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Algal Response and Ecosystem Perspectives

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Invited talks

Ecological and evolutionary challenges of life in suspension with implications of climate change

Judit Padisák

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Phytoplankton collects unicellular and colonial photosynthetic organisms differing both in shape and size, but all adapted to live in apparent, habitat-specific suspension in turbulent water masses. The amazing morphological diversity of phytoplankton has to be considered an evolutionarily-driven compendium of strategies to cope with the strong variability and unpredictability of the pelagic environment. Turbulence represents a key driver of phytoplankton dynamics in all aquatic ecosystems and phytoplankton morphological variability is the evolutionary response of this group of photosynthetic organisms to the temporal and spatial scales of variability of turbulence. This presentation is aimed at showing how deeply turbulence contributes to the shape, size, ecophysiological properties and distribution capacity to structure of phytoplankton assemblages to explore how these governs phytoplankton access to resources and, at the same time, how the shape structure of phytoplankton evolutionarily represents the way in which this group of organisms has optimized its chance to survive in the highly dynamic aquatic environment. Climate change substantially influence our lake habitats (extension, depth, stratification pattern, physical and chemical drivers) along with expectable changes in phytoplankton assemblages. Briefly: when the competitive arena changes, the actors must change.

Microalgae secondary metabolites – current knowledge and future prospects

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Secondary metabolites constitute a diverse group of natural products synthesised by all living organisms, including microalgae. While some of these compounds are shared across different taxonomic groups of microalgae, others are characterised and unique to specific strains. Their diversity is driven by factors such as the number of biosynthetic gene clusters (e.g. PKS and NRPS), regulatory mechanisms of gene expression, and variety of environmental conditions. Despite ongoing research, the functional roles of secondary metabolites in microalgal metabolism and their interaction with the environment remain incompletely understood.

This presentation addresses two aspects of microalgal secondary metabolites: their environmental functions and their biotechnological potential. Toxins are the most extensively studied group of bioactive compounds produced by microalgae. Although commonly investigated for their harmful effects on humans and ecosystems, they have been reported to play important role for the producing organisms, including allelopathy, competition, defence and predation. However, despite numerous reports, there is still a lack of studies elucidating the underlying mechanisms of action using integrated omics approaches. Even less is known about the ecological roles of many other microalgal secondary metabolites.

In contrast, substantial knowledge has been acquired regarding the bioactivity, mechanisms of action, and biotechnological application of these compounds. Cyclic peptides, polyketides, and alkaloids represent the most promising groups with significant pharmaceutical potential. The majority of microalgal secondary metabolites have previously been investigated primarily for their effects on a single specific target; however, recent findings indicate that they may exhibit a much broader spectrum of biological activities. The application of untargeted metabolomics, advanced computational approaches, and the development of comprehensive natural product libraries have offer new tools for the discovery of novel bioactive compounds. Concurrently, omics technologies provide valuable insights into their native biological functions and support their identification as high-value products.

Algal biodiversity knowledge as a foundation for understanding global environmental change

Frederik Leliaert

Meise Botanic Garden, Meise, Belgium

Algal biodiversity knowledge is important to understand and predict the impacts of global environmental change on aquatic ecosystems. However, our capacity to anticipate biodiversity responses is limited by incomplete knowledge of current diversity and distribution patterns. In seaweeds, advances in molecular systematics have shown that species diversity is often much higher than previously assumed, revealing widespread cryptic diversity and complex biogeographical patterns, as illustrated by the red algal genus *Portieria* and the brown algal order Dictyotales. Many regions, particularly in the tropics, are still poorly studied, but even in relatively well-studied regions such as Europe, taxonomic uncertainties continue to obscure true diversity. An example is the green algal genus *Ulva*, where morphological simplicity hampers reliable species identification. The EUlva project addresses this challenge by applying large-scale DNA-barcoding analyses to achieve a comprehensive understanding of *Ulva* diversity and distribution in European waters. Closing biodiversity knowledge gaps requires renewed investment in taxonomy, and herbarium collections play a central role in this effort. As permanent records of algal diversity collected over centuries, they provide critical reference material and historical baselines for studying temporal and spatial changes in species distributions. The ongoing digitization of these collections are transforming their use, enabling access to specimen data and facilitating their integration with molecular, ecological, and environmental datasets.

How diatoms respond to biotic and abiotic factors

Peter G. Kroth

Department of Biology, University of Konstanz, Germany

Diatoms are unicellular algae that play an important role in most aquatic ecosystems. Due to their evolution by secondary endosymbiosis, they show peculiar aspects with respect to their genomes, physiology, and metabolism. In the recent years, research on diatoms showed a breath-taking development, experiencing a strong boost from genome projects, the development of molecular tools, large-scale transcription analyses, transformation techniques, as well as gene silencing or genome editing approaches.

This seminar will deal with some aspects of diatoms to external triggers, including the role of (i) Stramenopile-specific photoreceptors, the (ii) interaction of diatoms with bacteria, as well as (iii) intracellular phosphate storage.

(i) Aureochromes are a relatively novel type of blue-light photoreceptors in algae, and they so far have only been found in Stramenopiles. They have a very peculiar structure: In addition to a blue-light sensing flavin-binding LOV-domain, they possess a DNA-binding bZIP domain, that is typically found in transcription factors. Therefore, aureochromes can be considered as light-driven transcription factors, allowing very fast responses. Our results show that aureochromes can affect a large number of genes very quickly.

(ii) Benthic diatoms often form biofilms on substrata. Such photoautotrophic biofilms are aggregates of heterotrophic bacteria and phototrophic algae, in which diatoms can be abundant. Specific interactions between diatoms and bacteria have recently been found to be necessary for biofilm formation of some diatoms.

(iii) Polyphosphates (polyP) are biomolecules that play a multitude of physiological roles in many organisms. We have studied the presence and role of polyP in the freshwater diatom *Achnanthidium minutissimum*. Using a combination of biochemical assays and stimulated Raman spectroscopy, we found that under the absence of exogenous P, the diatom rapidly consumed its internal polyP reserves and likely other non-polyP reserves, allowing diatom growth rate to be resilient against short-term P shortages.

Oral Presentations

Does it matter where we live? - The impact of climate zones and anthropogenic pressure on the diversity of toxic cyanobacteria and bacterial communities

Joanna Mankiewicz-Boczek[1,3], Francisco López-Hun[1,2], Arnoldo Font-Nájera[3], Magdalena Kluska[3], Tomasz Jurczak[1], Milena Skóra[4], Wiktoria Piestrzyńska[4], Bessie Evelyn Oliva Hernandez[5]

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The main drivers contributing to the rapid development of harmful cyanobacterial blooms (HCBs) and associated bacterial communities (ABCs) in freshwater systems are eutrophication, anthropogenic pressure and climatic conditions. We took all these elements into account when analysing bacterioplankton diversity and cyanobacteria hepatotoxicity in lakes representing i) different climatic zones (Amatitlan – AM and Laguna del Pino – LP, Guatemala, tropical zone; and Sulejow Reservoir – SU, Poland, temperate zone), ii) anthropogenicity (AM – urban and agricultural pressure; LP – lake in the National Park; SU – agricultural pressure) and iii) trophic status. Cyanobacteria and ABCs were analysed via 16S rRNA sequencing and microcystins via HPLC, in dry period (Guatemala) and summertime (Poland), in 2024 and 2025. The results of AM in comparison to LP confirm that nutrient enrichment from anthropogenic eutrophication is a key driver of cyanobacterial dominance. The urban and agricultural catchment surrounding AM contributes to hypertrophic condition, whereas the mixed forested/agricultural catchment with natural protected area of LP supports mesotrophic state. Notably, in AM, the available dissolved nutrients and stable temperature, yielded the highest *Microcystis* abundance and microcystins concentration exceeding WHO guidelines for recreational waters. In Lake SU, which has a temperate climate, temperature played a significant role in shaping the structure of the cyanobacterial community, besides nutrients. These environmental drivers contributed to a seasonal shift between coccoidal *Microcystis* and filamentous *Aphanizomenon*, with implications for water quality and ecosystem health. Regarding ABCs, *Flavobacterium* was consistently detected in both AM and SU, suggesting a broad ecological linkage with HCBs. Site-specific bacterial taxa were also identified, such as *Pseudomonas* in AM and *Limnohabitans* in SU. These taxa appear to engage in mutualistic or commensal relationships with cyanobacteria, with *Flavobacterium* and *Pseudomonas* also representing potential pathogenicity. In contrast, *Polynucleobacter* was highly abundant in LP, a genus typically associated with higher water quality.

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Diversity patterns – diatom communities in mountain streams of the Gorce National Park

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Small headwater streams play a crucial role in maintaining freshwater biodiversity, acting as refugia for rare taxa with specialized ecological preferences and supporting high species diversity. The Gorce range in Polish Carpathians is a distinctive and relatively isolated region, rising prominently above the surrounding valleys. Situated between Tatra Mountains, and lower ranges of Western Beskids, it represents a transitional landscape reflected also in the composition of diatom assemblages.

The investigated streams are mostly dominated by species typical for well-oxygened, fast flowing waters, including numerous representatives of the genus Achnanthidium. However, among the recorded taxa, alongside species typical known from similar types of streams in Bieszczady or Lower Beskid Mountains, there are also representatives commonly associated with alpine and alpine foothill freshwater environments.

Studies conducted on freshwater streams of the Gorce National Park (GNP) revealed a high species diversity and underlined the importance of fine-scale habitat heterogeneity in sustaining diverse assemblages within otherwise homogeneous systems. Studied waters provide suitable habitat for abundant populations of Didymosphenia geminata, a species of increasing global interest because of its capacity to form extensive blooms. Within the study area, it develops particularly well in shallow, sun-exposed parts of the Kamienica stream. Its presence in these otherwise relatively pristine systems highlights the importance of ongoing monitoring and a deeper understanding of its ecological preferences.

Overall, the results emphasize the significance of small undisturbed streams as biodiversity hotspots and their role in the conservation of rare diatom species in protected areas. They also emphasize the need for continued monitoring of key taxa to better understand ecosystem dynamics and anticipate possible shifts.

Amazing Novohradské mountains and their outstanding algae: checklist and stream dynamics pilot ecological study

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The diversity of algae and cyanobacteria in three streams (Černá, Lužnice, Veveřský potok) and ponds in their basins in the Novohradské Mountains was studied for two consecutive years (2023-2024). A special methodology for the identification of diatoms was used. A total of 1,126 taxa of algae and cyanobacteria were observed, of which 628 were new for the Novohradské Mountains, including a number of interesting and rare species. The results were evaluated with ordination methods, and simultaneously, diatom indices were used as well. In conclusion, the algal diversity and water quality significantly change along each stream. In addition, a complete to-date list of algal and cyanobacterial taxa of the Novohradské Mountains was compiled, where 1,565 taxa from 58 localities are listed.

