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ABSTRACT BOOK

Topic 6 Symposium

Sept 30 – Oct 1, 2026

Topic 6 Symposium 2026

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 **AWI**

I. TALK ABSTRACTS

Wednesday, 30 September 2026

Marine Ecosystem Futures: Biodiversity & Society – PART I

From customary tenure to capital: connecting ocean, water and fisher peoples' territorial struggles to global production networks, land politics and agrarian change

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The interconnectedness of oceans, inland waters and land is not reflected in dominant governance frameworks. Policy reforms on coasts, oceans and waters follow the same economic principles applied to land, facilitating their grabbing and incorporation into global production networks. Oceans and waters remain marginal in land and agrarian debates, where they are often cast as public goods the State allocates use and access. This has led to mosaics of state and private property regimes that manifest through one-size-fits-all spatial fixes, appropriating customary commons for extraction, energy production, conservation and infrastructure development. We examine fisher peoples' struggles in South Africa and Colombia, where policy reforms, co-management and legal instruments have been mobilised for the recognition of customary tenure. Due to competing political and economic interests, fisher peoples are navigating intensifying dispossession, criminalisation and militarised violence. Fisher movements face the challenge of aligning their struggles with existing land-based territorial frameworks, while articulating the distinctiveness of fishing ways of life, identities and territories across the land-water-ocean nexus. We call for theoretical and empirical imagination: oceans and waters are at the heart of land and agrarian change, excluding them misses a crucial part of capitalism and possibilities for reclaiming the commons and customary control.

For oblique engagement with tipping points: diversifying perspectives for governing a changing Earth

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'Tipping points' have become a bedrock of climate governance, perpetuating narratives of sudden and cascading environmental collapse, despite concern for the validity of their conceptual application. Challenging this dominant perspective, I propose greater oblique engagement with tipping points for engaging with and making sense of complex human-environment relations beyond metaphor. I do so by steering debate towards matters of scale and temporality in order to show how popular understanding of tipping reinforce linear understanding of space and time, by constructing a universal vision of a particular future that is often abstracted from the very real realities of climate change and its timescales. In advocating more careful use of term, and drawing attention to the impacts and dangers that universally ascribing a tipping point has, I argue that being more open to uncertainty, as well as other forms of knowledge, might allow for more equitable ways of highlighting the realities of climate change, particularly across climate policy which is often stifled by alarmism.

Calcium signaling: the missing link in the bleaching cascade

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Global warming is disrupting photosymbioses between heterotrophic hosts and phototrophic algal symbionts worldwide, a phenomenon commonly referred to as bleaching. Yet the mechanisms driving this symbiotic breakdown remain poorly understood. Here, using a cnidarian model system approach, we show that heat stress erodes the nutritional foundation on which photosymbiosis is built. Elevated metabolic energy demand under heat stress destabilizes host control over nutrient supply to the algal symbionts, driving rapid algal growth. This proliferation shifts symbiont metabolism toward retaining photosynthetically fixed carbon rather than sharing it with the host, and coincides with the release of calcium reserves stored within the algal cell wall. The resulting collapse of host calcium homeostasis, triggers the apoptotic breakdown of the symbiosis. Together, these results establish a mechanistic link between the collapse of mutualistic nutrient cycling and the breakdown of host calcium homeostasis that explains the breakdown of the cnidarian–algal symbiosis, and reveal bleaching as an inherent property of photosymbioses built on dynamic nutrient cycling.

Microbial seasonal succession in the Arctic surface ocean: a dance on a tightrope

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The stark seasonal contrast, meltwater stratification, and semi-enclosed setting distinguish the Arctic upper ocean from other surface marine ecosystems. With the growing inclusion of the Arctic in global ocean biogeographical surveys, the Arctic epipelagic microbiome is now recognized as highly specialized and enriched in genomic novelty, including a considerable fraction of endemic lineages. Yet little is known about how the microbial communities maintain seasonal succession and local dynamism despite the Arctic's intense selective pressure.

In this study, we investigate microbial succession from winter to summer in the Arctic surface ocean through deeply sequenced metagenomes collected during the Multidisciplinary drifting Observatory for the Study of Arctic Climate (MOSAIC) expedition.

The microbiome displayed pronounced seasonal patterns, closely matching the hydrographic partitioning of the upper water column. Beyond the hallmark algal bloom, we detected distinct compositional shifts in bacterial and archaeal communities. We show the year-round turnover was largely the result of replacement among closely related taxa within the same microbial families, the majority of which are cosmopolitan across the global ocean. Resolving a genome-independent metabolic landscape from metagenomic assemblies, we uncovered a coherent reorganization of the metabolic network in surface waters across the polar night-to-day transition. As the phytoplankton bloom sets in and floods the surface water with labile organic compounds, the bacterial and archaeal community transitions from a state of metabolic self-reliance towards optimized exploitation of bloom-derived substrates, fueling population expansion.

Overall, we present a high-resolution eco-evolutionary framework of microbial seasonal succession in the Arctic Ocean, demonstrating how the epipelagic microbiome modulates its genetic diversity to persist in one of the ocean's most selective environments.

Adaptation in Marine Organisms – PART I

Accumulation and clonal inheritance of epigenetic variation in Caribbean reef-building corals

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Corals experience widely fluctuating environmental conditions, yet the molecular basis of their response to such fluctuations remains poorly understood. Epigenetic mechanisms provide gene regulatory layers beyond genetic sequence, for instance through chemical DNA modifications and post-translational chromatin marks. In corals, differential DNA methylation has been associated with acclimatization to ocean acidification, light exposure, and bleaching. Here we aim to link phenotypic diversity and environmental history by studying patterns of coral DNA methylation, including their persistence and divergence across clonal lineages.

We present a framework to resolve epitypes by classifying DNA methylation patterns into dynamic and stable regions. We generated single-molecule long-read sequencing (PacBio HiFi) from two Caribbean reef-building corals, *Acropora palmata* and *Orbicella faveolata*. This approach allows for haplotype phasing and methylation identification on the same DNA molecule. We sampled multiple genets and ramets from locations with different thermal histories, enabling construction of a haplotype-resolved methylation atlas from which epitype classes can be defined. Dynamic epitypes are expected to vary across environmental or physiological contexts and may modulate transcriptional responsiveness, alternative splicing, or pathway activation. Conversely, stable epitypes are predicted to show minimal responsiveness during short-term acclimatization, such as constitutive gene-body methylation of housekeeping genes, and reflect long-term maintenance of cellular state. Such regions are also candidates for exploring a coral epigenetic clock, where stochastic deviations from canonical methylation patterns accumulate along somatic lineages. Identifying loci that exhibit progressive accumulation of epimutations would offer new tools to reconstruct relative lineage history and evaluate epigenetic inheritance in modular organisms.

In sum, we quantify how epitypes interact with genetic variation to generate phenotypic diversity, and assess their contributions to persistent population differences. This framework establishes a foundation for incorporating epigenetic variation into potential for environmental adaptation and coral reef resilience.

Synten-aware microbial pangenomes reveal blueprints of genomic variation

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Pangenomics quantifies the conserved and variable gene repertoire among genomes, but popular implementations ignore gene synteny. Graph-based approaches incorporate both gene homology and synteny, but become difficult to interpret due to pervasive rearrangements. Here we present network-pruning and graph-layout algorithms that enable interactive, synten-aware quantification and visualization of gene conservation and variability. Applied to 29 genomes of the marine genus *Undatipelagibacter* (formerly SAR11 subclade Ia.3.VI), we find that genomic variability forms not a few hypervariable islands against a static backbone but a structured continuum, whose variable regions differ in scale, topology, function, and evolutionary character. Genome variation spans from ancient, specialized regions of hundreds of genes whose propensity to vary is conserved across genera, to single hypervariable genes shaped by epistatic co-selection with partners dispersed genome-wide, and shows that chromosomal context carries evolutionary information synteny-unaware pangenomics cannot capture, and some evolutionary processes act on entire functional subsystems throughout a pangenome.

Biochemical capacities and limits of benthic marine invertebrates in the Arctic

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The Arctic is warming approximately four times faster than the global average, and marine heatwaves (MHWs) are becoming more frequent and more intense. As temperature strongly controls the metabolism and performance of ectothermic marine organisms, these changes may substantially affect the ecological role of a key grazer in Subarctic and Arctic fjords, the green sea urchin *Strongylocentrotus droebachiensis*. The AWI-INSPIRES project "Arctic Shift" was designed to investigate the temperature-dependent physiological, biochemical, genetic and behavioral adaptations to assess responses to future warming. Comparisons of Arctic and Subarctic populations revealed distinct adaptations to their local thermal regimes. Grazing rates peaked at the respective local summer temperatures, while differences in upper thermal limits indicated regional adaptation. Respiration rates and anaerobic metabolites increased exponentially with temperature, resulting in a higher risk of an energetic mismatch between food intake and metabolic demand. This risk was particularly pronounced in Subarctic sea urchins during MHWs due to their narrower thermal safety margin (TSM). Arctic sea urchins showed higher digestive enzyme activities and lower activation energies than Subarctic individuals, suggesting higher metabolic efficiency at low temperatures. Molecular analyses linked these differences to enzyme structure, providing evidence for genetic adaptation to local thermal conditions. However, this cold adaptation may become disadvantageous under warming because metabolic rates of Arctic individuals are expected to increase particularly rapidly with temperature. These population-specific adaptations suggest contrasting responses to climate warming. Arctic populations may maintain comparatively large TSM while experiencing enhanced metabolism and grazing pressure, potentially promoting the formation of sea urchin barrens. Conversely, Subarctic populations may increasingly exceed their physiological limits during extreme MHWs, resulting in energetic imbalance and population declines. Thus, future warming may drive a northward shift of sea urchin-dominated fjord ecosystems.

Unravelling deep pelagic predator prey interactions: a multi census approach

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Deep diving toothed are abundant predators of open ocean ecosystems that show high diversities in association with oceanic islands in the Atlantic. Squids are carnivorous invertebrates that are numerous in the deep sea with high diversity and biomass from the epipelagic to the bathypelagic zones. Toothed whales hunt in the deep sea for squid using an unprecedented weapon: echolocation. Squids avoid predation and detection by a range of species-specific traits including speed, agility, vision, body shape and position. The specifics of this arms race remain poorly known as squids can avoid ocean instruments and the predator-prey interactions occur in the deep sea and hence remain largely unwitnessed. In absence of direct observations, investigating these elusive fauna and their interactions relies on the application of diverse methods. Focussing on the prey side, we present highlights of an international collaborative effort that studies the interactions between toothed whales and squids off Terceira Island, the Azores. These efforts include 1) an overview of cephalopod diversity using a unique 8-year eDNA dataset in the foraging habitats of Risso's dolphins, Goose-beaked whales and Sowerby's beaked whales, 2) a comparison of toothed whale diets using DNA metabarcoding of faecal samples and 3) an analysis of the calorific value of cephalopods in relation to escape potential traits. The future of the study of whale-squid interactions relies on autonomous, quiet and non-intrusive ocean observations to help guide three dimensional conservation management in the deep pelagic realm.

Marine Carbon & Element Cycles Ahead – PART I

Biologically processed carbon drives the annual marine carbon sink over centuries after CO₂ emissions cease

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Physical-chemical uptake dominates the ocean uptake of carbon since preindustrial times. However, it remains unclear how the ocean carbon uptake will evolve after emissions cease and which mechanisms will drive these changes. Here we use Earth System models to study the evolution of the *annual growth rate* of the marine carbon uptake under ambitious CO₂ mitigation scenarios that achieve net zero CO₂ emissions within the upcoming decades. With net zero emissions, we find a rapid shift of the processes that govern the growth rate of marine carbon uptake. The physical- chemical uptake of anthropogenic CO₂ decreases in response to decreasing atmospheric CO₂. In contrast to the decreasing physical- chemical uptake, we observe a growing relevance of carbon uptake attributable to the biological carbon pump (DIC^{remin}). The time elapsed between turning net-zero and when marine carbon uptake is dominated by biological pump carbon ($\delta\text{DIC}^{\text{remin}} > 0.5 \cdot \delta\text{DIC}$) scales with cumulative CO₂-emissions since pre-industrial times. For scenarios with global warming targets of around +1.5°C, this point may be reached already around the turn of this century.

