementing additional components of the SWERVE work plans. Future work will include providing new training courses, creating an expert contact list with focus on technical expertise, creating a national equipment inventory and moving along with the research voyages. Ultimately, the work completed so far, along with our plans for continued efforts, demonstrates the value of SWERVE. We look forward to advancing the project's activities moving forward.

Day 3 November 28, 2024

Co-Creating a Blueprint for Integrated Ocean Science: Encouraging collaboration for a sustainable future

Lina M. Nordlund[1], Nina Lepola[1], Florian Lüskow[1], Artur Palacz[2]

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The BioEcoOcean project is co-creating a Blueprint for Integrated Ocean Science (BIOS), a guiding framework to advance collaborative and sustainable ocean observation. BIOS seeks to transform biological and ecosystem monitoring, supporting science-based conservation and informed policy. Through a question-based structure, BIOS fosters global collaboration across disciplines and sectors, addressing critical issues such as biodiversity loss, climate impacts, and invasive species. This approach enables stakeholders - including scientists, data managers, and policymakers - to contribute insights from each ocean observation value chain stage, from data collection and management to policy integration. BIOS aims to address critical conservation issues, such as biodiversity loss, climate impacts, and invasive species, by fostering collaboration across scientific, data management, and policy sectors. Central to this approach is the use of biology and ecosystem Essential Ocean Variables (EOVs), globally standardised metrics that, if adopted, would enable the consistent, open-access collection of data critical to conservation. For example, EOVs can generate distribution maps highlighting regions in decline, and areas of recovery, or serve as early-warning systems for invasive species. Participants from diverse regions and expertise are invited to engage in BIOS's development. Together, we will identify key challenges and form actionable questions that advance a unified, open-access approach to marine observation. BIOS's emphasis on integrating environmental, social, and economic factors ensures a comprehensive approach, providing tools essential for conservation. Scheduled for launch in 2027 via the Global Ocean Observing System (IOC-UNESCO), BIOS will be openly accessible and endorsed globally. Through BioEcoOcean, BIOS represents a shared commitment to ocean sustainability, aiming to guide the conservation, management, and sustainable use of marine ecosystems worldwide.

Ventilation of the Arabian Sea Oxygen Minimum Zone

Estel Font, Department of Marine Sciences, University of Gothenburg

Oxygen minimum zones are expected to change, yet climate models struggle to accurately represent their current coverage and future fate due to limitations in capturing processes at small temporal and spatial scales. For instance, misrepresentation of surface mixed layer variability, mode water formation and dense outflows from marginal seas, can result in large biases in oxygen ventilation. We bring together simultaneous observations of oxygen and ocean currents in the Arabian Sea Oxygen Minimum Zone, using gliders and floats, to understand how these physical processes influence oxygen ventilation.

Shear-driven mixing and oxygen fluxes in the upper thermocline in the Cape Basin

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As part of the QUICCHE (QUantifying Interocean Fluxes in the Cape Cauldron Hotspot of Eddy Kinetic Energy) project, an underwater glider was deployed in the Cape Basin to assess vertical and horizontal mixing, along with oxygen fluxes. The glider was equipped with sensors for temperature, salinity, dissolved oxygen, chlorophyll-a and optical backscatter, as well as a Nortek 1MHz AD2CP for high-resolution current measurements and a Rockland MR-1000G microstructure turbulence sensor. We also compared the in-situ current velocities with newly available high-resolution sea surface height data from the SWOT satellite during its calibration period revealing a dynamic eddy merging event. The Cape Basin, where Indian, Southern and Atlantic Ocean water masses converge, supports complex physical and biogeochemical interactions. Our analysis focuses on enhanced diffusivity in response to instabilities caused by the eddy merging event. Estimates of diffusive oxygen fluxes reveal significant variability under contrasting oceanic conditions in this energetic region. In particular, we observe the subduction of the near surface high-dissipation layer (from 20 m to ~100 m depth), highlighting the potential for strong and episodic ventilation and the capability of these phenomena to link the energetic surface with the ocean interior. These results highlight the ability of underwater gliders to capture turbulent diffusive fluxes and their variability across sharp ocean gradients and in strong ocean currents (mean ocean velocity > 0.3 m.s-1 between the surface and 1000 m), contributing to a better understanding of shear-driven mixing and oxygen dynamics in the Cape Basin.