Diatom-based reconstruction of extreme coastal events in a brackish lake from the Burin Peninsula (Newfoundland, Canada)

Cyprian Kowalczyk[1,2], Les C. Cwynar[3], John P. Smol[4], Mikołaj Kokociński[1], Witold Szczuciński[2], Krzysztof Pleskot[2]

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Extreme coastal events (ECEs), such as storm surges, tsunamis, and high-energy wave activity, are important drivers of environmental changes in coastal regions. While their impacts on terrestrial ecosystems are often well documented, their influence on coastal lakes remains less well constrained. These environments represent a unique interaction between marine and freshwater environments, creating brackish and saline conditions. Lake sediment records of these lakes provide continuous archives that allow to reconstruct past events and associated ecological responses to marine intrusions.

This study focuses on Broad Pond, a ~3m brackish lake located on the Burin Peninsula (Newfoundland, Canada), in close proximity (~25m) to the Atlantic Ocean and exposed to frequent storm activity. A 72-cm sediment core was collected in August 2022 to investigate past environmental changes and potential event layers associated with ECEs. Chronology is being established using radiocarbon accelerator mass spectrometry (C^{14} AMS) dating and gamma-ray measurements of the upper 20cm of the core. Sedimentological analyses include loss-on-ignition (LOI) and sand grain counts (SGC) to identify high-energy depositional events.

A previous study on this lake (Pleskot et al., 2024) established that diatom communities respond significantly to ECE. Therefore, the diatom analysis was conducted at a resolution of 0.5 cm (144 samples), with a count of 400 valves per sample to assess species assemblages and compositional changes downcore. Diatom total abundance (DTA) was quantified using the addition of a synthetic microsphere (Ø=7.8µm). The integration of sedimentological and biological proxies aims to assess the temporal relationship between diatom assemblage variability and sedimentological evidence of ECEs.

The sediment record spans approximately the last ~1000 years. The conducted analysis will enable a detailed reconstruction of environmental variability and contribute to a better understanding of the role of ECE's in shaping brackish lake ecosystems in the Burin Peninsula.

Biodiversity of algoflora of the Koshkar Ata river in shymkent, Southern Kazakhstan

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Water pollution is one of the most important environmental problems in Kazakhstan. The Koshkar-Ata River, which originates in the center of the city of Shymkent in southern Kazakhstan and flows through the city, is polluted by household and industrial waste, which has a negative impact on the habitat of aquatic organisms. The purpose of this study was to investigate the biodiversity of the algal flora in the Koshkar-Ata River. The study used chemical, microscopic, and taxonomic methods of analysis. It has been established that according to the degree of water pollution, the river can be divided into 3 conditional zones: *zone 1* is the beginning of the river, characterized by low water temperature and moderate pollution of the aquatic environment, with water pollution index values of -3.89±0.24, BOD_5 - 2.55±0.22 mg O_2/dm^3, content, mg/l: NO_2^- -0.02±0.001, NO_3^- - 9.50±0.11, Cu^{2+} - 4.22±0.21, Zn^{2+} - 4.03±0.21, Pb^{2+} - 0.004±0.000, Cd^{2+} - 0.002±0.000. 10 species of planktonic algae, 7 species of epiphytic algae, and 9 species of benthic algae have been identified in this area. *Zone 2* is the average distance of the 6 km long path where the river waters are polluted by municipal wastewater, characterized by a high rate of biochemical processes and related to dirty waters with water pollution index values of 5.71±0.78, BOD_5 - 48.12±0.42 mg O_2/dm^3, content, mg/l: NO_2^- -0.04±0.001, NO_3^- - 44.56±0.13, Cu^{2+} - 5.34±0.21, Zn^{2+} - 6.01±0.21, Pb^{2+} -0.004±0.000, Cd^{2+} -0.001±0.000. The number of planktonic species decreases to 6, epiphytic species – to 4, benthic species –to 7. *Zone 3* is the last area before the mouth of the river, where the level of BOD_5 -14.82±0.11 mg O_2/dm^3, ammonium, nitrate nitrogen and other mineral ions sharply decreases, which indicates a decrease in the decomposition process of organic matter. The number of planktonic species remains at 6 species, with a dominance of diatoms, 2 species of epiphytic algae, and an increase in the number of benthic species to 12. In general, diatoms dominate the river's algal flora: *Pinnularia viridis, Psammothidium, Planothidium, Nitzschia wuellerstorffii* and *Nitzschia ulnaria, Cocconeis placentula, Achnanthes biasolettiana, Gomphonema olivaceum, Navicula laterostrata,* green and blue-green algae were found in small quantities.

Diversity of diatoms in springs of the ecotonal zone

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Groundwater-fed springs at the land-sea interface represent poorly explored habitats for diatom diversity. These environments are characterised by highly dynamic conditions resulting from salinity fluctuations, storm events, coastal erosion, and variability in groundwater supplying. Despite their potential importance as ecotones linking freshwater and marine ecosystems, they remain insufficiently studied, particularly regarding the diversity of diatom communities.

Coastal springs located along the Chłapowo-Rozewie cliffs on the southern Baltic coast of Poland are unique environments where freshwater ecosystems are affected by seawater. To assess the influence of the mesohaline environment on diatom communities in these freshwater ecosystems, archival samples collected by Starmach in the 1960s were re-examined and compared with new material collected in 2014–2015 from selected springs along the Baltic coast. An important aspect of the study was the assessment of ecological preferences of the identified taxa, with particular emphasis on salinity and mineralisation.

High spatial and temporal variability in species quality and quantity composition was observed, reflecting the dynamic nature of the studied habitats. Archival material exhibited higher species richness than new samples. However, no clear differentiation between assemblages from two time periods was observed. Freshwater and brackish-fresh taxa dominated the diatom communities, as well as occasional marine-associated taxa, e.g., *Fallacia forcipata,* indicating a significant influence of seawater. The results confirm that coastal springs represent highly dynamic ecotone systems, where both the qualitative and quantitative composition of diatom assemblages is shaped by fluctuating environmental conditions and disturbances associated with coastal processes.

Morphological and molecular characterization of *Plagiogramma minus* var. *nanum* from tropical Sulawesi, Indonesia

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Plagiogramma minus var. *nanum*, is a species of araphid diatom species that has been reported from several continents, including Europe, North America, Africa, and parts of Asia. In Indonesia, it has so far been recorded from Java and South Sulawesi, without molecular data being currently available for the Indonesian populations.

The objective of this study was to characterize *Plagiogramma minus* var. *nanum* from Central Sulawesi Island, Indonesia. The specimen was collected, isolated and cultivated. Morphological identification was carried out using light (LM) and scanning electron microscopy (SEM), while molecular analyses were performed by the means of next-generation sequencing (NGS).

LM observation shows linear-elliptical valves with length between 13.2 and 18.0 µm and breadth from 4.0 to 7.4 µm. Striae density was 12–13 striae in 10 µm (n= 20). The sternum is narrow and linear, extending along the apical axis. Apical pore fields are present at both apices. SEM examination presents numerous branched spines along the valve face–mantle junction and a prominent central boss. Dense clusters of external granules are present in the apical pore fields.

The 6,168 bp long complete cluster of nuclear rRNA and complete 156,597 bp plastid genomes were obtained. There were massive differences in the gene content of the plastid inverted-repeat when compared to *Plagiogramma staurophorum.*

A multigene maximum likelihood phylogeny, using 124 concatenated plastid genes from 167 taxa (including *P. minus* var. *nanum*) and rooted with seven species of Triparmales, places *P. minus* var. *nanum* together with *P. staurophorum* within the same well-supported clade of the recently redescribed class Plagiogrammophyceae. A separate phylogenetic analysis performed using *rbc*L sequences and including only *P. minus* var. *nanum* populations indicates a closer genetic relationship between the Indonesian and Japanese populations, which are distinct from strains originating from southern Africa and the Caribbean Sea.

This work was supported by the Minister of Science the Republic of Poland under the Regional Excellence Initiative Program for 2024–2027 (RID/SP/0045/2024/01).

Horizontal gene transfer and reciprocal chimaerism in *Compactonostoc* (Nostocales, Cyanobacteriophyta) with evidence for two new species in the genus.

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The genus *Nostoc* has long been known to be polyphyletic, and recent taxonomic work has segregated several *Nostoc*-like lineages into new genera, including *Compactonostoc*. Until now, *Compactonostoc shennongjiaensis* was the only described species in the genus. In a survey of biological soil crusts from Santa Catalina Island (California, USA), we isolated two *Nostoc*-like strains that phylogenetically affiliate with *Compactonostoc*. A polyphasic approach based on morphology, 16S rRNA gene phylogeny, 16S–23S ITS secondary structure, and cloned ribosomal operons revealed that each strain harbors two highly divergent ribosomal operon types. One operon (Type 2) is closely related to *C. shennongjiaensis* and contains the two tRNA genes in the ITS region, whereas the second (Type 1) lacks tRNA genes and is strongly allied to the horizontally acquired Type 1 operon previously reported in *Kalymmatonema* (as *Scytonema hyalinum*), indicating an ancient HGT event from an unsampled nostocaceaen lineage. In *Compactonostoc chimaera*, we additionally detected two reciprocal chimaeric operons (Type 2/1 and Type 1/2), with crossovers in a conserved region of the 16S rRNA gene, demonstrating ongoing recombination between operon types. ITS percent dissimilarity, ITS domain structures, and 16S percent similarity, together with consistent morphological differences, support recognition of the two strains as new species, *Compactonostoc mediiheterocytium* and *C. chimaera*, both clearly distinct from *C. shennongjiaensis*. Our results document rare ribosomal-operon HGT and reciprocal chimaerism in *Compactonostoc* and highlight the need to examine multiple clones and operons when describing cyanobacterial taxa based on rRNA genes.

Genomic signatures of ecological speciation in globally distributed cyanobacterium *Microcoleus*

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Cyanobacteria have evolved for over three billion years and thrive in nearly all environments with sufficient light intensity. We recognize thousands of species, however, the genetic mechanisms underlying their adaptation and speciation remain poorly understood. Here, we used the globally distributed, filamentous cyanobacterium *Microcoleus* as a model to investigate how geography and ecological adaptation drive the species emergence in cyanobacteria. We analyzed population genomics data from over 200 newly sequenced genomes of cultured strains and herbarium specimens. *Microcoleus* comprised 12 distinct species, with extensive homologous recombination occurring between species with an intensity depending on their stage of divergence–speciation continuum. Both geographic isolation and environmental factors such as precipitation, temperature, solar radiation, and soil properties drove speciation. Using a reverse ecology approach, we identified strong positive selection on accessory genes involved in stress. Moreover, using genotype–environment associations on Oxford Nanopore sequenced strains, we identified insertions/deletions linked to adaptive loci involved in stress response as well.