Exploring further what drives the increasing contribution of the biological carbon pump, i.e., the 'gain' versus the 'loss' side (Frenger et al., 2024, <https://doi.org/10.1111/gcb.17124>) of DIC^{remin}, we find in output from CMIP6 models (Wilson et al., 2022, <https://doi.org/10.1073/pnas.2204369119>) that the increase in the biological pump carbon is driven by an overall slowing down of the ocean circulation leading to less re-emergence of DIC^{remin} at the ocean surface and a higher accumulation of DIC^{remin} below the surface ocean. This increase in DIC^{remin} is partly offset by a projected decrease in the export of organic matter into the interior ocean.

Large-particle regimes coincide with high carbon export but low mesopelagic transfer efficiency

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Large particles are traditionally assumed to enhance the efficiency of the biological carbon pump (BCP) due higher sinking velocities, yet observations increasingly challenge this relationship (Guidi et al., 2015; Stukel et al., 2024). Here, we use > 5,000 particle size distribution (PSD) profiles from the global Underwater Vision Profiler (UVP) dataset (Kiko et al., 2022) to investigate links between PSD, carbon export from the euphotic zone, and transfer efficiency.

Unsupervised clustering revealed a small-particle regime (< 0.5 mm equivalent spherical diameter, ESD) associated with oligotrophic open-ocean regions and low carbon export, and a large-particle regime (> 2 mm ESD) occurring mainly in coastal and polar regions with the highest carbon export. Transfer efficiency to 1,000 m decreased with carbon export ($R^2 = 0.42$) and affinity to the large-particle regime ($R^2 = 0.27$). In a subset with validated particle classifications (18% of profiles), the large-particle regime also showed elevated plankton concentrations and distinct particle geometry, suggesting differences in ecosystem processing. Small- and large-particle regimes were associated with pico- and microphytoplankton-dominated communities, respectively, with phytoplankton size structure explaining 18% of variance in regime affinity but only 1% in transfer efficiency. Environmental regression-tree models explained over half of in-sample variation in particle regimes and transfer efficiency, with transfer efficiency negatively associated with surface chlorophyll. Overall, high carbon export in large-particle regimes did not translate into high transfer efficiency, potentially reflecting enhanced mesopelagic processing. Although absolute carbon flux at 1,000 m remained higher in the large-particle regime, our results support an important role of small particles in efficient carbon sequestration.

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Cold storage: efficient trapping of iron in Greenland's fjords

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Ice sheets and glaciers supply iron (Fe), a bio-essential micronutrient, to the ocean. Yet, how glacier-fed fjords regulate this supply on annual timescales remains poorly constrained. Fjords may remove dissolved Fe (dFe) through particle scavenging, and/or resupply dFe through reductive dissolution in sediments, making their net effect uncertain. By combining pelagic, benthic, atmospheric and freshwater observations, we construct comprehensive dFe budgets for three glacier-fed fjords in southeast Greenland. All fjords showed dFe enrichment relative to adjacent shelf waters, primarily associated with additions from subglacial discharge and submarine melt. However, export of dFe to the shelf was limited due to intense scavenging. In 2024, we estimate southeast Greenland fjords received 'new' dFe inputs totaling 232 ± 21 Mg yr⁻¹ (excluding marine inflow), but $71 \pm 7\%$ of new dFe input was trapped rather than exported to the ocean. Greenland's fjords therefore act as efficient filters, strongly attenuating Fe delivery to the ocean.

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Microbial metalloenzymes shape biogeochemical nutrient cycles: trace metals and phosphorus

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Anthropogenic impacts threaten our oceanic planetary support system and its underlying microbial biogeochemical cycles. Elucidating how marine microorganisms drive these cycles on the molecular level is instrumental for predicting their responses to changing environmental conditions. Proteins, especially metal-containing enzymes, are biochemical machines that help microbes acquire, trade, transform, and recycle essential nutrients. One example of their importance pertains the phosphorus, a nutrient essential to oceanic phytoplankton which is predicted to become increasingly limiting due to climate-change induced ocean stratification and enhanced anthropogenic nitrogen pollution.^I To cope with phosphorus shortages, marine microbes express phosphatase enzymes to access the alternative nutrient source of dissolved organic phosphorus. These proteins often rely on trace metal cofactors and thus depend on metal availabilities in the marine environment. While current research focuses on alkaline phosphatases with iron or zinc cofactors, we showcase the roles of new metal centers and new protein families in regulating microbial phosphorus nutrition within natural phytoplankton communities. First, manganese was identified as active metal center in marine phosphatases through biochemical pure protein studies and environmental shipboard experiments. Second, uncharacterized phytases and phosphodiesterases were established to be main drivers of phosphorus utilization across different environmental habitats through metatranscriptomics analyses.^{II} This extended functional diversity in the utilization of different trace metals and organic nutrient sources can buffer marine phytoplankton against nutrient stress and increase the efficiency of the biological carbon pump.^{III} Overall, this work illuminates new nutritional mechanisms of marine primary producers and the coupling of phosphorus and trace metals in biogeochemical cycles, and highlights the potential of metalloenzyme studies in further understanding the controls on ocean ecosystem fertility.

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Ocean Pressures & Policy – PART I

Impacts of marine spatial planning in the German exclusive economic zone

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Marine Spatial Planning (MSP) is a policy tool designed to regulate and coordinate the spatial and temporal use of marine areas. Growing demands for energy production, data transmission, maritime transport, and security require a structured organization of multiple uses of marine space. In the German Exclusive Economic Zone (EEZ), MSP must accommodate a high density of offshore wind farms, submarine power and data cables, pipelines, fishing grounds, military exercises area and shipping lanes. Environmental pressures arise from the combined effects of multiple human activities; therefore, it is essential to assess the potential cumulative impacts induced by the expansion of the activities that shape this MSP. This study introduces a new framework that relies on the application of graph theory to evaluate the ecological pervasiveness of pressures generated by human activities through centrality indices. These indices enable the assessment of potential ecological consequences of MSP implementation in the German EEZ, identifying which pressures and trophic guilds should be prioritized to mitigate the cumulative impacts on marine ecosystems. The application of this framework highlights the pressures that become prominent with the implementation of MSP and clarifies the relative roles of different activities in driving ecosystem change.

How research triggers political decisions – the success story of marine munitions

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Large quantities of naval munitions and unexploded ordnance (UXO) from the First and Second World Wars remain on the seabed of European seas. They pose risks to shipping, fisheries, offshore infrastructure, public safety and the marine environment. While chemical munitions have long been recognised as a source of toxic substances, research has increasingly shown that conventional munitions can also release hazardous, carcinogenic and mutagenic compounds into the marine environment.

For more than ten years, research institutions in Germany have investigated marine munitions in the German North Sea and Baltic Sea. Research has focused on their detection and localisation, condition and degradation, the release of contaminants, their effects on marine organisms, and the resulting risks to humans and the environment. Communicating these findings has significantly increased public and political awareness of the scale and consequences of the problem.

This growing body of scientific evidence has contributed to a shift from recognising the problem towards taking political action. In Germany, this has culminated in a government-funded emergency programme for a pilot operation to recover and dispose of marine munitions from the North Sea and Baltic Sea, supported by €100 million. This development demonstrates how long-term research can provide the evidence needed to turn an environmental problem into a political priority and, ultimately, into concrete action.

Thursday, 1 October 2026

Marine Ecosystem Futures: Biodiversity & Society – PART II

Long-term satellite observations (1998–2025) reveal changing phytoplankton community structure and phenology in the Fram Strait

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The Fram Strait is the primary gateway between the North Atlantic and the Arctic Ocean, where ongoing Atlantification is reshaping hydrographic conditions and marine ecosystems. We applied ML-PhyTAO, a machine learning based retrieval model for Arctic phytoplankton functional types (PFTs), to generate a consistent 28-year (1998–2025) satellite record of total chlorophyll-a (TChl_a) and major PFT chlorophyll-a concentrations (Chl_a) in the Fram Strait. Trained with an extensive Arctic phytoplankton pigment dataset and ocean color and environmental products, the model provides robust performance for long-term analyses. Using a dynamic water mass classification based on sea surface temperature and sea ice fraction, the Fram Strait was partitioned into Atlantic Water (AW), Mixed Water (MW), and Polar Water (PW). Distinct seasonal cycles were observed among water masses, with later but more intense phytoplankton blooms in AW. Peak biomass timing advanced by 2–13 days decade⁻¹ for TChl_a, diatoms, and haptophytes in both AW and MW. Trend analyses revealed declining biomass primarily in MW and the AW–MW transition zone, while haptophytes and dinoflagellates increased within AW. Sea surface salinity, temperature, and sea ice fraction showed stronger and more spatially coherent relationships with PFT variability than modeled nutrient fields, indicating that Atlantification related hydrographic changes are driving shifts in phytoplankton phenology and community composition. This study highlights the unique value of long-term, consistent PFT observations for detecting climate-driven ecosystem change, linking hydrographic variability to community shifts, and supporting future ecosystem and biogeochemical assessments and modelling studies in the rapidly changing Arctic Ocean.

SEAKEY – a new identification key for the seaweeds of the German coasts

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Seaweeds are important components of coastal ecosystems. However, until now, an up-to-date and comprehensive resource about species along the German coastlines is missing. In order to fill this gap, the project SeaKey, in close cooperation between AWI and GEOMAR, pursues the transfer of knowledge about marine seaweeds to students, university teachers, monitoring agencies and the interested educated public. Information from regional sampling and other sources are included in order to establish a sound basis for an accessible approach to the difficult task of identification. Developed as a browser-based app, the identification aids and standardized taxon profiles are currently established for 68 species of brown algae from the German Wadden Sea and the island of Helgoland. Identification keys for green and red algae will follow. A parallel sister project has been launched in 2025, which will extend the approach to the German Baltic Sea. The SeaKey is based on a matrix concept, whose innovative approach offers variable access options. Users can enter the identification matrix at different levels, depending on their knowledge and on the difficulty to recognize the species characters. The SeaKey comprises three parts, i.e. the digital and printable matrix key, the SeaKey app, and a web and print version of a glossary comprising >1000 scientific terms. Version 1.2 from March 2026 is available at <https://seaweeds.awi.de/>, and the app in the Google and Apple App Stores. Both will be expanded continuously. Although with a regional German focus, all is available in English.

Topic 6 Symposium 2026

New findings on the CAO ecosystem and implications for policy and management

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Ecosystem change in the Central Arctic Ocean (CAO) often differs from that observed on the surrounding shelves. However, comprehensive data from this logistically challenging region have historically been scarce. Since the MOSAiC expedition, several research projects associated with Topic 6 have substantially advanced our understanding of the CAO ecosystem. Their findings include the discovery of unexpected fish and squid species in the CAO and new insights on the significance of the under-ice habitat for overwintering zooplankton. Research on the ecologically important polar cod has provided new insights into its population structure, feeding ecology, and presence in the CAO during the last ice age. The presentation illustrates how these findings contribute directly to management and governance processes related to the CAO, including those of the Arctic Council, the Central Arctic Ocean Fisheries Agreement, and relevant international working groups. We aim to stimulate discussion on how POF V can build on this progress in the lead-up to the International Polar Year and how the societal impact of this research can be further strengthened.