Glider Observations and Modeling of dissolved Methane from Nord Stream Leaks

*Martin Mohrmann1, 2 , Louise C. Biddle1, 2, Gregor Rehder3, Henry C. Bittig3, Bastien Y. Queste2**

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The study presents an analysis of elevated methane levels in the Baltic Sea, caused by ruptures in the Nord Stream gas pipelines. Observations of methane concentrations, collected through autonomous gliders and a Ship of Opportunity System (SOOP) complement each other to understand the distribution and pathways of dissolved methane. Using these measurements, a Lagrangian drift and fate model fills the gaps of the subsurface dispersion of methane in the water column. The initial quantity of dissolved methane from the leaks is estimated to be approximately 10 kt, constituting a substantial portion of the total emitted methane that escaped the pipelines. The glider observations show that dissolved methane concentrations are highest in intermediate depths, above a local halocline and below the seasonal mixed layer. Its dispersion is primarily controlled by advection. Elevated dissolved methane levels, from 2 to more than 100 times above natural levels, occured in 23 Marine Protected Areas. Some dissolved methane initially observed below the autumn mixed layer is subsequently entrained into the deeper winter-time mixed layer and released into the atmosphere. The impact of heightened dissolved methane levels in the Baltic due to the leaks is not yet completely understood. However, the majority of dissolved methane outgassed into the atmosphere within a three-month period, where it acts as a potent greenhouse gas. This study

emphasizes the importance of prompt and ongoing marine environmental observations, which can be achieved through the use of autonomous systems like gliders and SOOP.

Phosphorus strategies in the microbial-planktonic community across the Baltic Sea

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The Baltic Sea presents a north-south gradient in salinity, temperature, and nutrient limitation, with distinct regional characteristics impacting its ecosystem. In the Bothnian Bay, low temperature and salinity along with phosphorus limitation resemble a freshwater ecosystem. Moving south to the Bothnian Sea, there is a transition marked by higher salinity and seasonal nitrogen limitation. The Baltic Proper with higher salinity and temperature and nitrogen as limiting nutrients has more marine-like characteristics. Climate change scenarios suggest shifts such as decreased salinity and increased temperatures will lead to increased release of phosphorus from the sediments. This could translate into a shift in community composition in spring, higher filamentous cyanobacteria biomass in summer and increased microbial phosphorus recycling after the blooms. Previous research has scarcely examined microbial and phytoplankton strategies for phosphorus acquisition. To address this gap, recent metatranscriptomic analyses have begun to address this by mapping eukaryotic and prokaryotic responses across spatial-temporal scales in these regions, combining a year of monitoring in the Baltic Proper and cruises during spring and summer in the Bothnian Bay and Bothnian Sea. Despite differences in community composition across the basins, microbial and phytoplanktonic communities shared similar mechanisms in phosphorus acquisition. Across the Baltic, transporters are pivotal in both prokaryotes and eukaryotes, followed by intracellular processes like membrane remodelling. Our results highlight cellular adaptability in the microbial-plankton ecosystem despite fluctuating environmental conditions.

Carbon and nitrogen assimilation in individual cells can shed light on how diatoms survive diffusion limited nitrogen availability

Rickard Stenow, University of Gothenburg

Marine diatoms are responsible for 20% of global primary production They can form large seasonal bloom that greatly impact higher trophic levels and carbon sequestration. But what happens to them once the party is over? How do they survive nutrient or light limited conditions to seed next year’s bloom? I will present how chain forming diatoms can circumvent diffusion limited nitrogen transports by interactions with associated bacteria and luxury nitrate uptake. These nutrient dynamics were studied in two chain forming diatoms and associated bacteria on a single cell level using SIMS (secondary ion mass spectrometry) and nanoSIMS. Nitrogen assimilation was studied during diffusion limited nitrate availability in two chain forming diatoms, Chaetoceros affinis and Skeletonema marinoi. Both species avoided relying on the diffusion limited supply in a manner corresponding to their respective niche. S. marinoi which dominates early blooms quickly assimilated an excess of nitrate during high availability. This supply is presumably sufficient for the cells to survive transportation to the sediment and formation of resting stages. In contrast C. affinis which succeed S. marinoi recycled N from bacterial remineralization of inactive diatoms within the colonies as ammonium. This matches their respective niche, Skeletonema are commonly seen initially in spring blooms where they could assimilate much nitrogen. Chaetoceros are more common in late summer conditions when nitrate availability is low over extended periods.

Selective grazing on strains of the picocyanobacterium Synechococcus

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The picocyanobacterium Synechococcus is an abundant and significant primary producer with a world-wide distribution. The genus is highly diverse, consisting of more than twenty phylogenetic clades. Although ecotypes with distinct distribution patterns have been identified, multiple strains of Synechococcus frequently co-exist. The diverse characteristics of co-existing strains including differences in their pigmentation, may influence their grazing susceptibility, but little is known about energy transfer to higher trophic levels, selectivity or the response to grazing pressure of specific Synechococcus strains. In this study, we performed culture experiments to examine differences in the grazing of PC-rich and PE-rich Synechococcus strains and studied predator-induced formation of microcolonies as a possible defense mechanism. While the PE-rich strain was grazed, the PC-strain was not affected by the presence of the heterotrophic nanoflagellate Picophagus sp. We also observed differences in the extent of microcolony formation among the strains. We further inoculated stable isotope-labelled Synechococcus cells to coastal Baltic Sea seawater samples to identify active grazing. In total, 8 experiments were conducted in spring (April/May) and 8 experiments were conducted in summer (June) covering different productivity gradients and populations of grazers. The experiments allow for novel insights about interactions in the microbial food web and an increased understanding of the ecological consequences of within genus diversity.