Diversity and Adaptation: The Genomic Insights into Dryland Soil Crusts

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Filamentous soil cyanobacteria are one of the key ecosystem engineers, especially in arid and semi-arid environments. They form a crucial component of biological soil crusts (BSCs), complex microbial communities that sustain ecosystem processes under extreme conditions, including high UV radiation, low precipitation, and large temperature fluctuations. BSCs also play critical roles in soil stabilization, erosion prevention, water retention, and carbon and nitrogen cycling. Members of the genus *Microcoleus* are particularly important and often dominate BSC communities, driving their formation and persistence. Their production of extracellular polymeric substances (EPS) binds soil particles, enhancing crust cohesion and resistance to environmental stress. Despite their ecological significance, the diversity and taxonomy of filamentous cyanobacteria—particularly within *Microcoleus*—remain incompletely resolved; however, recent advances in whole-genome sequencing have begun to reveal that this apparent ambiguity reflects a global speciation continuum of closely related lineages, challenging traditional morphology-based classifications and exposing extensive cryptic diversity. In this study, we isolated over 150 filamentous cyanobacterial strains from biological soil crusts across multiple dryland sites in Utah (USA), with a focus on *Microcoleus*-like taxa. These isolates were analyzed using a polyphasic approach integrating morphological, ecological, and molecular data, including whole-genome sequencing. Preliminary genomic analyses reveal substantial diversity of filamentous cyanobacteria in Utah´s BSC communities, including distinct lineages that likely represent novel taxa.

Environmental drivers of freshwater microalgal diversity: large-scale metabarcoding and single-cell microbiome analyses

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Environmental drivers play a central role in structuring freshwater microalgal communities; however, traditional morphology-based approaches have limited taxonomic resolution. Metabarcoding offers a refined view of community composition, enabling detection of cryptic diversity and improved assessment of environmental influences. In addition, emerging single-cell approaches provide insight into microbiomes associated with individual algal cells, revealing potential host–microbe interactions that may further shape community dynamics.

Here, we investigated protist diversity across 15 lakes in the Masurian Lake District (Poland), sampled over three seasons during three years (2021–2023). Diversity was assessed using high-throughput sequencing of the 18S rRNA V4 region, complemented by single-cell analysis of dinoflagellate-associated prokaryotic microbiomes. We then evaluated diversity patterns across environmental gradients, including temporal and physicochemical parameters and lake morphometry, as well as their impact on the algal-prokaryotic associations.

Algal communities were dominated by Chlorophyta, Bacillariophyceae, other Gyrista, and mixotrophic groups including Cryptophyta and Dinoflagellata. Seasonal dynamics, rather than environmental variables, were the main drivers of community structure, as confirmed with Randam Forest analysis. Beta diversity showed strong seasonal clustering, with spring communities clearly separated from stratified periods. Interestingly, *Prymnesium parvum* was detected only in autumn 2022, suggesting recent dispersal, possibly via anthropogenic transport after its bloom in the Oder River.

Finally, single-cell analyses of dinoflagellates, including *Ceratium hirudinella,* revealed Rickettsiales-like endosymbionts, pointing to previously underappreciated host–microbe interactions. Comparison between single-cell and lake-water microbiomes further indicated that dinoflagellate-associated microbiomes are species-specific rather than environmentally driven.

Together, these findings demonstrate that freshwater microalgal communities are shaped not only by seasonal dynamics but also by host-associated microbiomes, while highlighting the importance of monitoring potentially invasive taxa in freshwater systems. Integrating high-resolution molecular approaches with ecological context provides a framework for understanding freshwater ecosystems under ongoing climatic and anthropogenic change.

Hidden diversity of autotrophic euglenids in southern Africa

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Despite the significant ecological role of autotrophic euglenids (Euglenida) in subtropical and tropical freshwater ecosystems, our knowledge of their diversity and distribution remains limited, particularly on the African continent. Only a few African countries have been covered by studies specifically dedicated to euglenids and supported by reliable documentation. Research on freshwater euglenids in South Africa has been sporadic, with most records dating back to the early twentieth century. These early works often lack adequate morphological documentation, and many of the described species have not been observed in subsequent studies. Furthermore, numerous species of euglenid, originally described in Africa, have not been reported elsewhere, suggesting a potentially high level of regional endemism. Existing observations also indicate that warm climates can promote the development of euglenids, including the formation of dense blooms, some of which may be toxic.

In 2025, we surveyed more than 100 freshwater bodies of various types throughout southern Africa, with most of the samples collected in South Africa. Most of the sites investigated were found to be highly rich in euglenid taxa. Our results include records of species that are rare in Europe, taxa not observed since their original descriptions, and several lineages likely new to science. Moreover, we identified a sessile loricate euglenid (*Lepocinclis loricata*) that differs from all known loricate taxa by a unique combination of features, including the presence of a lorica, monad morphology, sessile habit, and its phylogenetic position within the Phacaceae family. To further investigate diversity patterns, we analysed the genetic variability and phylogenetic placement of morphologically similar European and African isolates.

Diversity, taxonomic structure and functional potential of microorganisms in Biological Soil Crusts under hyperarid and nutrient-deficient conditions in high-altitude glacier valley in the Eastern Pamir, Tajikistan

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Biological soil crusts (BSC) constitute an extremely important community, especially in dry land environments such as mountains and deserts. BSC are formed by cyanobacteria, bacteria, fungi, lichens, bryophytes, and algae in various proportions. These complex assemblages are responsible for soil formation, nutrient sequestration and constitute a step in a succession of organisms. Cyanobacteria as autotrophs enrich soil with organic carbon and, together with some other bacteria, are responsible for N_2 sequestration. They also stabilize soil and increase its porosity and water retention capacity. Still the knowledge on diversity and structure, and on relationships between bacterial components in BSC, especially in extreme environments, is limited.

We investigated BSC on 11 study plots in Eastern Pamir Mountains at 4,400 m a.s.l. in July 2018 and 2019. We used amplicons sequence variants (ASV) approach recovered from a NGS analysis of hypervariable region V3-V4 of 16S rRNA gene followed by bioinformatic analysis using QIIME 2 with the SILVA database. Functional potential of the classified sequences was inferred by linking ASVs to reference databases (PICRUSt2, FAPROTAX).

The results showed that Actinomycetota (18% of ASVs), Pseudomonadota (14%), Bacteroidota and Chloroflexi (13% each) with Cyanobacteria (9%) formed the core community. However, the most numerous, single genus was a cyanobacterium - *Microcoleus vaginatus*. *Microcoleus* which isn't diazotrophic is known for its structure-forming role in BSC and creating "cyanosphere" which attracts heterotrophic bacteria, among which are N_2 fixing taxa. In each sample we identified presence of diazotrophic taxa. We also noticed increasing contribution of N_2-fixing cyanobacteria in more advanced BSCs.

The study demonstrated that BSCs are taxonomically and functionally diverse communities with complex interactions and with cyanobacteria playing a crucial role in their functioning.

Revealing the full picture - cyanobacterial and phototrophic diversity of ponds in eastern pamir mountains by comparison of amplicon-based and metagenomic methods

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Microbial diversity in extreme hypersaline environments remains poorly resolved due to historical reliance on non-genetic methods and methodological biases among molecular approaches. Here, we investigated bacterial communities in the sediments of small water bodies in the Pamir Desert using complementary metagenomic and V3-V4 16S rDNA amplicon sequencing to provide a more comprehensive assessment of taxonomic and functional diversity with special focus on cyanobacteria and other photrophic species. Microbial community structure in these habitats has largely been inferred without genetic methods, leaving gaps in our understanding of true taxonomic diversity.

Metagenomic analysis recovered 86 medium- to high-quality metagenome-assembled genomes (MAGs) spanning 26 classes, dominated by Bacteroidota, Gammaproteobacteria, and Alphaproteobacteria. We have found 3 Cyanophyceae genomes, one being na Oscillatoriales culture obtained from one sample. We have also compared new results with older analysis in the same place, revealing big changes related to ASVs creation and updated databases. Amplicon data indicated a high abundance of Pseudomonadota and revealed taxa omitted in earlier research due to a relatively low number of reference genomes and reported occurrences at that time insufficient citations (e.g., Vampirovibronia). Comparison of taxonomic profiles across amplicon, metagenome-extracted 16S rDNA, and MAG-based approaches revealed substantial discrepancies in richness estimates, highlighting methodological biases and the need for integrative approaches.

Metabolic reconstruction revealed genes connected with phototrophy in many groups: Cyanophyceae, Rhodobacterales, Sphingomonadales, or Burkholderiales. We have also found an interesting Gammaproteobacteria with two RC and Gemmatimonadota genome with RC I, not closely related to the only other phototrophic *Gemmatimonas phototrophica*. We have also found prominent sulfur metabolism pathways primarily in Alphaproteobacteria and Gammaproteobacteria, suggesting sulfur-based energy metabolism. Taxa consistently detected across methods were affiliated with halophilic or halotolerant lineages according to the literature, underscoring salinity as one of the importanta key environmental drivers shaping community composition.

Comparison of diversity and structure of cyanobacteria in microbial mats and biocrusts from cold and hot deserts

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The conditions on deserts can be harsh, ranging from water scarcity to high UV radiation, which drive microorganisms to develop specialized adaptations. One of such strategies is formation of structured communities in which organisms perform complementary functions that support collective survival. Examples include microbial mats (MMs) and biological soil crusts (BSCs). Bacteria, and particularly Cyanobacteria, play a key role in both systems contributing to carbon and nitrogen fixation, boosting nutrient availability, enhancing water absorption capacity, and producing UV protective pigments. In this study we analysed MMs and BSCs from hot deserts of California, USA, and cold deserts of the Pamir Mountains, Tajikistan. We identified bacteria based on the V3-V4 hypervariable region of 16S rDNA, using the SILVA database. We aimed to compare the taxonomic structure between community types (MM vs. BSC) and climatic regions (hot vs. cold deserts) to determine whether they are community- or location-specific. At the phylum level for both deserts and community types showed high similarities in bacterial structure. However, when we focused on Cyanobacteria, there were noticeable differences in structure on family level. Although Nostocaceae constituted a common percentage in all environments, the MMs from California were dominated by Geitlerinemaceae, BSCs from California by Nodosilineaceae, while both BSCs and MMs from Pamir had higher diversity and more even distribution of all families than the other two groups. Despite that, when we compared the presence of specific amplicon sequence variants, 25% of them were shared among BSCs from both desert types, while microbial mats shared only 14%. Within regions, there was a 23% overlap in mats and crusts from Pamir, whereas in California it was only 17%.

These findings indicate that the taxonomic composition of complex microbial communities vary substantially, even when functional roles are conserved, as multiple taxa can perform similar ecological functions across contrasting environments.