Adaptation in Marine Organisms – PART II

Heat adaptation of *Fucus* meadows from molecules to ecosystems

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The major Baltic Sea foundation species *Fucus vesiculosus* (bladderwrack) has strongly declined in recent history due to eutrophication and substrate removal, driving a retreat of extant populations into shallow depths. Facing rising temperatures and increasingly frequent and extreme heatwaves, it is yet unknown whether standing genetic variation may provide evolutionary rescue or if the adaptive capacity of the ecosystems cannot keep pace with the rate of change.

I will present an overview of the research conducted in the Algal Adaptation group which was established in January 2026. In the framework of the project FUBLUC, we aim to provide a holistic description of the temperature tolerance of Baltic *Fucus*, combining approaches of experimental ecology and evolutionary biology. Initially, we validated the concept of thermal damage accumulation in *Fucus*, which allows us to compare the critical thermal maximum (CT_{max}) of growth and photophysiology (F_v/F_m) in response to dynamic temperature ramping treatments. Next, we selected three pairs of closely located sheltered and exposed *Fucus* sites along the SW-Baltic coast, hypothesising that increased thermal amplitudes in sheltered sites are selecting for tolerance to extreme temperatures. Indeed, our first results show that sheltered *Fucus* populations on average express significantly higher CT_{max} in growth, and that this pattern is driven by few differentiated populations.

In parallel, we are using the Kiel Outdoor Benthocosms to subject *Fucus* juveniles from the same six sites to elevated temperature environments year-round, allowing us to investigate the potential of artificial selection for *Fucus* heat tolerance within near-natural community dynamics. Going forward, we aim to identify genomic loci associated with heat tolerance, using individual resequencing data and a novel *F. vesiculosus* reference genome. Our results will provide genomic resources for an important coastal foundation species, enhance the fundamental understanding of brown algal heat tolerance, and build the groundwork for innovative ecosystem reinforcement and restoration strategies.

Results overview from the MOSAiC ecosystem team

Clara Hoppe¹

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In 2019-2020, RV Polarstern drifted with the central Arctic pack ice for almost a whole year. In the framework of the MOSAiC expedition (Multidisciplinary drifting Observatory for the Study of Arctic Climate), hundreds of scientists studied the coupled Arctic ocean-sea ice-atmosphere system over the annual cycle. The ECOSYSTEM team focused on the diversity, activities and ecosystem functions of organisms ranging from microbes to fish. In this talk, an overview on some of the findings from this work will be presented. A focus will be put on those periods of the year that are usually considered less relevant for ecosystem dynamics and also severely understudied so far: the polar night between late fall to early spring.

Functional motifs in food webs and networks

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Understanding how complex systems respond to disturbances is one of the major questions we ask ourselves when working with them across disciplines. Complex systems can be thought of as networks of interacting units. Usually, their size and complexity demand numerical methods to find solutions. A way to simplify them and allow for analytical solutions is to use properties of the entire network that are rooted in small parts of it – so-called network motifs. If the occurrence of a motif in a network can guarantee that a network-level property like stability or reactivity behaves in a certain way without being negated by the rest of the network, we call these motifs functional.

A classic example in ecology is unregulated exploitative competition in food webs. Two species exploiting the same resource cannot stably coexist, whether we look at them as an isolated group of three species or as part of a larger network.

In our study [1], we explain why exploitative competition is a functional motif when it comes to system stability and why such motifs are rare in food webs and other networked systems, such as epidemic spreading and supply chain dynamics. Building on these results, we then discuss more broadly under which conditions functional motifs exist. Perhaps more importantly, we show that functional motifs with implications other than asymptotic instability are common in networks from applications using another dynamic property—reactivity. By distinguishing between emergent properties and functional properties, we are able to offer a necessary simplification for the mathematical modeling of complex systems.

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Marine Carbon & Element Cycles Ahead – PART II

Leveraging metagenomic data for genome-resolved inference of microbial metabolic interactions at scale

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Cross-feeding is a process by which metabolites produced by one organism can continue their biochemical transformation through complementary metabolic activities of another organism. Despite their fundamental role in shaping how communities assemble and function, which critically impacts global biogeochemical cycles and host-microbe interactions, such metabolic transfers have been predominantly studied in experimentally-tractable systems with a particular focus on interactions that are relevant to human health or biotechnology. Here we present a computational approach that leverages the increasingly available genomes and metagenomes from natural systems to investigate the ecology-informed, community-level cross-feeding potential of microbiomes at scale. We predict potentially-exchanged metabolites by reconstructing interconnected biochemical reactions from genomic data and identifying complementary metabolic capacities between community members. By employing metagenomic read recruitment to resolve global co-occurrence patterns, our approach effectively scrutinizes potentially interacting pairs and limits its focus to cohort-specific cross-feeding networks to identify the distribution and nature of metabolic exchanges throughout a community. Our application of this approach to over 9,000 publicly-available global metagenomes and 32,000 genomes from the Ocean Microbiomics Database demonstrates both the promise and challenges of identifying metabolic complementarities within marine microbial communities.

Seasonality and mineral type shape phytoplankton responses to ocean alkalinity enhancement in temperate waters – a mesocosm study

Juliane K. Tammen¹, Leila R. Kittu¹, Kai G. Schulz² & Ulf Riebesell¹

¹GEOMAR Helmholtz Centre for Ocean Research Kiel; ²Southern Cross University, Lismore, NSW, Australia

Seasonal variability of inorganic nutrient availability, light, and temperature are key drivers of phytoplankton dynamics in temperate waters. In these systems, spring is a period of high primary production and food web interactions, making planktonic communities potentially more sensitive to environmental change. Ocean alkalinity enhancement (OAE), a proposed carbon dioxide removal technology, alters seawater chemistry in ways that could disrupt these tightly regulated processes, yet its ecological impacts, especially across seasons and alkaline feedstocks, remain largely unexplored. We conducted three ~1 month mesocosm experiments in the Kiel Fjord during spring, summer, and autumn 2024. In each season, twelve 8 m³ mesocosms were used to test two alkalinity-enhancing minerals, brucite (Mg(OH)₂) and hydrated lime (Ca(OH)₂), applied along a total alkalinity (Δ TA) gradient from 0 to 750 $\mu\text{mol kg}^{-1}$ in 150 $\mu\text{mol kg}^{-1}$ increments. Responses in phytoplankton bloom dynamics and organic matter accumulation to OAE varied by season, mineral type, and alkalinity level, with the strongest effects observed in spring. There, alkalinity additions of $\geq \sim 450 \mu\text{mol kg}^{-1}$ delayed the onset of the phytoplankton bloom, as reflected in a delayed increase in chlorophyll *a*. In summer and autumn, chlorophyll *a* concentrations in all mesocosms declined rapidly after the start of the experiment and remained low thereafter, with no or minor effects of alkalinity and mineral type. Across all seasons, mineral additions induced shifts in phytoplankton community composition, as indicated by rapid declines in biogenic silica, reflecting reduced diatom biomass. These reductions were more pronounced with brucite and high Δ TA, possibly caused by high-pH driven silica frustule dissolution and enhanced aggregation with mineral particles leading to sedimentation. Our results highlight that season, mineral type, and alkalinity dose strongly shape phytoplankton responses to OAE, emphasizing the need for seasonally resolved, mineral-specific ecological assessments before large-scale deployment.

When microbes meet rocks: microbial responses to enhanced benthic weathering in coastal sediments

Stefanie Böhnke-Brandt¹, Andy Dale¹ & Mirjam Perner¹

¹GEOMAR Helmholtz Centre for Ocean Research Kiel

Enhanced benthic weathering (EBW) is a promising marine carbon dioxide removal (mCDR) approach, but its environmental consequences remain poorly understood. Over a series of experiments, we investigated how calcite addition affects microbial communities and their metabolic functioning in Baltic Sea sediments.

Initial laboratory sediment core incubation experiments comparing calcite-amended and untreated sediments under oxic and oxygen-limited conditions showed that responses were primarily observed in the upper 0-2 cm of the sediment. Total microbial cell abundance doubled under oxygen-limited conditions, where calcite dissolution was highest. Bacterial community profiling showed that the core bacterial community remained largely stable, while changes were particularly evident among less abundant taxa. Follow-up sediment core incubations combined with metatranscriptomics showed that calcite addition altered microbial functioning despite only minor changes in community composition. These functional shifts included increased potential for sulfate reduction without accumulation of H₂S, alongside upregulation of genes associated with denitrification and organic matter degradation. Similar effects were observed in closed benthic chamber incubations using the BIGO lander system, providing support for the transferability of some laboratory observations to more realistic *in situ* conditions.

Taken together, these experiments provide converging evidence that calcite addition can alter microbial functioning and, consequently, elemental cycling, even when the composition of the overall microbial community remains largely stable. However, experimental systems cannot fully capture the complexity and spatial variability of natural environments. Thus, determining the environmental relevance of microbial responses, require well-replicated field experiments and long-term observations under real-world conditions.

Ocean Pressures & Policy – PART II

Light pollution can influence growth in macroalgae and epiphytes

Mark Lenz¹

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About 20% of the world's coastlines are affected by artificial light at night (ALAN), while anthropogenic light emissions are expected to increase at a rate of 6 – 10% per year. Despite its abundance, a comprehensive understanding of the effects of ALAN on marine organisms, in particular photoautotrophs, is still lacking. In the framework of the international research and student training programme GAME (Global Approach in Marine Ecology), the influence of ALAN with an intensity of 10 - 30 lux ($0.20 - 0.46 \mu\text{mol m}^{-2} \text{s}^{-1}$) on the growth of macroalgae and epiphytic communities was investigated in standardized lab and field experiments that were implemented at 10 study sites along a latitudinal gradient from 5° to 60° N in 2024 (macroalgae) and 2025 (epiphytes). We found statistically significant effects of ALAN in both projects: Macroalgal growth was affected in 7 out of 14 tested species, while the abundance of epiphytes per surface area of the host alga was influenced in 13 out of 39 experiments. In both projects, however, the direction and the strength of the effects varied between study sites as well as between time points at the same site. Hence, it appears that the influence of ALAN on marine photoautotrophs is highly system-specific and season-dependent. Furthermore, the fact that light pollution can affect both, macroalgae and their epiphytes, in various ways makes forecasting its long-term impact on coastal benthic ecosystems very challenging.

Studies on the effects of (micro)plastics and alternative materials

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This presentation briefly summarizes our research on the interactions of marine organisms with synthetic microparticles and their biochemical, behavioral, and ecological consequences. Over two program periods, we studied diverse materials including conventional plastics, bio-based and biodegradable plastics, as well as nano-materials.

Our initial studies addressed microplastics and marine organisms under natural environmental conditions. We showed that mucus, secreted by seaweeds or gastropods, retains and accumulates microplastics, potentially facilitating their transfer into marine food webs. Uptake and effects of microplastics were studied in selected species. Various benthic crustaceans show morphological and behavioral adaptations to cope with indigestible natural and artificial microparticles. Nevertheless, smallest microplastics can induce biochemical stress responses in sensitive organs.

Within the European HORIZON 2020 project “Bioplastics Europe”, we investigated bio-based and biodegradable plastics as alternatives to conventional plastics, focusing on degradability and impact on marine organisms. Bio-based plastics degraded faster than conventional plastics but degradation rates in the marine environment were low. Certain enzymes, such as carboxylesterases, can hydrolyze biodegradable plastics. These enzymes are common in the marine environment and in various organism. Bio-based plastics induced different biochemical responses in marine organisms than conventional plastics.

Our current research within the EU HORIZON 2020 project CheMatSustain extends this work to the effects of nano-particles on aquatic organism. Our studies contribute to a mechanistic understanding of the complex interactions of marine organisms with synthetic micro- and nanoparticles, thereby supporting ecological risk assessment and the development of environmentally more sustainable materials.