Poster Abstracts

Submarine Landslides and Potential Tsunami Events in the Baltic Sea: Enhancing Geohazard Understanding for Submerged and Coastal Infrastructures

Elinor Andrén1 , Thomas Andrén1 , Jens Heimdahl2 , Martin Jakobsson3, Matt O'Regan3 , Carl Persson4 , Alar Rosentau5 , Johan Rönnby1 , Christian Stranne3 , Oscar Törnqvist1,6

1 Södertörn University 2 The Archaeologists 3 Stockholm University 4 Blekinge museum 5 University of Tartu, Estonia 6 Swedish Geological Survey

The discovery of extensive landslide scars in the southern Baltic Sea during the Swedish Geological Survey's sea floor mapping has raised questions regarding the timing and triggering factors of landslide events. The primary goal of this study is to conduct a comprehensive analysis regarding the areal extent and timing of submarine landslides, with focus on their potential to trigger tsunamis that could impact coastal regions. The research draws inspiration from historical events such as the Storegga slide off the coast of Norway ca. 8150 years ago which resulted in a tsunami that propagated across vast areas, leaving notable geological traces. By examining evidence from the Baltic Sea region, the study aims to shed light on the potential occurrence of tsunamis in this previously unexplored context. Various indicators, including disrupted stratigraphic offshore sediment profiles, sudden and rapid sea level rise and the abrupt inundation of Mesolithic settlements, suggest that a significant event in the region occurred in the past. Considering ongoing global warming and anticipated sea level rise, the southern Baltic Sea, lacking post-deglaciation land uplift, is particularly vulnerable to such changes. In essence, this research not only contributes to a deeper understanding of geohazards in the Baltic Sea but has important implications for coastal infrastructure planning in the face of climate change and sustainable mitigation strategies.

Life Among the Cod: Sessile Communities on Artificial Reefs in the Baltic Sea

Clara Palmer, Lou Cloix, Josefine Larsson, Hampus Söderberg, Hannes Kindeberg, Anders Tengberg, Anders Persson, Peter Ljungberg, Helena L. Filipsson.

Lund University, Marin center Simrishamn, Hanö torskrevsförening

The Baltic Sea has a generally low biodiversity, and several species are declining due to high anthropogenic pressure. One example is the Baltic Sea cod (Gadus morhua, L.), the cod has decreased since the 1980s in both biomass and abundance. One potential solution to increase the cod population is to improve settling ground and provide shelter for juveniles in artificial reefs. The Hanö Cod Reef project aims to increase the carrying capacity of cod in the southern Baltic Sea. The man-made structures could however benefit more than cod and an increase in settling ground for example epiphytic organisms could lead to a positive bottom-up effect on the ecosystem. In this study we aimed to investigate the colonization of epiphytic organisms on Hanö Bay cod reef over time. In February 2023 14 reefs were installed and an additional 20 reefs in 2024. The reefs were documented using an underwater ROV. The video footage was analyzed and the epiphytic organisms were categorized into groups of: blue mussel (Mytilus edulis), Hydroids (life stage of Hydrozoa spp.), Barnacles (Amphibalanus improvises), Bryozoa spp., Rhodophyta spp., Chlorophyta spp. and "No organisms". The result showed that blue mussels are the first to colonize the reefs while macroalgae

(Rhodophyta spp. and Chlorophyta spp.) had the slowest colonization rate. Blue mussel, both as migrating older individuals and as settlement by new individuals increased the competition for space. Bryozoa spp. was not detected until March 2024 emphasizing the importance of time for high biodiversity to accumulate. These findings suggest that, beyond supporting cod populations, the artificial reefs in Hanö Bay provide valuable habitat for a variety of sessile organisms, which in turn may contribute to increased biodiversity and ecosystem complexity in the area. As colonization progresses, the reefs could attract an even wider array of species, potentially creating new niches and enhancing the resilience of local marine life.

Assessment of algal toxins in Mytilus edulis from mussel farms in the Baltc Sea – Seasonal observatons

Manuela Seehauser, SLU

Algal blooms are a prominent natural phenomenon in the Baltic Sea, especially during summer months when temperatures favor the overgrowth of algae and cyanobacteria. With increasing anthropogenic pressures on the Baltic Sea, algal blooms are predicted to intensify, potentially leading to a shift in the functionality and structure of the entire ecosystem. Besides that, their toxic potential poses a health risk to other aquatic organisms, particularly those that feed on phytoplankton, like mussels, and are thus also of concern for aquaculture and food safety. Although the risks of harmful blooms are well known, knowledge about the seasonal dynamics of harmful algal species in the Baltic Sea and the conditions triggering toxin production remains limited. In this study, we investigate the seasonal patterns of harmful algal blooms at two mussel farms in the Baltic Sea in relation to environmental drivers, such as temperature and nutrients. We aim to disentangle the composition of the microbial community over the entire season by applying a combination of metagenomic tools and microscopy. The genetic repertoire related to toxin production, as well as the regulation of toxin-relevant genes, is further investigated using multi-omic approaches. Key toxins extracted from mussel tissues and water samples are identified and quantified using advanced analytical methods, including LC-MS. Our investigations aim to support the adaptation of regulatory frameworks and assist stakeholders in managing their cultivation and harvesting strategies under bloom events in the Baltic Sea, with the ultimate goal of ensuring safe aquaculture practices under challenging environmental conditions.