Hidden threats in cyanobacterial blooms: Intercontinental evidence of potential pathogens and antibiotic resistance genes

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Harmful cyanobacterial blooms (HCBs) and their toxigenic effects are well documented; however, emerging evidence indicates that their associated microbial communities (phycosphere) may present additional and underexplored threats. These communities can include potentially pathogenic bacteria and reservoirs of antibiotic resistance genes (ARGs), indicating that HCBs may act as environmental hotspots for additional hazards. Despite this potential, intercontinental comparisons across climatic zones and varying anthropogenic pressures are lacking. Here, we conducted a study of HCBs across tropical and temperate regions, including water bodies in Singapore, Guatemala, Poland, the United States, and the Republic of Korea. Sampling was performed during peak bloom events in 2024 and 2025. Shotgun metagenomics was used to assess bacterial community composition and ARG occurrence. We detected many genera recognized by the World Health Organization as containing "bacterial pathogens of public health importance", including *Pseudomonas*, *Acinetobacter*, *Aeromonas* and *Mycobacterium* (up to 4.25, 2.63, 1.85, and 0.73 % of the bacterial community, respectively), as well as members of the order Enterobacteriales (up to 0.95%). Potentially pathogenic species such as *Pseudomonas aeruginosa*, *Acinetobacter johnsonii*, and *Aeromonas veronii* were also detected occasionally and are known to affect a broad range of organisms in aquatic ecosystems. These bacteria were most abundant at Lake Amatitlán, Guatemala, likely linked to anthropogenic stressors. ARG analysis further examined whether phycosphere-associated taxa act as primary reservoirs, including environmentally abundant genera commonly linked to blooms, such as *Flavobacterium*, *Roseomonas* and *Limnohabitans* (up to 7.18, 4.35 and 3.75 %, respectively). These findings highlight HCBs as potential reservoirs of pathogenic bacteria and ARGs, emphasizing the potential benefits of integrating microbial threat assessment into bloom monitoring and management strategies.

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Ecosystem modelling to understand and predict cyanobacterial blooms in freshwater lakes

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Cyanobacterial blooms represent one of the most pressing ecological challenges in freshwater ecosystems, driven primarily by nutrient enrichment and climate warming. These blooms threaten water quality, ecosystem functioning, human health, and have economic impacts on water supply and recreation. Understanding the mechanisms controlling cyanobacterial dominance and predicting bloom dynamics are therefore essential for effective lake management. Ecosystem modelling provides a powerful tool to integrate environmental drivers and explore future scenarios. Two ecosystem models were applied to investigate mechanisms driving cyanobacterial blooms and to support evidence-based management decisions.

The AQUATOX model was used to explore how warming and nutrient availability influence cyanobacterial community structure in lakes with contrasting ecological conditions, including systems dominated by a single species and those with polydominant communities. Model simulations indicate that temperature increases, consistent with climate change projections, can substantially alter cyanobacterial community composition. Warming of 2–4 °C favours nitrogen-fixing Nostocales over Oscillatoriales and Chroococcales, particularly in nutrient-rich conditions. In phosphorus-limited systems, however, nutrient availability played a stronger role in determining species dominance, highlighting the importance of ecosystem productivity in shaping bloom dynamics.

Dynamic modelling was used to evaluate management strategies for a shallow eutrophic lake frequently affected by cyanobacterial blooms. The modelling scenarios evaluated in-lake restoration measures, including cyanobacterial biomass removal and macrophyte harvesting, as well as reductions in external nutrient loading. Results indicated that biomass removal alone has a limited effect on chlorophyll-a and total phosphorus. In contrast, a 50% reduction in external phosphorus inputs led to substantial improvements in simulated water quality, including decreases in nutrient concentrations and bloom intensity.

Together, these studies highlight the importance of nutrient management. By integrating climate and nutrient scenarios, modelling allows to evaluate restoration strategies, anticipate ecological responses, and identify the most effective measures for the long-term mitigation of harmful blooms in freshwater systems.

Detection of structurally diverse cyanopeptides in environmental samples using mass spectrometry query language (MassQL) – the case of microcystins

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Cyanobacteria produce a diverse array of potent toxins, among which microcystins are of primary global concern for water quality and public health. Rapid and accurate detection of these hepatotoxins in complex environmental and biological matrices using mass spectrometry (MS) is essential for hazard assessment and monitoring. However, the extreme structural variability of microcystins (with hundreds of known congeners) often leads to incomplete detection when relying solely on matching with publicly available spectral libraries, which are inherently limited and incomplete.

To address this analytical gap, we have developed a computational screening approach tailored specifically for the detection of microcystin variants. The workflow begins with feature-based molecular networking (FBMN) to map and categorize known and potential microcystins within MS datasets. While FBMN successfully reveals clusters of related compounds, this project develops microcystin-specific Mass Spectrometry Query Language (MassQL) queries [1]. Deployed within the Global Natural Products Social Molecular Networking (GNPS2) ecosystem, this approach provides a robust, complementary, and transferable methodology for comprehensive screening across diverse MS2 datasets.

Our approach centers on systematically identifying and incorporating the minimal set of required and excluded MS2 fragmentation patterns characteristic of microcystins (e.g., diagnostic fragment ions and specific neutral losses). The core objective is to simultaneously minimize Type A errors (false negatives), ensuring near-comprehensive coverage of microcystin analogs, and Type B errors (false positives), maximizing specificity against unrelated environmental compounds.

The resulting microcystin-focused MassQL queries are designed for direct implementation across both proprietary in-house libraries and vast publicly accessible metabolomics repositories. This work demonstrates the power of a standardized, pattern-matching query language to transform high-throughput screening, providing the phycological and environmental health communities with a much-needed tool for the rapid and comprehensive detection of microcystins.

Strain-specific growth strategies in the harmful alga *Prymnesium parvum*

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Invasive and toxic algae pose a significant threat to ecosystems and public health due to their rapid spread, competitive displacement of native species, and production of harmful metabolites. This study investigates the environmental factors regulating the growth of the harmful species *Prymnesium parvum*, a toxic, bloom-forming haptophyte that produces ichthyotoxins responsible for major fish kills and severe disruption of aquatic food webs. The species was also implicated in the ecological disaster in the Odra River in 2022. Two strains of *P. parvum* were used to assess environmental conditions supporting maximal growth: a strain isolated from the Kłodnica River in Poland in 2023 and a reference strain from Scotland (CCAP 946/6). Growth was evaluated over a 15-day period across a broad range of environmental conditions, including temperature, conductivity, pH, total nitrogen, total phosphorus, and iron concentration, with daily microscopic analysis of cell abundance. The results revealed distinct strain-specific responses; however, temperature, total nitrogen, total phosphorus, and iron concentration produced broadly similar patterns in both strains, with both favouring comparable conditions. Maximum growth occurred at 27.5 °C, an intermediate temperature within the tested range, while elevated nutrient concentrations generally enhanced growth. The optimal conductivity was higher for the Scottish strain (13.50 mS/cm), although the Polish strain also exhibited strong growth under elevated conductivity conditions (10.50 mS/cm), which exceeded those recorded during the Odra River catastrophe (4.50 mS/cm) and in the Kanał Gliwicki (around 7.50 mS/cm). Nevertheless, the conductivity levels recorded in these regions were also sufficient to support growth under experimental conditions. Contrary to common assumptions, both strains favoured relatively lower pH values, with the Scottish strain preferring even lower conditions. This study highlights the importance of continuous monitoring of toxic, invasive algae and the development of mitigation strategies tailored to strain-specific responses.

Comparing aquatic environmental dna, microscopy and sedimentary DNA to investigate cyanobacterial community dynamics across a trophic gradient

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As a result of increasing temperatures and anthropogenic stressors, freshwater biomonitoring indicates that toxigenic and non-native cyanobacterial species are increasing globally. Because of the high-effort nature of traditional microscopy, aquatic Environmental DNA (eDNA) metabarcoding as a form of biomonitoring is becoming commonplace. While eDNA has been found to complement microscopic phytoplankton analysis, it has also been demonstrated that recent eDNA from surficial sediments (sedDNA) can also be a powerful tool to monitor a variety of organisms including benthic and planktonic microorganisms. However, comparisons between all three methods are rare.

Therefore, we compared cyanobacterial metabarcoding data derived from aquatic eDNA and sedDNA to cell density and biomass determined by traditional planktonic microscopic analysis on samples taken from more than 20 lakes in the Masurian and Suwałki Lakelands of north-east Poland; an area composed of thousands of lakes with diverse morphologies, land-use histories, and varying trophic states.

We found that there was a high degree of within method (eDNA/sedDNA, cell density/biomass) correspondence between the approaches, with trophic changes plausibly driving general patterns in taxa leading to these underlying agreements. Between methods, cell density proved to be more closely associated with eDNA, but was not found to be statistically significant. We postulate that cell numbers are a more similar metric to sequence read numbers than biomass, but that unique qualities of each measure mean that the approaches examined are complementary, rather than redundant. We detected several invasive taxa, which appear to have increased in abundance along the trophic gradients, and postulate that the accumulating nature of sediments may prove useful in detecting invasive taxa, particularly in the low-abundance early introductory stages.

The life force of unicellular organisms

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It is common knowledge that the most numerous group of living organisms on Earth, both historically and currently, are unicellular organisms. These include both prokaryotes and eukaryotes. Undoubtedly, bacteria/archaea/cyanobacteria have dominated the entire globe. These incredibly tiny organisms independently perform all essential life functions, including metabolism, reproduction, and environmental responses. They possess remarkable adaptive abilities, allowing them to thrive in diverse and extreme environments, from high-temperature hydrothermal vents to highly acidic habitats. Our research confirm the extraordinary strength of one representative of these microorganisms. The samples were collected from freshwater reservoirs in Southern Europe, mostly contaminated with compounds such as aluminum (Al), arsenic (As), bromine (Br), cadmium (Cd), cobalt (Co), chromium (Cr), copper (Cu), nickel (Ni), selenium (Se), and zinc (Zn), most of which are toxic in excess. The samples were identified using integrative taxonomy techniques, including light microscopy phenotypic analysis and molecular metabarcoding. Interestingly, after five years of storage, without specialized culturing procedures, only one eukaryotic unicellular organism survived the unfavorable environmental conditions and recovered in microscopic slides prepared years later.

Contrasting responses to insularity in fen habitat islands: divergence within protists and across other groups

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Habitat fragmentation is often assumed to have weak effects on microorganisms due to their high dispersal ability, yet comparisons across microbial groups remain limited and rarely embedded in broader multi-taxon studies. Here, we examine diatoms, non-diatom algae and testate amoebae within a larger dataset covering nine groups of organisms in insular temperate fens. Across 30 habitat patches, insularity explained only a minor fraction of variation in all three groups, indicating weak spatial structuring. However, responses differed: diatoms were strongly shaped by environmental conditions (and especially vegetation type), non-diatom algae showed weak structuring overall, and testate amoebae exhibited intermediate patterns. In contrast to other organismal groups in the same system, which depend on habitat continuity and connectivity, microbial communities appear largely driven by local conditions. This suggests that conservation strategies should not rely solely on connectivity, but must also reflect fundamental differences in dispersal and persistence across taxa.