AI MareExplore: utilizing AI for marine enzyme discovery to address human-made grand challenges

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The Innovation pool project AI MareExplore brings together four Helmholtz Research Centres to work across topics on human-made grand challenges utilizing artificial intelligence. The project leverages extensive marine metagenomic datasets to prospect for novel biocatalysts capable of degrading plastic waste as well as fixing atmospheric carbon. AI is used in this project to tap into the microbial dark matter and provide in depth enzyme characterization before a single step is made into the laboratory.

More than 140.000 marine metagenome assembled genomes (MAGs, i.e. bacterial genomes) have been investigated with large language models and Hidden Markov Model profiles, yielding more than 430.000 dereplicated putative enzyme candidates for the thought after activities. For the analysis of these candidates a bioinformatic pipeline has been developed, that automatically invokes different machine learning algorithms to provide a first glimpse into the catalytic properties of these enzymes. With respect to biotechnological applications the predictions currently encompass putative temperature stability as well as expected pH optimum, but will be further extended over the course of the project. The implementation of this pipeline allows for careful selection of candidates with desired properties for heterologous expression trials. First enzymes for the degradation of poly(ethylene) terephthalate (PET), polyamide (Nylon), poly(butylene adipate-co-terephthalate) (PBAT – bioplastic) and ribulose-1-5-bisphosphate carboxylase/-oxygenase (RuBisCo) for the fixation of carbon have been selected, cloned and successfully expressed and are currently being characterized. The initial results highlight the power of this AI-integrated bioinformatic pipeline for the targeted and thus sustainable bioexploration of marine genomic resources to mitigate human pollution pressures. Further, the project is integrated via collaborations in other Helmholtz (SynCom) and European initiatives (EU Horizon) to provide policy and management advise.

II. POSTER ABSTRACTS¹

¹Listed alphabetically by poster presenter

Small-scale biogeochemical cycles in the surface ocean and their potential role in the formation of marine aerosols in the Southern Hemisphere

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Theresa Barthelmeß¹, Hendrik Feil^{1,2}, Riel Carlo Ingeniero¹, Dennis Booge¹, Christa Marandino¹, Hermann Bange¹ & Anja Engel¹

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The Southern Hemisphere Oceans play a unique role in cloud formation and, hence, climate regulation. During the last years we have explored small-scale biogeochemical cycling in the surface ocean and found preliminary evidence that the emission in secondary aerosol precursors follows similar diel cycles. Secondary aerosols, in turn, influence cloud formation. These features manifested within the subtropical front, including the Western Pacific and the Indian Ocean (TAN2003, MD247), and were tentatively related to trophic interaction. Small-scale biogeochemical cycles in the surface ocean may thus provide a key to decipher aspects of microbial ecosystem functioning and its impact on e.g., the emission of climate relevant trace gases such as dimethyl sulfide (DMS) or nitric oxide (NO). Studies focusing on these small-scale pattern and related interdisciplinary linkages are only starting to emerge. Rapid environmental changes preclude knowledge of existing ecosystem services, especially in remote and threatened areas such as Antarctica. Under the umbrella of Antarctica InSync, we are planning to explore seasonal and diel biogeochemical variability in relation to the emission of primary and secondary aerosols and their precursors in 2028.

Interdisciplinary observations of a changing Central Arctic Ocean

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Antje Boetius^{1,2,3,4}, Christina Bienhold^{1,2} & the extended PS138 Scientific Crew

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The amplified warming and substantial sea-ice loss in the Arctic affect the hydrography of the Arctic Ocean, and lead to increased primary productivity in the shelf seas, with cascading effects throughout the ecosystem. Yet, long-term trends in productivity and the biological carbon pump in the highly oligotrophic Central Arctic Ocean (CAO) basins remain poorly constrained. Previous expeditions to the CAO documented the extensive under-ice growth and export of the sea-ice algae *Melosira arctica*, contributing significant amounts of fresh carbon to pelagic and benthic food webs (Boetius et al. 2013). More recent missions in 2023 (ArcWatch-1; Boetius & Bienhold, 2024) and 2024 (ArcWatch-2; Rabe & Geibert, 2025) encountered altered atmospheric circulation and sea-ice drift regimes with profound consequences for ecosystem functioning. In 2023, an atmospheric circulation anomaly shifted the Transpolar Drift westwards, reducing the contribution of ice originating from shallow Siberian shelves to the investigated regions and thereby limiting the incorporation of *Melosira* cells during ice formation. As a result, large algal deposits were absent from the seafloor across the northern Eurasian basins including the North Pole. Consequently, benthic communities received substantially less fresh organic matter compared to 2012, leading to reduced benthic activity. Our interdisciplinary observations demonstrate direct links between atmospheric circulation, sea-ice provenance, biological connectivity and the vertical transfer of carbon to the abyssal seafloor. Further investigation of these coupled processes is therefore critical to better constrain their implications for Arctic ecosystem functioning under ongoing environmental change.

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Urban environments select for adaptation to multiple stressors: a case study of *Fucus vesiculosus*

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Anthropogenic activities have radically changed environmental conditions worldwide, negatively impacting biodiversity and ecosystem services. At the same time, most of the human population lives in urban areas that are greatly altered from natural habitats. Nevertheless, many species prosper in those environments. Stressful habitats may not only force additional pressures on biological communities, but they may also promote adaptation of taxa to those turbulences. For example, Briski et al. (2025) demonstrated an intraspecific difference among populations of *Gammarus* sp. and *Mytilus* sp. from three urban and one pristine habitat, with those from urban habitats performing much better.

To determine the generality of the pattern across taxa and space, here we conducted a comparative assessment of stress tolerance of seven brown alga *Fucus vesiculosus* populations. The populations were collected along the Baltic coast of Schleswig-Holstein in urban and pristine environments, allowing for testing whether populations from urban environments would perform better to induced stress than those from pristine habitats. The experiment was fully crossed factorial design, consisting of two temperatures (14 and 17°C) and seven copper concentrations (0, 3, 5, 10, 20, 40, and 80 µg/L). Two variables were followed during the experiment: growth rate and mortality of algal germlings. Both increased temperature and copper concentrations decreased the relative growth rate of germlings. However, the differences among populations were marginally significant ($p = 0.016$), with temperature - population interaction leading those differences. In the case of mortality, populations from urban habitats significantly outperformed pristine habitat populations, with germlings from the most impacted habitat being the most robust. We propose that urban populations are adapting to life in disturbed environments — this adaptation concurrently promotes more resilient rescue populations but potentially confers increased invasion risk from non-native species.

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Is the biological carbon pump still in a steady state?

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The biological carbon pump (BCP) transfers carbon from the surface ocean to the ocean interior and, ultimately, a small fraction to marine sediments, thereby influencing ocean carbon storage and atmospheric CO₂ concentration. Model experiments eliminating ocean biology from preindustrial steady state result in atmospheric CO₂ concentrations approximately 160–200 ppm higher than in corresponding simulations with an active BCP (Maier-Reimer et al., 1996; Tjiputra et al., 2025). Anthropogenic perturbations are altering the physical, chemical, and biological processes regulating these carbon fluxes. We therefore assess whether the BCP is departing from steady state.

We synthesize observational, experimental, and modelling evidence for changes in primary production, plankton community structure, particle export, zooplankton-mediated transport, dissolved organic matter cycling, remineralization, sedimentary carbon burial, and the physical redistribution and re-emergence of remineralized carbon. The evidence indicates substantial regional heterogeneity and strong coupling among these processes.

Global primary production shows signs of decline, whereas regional trends differ, with increases observed or projected in some high-latitude regions. Climate-driven shifts in plankton community composition can modify export and transfer efficiencies independently of changes in primary production. Warming, deoxygenation, and circulation changes further affect remineralization, carbon residence time, and the return of remineralized carbon to the surface ocean. Zooplankton-mediated fluxes, community restructuring and feedbacks between biological processes and circulation remain particularly uncertain.

Importantly, changes in carbon export do not directly translate into equivalent changes in BCP-mediated carbon storage. Reduced export can coincide with increased storage when circulation changes prolong the residence time of remineralized carbon in the ocean interior. Observed increases in global apparent oxygen utilization provide evidence for an accumulation of respired carbon in the ocean interior, consistent with enhanced BCP-mediated carbon storage (Koeve et al., 2020).

Collectively, available evidence indicates that the BCP is already responding to climate change and is no longer strictly in a steady state. However, the magnitude, spatial structure, and mechanisms of this departure from steady state remain poorly constrained. Opposing regional responses, natural variability, limited long-term observations, and model uncertainties continue to impede robust quantification and attribution. Resolving the evolving BCP requires sustained observations and biogeochemical models integrating changes in biological export, remineralization, circulation, and carbon re-emergence.

Topic 6 Symposium 2026

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Interactive effects of warming and anthropogenic pollutants on overwintering Arctic copepod *Calanus hyperboreus*

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Arctic marine ecosystems are increasingly exposed to multiple anthropogenic stressors, including ocean warming and emerging contaminants such as per- and polyfluoroalkyl substances (PFAS) and microplastics. The lipid-rich copepod *Calanus hyperboreus* is a key Arctic zooplankton species whose survival and reproduction depend on successful overwintering during prolonged periods of darkness and food limitation. Here, we investigated how environmentally relevant exposure to warming, perfluorobutane sulfonate (PFBS), and polyethylene terephthalate (PET) microplastics affects overwintering performance in *C. hyperboreus*. Individuals were incubated for 60 days under simulated overwintering conditions in a full factorial $2 \times 2 \times 2$ design crossing temperature (-1°C and 4°C), PFBS exposure, and PET microplastics exposure. Survival, egg production, lipid-sac condition and developmental stage were assessed throughout the experiment. In addition, enzyme assays targeting superoxide dismutase (oxidative stress), alkaline phosphatase (metabolic activity), and acetylcholine esterase (neurotoxicity) were conducted following short-term exposure (8 h), midway through the experiment, and after 60 days to evaluate both acute and chronic physiological responses to combined stressors. Preliminary results indicate that elevated temperature had the strongest overall effect on overwintering performance, while environmentally relevant concentrations of PFBS and PET microplastics produced comparatively limited effects and did not substantially exacerbate warming impacts. Interestingly, copepods exposed to combined stressors showed increased egg production, suggesting potential stress-induced reproductive responses despite otherwise limited physiological impacts. Enzyme analysis show limited acute stress responses but increased oxidative stress and metabolic activity after 60 days, showing the importance of long-term experiments when trying to assess relevant responses to environmental stressors.

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Remediation – recommendations towards policy and decision makers

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The remediation of underwater munitions in the Baltic Sea requires science-based decision-making to ensure safety, efficiency, and sustainability. In this Poster we present some of our efforts to provide support and recommendations for the politicians and decision makers. The CONMAR project addresses this challenge by developing a structured approach to support policymakers. A priority list of munition piles that should be cleared first has been generated using a Multi-Criteria Analysis (MCA). Developing the MCA involved criteria identification, data collection, weight assignment, and integration of findings using GIS-based analysis. In parallel, stakeholder engagement plays a crucial role in enhancing transparency and public acceptance by facilitating collaboration with experts and policymakers, acquiring relevant data, and promoting knowledge transfer. Co-creation and stakeholder workshops are one of the main parts of our munition projects (CONMAR, MMinE-SWEEPER, MUNI-RISK, ProBaNNt and BASTA) that contributed over several years to the MCA.

A key outcome of our efforts to provide decision-support was the establishment of the first Quality Guideline for Offshore Explosive Ordnance Disposal (EOD), published within the RoBEMM project. This guideline defines best practices and standardized procedures to improve safety, efficiency, and sustainability in clearance operations. Furthermore, CONMAR provided direct support for the new German Immediate Action Program for munitions clearance, contributing sonar and image data, as well as a multi-criteria prioritization of munition piles, with a specific focus on Lübeck Bay.