Gas transfer velocity of methane in coastal settings at low wind speeds

Thea Bisander[1], Volker Brüchert[2,3], John Prytherch[4]

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The coastal zone is a significant source of methane (CH_4) emissions, accounting for the majority of oceanic contributions to atmospheric CH_4 concentrations. Gas flux across the water-air boundary relies on two main components: the concentration gradient between water and atmosphere and the gas transfer velocity (k), which determines flux efficiency. Existing parameterizations of k, primarily developed for open-ocean environments with wind as the sole contribution to turbulence, often focus on moderate to high wind speeds scenarios. However, accurately characterizing k under low-wind conditions is essential for coastal CH_4 assessments, especially in shallow nearshore zones where wind-driven turbulence might be limited. This study examines CH_4 fluxes and k_{660} in shallow, sheltered marine environments of the Baltic Sea under low wind (< 5.8 m s^{-1}), with a focus on (1) understanding the behaviour of k_{660} as wind approaches zero, and (2) identifying variations in k_{660} across sites with different exposure and vegetation cover. Using floating chamber incubations, we observed a quadratic relationship between k_{660} and wind speed, with results supporting a non-zero intercept, indicating the role of alternative turbulence drivers in CH_4 transfer under these conditions. Differences in k_{660} between sites were linked to factors such as water movement and emergent vegetation. Further, onshore winds produced a stronger correlation with k_{660} than offshore winds. These findings suggest that accurate coastal CH_4 flux estimates may require region-specific k parameterizations and at minimum, the inclusion of non-zero intercept models.

Do picophytoplankton sink? The Baltic Sea as a case study

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Primary production by phytoplankton plays a crucial role in the global carbon cycle by converting carbon dioxide into biomass, by which a fraction is exported into the deep. Picophytoplankton often dominate phytoplankton biomass, but the long-standing paradigm is that their small size (< 2µm) prevents them from sinking. This paradigm, however, is challenged through modelling studies, but observational field data confirming picophytoplankton sinking is still largely lacking. Picophytoplankton in the Baltic Sea encompasses diverse groups, including both picocyanobacteria and photosynthetic picoeukaryotes. Aggregate formation is expected to play a fundamental role in the potential export of picophytoplankton. The high diversity of picophytoplankton corresponds to a range of ecophysiologies, which, therefore, necessitates high taxonomic resolution when studying their sinking patterns. In this study, we assess species-specific sinking patterns of picophytoplankton through amplicon sequencing of 16S and 18S rRNA genes. We investigate natural picophytoplankton populations on sinking aggregates in the brackish Baltic Sea through the deployment of marine snow catchers at two different depths (5 and 30 m) at 23 stations during two cruises with R/V Aranda in the spring (April) and summer (June) of 2024. This technique enabled the targeted study of suspended cells and actively sinking marine snow (aggregates) as two separate fractions. By covering temporal (spring and summer) as well as abiotic and biotic gradients (e.g. salinity, inorganic nutrients, and phytoplankton biomass) in the Baltic Proper, Gulf of Finland, Bothnian Sea and Bothnian Bay, we examine the environmental regulation of picophytoplankton associated with sinking aggregates. Ultimately, the data generated will help elucidate the role of picophytoplankton in carbon export, which is of global importance due to an expected increase in picophytoplankton abundance and distribution with progressing climate change.

Community assembly under stable temperatures compared to seasonal drivers

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Marine bacteria are the main contributors to organic carbon turnover in the microbial loop and via their respiration directly influence how much carbon is stored or excluded from long-term storage in the ocean. Yet, they receive little consideration within ocean change research. In addition, the high complexity of marine ecosystems impedes the disentanglement of long-term microbial observations to identify the mechanisms behind bacterial community assembly, its persistence and thus, how it is impacted by climate change. Nonetheless, recent work has indicated that marine microbial communities are especially impacted by temperature (e.g., in terms of community composition and gene expression), albeit it is still unknown how this affects specific community dynamics and bacterial interactions. For this study, we are currently implementing a microbial time-series with weekly sampling using aquaria tanks as a model system. In collaboration with the Maritime Museum Aquarium in Gothenburg, we are sampling the bacterial biodiversity of four aquaria since January 2024 to: i) assess the bacterial community dynamics in four model ecosystems (two tropical and two temperate) on a structural (16S rRNA amplicon sequencing) and functional (metagenomics) level, ii) generate ecological understanding on mechanisms and drivers of change of bacterial community assembly and its persistence under stable temperature conditions, and iii) transfer this knowledge to ocean time-series conducted in similar ecosystems to understand the observed temporal dynamics in the bacterial community. Our findings will help us to explain the long-term structural and functional community dynamics that we observe in natural marine microbial communities but struggle to understand due to the high complexity of natural ecosystems. This will facilitate our ability to predict how microbes and their provision of essential ecosystem services will be affected by events such as global warming.