Does periphyton reflect anthropogenic pressure better than trophic indices? A comparison between Carlson's Trophic State Index and field-based assessment of pond disturbance

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Small water bodies are highly sensitive freshwater ecosystems strongly influenced by surrounding land use and local habitat conditions. The trophic state of standing waters is commonly assessed using Carlson's Trophic State Index (TSI), which was originally developed for lakes. However, due to the structural and ecological differences between lakes and ponds, trophic indices may not fully reflect anthropogenic disturbance in these systems. Periphyton communities, which rapidly respond to local environmental conditions, may provide a more sensitive indicator of human impact.

This study examined whether periphyton community structure reflects anthropogenic pressure, evaluated through field-based classification considering catchment land use, shoreline modification and visible nutrient inputs, more consistently than trophic state estimated using Carlson's TSI. A total of 48 small and shallow ponds located in agricultural and forested catchments were investigated. The water bodies differed in origin, hydroperiod, macrophyte cover and trophic status. Periphyton biomass and taxonomic richness of major algal groups were analysed and compared using non-parametric statistical tests and regression analyses.

Although anthropogenic ponds showed higher mean TSI values, a considerable overlap occurred between disturbed and non-disturbed systems, indicating that trophic indices do not fully correspond with field-based disturbance classification. TSI values were strongly influenced by natural environmental factors such as water transparency, depth and shading. In contrast, periphyton structure showed clearer responses to anthropogenic disturbance, particularly through reduced diatom biomass in impacted ponds. The explanatory power of anthropogenic classification was higher than that of TSI in explaining variation in periphyton communities.

These results suggest that periphyton reflects anthropogenic disturbance more effectively than trophic indices in pond ecosystems and underline the importance of incorporating littoral bioindicators into ecological assessments of small water bodies, where pelagic trophic metrics may underestimate human impact.

An ecological and seasonal assessment of cyanobacterial oligopeptide variability

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Oligopeptides represent a structurally diverse group of bioactive secondary metabolites commonly produced by many cyanobacterial taxa. Among them, microcystins have been studied most extensively due to their well-established toxicity and the risk they pose to public health and water quality. However, other ecologically significant oligopeptides remain comparatively poorly characterised, despite their documented importance and biological potential. Understanding the variability of these metabolites is essential for recognition of their ecological roles and impacts on aquatic ecosystem functioning.

We aimed to characterise cyanobacterial oligopeptides in three shallow, eutrophic freshwater bodies and to examine how environmental conditions influence their abundance, richness and seasonal patterns. Metabolite composition was analysed in 117 samples collected between 2022 and 2025 using LC-MS/MS, while cyanobacterial community composition was identified by light microscopy.

The dominant cyanobacterial species varied between water bodies: *Microcystis aeruginosa* (Kützing) Kützing was predominant in Tyniec, while *Aphanizomenon gracile* Lemmermann and *M. aeruginosa* dominated in Podkamycze 1. In Podkamycze 2, the community composed of *M. aeruginosa* and *Microcystis flos-aque* (Wittrock) Kirchner. Analysed samples showed variety of oligopeptides beyond microcystins, including anabaenopeptins, aeruginosins, aeruginosamides, microginins, micropeptins, cyanopeptolins and planktocyclins. Over the four-year period, metabolite composition varied between years and among water bodies and showed distinct seasonal patterns. While oligopeptide richness and abundance peaked in 2024, microcystin concentrations declined. Moreover, water temperature and cyanobacterial biomass were identified as key factors significantly influencing cyanopeptides profile.

Examining seasonal variations of cyanobacterial secondary metabolites offers crucial information on the functioning of aquatic ecosystems, as well as the potential risks and benefits associated with the expansion of cyanobacterial blooms. These results emphasise the significance of metabolite composition as a sensitive indicator of changes in cyanobacterial community structure, challenge the simplified assumption that bloom intensity directly determines toxicity and highlight the need to consider the full chemical diversity in ecological and environmental studies.

Resilience and adaptive mechanisms of terrestrial green algae on building surfaces as direct drivers of substrate deterioration

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Terrestrial (aerial) green algae are recognized as potential contributors to the deterioration of building materials in temperate climate, primarily affecting their aesthetic value. This study combines physiological, structural, and metabolomic approaches to evaluate the direct role of early-stage algal colonizers in the physical and chemical deterioration of brick-and-plaster man-made objects. Five taxa—*Chloroidium saccharophilum*, *Klebsormidium nitens*, *Bracteacoccus minor*, *Diplosphaera chodatii*, and *Stichococcus bacillaris*—were isolated, identified using classical and molecular methods, and cultivated on brick and plaster under laboratory and environmental conditions over a year. Algal colonization was monitored using chlorophyll a concentration, fluorescence intensity, and substrate surface profiling. After a year, algal metabolites on the substrates were examined using UHPLC–MS/MS.

All taxa successfully colonized both substrate types, penetrating their interiors and forming compact biofilms that frequently filled pores and overgrew surface cavities. In several cases, membrane-like layers developed, overgrowing the pores and cavities. Mechanical deterioration was evident, as the biofilms of taxa with thick cell walls (*Chloroidium*, *Diplosphaera*, *Stichococcus*) and filamentous *Klebsormidium* were capable of detaching mineral grains from brick surfaces during biofilm disruption. Except for *B. minor*, all species exhibited substantial direct geophysical deteriorative activity.

Metabolomic analyses revealed pronounced strain-specific and substrate-dependent metabolic profiles. Plaster substrates induced higher metabolic heterogeneity and stress-related pathways, while brick supported more stable growth-associated metabolism. Across taxa, consistent production of low-molecular-weight organic acids—such as citric, acetic, and oxalic acids—was detected, implicating these compounds in geochemical deterioration *via* acidification and metal chelation. Additional enrichment in flavin nucleotides, fatty acyls, and aromatic metabolites highlights the importance of redox activity, stress adaptation, and biofilm resilience in colonization success.

Together, these findings demonstrate that terrestrial algae contribute to material deterioration through synergistic mechanical and biochemical mechanisms, even at early stages of colonization.

Influence of brown coal waste on species diversity of algoplant of lenger river in Southern Kazakhstan

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Brown coal waste contains toxic components that can enter surface water, which has a negative impact on the hydrobiocenosis. The aim of this study was to investigate the effect of brown coal waste from the Lenger deposit on the composition of the algal community in the Lenger River. The study used FTIR, diffraction, chemical, SEM, and microscopic analysis methods. It was found that the brown coal waste consists of quartz /Silicon Oxide SiO_2, Gypsum $CaSO_4 \times 2H_2O$, Kaolinite - $Al_2Si_2O_5(OH)_4$, Cronstedtite- $Fe_3((Si0.74Fe0.26)_2O_5)(OH)_4$, Margarite- $CaAl_2(Si_2Al_2)O_{10}(OH)_2$, Muscovite $H_2KAl_3(SiO_4)_3$, Calcite $CaCO_3$, Laumontite $CaAl_2Si_4O_{12}(H_2O)_2$, Lead Aluminum Sulfate Hydroxide $Pb_{0.5}Al_3(SO_4)_2(OH)_6$, which occur in different ratios depending on the sample. The toxicity of waste is due to the multifactorial nature of the following: low pH values, high content of active forms of aluminum, iron, and manganese, high electrical conductivity, low content of biogenic elements, and an arid climate, which all contribute to the strong negative effects of waste. It has been established that the metals in waste are arranged in the following sequence based on their content and form: Al(pyrophosphate) > Fe(pyrophosphate) > Fe(oxalic acid) > Al(CuCl2) > Mn(CuCl2) > Fe(CuCl2) > Mn(pyrophosphate) > Al(KCl) > Mn(KCl) > Fe(KCl). In the Lenger River, in the area where coal waste is stored, the Mn content is 9.0 times higher and the Al content is 2.0 times higher than the recommended standards for irrigation water. There is a decrease in the species diversity of the algal flora from 11 species in the initial section of the river (*Cymbopleura apiculata, Neidium sp., Fragilaria capucina var. Rumpens, Brachysira sp., Craticula sp., Navicula notha, Navicula tripunctata var. arctica, Diatoma vulgare, Pinnularia sp., Meridion circulare, Oscillatoria chalybea)* up to 4 sustainable species in the area near the waste storage site *(Cymbopleura apiculata, Craticula sp., Diatoma vulgare, Oscillatoria chalybea)*. As the distance from the waste storage sites increases, the species diversity of the algal flora returns to the initial section of the river, and new species appear: *Aphanizomenon flos-aquae, Toxarium undulatum.*

Benthic algal communities in post-mining lakes: diversity, functioning and bioremediation potential

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Our team studied oligotrophic post-mining lakes in northern Bohemia (Czech Republic, Europe) using a holistic approach to reveal diversity and functioning of primary producers across the entire euphotic zone (up to 10 m), with main emphasis on periphyton. These novel ecosystems, formed by flooding abandoned lignite pits (lakes Most, Medard, Milada), host diverse communities dominated by algae and cyanobacteria, creating substantial biomass that influences nutrient cycles.

A year-round study revealed overwintering biomass and cumulative development, with lake-specific seasonal dynamics: diatoms decreased as lakes aged and trophic levels rose. Periphyton composition was driven by lake identity, season, year, and calcium, showing three successional patterns tied to internal nutrient recycling (P, C). Phosphorus uptake kinetics declined seasonally (high C:P ratios indicating P-limitation), with orthophosphate uptake dominating early season and alkaline phosphatase activity/internal recycling rising in summer/autumn, enabling niche separation from phytoplankton. In situ primary productivity (measured via novel floating barge) was controlled by light, temperature, and P-availability.

Macroalgae (*Vaucheria* sp., Xanthophyceae; *Chara* spp., Charophyceae) from deeper euphotic zones showed high bioremediation potential: laboratory experiments (ICP-MS) confirmed efficient accumulation of rare earth elements (REEs) from lake water under natural conditions, with *Vaucheria* outperforming *Chara* and capacities comparable to hyperaccumulators like fern *Dicranopteris*. REE content varied by lake and season.

These insights on high water quality, ecological roles, and contaminant removal contribute to restoring and sustaining post-mining lakes in recultivated landscapes.

Brassinosteroid-mediated regulation of biochemical composition and growth of *Chlamydomonas reinhardtii*

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Brassinosteroids (BRs) are crucial plant growth regulating phytohormones, metabolism, and stress responses, present throughout whole plant kingdom; however, their role in algae remains insufficiently explored. In this study, we investigated the dose-dependent effects of 24-epibrassinolide (24-epiBL) on growth and biochemical composition of the green microalga *Chlamydomonas reinhardtii*. Cultures were exposed to a wide range of 24-epiBL concentrations (0.1–1000 nM), and changes in cell proliferation, protein and monosaccharide content, fatty acid profiles, and photosynthetic pigments were monitored over a 17-day cultivation period. Low concentrations of hormone elicited a pronounced hormetic response, with 1 nM identified as the optimal dose, enhancing cell growth, protein and monosaccharide accumulation, and shifting lipid composition toward a higher proportion of polyunsaturated fatty acids (PFA). This concentration also promoted the accumulation of photosynthetic pigments and carotenoids. In contrast, higher 24-epiBL concentrations inhibited growth and altered metabolic profiles leading to accumulation of saturated and monounsaturated fatty acids, consistent with metabolic stress. Our findings show, that BRs modulate growth and metabolism in *C. reinhardtii* in a concentration-dependent manner and highlight their role as regulators in algae. These results expand current knowledge of BRs signaling beyond higher plants and suggest applications of controlled BRs treatment in algal biotechnology.