Looking toward the future, long-term decision-making support will be ensured through MUNIMAR, a dedicated center for marine munitions management established with the support of GEOMAR and the Environmental Ministry of Schleswig-Holstein. MUNIMAR will facilitate continuous monitoring, adaptive risk assessment, and cross-sector collaboration, strengthening strategic remediation efforts in the marine environment. By integrating scientific methodologies with policy needs, we can provide a robust framework for sustainable and effective munitions clearance.

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Who shakes the web? Disturbers, vulnerables, and dynamical centralities in food webs

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Quantifying species importance in food webs is core for biodiversity conservation and ecosystem management, yet structural network indices fail to capture perturbation dynamics. Using generalized ecological modeling across 200 niche-model food webs and 500 stable parameter configurations per topology, we systematically evaluate pairwise redundancies, parameter dependencies, and ranking stability across eleven structural and nine dynamical centralities. Dynamical centralities separate into disturber-identifying and vulnerability-identifying regimes. Disturber-identifying centralities (influence, L^2 -influence, and absolute impact) scale inversely with intrinsic turnover rates, rendering them largely redundant under standard unit-vector formulations. In contrast, vulnerability centralities remain sensitive to specific network structures and can distinguish effects due to diffuse environmental noise from targeted pressure. Furthermore, we reveal an inverse relationship between perturbation propagation and extinction cascades: basal species prone to triggering secondary extinctions cause minimal systemic disruption under transient perturbations, whereas potent disturbers rarely cause secondary extinctions. Ultimately, the ensemble of dynamical centralities condenses to four non-redundant indices: mean deviation, initial amplification, L^2 -sensitivity, and absolute displacement.

Nutritional flexibility in the cold-water diatom *Thalassiosira nordenskioeldii* – how does resource allocation shape particle aggregation and remineralization rates?

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Arctic phytoplankton blooms are a cascading succession of phytoplankton taxa that vary temporally and spatially in their extant (Bracher et al., 2026). During the warm, high light summer months, nutrient availability is likely a limiting factor to phytoplankton growth, contributing to the decay phase of a bloom. Nutrient availability also influences cellular resource allocation and macromolecular composition, with potential consequences for the fate of phytoplankton-derived organic matter (Inomura et al., 2022). In the Fram Strait, diatom-derived sinking aggregates are one important factor in determining sinking rates of particulate material (Hufnagel et al., 2026). We hypothesize that the elemental and macromolecular composition of phytoplankton-derived particulate material impacts the fraction exported to the benthos or remineralized in the mesopelagic zone.

As an initial case study, we cultured the cold-water diatom *Thalassiosira nordenskioeldii* under varying macronutrient concentrations to examine effects on particulate organic matter. Batch cultures were grown in autoclaved Arctic seawater amended with modified F/2 medium containing varying concentrations of NO₃ (0-0.88 µM), PO₄ (0-0.036 µM), and SiO₄ (0-0.106 µM), and incubated in triplicate at 6°C. Preliminary results indicate that growth was primarily inhibited by NO₃ availability, with a reduced growth at zero PO₄ addition and no significant response to varying SiO₄ additions. Particulate carbon, nitrogen, carbohydrate, and amino acids were also sampled to assess nutrient-driven changes in biochemical composition. These measurements will guide subsequent roller-table experiments examining particle aggregation and export potential. Here, we present the experimental framework and preliminary growth responses that form the basis for subsequent experiments examining how nutrient-driven changes in phytoplankton composition influence particle aggregation and potential export.

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Deep-sea benthic microbial communities reflect environmental change at the Arctic long-term observatory HAUSGARTEN

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In 1999, the Alfred Wegener Institute established the Long-Term Ecological Research (LTER) observatory HAUSGARTEN in Fram Strait, the only deep-water connection between the central Arctic Ocean and the North Atlantic. Spanning major gradients in depth, water-mass and sea-ice regimes within both Atlantic and Arctic oceanographic regimes, LTER HAUSGARTEN includes 21 annually sampled sites. Within this infrastructure, researchers record comprehensive time-series of environmental variables from surface waters to the ocean floor. Over the past years, pronounced surface water temperature anomalies and warming, loss of sea ice and shifts in plankton community composition took place alongside significant changes in marine biogeochemical characteristics. Trends within the deep-sea benthos include significant decreases in faunal abundances as well as a 28% loss of microbial cellular biomass. Yet, how these changes affect benthic microbial community composition and ecology remains poorly understood.

Therefore, we leveraged an archive of frozen deep-sea sediment samples collected at water depths between 1000 and 5500 m over a 23-year period and applied next-generation amplicon sequencing to characterize the taxonomic composition of microbial communities. We investigated effects of environmental change on microbial communities using time-resolved data on sea ice, upper ocean temperature, plankton communities, sinking particulate organic matter and benthic geochemistry. Diffusion map analyses revealed strong biogeographic structuring of microbial communities, with environmental variables as well as spatial and temporal structure explaining 76% of variation in community composition. Additionally, we identified two recurring community compositional states that were significantly associated with pigment concentrations, as well as timing of the sampling event. Therefore, both states likely represent benthic microbial communities before and after bloom settlement events. Our results provide new insights into the response of deep-sea benthic microbiomes to environmental change, and highlight the value of interdisciplinary, long-term infrastructure projects like the LTER HAUSGARTEN to study ecosystem change in the Arctic.

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The role of sponges for the Antarctic environment

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Antarctic sponge grounds are important components of benthic ecosystems, yet their roles in sustaining biodiversity, mediating biotic interactions, and contributing to biogeochemical processes remain poorly understood. Here, we investigate the ecology and functioning of the Antarctic glass sponge *Anoxycalyx joubini* in the Ross Sea, focusing on how this species interacts with its physical and biological environment.

We combine long-term in situ observations with hydrodynamic measurements, analyses of sponge pumping and surprising contraction behaviour, incubation experiments, and stable isotope and tissue composition analyses. These approaches allow us to investigate sponge–environment interactions, metabolic activity, feeding strategies, and the cycling of carbon and nitrogen within sponge grounds. In particular, we explore how environmental conditions, water movement and food availability may influence sponge activity, and how the distinctive structural and metabolic characteristics of *A. joubini* contribute to its ecological role.

By linking organismal behaviour with physiological and biogeochemical processes, this work aims to better understand the functions of Antarctic sponges and their contribution to the resilience and functioning of polar benthic ecosystems.

Data2AI Compass: framework, training, and tooling for AI-readiness for research data

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Artificial intelligence is central to research, but algorithmic sophistication cannot compensate for inadequate data: model performance is constrained by data readiness. Yet AI-readiness remains inconsistently defined and lacks frameworks comparable to FAIR. Without a coherent definition and criteria, researchers cannot assess AI-readiness systematically, hindering use and cross-domain comparison and reuse. We build the Data2AI Compass: 1) operationalizes existing taxonomies into a machine-actionable criteria catalog spanning four dimensions (data quality, task fit, governance/documentation, intended use), developed by a Helmholtz-wide working group; 2) makes the catalog testable, validated against outcomes, and community-extensible via a contribution schema and versioned repository; 3) provides training materials embedding AI-readiness across Helmholtz centers; 4) offers a prototype tool (Data2AI Companion) running auditable tests with remediation guidance via a conversational interface.

AMPBA & sedaECHO: modular Snakemake workflows for reproducible amplicon and ancient DNA metagenomic analysis

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High-throughput sequencing has become central to both biodiversity assessment and paleoecological reconstruction. Both fields depend on multi-step pipelines spanning preprocessing, taxonomic assignment, and statistical or authentication filtering, in which each methodological decision can shape the resulting ecological interpretation. Existing solutions are either flexible but poorly documented single-use scripts, or standardized but rigid and infrastructure-heavy platforms, leaving little room for tools that are both adaptable and reproducible. We address this gap with two complementary, Snakemake-based workflows tailored to different sequencing strategies.

AMPBA (Accessible Metabarcoding Platform for Biodiversity Analysis, <https://helmholtz.software/software/ampba-workflow>) addresses amplicon metabarcoding, sequencing taxonomically informative marker genes for biodiversity assessment and monitoring. Because markers differ in target taxa, evolutionary rate, and resolution, AMPBA decouples feature generation from any single, fixed biodiversity unit: denoising, clustering, and cooccurrence collapse each build a new unit (ASVs, swarm/OTU clusters, cASVs/cOTUs) from whichever precedes it, while NUMT filtering, decontamination, and replicate merging refine it, not redefine it; taxonomic assignment separately switches between marker-specific classifier/database pairs. This supports diverse markers, strategies, and study designs while keeping results reproducible across environments and reruns.

sedaECHO (<https://gitlab.awi.de/data-science-team/sedaecho>) addresses shotgun metagenomic analysis of sedimentary ancient DNA (sedaDNA), which enables high-resolution reconstruction of past ecosystems by capturing taxa that rarely appear in the fossil record. It ensures reproducibility through explicit rule definitions, pinned software versions, and traceable provenance, integrating established tools for taxonomic and functional classification and for damage pattern authentication, and allowing multiple methods to run side by side under identical conditions.

Both pipelines share the same design philosophy: locally installable, workflow-managed, and modular, reducing setup complexity while enabling systematic comparison of methodological choices. AMPBA and sedaECHO make this approach usable across sequencing-based ecological and paleoecological research, supporting standardized and reproducible analysis of environmental and ancient DNA.

A novel mesocosm facility to study phytoplankton fluorescence signals detected by satellite sensors

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Understanding the environmental drivers controlling primary productivity and how they vary across time and space is essential for assessing ecosystem function and predicting future change. Current observational approaches range from shipboard measurements and autonomous platforms to satellite remote sensing.

Whilst remote sensing has revolutionized the observational capacity of phytoplankton abundance and productivity, physiological insights remained restricted. However, passive chlorophyll a fluorescence has shown potential as a satellite-based proxy for phytoplankton physiology. Passive fluorescence occurs naturally in all phytoplankton cells when they are exposed to more sunlight than they can use for photosynthesis and is regulated by chlorophyll a concentration, absorbed light, and fluorescence yield. The latter is influenced by the physiological state of phytoplankton (modulated by temperature, light exposure, and nutrient availability). Although recent field studies have advanced our understanding of how, for instance, nutrient limitations affect passive chlorophyll fluorescence, these observations alone often cannot disentangle co-varying biotic and abiotic fluctuations; hence, key questions remain unresolved. Experimental approaches are therefore needed to identify the roles of these variables on passive fluorescence.

Building on previous approaches, we developed a novel indoor mesocosm facility designed to measure passive fluorescence while independently manipulating temperature, light, and nutrient availability. The facility was specifically designed to tackle key limitations of previous studies: (i) replicating realistic ocean conditions of light availability; (ii) detecting weak fluorescence signals under realistic low chlorophyll concentrations; and (iii) enabling simulations of major oceanic nutrient limitations (nitrogen and iron) under trace-metal-clean conditions. Initial tests using the ubiquitous diatom *Chaetoceros calcitrans* demonstrate the potential of this facility to advance our understanding of phytoplankton physiology at global scales.

Biological and physical influences on marine snowfall at the Atlantic equator at 23°W

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The biological carbon pump transfers organic carbon from the surface ocean to depth, but the processes controlling its variability remain poorly resolved, particularly on intraseasonal timescales. Here, we investigate the biological and physical drivers of marine snowfall in the central equatorial Atlantic using a unique long-term time series from the mooring at 0°N, 23°W.

Since October 2019, Underwater Vision Profilers deployed at approximately 300 and 850 m depth have continuously quantified particle abundance and size distributions, from which particulate organic carbon (POC) fluxes were estimated. We combine these observations with moored hydrographic and current measurements and satellite-derived sea-surface temperature and chlorophyll-*a*. Frequency decomposition and cross-correlation analyses are used to distinguish processes operating from intraseasonal to interannual timescales.