Baltc Sea Coastal Sediment-Bound Eukaryotes Have Increased Year-Round Actvites Under Predicted Climate Change Related Warming

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Climate change related warming is a serious environmental problem attributed to anthropogenic actvities, causing ocean water temperatures to rise in the coastal marine ecosystem since the last century. This particularly affects benthic microbial communities, which are crucial for biogeochemical cycles. While bacterial communities have received considerable scientific attention, the benthic eukaryotic community response to climate change remains relatively overlooked. In this study, sediments were sampled from a heated (average 5 °C increase over the whole year for over 55 years) and a control (contemporary conditions) Baltic Sea bay during four different seasons across a year. RNA transcript counts were then used to investigate eukaryotic community changes under long-term warming. The composition of active species in the heated and control bay sediment eukaryotic communities differed, which was mainly attributed to salinity and temperature. The family level RNA transcript alpha diversity in the heated bay was higher during May but lower in November, compared with the control bay, suggesting altered seasonal activity patterns and dynamics. In addition, structures of the active eukaryotic communities varied between the two bays during the same season. Hence, this study revealed that long-term warming can change seasonality in eukaryotic diversity patterns. Relative abundances and transcript expression/count comparisons between bays suggest that some taxa that now have lower mRNA transcripts numbers could be favored by future warming. Furthermore, long-term warming can lead to a more active metabolism in these communities throughout the year, such as higher transcript numbers associated with diatom energy production and protein synthesis in the heated bay during winter. In all, these data can help predict how future global warming will affect the ecology and metabolism of eukaryotic community in coastal sediments.

The need for health monitoring of Kalmarsund harbour seals

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The small and genetically distinct population of harbour seals (Phoca vitulina) from Kalmarsund is classified as vulnerable due to hunting and disease outbreaks, emphasizing its need for unique conservation and management efforts. Since the 1970s, a research and health monitoring program on all three seal species occurring in Sweden has been conducted at the Swedish Museum of Natural History (NRM). The focus has been pathological- and reproductive changes in combination with environmental contaminant effects. Nowadays NRM, in collaboration with the Swedish Veterinary Institute (SVA), coordinates health and disease monitoring programs, which require collecting stranded seals with unknown cause of death to SVA and unintentionally bycaught and hunted seals to NRM. Due to hunting and fishing restrictions, as well as low number of stranded harbour seals, NRM and SVA receive very few individuals from Kalmarsund, which poses difficulties in assessing the health of this particular population. Collected bycatches tend to be biased towards very young individuals, since collecting older seals is laborious. Here we present the age distribution and pathological changes in harbour seals collected from Kalmarsund (n=41) to NRM during the last 10 years and compare them to the population on the Swedish west coast (n=713). Notably, our findings indicate a higher prevalence of mild mucosal erosions in the colon of Kalmarsund harbour seals compared to their west coast counterparts, as well as a much higher colonic parasite burden (Corynosoma spp.). When taking the bottleneck effect and inbreeding of the Kalmarsund population into account, they might be more susceptible to pathological changes than other populations. To gain a comprehensive understanding of the Kalmarsund harbour seals' health and dynamics, we emphasize the need for collecting more individuals (particularly older ones) for future research and monitoring.

Food quality vs. quantity: Effects on health status in Eastern Baltic Cod

Johanna Fröjd, Stockholms Universitet

The Eastern Baltic Cod (Gadus morhua) is in a poor condition and experience low growth rate . Food limitation from overfishing of its main prey sprat and herring, a nutritional imbalance of prey, hypoxia or parasite infestations from the increasing seal population has been put forward as potential explanations. This study investigates the influence of food quality and quantity on body mass increase, condition status (Fultons index, liver index and gonado-somatic index) as well as parasite infestation rate in cod. We conducted an experiment at the Ar research station, Gotland, where cod were fed with sprat from the Baltic Sea and sprat from the North Sea until satiation (equal mass of sprat per cod, testing quality), and one group that got limited access to sprat from the Baltic Sea (testing quantity effect). The results indicated that cod fed until satiation of either sprat source exhibited similar growth rates, and condition status as well as liver index, indicating that sprat from the Baltic is not inferior in nutritional quality to North Sea sprat. However, cod that received limited amount of (Baltic) sprat demonstrated significantly reduced growth and condition status as well as liver index underscoring the importance of food availability. These findings suggest that food scarcity may be the primary driver of the poor growth for the Eastern Baltic cod and hence the necessity of reversing the negative sprat stock development in the Baltic to support the recovery the cod population in the Baltic Sea.