Baltic cyanobacteria as a source of antibacterial compounds – a promising yet challenging path

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Cyanobacteria are a well-known source of biologically active compounds. Among the activities exhibited by these compounds, antibacterial effect is the third most frequently reported, accounting for approximately 10% of all described bioactivities, following cytotoxicity and enzyme inhibition. The Baltic Sea, characterized by a pronounced salinity gradient and significant anthropogenic pressure, constitutes a unique environment that promotes the evolution of distinct adaptive mechanisms in microbial communities, including the production of specialized metabolites.

The aim of this study was to identify cyanobacterial strains isolated from the southern Baltic Sea (mainly Gulf of Gdańsk and Curonian Lagoon) for their ability to produce antibacterial compounds under *in vitro* conditions, with potential for future development of antimicrobial agents.

Over several years, a total of 48 strains were screened against a panel of Gram-positive and Gram-negative bacteria, including both environmental and clinical isolates. During the initial screening of crude extracts, the highest antibacterial activity was observed in five strains, including two assigned to the Pseudanabaenaceae family, two to the genus *Aphanizomenon*, and one to the genus *Anabaena*. These extracts, along with their subsequently obtained polar fractions, exhibited activity primarily against Gram-positive bacteria representing *Streptococcus*, *Clostridium*, *Staphylococcus*, and *Mycobacterium* genera, including drug-resistant strains. The second type of activity identified was associated with quorum sensing inhibition and was detected to a different extent in 30% of the tested extracts. Bioassay-guided fractionation of the most active extract derived from *Aphanizomenon* sp. KUCC C1, combined with LC–MS/MS analysis, revealed the presence of glycerolipids and glycolipids as major constituents of fractions exhibiting quorum sensing inhibitory activity in *Chromobacterium violaceum.*

The discovery and characterization of cyanobacterial metabolites remain challenging due to extract complexity, low compound yields, and limitations associated with cultivation and isolation. However, Baltic cyanobacteria constitute a promising and still insufficiently explored reservoir of bioactive compounds, and the Curonian Lagoon may represent a particularly valuable yet underexplored niche for the discovery of novel antibacterial agents.

Where is the cytotoxic activity? Insights from molecular networking of *Nostoc edaphicum* fractions

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Cyanobacteria of the genus *Nostoc*, characterized by large genomes and an extensive repertoire of biosynthetic gene clusters, are a rich source of structurally diverse secondary metabolites with a wide range of biological activities, including cytotoxic and anticancer effects. However, the identification of bioactive compounds is often limited by their low abundance and challenges associated with isolating sufficient quantities for individual testing.

In this study, we evaluated the cytotoxic potential of chromatographic fractions derived from *Nostoc edaphicum* CCNP1411 using a combination of bioassay-guided fractionation and LC–MS/MS-based feature-based molecular networking (FBMN). Cytotoxicity was assessed using the MTT assay on a panel of epithelial and neuronal cancer cell lines, alongside normal human dermal fibroblasts. The highest activity was observed in fractions eluted with 80–90% methanol, which exhibited broad cytotoxic effects across all tested cancer cell lines.

Molecular networking analysis revealed that these active fractions were predominantly composed of lipid derivatives, including lysophospholipids, monoacylglycerols, and free fatty acids. In contrast, previously reported peptide metabolites were distributed across all fractions and are unlikely to be the primary contributors to the observed bioactivity. Targeted evaluation of selected commercially available lipid compounds confirmed their cytotoxic effects, with lysophospholipids showing the highest potency in selected cell lines. Nevertheless, dose–response analysis indicated limited activity at lower concentrations, as reflected by relatively high IC_{50} values.

Overall, our findings demonstrate that lipid constituents, previously overlooked as bioactive metabolites in *N. edaphicum* CCNP1411, play a significant role in the cytotoxicity of its extracts. Furthermore, the application of molecular networking proved to be a powerful tool for prioritizing bioactive metabolites and linking chemical composition with biological activity in complex cyanobacterial matrices.

Nodularin, the Dr Jekyll and Mr Hide of cyanobacterial metabolites

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In summer months, the Baltic Sea is subject to massive harmful water blooms, typically dominated by filamentous, nitrogen-fixing species. Among these, *Nodularia spumigena* is the primary toxin-producing cyanobacterium.

N. spumigena produces nodularin (NOD), a potent hepatotoxic cyclic pentapeptide which exerts its toxicity mainly through inhibition of serine proteases and protein phosphatases, leading to disruption of critical cellular signalling pathways. Nodularin also induces oxidative stress, reactive oxygen species (ROS) generation, DNA damage, and apoptosis in human hepatocytes (HepG2) and fish leukocytes. The negative effects of the compound have been documented in various organisms including zooplankton, fish larvae, mussels, as well as higher trophic levels through bioaccumulation and disruption of the food web.

In the current study, the cellular extract from the Baltic cyanobacterium *Nodularia spumigena* CCM N0001 was tested for activity against lung cancer cells (A549), human dermal fibroblasts (HDFa), and rainbow trout gill (RTGill-W1) cells. The extract was subsequently fractionated, using chromatographic techniques, resulting in the isolation of two nodularin variants, NOD 811 and NOD 825. The biological activities of the isolated compounds were then assessed against the same cell lines. The results demonstrated that nodularin was active against all tested cell types. Notably, significant differences in sensitivity between the cell types were observed, along with distinct differences in potency between the two nodularin variants.

Waste algal biomass in water treatment systems: characterization and prospects – preliminary studies

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Waste algal biomass is used in this study as the primary research material and is considered a promising and valuable resource within the framework of the circular economy (CE). This work aimed to identify effective and sustainable methods for managing biomass generated by eutrophication processes and natural water self-purification. This issue is of increasing importance in the context of climate change and the continuous emission of pollutants and nutrients into aquatic environments, which intensify uncontrolled algal blooms.

The research material was collected from a pond located in Park Krakowski im. Marka Grechuty. The collected biomass was properly prepared and subsequently subjected to thermal transformation under fluidized conditions for its subsequent utilization. Both the raw biomass and the ash obtained after thermal treatment were analyzed in terms of morphology (SEM-EDS), heavy metal content, heavy metal leachability, phase composition (XRD), surface properties (FT-IR, BET), and sorption properties.

The biomass consists mainly of freshwater filamentous algae. Both the biomass and the resulting ash contain heavy metals (Pb, Cd, Zn) at levels comparable to those reported in the literature, while elements such as Mn, Cr, Ni, and Cu are present in significant amounts. The leachability of the analyzed elements (Cd, Cu, Mn, Ni, Pb, Zn) is low. FT-IR analysis of the algal biomass revealed the presence of numerous functional groups (O–H, CH_2, CH_3, N–H, O–C–O), indicating the occurrence of nutrients such as proteins, lipids, and carbohydrates, as well as suggesting the potential for binding contaminants from water.

Phase composition analysis confirmed the presence of cellulose in the raw biomass, along with mineral phases such as quartz, sylvite, gypsum, and calcite. After thermal transformation, new sulfate phases, including langbeinite and anhydrite, are formed, which may be relevant for further applications. Preliminary sorption studies indicate the potential use of these materials in water treatment processes. Moreover, the ash composition, similar to that of coal fly ash, together with a favorable Si/Al ratio, suggests the possibility of synthesizing functional composites with zeolite-like structures.

The obtained results indicate a broad, multi-directional potential for the valorization of waste algal biomass as a valuable secondary resource.

Baltic diatoms as novel sources for biofabricated nanomaterials: an overview

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Diatom are unicellular microalgae with unique silica cell walls that make them attractive for applications in environmental protection and nanotechnology. Their porous biosilica structure and ability to interact with metals allow their use both in water treatment and as natural templates for nanomaterial production. This study presents an overview of our previous and ongoing research on selected Baltic diatoms, focusing on *Pseudostaurosira trainorii* as a potential model species and new work on *Cyclotella* sp. Earlier studies showed that diatom-derived biosilica can be modified into functional materials with good sorption properties for metal ions (i.e., Ag, Au) and organic pollutants (i.e., nitrophenol or methylene blue). Our recent work explores the biofabrication of iron oxide nanoparticles (IONPs) using *Cyclotella* sp. Incubation in Fe^{3+} solution leads to the formation of spindle-shaped nanoparticles located both on the frustule surface and in the surrounding medium. Microscopy (SEM, TEM) and elemental analysis (EDAX) confirmed the presence and distribution of iron-based nanoparticles on biosilica structures. The produced nanomaterials showed promising performance in water treatment experiments with over 50% removal of Cr(VI) observed within 180 min, and Hg removal up to 98% under similar conditions. These results shows that the Baltic diatoms can play a dual role as both biological models and sustainable biofactories. Their ability to support low-cost and environmentally friendly nanoparticle synthesis makes them promising tools for future applications in water purification and functional material development.

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Poster presentations

A hidden taxonomic diversity of terrestrial algae in biofilms growing on metal surfaces

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Algae have developed numerous adaptations to terrestrial environments of both natural and anthropogenic origin. They are capable of inhabiting man-made substrates such as concrete, metal, plastic, and glass. One of their strategies that enable them to thrive on these potentially inhospitable surfaces is the formation of biofilms, which provide algae with more stable conditions and protection against desiccation.

In this study, algal biofilms were collected from two metal substrates exposed to different environmental conditions at three-month intervals over the course of one year. The taxonomic diversity of these biofilms was assessed through microscopic examination of environmental samples. Additionally, four cultures (each grown in a different medium) were established for each environmental sample to facilitate for the growth of less adapted taxa; these cultures were subsequently analysed using light microscopy.

Chlorophyta were the only group found in fresh environmental samples, with *Apatococcus lobatus* constant in all samples. However, analysis of the cultures revealed a previously "hidden" taxonomic diversity. Along with Chlorophytes that revealed higher diversity than in the environmental samples, taxa representing Cyanobacteria, Bacillariophyta, and Heterokontophyta were also identified. The use of cultures increased the number of taxa by up to 233%. Furthermore, examination of the cultures allowed for the assessment of seasonal variation, identifying humidity and radiation as key factors influencing the taxonomic diversity throughout the year.

Fantastic Algae and Where to Find Them into Czech Republic. And what does that mean?

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Local studies of flora and fauna, although sometimes underrepresented in broader scientific discussions, play a crucial role in documenting biodiversity, informing conservation strategies, and improving public awareness of the natural world. This is especially important for microscopic organisms such as cyanobacteria and algae, whose ecological roles often exceed those of more conspicuous species.