Marine snowfall at 300 m exhibits pronounced variability across multiple frequency bands. Annual variability accounts for approximately 12% of flux variance and is associated with a lag of about one month between upper-ocean variability and POC flux. Semi-annual and shorter seasonal variability accounts for approximately 24%, with lags of 5–7 days, while 1–2-month variability contributes approximately 25%, with lags of 8–9 days. These timescales point to a combination of seasonal upwelling, changes in Equatorial Undercurrent structure, and equatorial wave activity as important controls. The exceptionally warm conditions of 2023–2024 coincided predominantly with low POC flux.

Our observations demonstrate that equatorial marine snowfall responds to physical forcing across distinct timescales, linking rapidly varying upper-ocean dynamics to carbon transfer into the mesopelagic ocean.

Unveiling the trophic marker composition of *Melosira arctica*: bridging field observations and cultured isolates

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The centric diatom *Melosira arctica* grows in long strands underneath Arctic sea ice. Despite its ubiquitous distribution across the Arctic Ocean, little is known about its biochemical composition and importance as a food source for grazers, particularly in light of a decreasing icescape. We analysed the composition of different lipid-based trophic markers in *M. arctica* collected during three research expeditions and contrast their trophic marker content with that of unialgal *Melosira* cultures. To test whether there are differing biochemical characteristics between *Melosira* and typical pelagic and ice-associated (sympagic) algae assemblages, we additionally compared the trophic marker content of *Melosira* field samples to that of pelagic and ice-associated particulate organic matter (POM) as well as to pelagic and sympagic diatom-dominated communities during bloom situations. Despite pronounced variability in trophic marker content among *Melosira* field samples, some common patterns emerged, including overall high contributions of typical diatom-associated fatty acids (FAs) such as 16:1(*n*-7) and 20:5(*n*-3). Polyunsaturated FAs (PUFAs), an indicator for nutritional quality, contributed up to 30% of total FAs in the *Melosira* field samples from the Fram Strait and Yermak Plateau/Nansen Basin as well as in the cultures. PUFA proportions were distinctly lower in the central Arctic Ocean (CAO; 17%), likely reflecting differences in cell developmental stages, nutrient supply and ice properties. CAO *Melosira* assemblages had developed over a longer time than those collected from the other locations, likely exhibiting first indications of senescence. This state potentially hampers the diffusion of inorganic carbon into actively growing cells within the strands, resulting in highly enriched FA stable isotopes. Overall, the chemical composition of *Melosira* was found to be typical of a centric diatom; solely the sterol composition differed largely from that of pelagic and ice-associated POM. From experimental work with sympagic amphipods, we observed varying degrees of *Melosira* consumption.

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Food-web dynamics in the Arctic: insights from trophic markers in a rapidly changing region

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The Arctic is severely affected by climate change and warming at a faster rate than any other region in the world. Increasing water temperatures, sea ice loss, ocean acidification, and the potential poleward shift of boreal taxa place polar communities under significant pressure. In particular, the decline of habitable sea ice due to the onset of earlier, longer, and more extensive low-ice periods in the Arctic is expected to alter the functioning of the sea ice-water interface. This area constitutes an essential habitat for ice-algal growth and a shelter for many resident taxa as well as early-life stages of various species. Sea-ice decline is affecting the availability and transfer of sympagic (ice-derived) carbon, trophic pathways and community connectivity. While the importance of sympagic carbon has been determined for some Arctic species, further investigations are needed to better understand species-specific responses to anticipated changes in sympagic carbon availability over latitudinal and interannual patterns. In this aim, this study provides new insights about food web dynamics in two different areas: the Barents Sea (seasonal ice-cover) and the Central Arctic Ocean (perennial ice-cover). Samples were collected on two ship-based expeditions in the Barents Sea and Central Arctic Ocean during the summer months. Trophic marker analyses on lipids of primary producers and dominant zooplankton taxa were used to elucidate trophic relationships and the reliance on sympagic versus pelagic carbon sources across multiple trophic levels. Based on previous findings, we expect to detect distinct uses of pelagic and sympagic resources across taxa, as well as emerging trophic links that reflect clustering along sympagic- and pelagic-based carbon food webs. These findings will contribute to a deeper understanding of Arctic food web functioning and of potential future developments under continued sea-ice decline.

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Electron to carbon efficiency and phytoplankton community composition changes at Boknis Eck

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Fast Repetition Rate Fluorometry (FRRf) offers a rapid, non-radioactive alternative to ¹⁴C incubation for estimating primary productivity. However, electron transport rates do not directly translate to carbon assimilation. This relationship is captured by the electron requirement for carbon fixation ($\Phi_{e,C}$), the number of electrons transported through Photosystem II per carbon atom fixed. $\Phi_{e,C}$ varies with community composition and physiological state, introducing uncertainty into productivity estimates derived from FRRf alone. In this study, we address this uncertainty by quantifying electron-to-carbon efficiency and linking its temporal variability to the relative contribution of dominant phytoplankton groups, particularly diatoms and cryptophytes. Boknis Eck, a long-term monitoring station in the southwestern Baltic Sea, provides a well-characterized time series of physical, chemical, and biological parameters. Between November 2025 and July 2026, we deployed LabSTAF for FRRf-based electron transport measurements alongside CytoSub for phytoplankton community composition, paired with ¹⁴C incubations to determine particulate and dissolved carbon fixation rates. From these paired measurements, we calculated $\Phi_{e,C}$ at multiple depths across the sampling period to characterize its temporal dynamics and assess whether shifts in $\Phi_{e,C}$ coincide with changes in diatom and cryptophyte dominance. Preliminary results show an increase in electron-to-carbon efficiency from December to February, coinciding with a diatom-dominated bloom period.

Ecology of marine diversity-generating retroelements

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Microbial evolution via the accumulation of variants within a population is often a slow process, however, a group of dynamic genetic mechanisms exist and have the capacity to alter the within-population and individual's genomes by different means, including genomic rearrangements, excision and inclusion of various elements, and the introduction of single nucleotide variants. Diversity-generating retroelements (DGRs) are one such mechanism in which microbes and viruses uniquely guide site-specific protein hypervariability through an error-prone reverse transcription process, rapidly increasing the number of genetic variants that adaptive processes of evolution can act upon. DGRs have largely been studied in genomes of organisms in culture, and recent efforts to characterize their distribution in marine metagenomes demonstrated their ecological importance. So far, the detection of DGRs only relied on the correct identification of homologous reverse transcriptases. We developed a new program, in *anvi'o*, to find DGRs based on their unique pattern of single nucleotide variants, along with the typical reverse transcriptase homology approach. We apply this new program to the current large collection of marine metagenomic assembled genomes, which enables the characterisation of DGRs in naturally occurring microbial populations, across marine biomes, and offers opportunities to find new DGRs and quantify their activity as a function of environmental parameters. We investigate the targeted functions of DGRs across marine biomes, revealing those that are unique to particular environments.

Harmonising historical and recent observations of the Western Baltic Sea phytoplankton

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The environmental health of Western Baltic Sea is under pressure: algal blooms, oxygen depletion and fish kills linked to eutrophication and warming are becoming more frequent. Robust, long-term phytoplankton data are essential for tracking these changes, yet such data are scattered across institutions, languages, and formats, varying widely in methodology and quality.

Within the project RECOVER (**RE**silience of **CO**astal **V**ital **E**cosystems through innovative management solutions in the Danish-German border **R**egion), we are compiling and harmonising phytoplankton observational data from various historical and recent sources to assess how phytoplankton can be used as an indicator of environmental health and how environmental monitoring can be improved. Historical records reach back several decades but are often temporally and spatially sparse, with inconsistent methodology, while data coverage becomes denser and more standardised from the 2000s onward.

So far, we have compiled around 61.000 data points from six major sources (EurOBIS, SeaDataNet, MUDAB, KEMIDATA, ODIN, and monitoring data from LfU/MEKUN), supplemented by our own expeditions, open data repositories, and personal communication with regional experts. Quality control, cleaning, de-duplication, and aggregation are still ongoing.

The compiled dataset combines phytoplankton community composition and abundance from microscopy with observations from high-throughput methods such as eDNA, CytoSub/CytoBuoy and the Planktoscope. Furthermore, chemical and physical water properties (nutrients, stratification, Chl-*a*, water clarity) and primary productivity (¹⁴C incubations, LabSTAF) data are included.

By integrating historical and recent observations, this harmonised dataset will support the detection of long-term trends or regime shifts, help distinguish natural variability from directional change, and inform evidence-based protection and restoration targets. It will further facilitate the development of AI-supported real-time data analyses and a Digital Twin of the Western Baltic Sea within RECOVER.

Molecular composition of organic matter shapes microbial metabolism and alters carbon and nitrogen acquisition strategies in the ocean

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Dissolved organic carbon (DOC) is one of the largest active carbon reservoirs in the ocean, yet the extent to which its molecular composition influences microbial metabolism remains poorly understood. We investigated relationships between dissolved hydrolyzable amino acid (DHAA) composition, heterotrophic bacterial production (BP), and extracellular enzymatic activities (EEA) in the southwest Indian Ocean. DOC and DHAA concentrations decreased with depth as organic matter shifted from leucine-rich (leu), protein-like material toward glycine-enriched (Gly), diagenetically altered forms. The BP:DOC ratio, used here as a proxy for microbial carbon utilization relative to substrate availability, increased with Leu mol% but decreased with Gly enrichment. The relationship between Leu mol% and BP:DOC remained significant after accounting for DOC concentration and depth. Increasing organic matter degradation was accompanied by a shift from microbial biomass production toward extracellular resource acquisition, reflected by increasing cell-specific EEA relative to BP. Proteolytic enzyme activity consistently exceeded carbohydrate-degrading enzyme activity across stations and depths, suggesting greater microbial investment in organic nitrogen-acquisition than carbohydrates in the ocean interior. Together, our results show that amino acid composition is not only an indicator of organic matter degradation but is also closely linked to microbial metabolic allocation, connecting substrate biochemistry with microbial carbon processing and long-term carbon storage in the ocean.

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Pteropods as early-warning indicators of ocean acidification in the Antarctic Weddell Sea

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Aragonite undersaturation ($\Omega_{ar} < 1$) events are projected to rapidly increase in frequency and duration in the Antarctic Weddell Sea by 2050. Thecosome pteropods (pelagic snails) are bio-indicators of ocean acidification (OA) because their aragonite shell dissolves easily at low Ω_{ar} saturation states. Here, we describe the shell dissolution state of the pteropod *Limacina helicina antarctica* in relation to the water column Ω_{ar} in the southern Weddell Sea during austral summer 2018 as benchmark for future monitoring of ongoing OA. Ω_{ar} depth profiles at the sampling sites were consistently close to or in the range of threshold levels ($\Omega_{ar} \sim 1.1$ – 1.3) for pteropod shell dissolution. Pteropods contributed up to 69% of total mesozooplankton biomass, and their distribution correlated positively with Ω_{ar} and chlorophyll *a* concentration. When analyzed with scanning electron microscopy, 78% of the investigated shells exhibited dissolution, and 50–69% showed the more severe Type II dissolution exceeding current projections of pteropod shell dissolution for the Southern Ocean. But importantly, in our study, only two specimens had the most severe Type III dissolution. Dissolution often co-occurred with and occurred in scratch marks of unclear origin supporting notions that an intact periostracum protects the shell from dissolution. Where dissolution occurred in the absence of scratches or absence of evidence of periostracum breaches, micro-/nanoscale breaches may have been an important pathway for dissolution commencement supporting recent findings of a reduction of the organic shell content caused by low Ω_{ar} / low pH. The dissolution benchmark we provide here allows future application of pteropods as early-warning indicators of presumably progressing OA in the Weddell Sea.