Role of (sub-)mesoscale processes in diapycnal mixing in the Baltic Sea

Martin Mohrmann, Voice of the Ocean Foundation

The Baltic Sea is a large estuary with a surface layer of brackish water and a deep layer of saltier water. The strong vertical density gradient inhibits vertical mixing and a limited connectivity to the ocean reduces water mass exchange. The turnover times of the saline deep waters are in the order of 30 years. Existing estimations are mostly based on numerical modeling, tracer release experiments and anthropogenic radiotracers analysis. Recent continuous, long term and high resolution glider sampling observatories in the Baltic Sea enable us to see and quantify submesoscale processes, that contribute to diapyncal mixing and an exchange of dense saline water masses over time. The speed of the gliders and the set of observation variables (CTD, currents, oxygen, Chl-A) as well as the relatively short transects allow an identification of energetic processes such as eddies, internal waves, and shear mixing. In this project, we estimate the importance of (at least some of) these individual processes for vertical mixing. Prior to analysis, the glider observations are split into individual short transects and are reprojected onto a 2 dimensional grid along the observatory line, resulting in a collection of hundreds of individual short transect for each observatory. Distinct patters such as transient eddies or large internal waves are easy to recognise and follow through a series of individual transects and their respective potential and kinetic energies are derived from wave theory. Processes with wavelengths or phase speed faster than the gliders lateral motion can be analysed by spectral analysis methods (Fourier transformation or wavelet analysis). The energy of the observed processes allows the estimation of dissipation rates, within the limited extend of the Baltic Basins, and finally the turbulent diapycnal exchange coefficients. These coefficients are essential for the salinity balance of the Baltic Sea, the transport of oxygen into the depth and the nutrient availability.

Degradation of coarse organic matter and dynamics of macroinvertebrate communities in a climate change scenario

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Climate change will likely lead to altered biodiversity and changes in biochemical processes, for example carbon flows. The magnitude of these changes and the resultant effects on carbon dynamics and production in food webs remaining unknown. In our study we are focusing on a rarely investigated aspect of marine carbon flows in coastal areas, the breakdown of coarse organic matter. We study rates of degradation and the organisms involved in this process, in a climate change scenario. With leaf matter degradation experiments in the field in combination with macroinvertebrate community samplings over different seasons we can identify main differences between a heated and non-heated natural environment. First results indicate that the natural, non-heated environment performs better in coarse organic matter degradation and has higher biodiversity and abundance of macroinvertebrate communities. The sampling campaign and field experiments are still ongoing. These findings will give insights into the process of breaking down coarse organic matter in the coastal zone and how this process will change during climate change.

Phosphorus addition promotes silica accumulation in diverse Baltic Sea picoplankton communities

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In recent years, new contributors to the marine silica cycle have emerged, including pico-sized phytoplankton (3 µm) in the silicic acid (dSi) rich (>8 µM) Baltic Sea over a biweekly time series at the Linnaeus Microbial Observatory (LMO) station over two years. Additionally, we performed four microcosm incubation experiments, at different seasons, with differing bacterial and phytoplankton community compositions, wherein we alleviated nutrient limitation. LMO time series data showed strong seasonal variation in bSi stock in both picoplankton and microplankton, with a substantial but brief contribution (up to 22% of total bSi) by the pico fraction in the summer. While bSi stocks in the >3 µm were strongly correlated to microplankton biomass concentrations, the microcosm experiments showed that phosphorus availability positively correlated with bSi accumulation in the pico fraction. Our results identify a potential control of bSi accumulation in picoplankton, which can help us understand the cellular mechanisms behind this process in picoplankton and uncover their role in marine silica cycling.

Reproducible analysis of metatranscriptomics either through nf-core/metatdenovo or nf-core/magmap

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In the last decade, the study of microbial communities through RNA sequencing from various environments has significantly increased. Metatranscriptomics offers insights into metabolic processes within microbial communities, providing a snapshot of gene expression based on in situ environmental conditions. To support biologists in this endeavor and to promote reproducibility and standardization in data analysis, we developed two complementary pipelines with the help of the nf-core community: nf-core/metatdenovo and nf-core/magmap. These pipelines, designed to be user-friendly and reproducible, aim to investigate the activity of microbial communities with varying levels of genomic knowledge. The nf-core/metatdenovo pipeline applies a de novo assembly approach to annotate metatranscriptomic data. This approach constructs transcriptomes directly from RNA sequencing reads without requiring a reference genome, followed by quantification of active genes and the assignment of both taxonomy and functional annotation. This approach makes nf-core/metatdenovo particularly advantageous for studying environments where genomic resources are scarce or incomplete. Such environments could include extreme habitats like the deep sea or soils, where many organisms remain uncultured and uncharacterized. The nf-core/magmap pipeline instead is applicable for communities for which genomes are available – e.g. gut microbiomes or surface water – either in the form of metagenomeassembled genomes (MAGs) or reference genomes. The pipeline identifies references genomes using a kmer-based approach using Sourmash, to continue with mapping reads to identified genomic references, to allow quantification of expressed genes. By developing these pipelines, we aimed to provide biologists with robust, flexible tools that cater to different research needs and environmental contexts. To demonstrate the utility and performance of these pipelines, we will show a comparative analysis using a dataset derived from a complex microbial community. Our results show the distinct advantages of the nf-core/metatdenovo and nf-core/magmap pipelines in different ecological contexts.