Across Europe, a number of regional floristic surveys have been published in recent years, significantly advancing knowledge of these groups in diverse habitats. In the Czech Republic, research on cyanobacteria and algae has a long tradition dating back to the late 19th century, with the most recent comprehensive inventory completed in 1997. Since then, however, both the ecological conditions at many sites and the taxonomic understanding of these organisms have changed substantially, making an updated synthesis necessary.

This study compiles data gathered by a wide team of authors and critically evaluates previously published records, including those found in grey literature. In total, 2419 localities were analyzed, documenting 4844 species of algae and cyanobacteria, including Cyanobacteria (578), Cryptophyta (31), Dinophyta (76), Euglenophyta (263), Haptophyta (4), Raphidiophyceae (7), Chrysophyceae (272), Phaeothamniophyceae (1), Eustigmatophyceae (112), Xanthophyceae (223), Diatomae (1168), Phaeophyceae (1), Synchromophyceae (1), Glaucophyta (3), Rhodophyta (22), Prasinophyceae s.l. (19), Ulvophyceae (69), Trebouxiophyceae (232), Chlorophyceae (1097), Mesostigmatophyceae (1), Chlorokybophyceae (1), Klebsormidiophyceae (30), Coleochaetophyceae (9), Zygnemophyceae (602), and Charophyceae (22).

The findings underscore the dynamic nature of these ecosystems and highlight the importance of their continued investigation.

A reservoir of contrasts: winter habitat diversity and phytoplankton responses

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Primary producers in aquatic environments are constantly competing for resources. This relationship is disrupted during the winter months, when the phytoplankton community can continue to grow, whereas the role of macrophytes is diminished. The aim of this study is to describe the dynamics within the phytoplankton community in winter under the influence of habitat conditions in a specific shallow subsidence reservoir (Nadrybie, eastern Poland) formed by coal mining activities. The reservoir currently covers an area of about 30 ha and is divided by a dyke made of coal gangue into two unequal parts: a larger western part, with phytoplankton domination in summer, and a much smaller eastern part dominated by submerged aquatic vegetation. The study was conducted over four consecutive winter periods between 2020 and 2023. The results showed that the two parts of the reservoir did not differ in terms of dissolved nutrient content but differed significantly in terms of total nutrient content, with significantly higher values in the western part of the reservoir. These values were influenced by the phytoplankton community, which developed much more intensively in the western part, where chlorophyll-a concentration and phytoplankton biomass were significantly higher. The western part of the reservoir was dominated by cyanobacteria, cryptophytes, euglenophytes, diatoms, and chlorophytes, whereas dinoflagellates and chrysophytes predominated in the eastern part, with cyanobacteria being completely absent. Differences in phytoplankton composition, despite no variation in the concentrations of dissolved biogenic compounds, suggest that it was not the abiotic conditions in winter that influenced the variability of the phytoplankton community in the Nadrybie reservoir, but rather the presence of extensive submerged aquatic vegetation in the eastern part during the summer and the persistence of its secondary metabolites in the water even during the winter dormancy period. These findings may be applicable to the restoration of water bodies affected by phytoplankton blooms.

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Live in the shadow of a forest: diatoms of water bodies in the Turzański Forest (SE Poland)

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The Turzański Forest complex is located approximately 30 km north of Rzeszów, surrounded predominantly by agricultural land, privately owned forests, and urbanized areas. The forest itself is composed mainly of mixed coniferous forests, with patches of oak-hornbeam forests and Carpathian beech forests. In terrain depressions, alder carrs and raised peatbogs also occur.

Field studies conducted in 2023–2024 encompasses five sampling sites. Four of these were located in post-peat extraction depressions, while one site was situated in a small water reservoir designated as a forest water intake point (a basin with anthropogenic origin). Studied water bodies were characterized by specific environmental conditions, including acidic pH (4.0–6.4) and very low electrolytic conductivity (56–134 µS/cm).

Diatom analyses revealed considerable variation in species richness and community composition. In total, more than 200 diatom taxa were identified, including over 40 taxa in the post-peat depressions and more than 160 taxa in the anthropogenic reservoir. Two types of water bodies exhibited clear differences in diatom assemblages, reflecting contrasting environmental conditions and ecological processes. Small post-peatbog bodies were dominated by *Eunotia sphagnicola* (10-92% of share), *Pinnularia subcapitata* var. *elongata* (5–75%) and *Pinnularia* sp. (up to 10%), whereas in water reservoir the largest populations were formed by *Aulacoseira tenella* (15–80%) and *Achnanthidium minutissimum* (10–20%).

The studied water bodies were characterized by the presence of rare, threatened species including *Pinnularia brauniana*, *P. rupestris*, *P. subgibba*, *Fragilariforma virescens*, *Psammothidium subatomoides*, *Entomoneis ornata*. Additionally, taxa new to Poland were recorded, including *Psammothidium scoticum*, *Pinnularia subfalaiseana*, as well as *Aulacoseira tenella*, which was particularly noteworthy due to its dominance and high abundance within the assemblages.

Forest water bodies constitute valuable retention features, particularly during increasingly frequent drought episodes. Our study also confirms their significant ecological role in supporting and maintaining biodiversity.

Plankton of pit lakes in post-mining locations of Wielkopolska

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Open-pit lignite mines cause severe environmental impacts by removing vegetation and soil, completely transforming the landscape, and creating large areas of barren depressions. Reclamation is the practice of restoring land after mining activities have ceased, aiming to mitigate environmental damage and enable alternative land uses. The common method of reclamation is to convert abandoned pits into lakes by artificially flooding them or allowing natural filling through processes such as rainwater and groundwater infiltration. The formation of these post-mining lakes offers a possibility to observe the various phases of colonization by different plankton communities. Our study presents hydrological, physicochemical, and biological parameters of three lakes – Roztoka, Kleczew, and Jóźwin - created in the area of the Konin S.A. lignite mining pits, in the years 2003, 2013, and 2023, respectively. The research was conducted in the summers of 2024 and 2025. The variation in abiotic conditions was visible in the degree of salinity (Kleczew: conductivity ca. 540 µS/cm; Roztoka and Jóźwin: 861-952 µS/cm), while in all investigated post-mining reservoirs, eutrophic conditions were stated (TP 0.082-0.130 mg P/L; TN 2.83-8.47 mg N/L), not reflected in the algal density (chlorophyll a < 2 µg/L; total biomass <3 mg/L). Similarly, zooplankton abundance was also relatively low, with the lowest values recorded in Jóźwin (about 100 ind./L) and the highest in Roztoka (above 700 ind./L). The Jóźwin and Kleczew reservoirs are dominated by small flagellates belonging to cryptophytes and chrysophytes. The domination of euglenoids and chlorophytes in the summer was stated in Roztoka.

Biomineralization in the trachelomonad lorica: a comparative analysis of its chemical composition

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The genus *Trachelomonas* comprises unicellular euglenophytes distinguished by the presence of a rigid external covering, the lorica. This structure consists of an organic polysaccharide matrix onto which inorganic components are deposited. Lorica formation begins with the secretion of mucilaginous material by the protoplast, followed by the incorporation of metals, initially ferric hydroxides, then manganese oxides, and the subsequent adsorption and precipitation of dissolved ions from the surrounding water. The inorganic fraction of the lorica is predominantly composed of iron (Fe) and manganese (Mn). In our study, we observed an intriguing relationship concerning differences in lorica mineralization among *Trachelomonas* specimens coming from the same water body. The lake water was characterized by high concentrations of calcium and magnesium, indicating hard water conditions associated with strong geological influence. Trace elements such as Mn, Fe, Cu, Zn, and Ni were also present, with Fe and Mn occurring at moderate and relatively stable concentrations (approximately 0.23 and 0.19 mg L^{-1}, respectively). Despite these relatively stable environmental concentrations, the incorporation of Fe and Mn into *Trachelomonas* loricae differed markedly. We analyzed the chemical composition of loricae with smooth surfaces, occasionally possessing fine pores, depressions, or folds, and those bearing spines or wart-like projections. The first group included *T. compacta*, *T. lomnickii*, *T. manginii*, *T. rotunda*, *T. rugulosa*, *T. volvocina*, and *T. volvocinopsis*, while the second group comprised *T. australica*, *T. hispida*, *T. neotropica*, and *T. subverrucosa*. Smooth loricae were more strongly mineralized and characterized by high iron content and negligible manganese levels. The Fe:Mn ratio in these forms consistently exceeded 20:1, often reaching 40–60:1, and in some cases surpassing 100:1. In contrast, ornamented (spines, warts) loricae showed lower mineralization and significantly lower Fe:Mn ratios, generally between 2:1 and 3:1, and reaching a maximum of approximately 10:1. These results suggest that lorica morphology is closely linked to species-specific biomineralization strategies and differential metal incorporation in *Trachelomonas*.

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Phytoplankton diversity in post-mining subsidence reservoirs in the Lublin region

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In the Lublin region, the Earth's surface is undergoing transformations as a result of hard coal mining, leading to the formation of subsidence reservoirs. The development of new reservoirs provides an opportunity to investigate the early stages of colonization by various freshwater communities, including phytoplankton.

The aim of the study was to identify phytoplankton communities in seven post-mining subsidence reservoirs of varying ages (from 1 to nearly 30 years) in relation to their physicochemical conditions. Phytoplankton abundance and biomass were analyzed. Biomass was expressed as fresh biomass and the concentration of total and cyanobacterial chlorophyll, which is necessary to assess trophic status. The basic physicochemical parameters of the water in these reservoirs were also analyzed.

All of the post-mining reservoirs studied were shallow (<2 m) and small in size (<40 ha). Their waters were characterized by a trophic state ranging from eutrophy to hypertrophy: TSI from 58 in one of the youngest reservoirs (Bogdanka I) to above 90 in the oldest reservoirs (Szczecin and Nadrybie). The high trophic potential of the waters favored the intensive development of phytoplankton, including blooms caused by cyanobacteria (Nadrybie1, Bogdanka-heap) or green algae (Szczecin, Nadrybie2). In terms of abundance and biomass, phytoplankton in the reservoirs was dominated by cyanobacteria (e.g., *Planktolyngbya limnetica, Chroococcus limneticus, Romeria* sp.) and green algae (e.g., *Desmodesmus opoliensis, D. communis, Dictyosphaerium tetrachotomum, Monoraphidum contortum*), with a substantial contribution of diatoms (e.g. *Cyclotella meneghiniana*) and euglenoids (e.g. *Euglena viridis*, *Trachelomonas* spp.). In terms of species richness, green algae were dominant. Phytoplankton communities were highly variable between sites, and the species composition, abundance (up to 600 × 10^3 indiv./dm^3), and biomass (up to 250 mg/dm^3) in the older reservoirs indicated a high trophic status. Among the cyanobacteria, an invasive species in Europe, *Sphaerospermopsis aphanizomenoides*, was recorded – its expansion is associated with climate change.