Synergistic effects of artificial light at night (ALAN) and heat stress on corals

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Artificial light at night (ALAN) modifies natural light regimes and represents a pervasive type of sensory pollution affecting many coral reefs. In Indo-Pacific corals, ALAN has been shown to disrupt circadian rhythms, feeding strategies, photosynthesis, and gametogenesis (Marangoni et al., 2022); however, its physiological effects on Atlantic species remain untested. Moreover, given the rising frequency of heat waves, investigating impacts of concurrent ALAN and increasing temperature is of critical importance. This study investigates the combined effects of light pollution and heat stress on the Atlantic coral *Madracis decactis*. Six colonies were collected from the Alcatrazes Archipelago, Southeast Brazil. The colonies were fragmented and distributed in 24 indoor aquaria in a flow through system with filtered seawater, and artificial illumination. After acclimation, the corals were exposed (15-days) to four conditions: (1) Control (12L/12D, 24°C), (2) ALAN (12L/12L, 10lux), (3) Heat Stress (12L/12D, 29°C), and (4) ALAN + Heat Stress. There was a synergistic effect of ALAN and Heat on the photosynthetic efficiency (Fv/Fm). The combined treatment caused 1.6 times more inhibition than temperature alone. Despite reduced Fv/Fm and therefore potentially impaired metabolic performance, corals upregulated antioxidant capacity under Heat, likely as an adaptive response. However, co-exposure with ALAN dampened this response, suggesting a compromised capacity to cope with oxidative stress under light pollution. Further analyses are underway to better characterize the pigments and antioxidant pools, as well as damage to lipids, protein and DNA, and transcriptomic response. These results will help characterize the broader molecular and physiological basis of coral resilience to combined ALAN and Heat. Determining whether these processes response synergistically, additively, or antagonistically to combined stressors will enable more accurate predictions of the impacts of urbanization-related light pollution and climate change on coral health, ultimately supporting more informed conservation strategies.

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Temperature-driven biochemical and physiological responses in the Arctic diatom species *Melosira arctica* and *Thalassiosira nordenskioeldii*

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Increasing Arctic Ocean temperatures are imposing substantial stress on marine ecosystems. Diatoms contribute approximately 40% of global marine primary productivity and form the foundation of marine food webs. Phytoplankton productivity is strongly influenced by the abiotic environment, particularly temperature, controlling physiological processes, rates and biochemical composition. The objective of this study is to investigate the relationship between thermal performance and the biochemical composition of diatoms.

We investigated the effects of temperature on the physiology and biochemistry of the Arctic diatom species *Melosira arctica* and *Thalassiosira nordenskioeldii*, using batch culture experiments. Cultures were grown at five temperature treatments (0°C, 3°C, 6°C, 9°C, 12°C), representing ambient conditions and projected warming scenarios. Samples were collected during exponential and stationary growth phases. Cell abundance and growth rates were determined by microscopic counts. To characterize changes in biochemical composition, we measured particulate organic carbon (POC) and quantified the concentration and composition of carbohydrates, amino acids, and lipids.

Our results reveal pronounced species-specific responses to temperature, with both species exhibiting maximum growth rates at approximately 11°C, indicating they naturally grow below their thermal optimum. However, increases in growth rates were accompanied by substantial shifts in biochemical composition. A pronounced decline in glucose content was observed in *T. nordenskioeldii* with increasing temperature, whereas *M. arctica* exhibited only minor biochemical changes in POC composition. Glucose represented the dominant carbohydrate at lower temperatures, but its concentration decreased progressively with warming in *T. nordenskioeldii*, becoming undetectable at 12°C. This indicates a warming-induced reallocation of carbon within the cell, suggesting that the maintenance of high growth rates under warming conditions may occur at the expense of key biochemical traits linked to nutritional quality. This may alter the transfer efficiency and availability of energy and nutrients to higher trophic levels, as well as carbon cycling.

O2A SAMPLES: from expedition to digital database – a unified framework for sample digitization and interoperability

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Field campaigns produce a wide range of physical samples, but fragmented data management and inconsistent workflows frequently limit the usability of these samples over time and across different workgroups. The O2A Sample Management System ([O2A SAMPLES](#)) provides a sustainable, interoperable platform for FAIR-compliant (Findable, Accessible, Interoperable, Reusable), and AI-ready sample metadata across disciplines. O2A SAMPLES enables standardized sample registration following the [DataCite](#) metadata schema, storage management, sample loans, and transparent availability for collaborative use. Established research infrastructures, including the [O2A REGISTRY](#), [PANGAEA](#), [DSHIP](#), and the [Marine Data Portal](#), are integrated into the workflows. This integration allows automated metadata enrichment to reduce manual work while boosting both the completeness and consistency of metadata, and links to [Nagoya Protocol](#) documentation to support legal compliance. Standardized workflows, standard operating procedures (SOP), and QR code-based tracking further strengthen reproducibility and accessibility across the entire sample lifecycle.

O2A SAMPLES functions as a sustainable, long-term service. It establishes a unified digital framework to support easy sample discovery, interoperability, and cross-institutional collaboration from field acquisition to digital repository for environmental research.

The Wall of Mouths: *in situ* heterotrophy of deep-sea corals in shallow fjord waters

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The north Patagonian fjords of Chile feature the phenomenon of deep-sea emergence, providing a unique opportunity to access dense populations of deep-sea cold-water corals (CWC) by shallow-water scientific diving. The existence of CWC in the naturally acidified and aragonite-undersaturated waters suggests that CWC growth is sustained by an ample supply of food and rich energy stores^[1]. However, corals paradoxically appear to perform better and grow faster in the aragonite- and plankton-depleted deep parts of the fjord^[2]. These counter-intuitive findings may be related to differences to energy allocation into reproduction vs other energy expenditures (e.g. calcification, defense), but a test of this hypothesis is wanting. Here, we examine how CWC abundance and currents drive suspended organic matter distribution and fluxes of food to the corals.

1. Our study pioneers the use of Underwater Vision Profilers (UVP) to assess benthopelagic coupling by cold-water corals *in situ*.
2. UVP6 deployments show lower particle concentrations near CWC, specially for larger particles (>2 mm).
3. Small particles (<1.65 mm) show consistent but smaller depletions (1.5–3.5 ml/m³).
4. Combining measured depletions with average boundary layer currents, we calculate particle fluxes of 2.1–4.8 l/m²/day to the coral “Wall of Mouths”.
5. At 199 ± 30 CWC/m², daily retention is 11–24 ml/CWC.

Enhanced heterotrophy may help CWC cope with climate change and anthropogenic stressors^[3].

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Ocean Glow: nutrient limitation and contrasting fluorescence responses across ocean environments

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Phytoplankton productivity in the open ocean is strongly influenced by nutrient availability, yet nutrient limitation remains difficult to monitor at basin and global scales. Ocean Glow investigates whether sun-induced chlorophyll fluorescence measured by above-water radiometry can provide information on phytoplankton nutrient stress. Across a series of research cruises, we have observed contrasting fluorescence responses between low- and high-latitude environments. Here, we use observations from the M187 and DY172 cruises to examine these different responses, combining high-resolution radiometry with nutrient-addition bioassays, phytoplankton pigments, active fluorescence measurements, nutrient concentrations, and environmental observations.

During M187 in the South Atlantic, the fluorescence response was approximately threefold higher in iron-limited than nitrogen-limited waters, consistent with previous observations from the equatorial Pacific. In contrast, DY172 showed a different expression of the fluorescence signal at high latitudes, where phytoplankton experienced lower and more variable mixed-layer irradiance and showed enhanced fluorescence responses alongside strong photoprotective capacity. Similar broad patterns have subsequently been observed during other Ocean Glow campaigns, suggesting that the way nutrient limitation is expressed through passive fluorescence differs across ocean environments. These observations highlight the importance of the light environment and phytoplankton photoacclimation or adaptation in determining how nutrient stress appears in sun-induced fluorescence, and therefore how fluorescence-based indicators of nutrient limitation may be applied across different regions of the ocean.

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Robinson, T. B., Liu, H., Garaba, S. P., Voss, D., Schuback, N., Moore, C. M., ... & Browning, T. J. (2025). Nutrient limitation regimes control sunlight-stimulated chlorophyll fluorescence in the South Atlantic Ocean. *Communications Earth & Environment*, 7(1), 43.

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O2A SEQUENCES: a FAIR platform for end-to-end metabarcoding data management

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Metabarcoding, the sequencing of marker genes from environmental samples to identify the organisms present, is central to biodiversity and environmental research, and its data volumes are growing quickly. Turning these data into a lasting, shareable resource depends on keeping sequences, their metadata, and analyses connected and archive-ready, which remains difficult to do consistently across groups and tools.

O2A SEQUENCES (<https://sequences.o2a-data.de>) provides this missing layer. Embedded in AWI's O2A (Observations to Analysis and Archives) framework, it manages raw sequences from ingestion to archive submission. Researchers upload their sequences and complete a standardized set of metadata fields aligned with the HARMONise schema (<https://harmonise.awi.de>), which builds on the MIxS standard. The platform runs standard, preconfigured workflows reproducibly, and it lowers the barrier to archiving by assembling raw sequences together with their metadata into submission-ready files that follow European Nucleotide Archive (ENA) and German Federation for Biological Data (GFBio) conventions.

Offered as software-as-a-service, O2A SEQUENCES makes metabarcoding data FAIR, AI-ready, and reusable across centers, providing a foundation for sustainable research-data management that extends to other environmental data types.

A standardized framework for comparing POC-SPM relationships in coastal systems

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The ratio of particulate organic carbon (POC) to suspended particulate matter (SPM) is a key indicator of the formation and decay of particulate carbon in coastal waters and across the transition to the open-ocean. A meaningful assessment of the relationship between POC and SPM in coastal regions is challenging due to the distinction between the inorganic and organic components of SPM. Furthermore, statistical comparisons are often complicated by differences in data coverage. Here, we present a novel and robust approach that standardizes the analysis of POC relationships by describing the POC:SPM ratio as a function of SPM concentration.

The method builds on the semi-empirical model proposed by Schartau et al. (2019), which was refined in Fettweis et al. (2022). Here, we introduce an updated model formulation together with a standardized workflow for data assimilation, i.e. the process of adjusting the model's solution to fit the observational data. This approach provides a consistent basis for comparing POC relationships across diverse coastal environments.

Applications to contrasting coastal systems demonstrate that the standardized analysis not only reveals common characteristics of POC partitioning but also highlights systematic regional differences. The proposed framework separates the high variability from the more meaningful environmental signals, thereby facilitating an objective comparison between coastal regions. It also provides a consistent basis for linking POC-SPM relationships to optical remote sensing signals. This opens up the potential for improved retrievals of SPM concentrations from satellite observations, and for the development of more robust POC estimates from remote sensing in coastal and shelf seas.

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Bringing the meadow ashore: a 3D-printed, life-size seagrass model for science outreach

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Seagrass meadows are among the most valuable yet least visible coastal ecosystems: submerged in often turbid waters and rarely accessible to the public eye. To close this gap, we present a novel outreach exhibit: a life-size, 3D-printed model of a seagrass meadow (*Zostera marina*) complete with sediment layer that visitors can look directly into. The model is fully hand-painted and populated with the meadow's characteristic fauna — among others bivalves, shore crabs, fish, snails, and lugworms — recreating the structural complexity and biodiversity of a real meadow in a format that is tactile, durable, and immediately legible without diving or snorkeling gear.

The exhibit offers a new, low-barrier way to open conversations about seagrass ecosystems with non-specialist audiences, including school pupils, university students, and members of the public. The exhibit is modular, comprising four independent cubicles that can be displayed individually or combined into the full installation, depending on transport, space, and audience requirements. Thereby, it supports multiple modes of engagement: as a visual entry point to discuss seagrass ecosystem services; as a hands-on search-and-discover activity for children hunting for hidden animals; or simply as an immersive, scenic representation that lets visitors imagine what a real subtidal meadow looks like underwater.

By translating an underwater habitat into a physical, explorable object, the model lowers the threshold for public engagement with seagrass science and can be flexibly adapted to audiences ranging from young children to university-level students.