Investigating the long-term effects of thermal discharge on coastal microbial communities and copepod gut content in the Baltic Sea

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Climate change is expected to alter coastal ecosystems by increasing water temperatures, potentially reshaping microbial communities. The marine microbial food web is primarily composed of phytoplankton, zooplankton, heterotrophic bacteria, and viruses. How marine microbial food web components will respond and interact under climate change-induced warming is a crucial research question. Understanding these responses is essential, as changes in microbial interactions can disrupt energy flow, nutrient cycling and impact carbon sequestration, ultimately influencing the stability and resilience of marine ecosystems in a warming climate. This study examined the effects of thermal discharge from a nuclear power plant on coastal microbial communities and copepod gut content in the Baltic Sea. By comparing a bay impacted by warm water discharge (Warm Bay) to a nearby unaffected bay (Control Bay), we analyzed water temperature, chlorophyll a, and prokaryotic and eukaryotic microbial community composition in seawater, as well as prokaryotic communities in copepod guts (Acartia and Eurytemora), between December 2022 and May 2023. Chlorophyll a concentration was higher in the Warm Bay in early spring than in the Control Bay. Distinct differences in the prokaryotic and eukaryotic community composition of seawater between the bays were found. The phyla Proteobacteria and Actinobacteriota were the most prevalent bacteria found in the copepods' guts from both bays. However, the bacterial community structure at the phylum level in copepod guts did not show a distinct difference across bays, dates, or genera. These findings contribute to our understanding of how warming may differentially influence microbial community dynamics and energy transfer in coastal food webs, highlighting potential shifts in microbial community structures under future climate scenarios.

New ways are urgently needed for gelatinous zooplankton monitoring in the Baltic Sea

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Our understanding of gelatinous macro-zooplankton (jellyfish and comb jellies; GZ), in the Baltic Sea is limited. While GZ organisms can be a nuisance, they play essential roles in regional food webs and biogeochemical cycles. These organisms are known to tolerate increasing temperature and dropping oxygen concentration better than other invertebrates and fish. There is much speculation about recent increases in seasonal bloom extent and frequency. However, the lack of long-term data and consistent sampling protocols makes projections and distribution models unreliable. Research has focussed mainly on western Baltic native species, leaving central and eastern regions and additional species understudied. Recently introduced species like Blackfordia, Maeotias, and Craspedacusta have highlighted the need for further research. Furthermore, new approaches are required to enable marine ecologists, stakeholders, and policymakers to acquire data. Essential Ocean Variables (EOVs), identified by the Global Ocean Observing System (IOC-UNESCO), are key for globally coordinated marine data. GZ fall under the zooplankton EOV and the recommended variables to be measured are overall biomass, biomass or abundance (or presence/absence) by taxon, functional group or size class and should follow the data standards. By following FAIR data standards (Findable, Accessible, Interoperable, and Reusable), GZ monitoring could significantly enhance global understanding. It is recommended that these variables are incorporated in existing/planned observations and/or monitoring of GZ along with locally/regionally relevant variables. The coordinated observations along with innovative ideas and combinations of approaches (e.g., large-scale polls, fishers, ferries), social media data mining, and sampling for environmental DNA may provide new platforms for studying spatial and temporal distributions of GZ in the central and eastern Baltic Sea.

Allocation of Thiamine throughout the Reproductive Cycle of Atlantic Cod

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Since the 1960s, several fish species have been suffering from periodic thiamine (vitamin B1) deficiency. Depending on its severity, the lack of this essential micronutrient leads to neurological issues or death. Early life stages are especially vulnerable, which has led to largescale die-offs in European and North American salmonid populations. Although research has identified potential causes for thiamine deficiency, our understanding remains limited about how ecological factors influence thiamine dynamics among and within species. A key aspect in this regard is the fluctuation in thiamine levels over different life-history stages, including the allocation of thiamine to the soma and gonads at various maturation stages. To investigate these life history effects on thiamine dynamics, we sampled 193 Atlantic cod, a species that has recently been suggested to suffer from thiamine deficiency, in the North and Baltic Sea. We selected individuals of varying sizes/maturities and measured their thiamine content in muscle, liver and gonad tissues. This poster presentation will focus on how reproduction affects tissuespecific thiamine dynamics in cod.