The exhibit was funded by GEOMAR's internal EngageComm-Award (2024), a grant supporting innovative approaches to science communication.

Global prevalence of intermediate particle maxima in *in situ* imaging data

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The Biological Carbon Pump plays a key role in regulating the ocean carbon cycle by transporting particulate organic carbon (POC) from the surface into the deep ocean. Understanding how particle flux attenuates with depth is therefore critical for quantifying carbon sequestration. While flux attenuation is commonly described using a power-law (Martin curve) or exponential decline, high-resolution *in situ* imaging reveals substantial deviations from these idealized profiles.

Here, we present a global analysis of Intermediate Particle Maxima (IPM) identified in fine-resolution *in situ* imaging data. Using a newly developed algorithm, we characterized the prevalence, depth, intensity, and particle size structure of IPM, and assessed their influence on commonly used flux attenuation metrics. IPM were widespread, occurring predominantly between 300 and 500 m depth, with highest prevalence in coastal and equatorial regions. IPM generally exhibited flatter particle size spectra slopes than surface waters, indicating a relative enrichment in larger particles. However, independent semi-automatically annotated UVP data (Nocera et al., 2025) showed no significant increase in copepods or fecal pellets within IPM, instead suggesting that these maxima were predominantly composed of non-living detrital particles.

Importantly, the presence of IPM significantly affected all tested measures of flux attenuation, including Martin curve fits, transfer efficiency, and remineralization depth. Our results demonstrate that IPM are a widespread feature of *in situ* imaging profiles and highlight their potential importance for interpreting and quantifying vertical carbon flux attenuation.

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Environmental controls on benthic microbial sulfide production in seasonal hypoxic locations of Kiel Bight

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The Kiel Bight is exposed to multiple anthropogenic pressures that promote warmer water, high nutrient load, intensified algal blooms and prolonged seasonal stratification. These conditions increase organic matter flux and contribute to bottom waters deoxygenation, while stratification prevents re-oxygenation and allows hydrogen sulfide to accumulate first in the benthic system and subsequently in the bottom water. This can create toxic conditions at the seafloor and may ultimately contribute to fish kill events.

Over three years, we collected sediment and water column data from the Kiel Bight during seasonal hypoxia to investigate benthic microbial communities and their role in sulfide production, with sulfate reducing bacteria (SRB) as key organic matter degraders. Abundances of putative SRB varied substantially among sites and years. Sulfate reduction rates (SRR) were detected in the sediment, particularly in the upper sediment centimeters, but not in the sulfidic bottom water samples. However, the relative abundance of putative SRB did not consistently correspond to high SRR or sulfide accumulation, indicating that SRB abundance alone is not a reliable proxy for sulfide production or release. Organic matter composition, cell abundance and activity, sulfide oxidation by sulfur oxidizing bacteria, microbial mediated iron-sulfur reaction and local hydrographic and geochemical conditions likely jointly influenced whether sulfide accumulated or was reoxidized at the seafloor.

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Not one history but many: evolutionary rate and gene coupling across the SAR11 core genome.

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The core genome of a microbial clade is usually treated as a single unit, a block of shared genes used to track the history of the organism. But each of those genes has its own evolutionary rate and its own trajectory. That core is defined by amino acid sequence similarity, so the fastest-evolving genes fall out of it, not because they are absent from the genomes, but because we can no longer recognise them. Because selection acts on protein function rather than on sequence itself, structural similarity outlives detectable sequence similarity, and much of the missing fraction is still there to be found, once genes are grouped by structure. We took this approach to SAR11 where streamlined genomes carry few paralogs and little redundancy, so a dependency between two proteins is visible and large populations let selection resolve it. We recently found that some of the most variable genes in this clade are shaped by epistatic co-selection with partners scattered across the genome (Hench et al. 2026). Whether the same coupling reaches into the conserved fraction is unknown. If the genes that all appear essential still move together, coupling is not a feature of variable regions but of how the genome is wired throughout. We ask three questions of the same set of gene trees: how fast gene evolves relative to the organism, how closely its topology follows the organism's and which genes accelerate and slow in step with one another.

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Zooplankton C:N stoichiometry and its influence on carbon cycling in a global ocean model

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Ecological stoichiometry predicts stronger homeostasis in zooplankton than in phytoplankton, but also acknowledges that zooplankton stoichiometry is not fixed but varies to some extent. Albeit smaller than in phytoplankton, flexible homeostasis in zooplankton may influence biogeochemical cycles. Global biogeochemical models are increasingly able to describe flexible phytoplankton stoichiometry, both in carbon:nutrient and chlorophyll:carbon ratios, caused by acclimation to variable nutrient and light availability. Very little attention, however, has been paid to how the interaction of variable food stoichiometry with zooplankton homeostasis affects carbon and nutrient fluxes. Expectations from ecological stoichiometry are that generally the dietary carbon:nutrient requirements of zooplankton have a maximum at somewhat lower ratios, and their allowable range becomes narrower with increasing trophic level. Here we show results from a global ecosystem model, REcoM, that allows for flexible C:N stoichiometry, and that represents three zooplankton size classes, micro- meso- and polar macrozooplankton. We show that even without explicit homeostatic regulation of zooplankton stoichiometry in the model, the model produces an overall decrease of both the mean and the breadth of the C:N ratio distribution with trophic level from phytoplankton to polar macrozooplankton. Respiration can, however, lead to unrealistically low C:N ratios in the highest trophic level, if not tuned appropriately. We explore the effects of several possible processes suggested for regulating zooplankton homeostasis. Finally, we discuss the role of zooplankton stoichiometry for the biological carbon pump.

Assembly transitions and multistability dynamics in the Arctic marine plastisphere: Insights from long-term mesocosm succession and field validation

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The Arctic Ocean serves as an increasingly critical sink for marine plastic pollution, yet the spatiotemporal assembly processes and multistability dynamics governing the Arctic plastisphere remain poorly understood. Here, we integrated long-term mesocosm experiments (D40 and D135) with natural field-collected plastics (Field) in the Arctic Ocean to unravel the compositional succession, assembly mechanisms, and potential energy landscapes of plastisphere communities. Plastic substrate types had no significant effect on microbial community diversity and composition ($p > 0.05$), whereas exposure time and environmental regime were the primary drivers of community succession. Alpha diversity increased monotonically along the successional trajectory, peaking in natural Field plastispheres. Taxonomic succession was overwhelmingly dominated by species turnover (>83%), driven by a transition from early generalist pioneers (*Pseudoalteromonas*) toward late-stage, specialized micro-niche dwellers (*Yoonia* and *Dokdonia*). Dissolved nutrients (DOC and TDN) were associated with early stage of community succession (D40), whereas mature biofilm differentiation (D135) was associated with total organic carbon (TOC) and ambient bacterial abundance (LNA cell abundance). Quantitative null-model analyses (iCAMP) revealed a fundamental transition in community assembly, shifting from early stochastic drift (58.9% at D40) to predominant dispersal limitation (79.6% in Field). Three-dimensional energy landscape and bimodality analyses further revealed a non-linear state bifurcation of plastisphere communities, from an initial single-basin transient state (BC = 0.54 at D40) toward alternative stable sub-states (BC = 0.64 at D135), ultimately converging on a distinct field equilibrium (BC = 0.57) that was topologically decoupled from the laboratory microcosm regimes. Overall, this study demonstrates that physical migration barriers and micro-niche adaptation lock mature plastispheres into topologically independent alternative stable states, providing critical insights for predicting the ecological persistence and fate of plastic debris in changing polar ecosystems.

Insights into antibiotic resistance of bacteria associated with wild fish from Baltic Sea and Cape Verde

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Antimicrobial resistance (AMR) poses a serious global threat to human health (WHO, 2025). In this context the potential role of wildlife as reservoirs, disseminators, amplifiers, and sentinels of AMR is discussed. Research on antibiotic resistance bacteria associated with wild marine fish has not yet progressed very far. Antibiotic resistance profiles of bacteria associated with commercially important fishes were studied. Cod, herring, and sprat were collected from the Baltic Sea and bluespotted seabass from the Atlantic Ocean. Among 100 fish-associated strains were 11 isolates from the genera *Shewanella*, *Psychrobacter*, and *Glutamicibacter* which were selected for genome phylogeny, agar-disc diffusion assays (phenotype) and genome analyses (resistome). These genera are common parts of the microbiome of wild marine fishes (*Shewanella*, *Psychrobacter*), been rarely studied (*Glutamicibacter*), and belong to clusters of phylogenetically closely related bacteria from both habitats, Baltic Sea and Cape Verde. A comprehensive spectrum of 60 antibiotics used in human medicine from 18 compound classes was tested. Among them were last resort antibiotics (WHO, 2022) and 30 antibiotics listed in the WHO Essential Medicine List (WHO, 2023). *Shewanella* sp. strains showed the highest resistance rates (38%), followed by *Psychrobacter* sp. strains (28%), and *Glutamicibacter* sp. strains (20%). Resistance was shown at least for one representative of 14 out of 18 drug classes, such as last resort antibiotics colistin and fosfomycin. Antibiotic resistance genes conferring resistance to almost all antibiotics tested were found. Genes related to multi-drug efflux pumps dominated, followed by genes related to resistance to β -lactams. Both, phenotypes and resistomes were very similar among members of *Psychrobacter*, *Glutamicibacter*, and *Shewanella*, independently of host and geographic origin. Multi-drug resistance patterns of the wild fish-associated bacteria demonstrated the natural occurrence of antibiotic resistance which should be considered in matters of development, transmission, and spreading of antimicrobial resistance.

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Equatorial Pacific iron-nitrogen co-limitation driven by nitrogen-limited *Prochlorococcus*

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Phytoplankton growth in the Equatorial Pacific contributes ~17% to global ocean primary production^I. Concentrations of nitrate in this region are elevated and phytoplankton growth is considered to be iron-limited. Here we show that phytoplankton are co-limited by iron and nitrogen over >8,000-km of the Equatorial Pacific, where experimental supply of either nutrient stimulated growth. This was driven by *Prochlorococcus* being stimulated by ammonium supply whereas other phytoplankton responded to iron. Consistent with this, sites in the far east of the basin—where both nitrate and ammonium were initially elevated—showed iron limitation only. Mechanistically, we find that co-limitation was regulated by the predominance of high-light (HL)-adapted HLIII and HLIV *Prochlorococcus* ecotypes, which lack iron-dependent enzymes required to utilize the abundant nitrate^{II,III}. These results have implications for how phytoplankton growth is modelled in the ocean and emergent phytoplankton community structures, with impacts on ocean biogeochemistry and food webs.

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Aggregation and sinking parametrizations of transparent exopolymer particles in FESOM2.1-REcoM3

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Transparent exopolymer particles (TEP) play an important role in the Arctic Ocean carbon cycle by facilitating the transfer of dissolved organic carbon to particulate organic carbon, enhancing particle aggregation through their stickiness, and influencing the vertical flux of organic carbon to the deep ocean. Furthermore, TEP in the upper ocean can also serve as marine biogenic aerosol precursor when they are transported into the atmosphere. As the data availability of TEP is scarce globally and even more limited in the Arctic, we implemented dissolved acidic polysaccharides and TEP into the AWI-developed global ocean biogeochemistry model FESOM2.1-REcoM3 that resolves two phytoplankton classes and allows for flexible stoichiometry (Zeising et al., 2026). This framework enables the representation of carbon overconsumption as a major pathway for PCHO formation and thus, explicit simulation of carbon exudation under nutrient-depleted conditions. In our ongoing work, we address different interaction and sinking schemes of TEP with other organic carbon particles in the water column. In Zeising et al. (2026), TEP only contribute to the aggregation of phytoplankton by their stickiness, but they do not interact further with thereby formed detritus particles. In an updated parametrization, we test how particles fluxes are influenced by, first, TEP being transferred into the detritus pool as well, and second, TEP being simulated based on their own sinking parametrization.

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