Nitrous oxide dynamics in the eastern tropical South Pacific

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The oceans are a major source of atmospheric nitrous oxide, a potent greenhouse gas which has 300-fold the global warming potential of carbon dioxide, and oxygen depleted waters are known to be areas with high nitrous oxide emissions. Oxygen depleted zones are expected to expand due to global warming, which may further enhance nitrous oxide accumulation and emissions. Nitrous oxide is produced and consumed by microbial nitrogen transformations, but we lack an in-depth understanding of the biogeochemical pathways and their environmental controls. Previous studies have shown that denitrification is the dominant production pathway, with indications that microbes are performing this pathway in a manner such that intermediates do not exchange with the ambient pools. Yet the details of the pathway remain unknown. In this study we have undertaken work in the eastern tropical South Pacific oxygen depleted zone utilizing novel tracer labelling techniques and highly sensitive optical oxygen sensing techniques. Nitrous oxide production and consumption rates were quantified to elucidate relevant pathways, and their environmental controls investigated. These results contribute to a better understanding of nitrous oxide dynamics in oxygen depleted waters.

Seasonal Dynamics, Genetic Variation and Host Range of Baltic Sea Phages Infecting Different Strains of Rheinheimera Bacteria

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Marine phages (viruses that infect bacteria) and their hosts are the most and second most abundant entities in the ocean, respectively. Bacteria are crucial for aquatic biogeochemical cycles, and their phages are of importance by serving as microbial modulators through infection and lysis. However, little is known about numeric and genetic shifts of phages over temporal scales and the influence on phage-host interactions. This project aims to investigate the seasonal abundance dynamics of phages that infect different strains of Rheinheimera sp. derived from the Baltic Sea. In addition, their phylogenetic relationships and the number of hosts they can infect (also called host range) will be explored. Plaque forming unit data showed that phage abundances peaked repeatedly during late summer, with a steep increase and slow decline. Phages infecting strain BAL341 phages dominated in the years 2022 and 2023. However, in 2024, phages infecting the strains LMO12 and LMO14, outnumbered phages infecting BAL341. Genomically, the phages primarily clustered based on the host from which they were originally isolated. An exception was two BAL341 phages, which were more similar to LMO12 phages. There was a large variation in the sensitivity of the different host strains towards the phages, where BAL341 could be infected by all viral candidates. In contrast, SMS3, could only be infected by its original phages. All phages showed highest efficiency of infection on the host from which they were originally isolated, and phages isolated from the same host generally shared a similar host range. However, one BAL341 phage that was genomically similar to the LMO12 phages, also had a host range more similar to that of LMO12 phages. This project deepens our understanding of temporal variations of phages infecting ecologically important bacteria in the Baltic Sea and how phage phylogenies relate to host ranges.

Air-Surface Exchange of Halomethoxybenzenes in Northern Sweden

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Halomethoxybenzenes (HMBs) are “semivolatile” and exchange between the atmosphere, oceans and seas, and terrestrial surfaces (soil, vegetation, rivers, lakes). (1,2). Here we focus on natural brominated anisoles (BAs), produced in marine ecosystems by algae and bacteria (3), and drosophilin A methyl ether (DAME = 1,2,4,5-tetrachloro-3,6-dimethoxybenzene), a secondary metabolite of terrestrial fungi (4).

Studies were conducted in Lake Torneträsk (LT) (68o 22’N, 19o 06’E) and streams in subarctic Sweden (2) and in rivers and Baltic estuaries of Västerbotten County (VC) (3). HMBs in air, soil and ground litter were also measured. Sampling and analytical methods are reported in (2-4). Air-surface exchange was assessed by calculating the water/air and soil/air fugacity ratios (FRWA, FRSA) from their environmental concentrations and physicochemical properties of the HMBs (1,2). FR=1 indicates equilibrium, while net deposition and volatilization are indicated by FR<1 and FR>1.

Concentrations of BAs in water and FRWA followed the order: estuaries > offshore > VC rivers > LT and streams. The highest concentrations and FRWA in estuaries can be attributed to local production. DAME concentrations were highest in VC rivers (land runoff) followed by estuaries > offshore > LT and streams. Net volatilization was found at most sites (FRWA >1), in agreement with studies in Canada, where DAME in air was related to proximity to water bodies (1). Exchange of DAME with soil/litter was assessed at 8 sites in VC and 7 sites near LT. Net volatilization (FRSA>1) was found at 11, net deposition (FRSA<1) at 2 and near-equilibrium (FRSA~1) at 2 sites.

These HMBs volatilize from sea and land, disperse through the atmosphere, and return via precipitation and rivers, cycles that connect ecosystems and provide widespread exposure to organisms (1,5). HMBs bioaccumulate (6,7) and DAME has the potential for toxicity that is characteristic of persistent organic pollutants (POPs) (1).

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