Extremophilic *Nitzschia* species in a man-made environment: phylogenetic link to Crimean volcanic isolate

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This study documents the occurrence of extremophilic *Nitzschia* aff. *anatoliensis* population inhabiting a highly unusual, man-made microhabitat in southern Poland (Poręba Wielka, buffer zone of Gorczański National Park). The species was found in a hypersaline seepage emerging from a remnant borehole pipe associated with historical geothermal exploration. The habitat is characterized by extremely limited water availability (a thin film of a few millimeters), high salinity, exposure to a metal substrate, and strong temperature fluctuations.

Morphological analyses based on light microscopy and scanning electron microscopy revealed striking similarity to the widespread *N. communis*. However, molecular data (*rbc*L) demonstrated that the studied population is only distantly related to this taxon. Instead, it shows a close phylogenetic affinity to *N.* cf. *thermaloides* isolated from Crimean mud volcanoes, and a related position to *N. anatoliensis* described from Turkey.

Despite this phylogenetic proximity, *N. anatoliensis* exhibits morphological differences compared to both the Polish and Crimean populations, suggesting unresolved taxonomic relationships within this group. Further integrative studies will be necessary to clarify species boundaries and confirm the taxonomic status of these taxa.

Our findings highlight that even extremely small and transient anthropogenic habitats can support stable populations of extremophilic diatoms, including unrecorded taxa.

Revisiting *Colacium* (Euglenaceae): molecular and morphological species delimitation and epitypification of the type species *Colacium vesiculosum*

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Colacium is the only genus among autotrophic euglenids capable of attaching to substrates and forming colonies. Although its representatives occur commonly in environmental samples, its taxonomy and phylogenetic relationships within the genus remain poorly resolved. Reliable species delimitation is hindered by the small cell size, the scarcity of clear diagnostic morphological characters, and the presence of mucilaginous structures that may lead to misinterpretation. Furthermore, the type species*,* *Colacium vesiculosum*, has been incorrectly represented in molecular datasets by a strain belonging to a different species. To clarify species boundaries and the phylogenetic relationships within the genus, we conducted an integrative taxonomic study. Herein, we present 60 new *Colacium* sequences obtained from samples collected in Poland and strains from culture collections, representing four molecular markers: nSSU (20), nLSU (6), cpSSU rDNA (17), and cpLSU (17) rDNA. Phylogenetic analyses incorporating 61 additional sequences retrieved from GenBank enabled species delimitation and accurate identification. By integrating phylogenetic evidence with detailed morphological observations and a critical review of the available literature, we recognize and revise five species (*C. arbuscula*, *C. calvum*, *C. elongatum*, *C. epiphyticum*, and *C. mucronatum*), as well as the type species C. vesiculosum, for which an epitype is designated.

From the Baltic Sea to land: airborne transport of cyanometabolites via sea spray aerosols

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Cyanobacteria in the Baltic Sea produce a wide range of bioactive compounds, including hepatotoxic peptides such as nodularin and microcystins, as well as other metabolites (e.g., spumigins and anabaenopeptins). While their occurrence in surface waters is well documented, far less is known about their transfer to the atmosphere and subsequent inland transport. This study investigates the airborne transport of cyanometabolites via sea spray aerosols from coastal waters to inland areas.

Multi-day field studies were conducted during the summer of 2025 in the Gulf of Gdańsk region. Sampling included marine waters, aerosols collected at the beach and over the open sea, as well as inland sites, allowing for the assessment of spatial variability. Aerosol samples were collected using a Coriolis air sampler for bulk bioaerosols and an Andersen cascade impactor for size-segregated particles. Water samples were collected in parallel to evaluate source concentrations.

Chemical analyses were performed using LC-MS/MS to quantify nodularin, microcystins, and additional cyanobacterial metabolites, including spumigins and anabaenopeptins. Meteorological parameters-wind speed and direction, temperature and precipitation-were recorded and assessed in relation to aerosolization and inland transport of cyanometabolites.

Cyanometabolites were detected not only in coastal air but also at inland location, confirming their transfer from sea to land. Concentrations varied with wind conditions and bloom intensity. The presence of different metabolite classes suggests that sea spray aerosols act as efficient vectors for cyanobacterial metabolites. These findings provide new evidence for the inland dispersion of marine cyanometabolites and highlight sea spray aerosols as a potential pathway of human exposure in coastal regions.

The role of DNRA and ANRA bacteria in the development of cyanobacterial blooms with different physiological strategies and distinct morphologies

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Anthropogenic eutrophication, driven by excessive nutrient inputs, alters freshwater ecosystems by promoting cyanobacteria dominance, reducing water transparency and oxygen levels, and increasing toxin production. The persistence of blooms is closely linked to nitrogen availability, including ammonium (NH_4^+), the preferred nitrogen source for non-diazotrophic cyanobacteria such as *Microcystis* and *Planktothrix*. Ammonium production by bacteria begins with nitrate (NO_3^-) reduction to nitrite (NO_2^-), catalysed by nitrate reductase encoded by the *nar*G gene (the initial, potentially rate-limiting step of the entire process). Subsequent nitrite reduction occurs via two pathways: assimilatory nitrate reduction to ammonium (ANRA), involving *nir*BD genes and incorporation into bacterial biomass (reservoir); whereas in dissimilatory nitrate reduction to ammonium (DNRA), mediated by the *nrf*A gene, releases ammonium to the environment enhancing nitrogen availability for cyanobacterial development.

This study aimed to assess the prevalence of nitrate reduction to ammonium, indicated by *nar*G and *nrf*A genes, across pre-, mid-, and post-bloom stages in freshwater systems, and evaluate the potential impact of ammonium availability for cyanobacterial development. The water bodies were represented by phytoplankton communities dominated by cyanobacteria with different physiological strategies (diazotrophic/non-diazotrophic), morphology (coccoidal/filamentous), or non-cyanobacterial communities. Water was collected from three freshwater ecosystems: Sulejów Reservoir (*Microcystis* and *Aphanizomenon*), Lake Lubosińskie (*Planktothrix*), and Stefański Ponds (non-cyanobacterial phytoplankton). qPCR, targeting *nar*G, *nrf*A, and cyanobacterial 16S rRNA genes, was performed to determine the proportion of ANRA/DNRA bacteria during blooms. Results showed consistently high *nar*G gene copy numbers throughout the season, while *nrf*A gene increased markedly during bloom development. This suggests that although the potential for nitrate reduction remains stable, the importance of the DNRA pathway rises when cyanobacterial growth intensifies, enhancing ammonium availability. Consequently, DNRA-bacteria may play a key role in sustaining cyanobacterial blooms and influencing their adaptation, persistence and toxicity in eutrophic waters.

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Current and future chloride concentrations in the Vistula River as a driver of *Prymnesium parvum* bloom risk

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The ecological disaster in the Oder River in 2022, driven by the toxic bloom of Prymnesium parvum, highlighted the critical role of elevated salinity—particularly chloride concentrations—in triggering harmful algal blooms in freshwater systems. Given that the Vistula River, Poland's largest river, receives substantial saline discharges from mining activities in the Upper Silesian region, concerns have emerged about the potential for a similar event.

This study aims to assess current and future chloride concentrations in the upper Vistula River and evaluate their implications for the development of Prymnesium parvum. The analysis integrates in-situ monitoring data (2013–2019) from the Grunwaldzki Bridge cross-section in Kraków with hydrological projections derived from the CHASE-PL dataset. A statistically significant inverse relationship between river discharge and chloride concentration was used to simulate future salinity conditions under two climate scenarios (RCP 4.5 and RCP 8.5) and two time horizons (2024–2050 and 2074–2099).

Observed chloride concentrations ranged from 52 to 1910 mg/L, with an average of approximately 750 mg/L, already exceeding thresholds associated with elevated risk of golden algae blooms. Model projections indicate that, regardless of the climate scenario, future chloride concentrations will remain within or above ranges conducive to P. parvum development. Under low-flow (dry) conditions, concentrations may exceed 1200 mg/L on average and reach extreme values above 3000 mg/L, while even in high-flow (wet) scenarios, dilution is insufficient to eliminate bloom risk .

The results demonstrate that the Vistula River is already in a state of elevated vulnerability and that climate change may exacerbate salinization through altered flow regimes. Without significant reduction of chloride-rich mining discharges and implementation of adaptive water management strategies, the recurrence of a large-scale ecological disaster similar to that observed in the Oder River cannot be excluded.

Cyanobacterial drivers in Poland and Lithuania

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Cyanobacterial blooms are a persistent and recurring problem, particularly in freshwater ecosystems. Paleolimnological and contemporary data indicate that their severity has increased as a result of progressing eutrophication and climate change. Ongoing global warming, also observed in temperate regions of Europe, may further intensify cyanobacterial proliferation and toxin production. This study investigated the environmental and spatial factors influencing cyanobacterial toxin occurrence in lakes across Poland and Lithuania. We analysed the distribution and diversity of cyanotoxins in approximately 90 lakes, with particular emphasis on geographic and climatic gradients. Cyanotoxins were analysed in untreated water samples using HPLC and LC–MS/MS with an Agilent 1200 chromatograph coupled to a hybrid triple quadrupole/linear ion trap mass spectrometer. We identified 41 microcystin congeners, two variants of anabaenopeptins, and micropeptins, whereas cylindrospermopsin and nodularins were not detected. Statistical analyses, including Principal Component Analysis, Factor Analysis, and Peter–Clarke regression, revealed the key drivers of cyanotoxin production. Cluster analysis indicated competitive interactions among cyanobacterial taxa, relationships between cyanobacteria and eukaryotes, and the existence of shared ecological niches. These findings contribute to a better understanding of cyanobacterial bloom dynamics and may support the development of evidence-based strategies for freshwater ecosystem protection.

Cyanobacterial blooms and associated cyanometabolites in water, phytoperiphyton, and gastropods of the hypertrophic Lake Syczyńskie (Eastern Poland)

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Shallow, eutrophic lakes are particularly prone to persistent cyanobacterial blooms. Small (8.15 ha) and shallow (mean depth 1.54 m) Lake Syczyńskie is a hypertrophic water body (0.213–0.445 mg P_tot/L) with recurrent cyanobacterial dominance. This study aimed to assess the abundance and biomass of bloom-forming cyanobacteria and to characterize the occurrence and distribution of microcystins (MCs) across various ecosystem compartments in May, August, and November 2025, and January 2026. The production of oligopeptides other than MCs was also investigated.

From May to November, phytoplankton biomass was dominated (63.4–99.0%) by the filamentous cyanobacterium *Planktothrix agardhii* (Gom.) Anagn. & Kom. The species reached the highest densities (50.78×10^6 ind./L) and biomass (117.78 mg/L) in August and occurred (0.05×10^6 ind./L) in winter, under the ice cover (30 cm). In January, cyanobacteria *Limnothrix redekei* (Goor) Meffert and *Planktolyngya limnetica* (Lemmerm.) Komárk.-Legn. & Cronberg co-dominated (14.65×10^6 ind./L) the water bloom. HPLC and LC-MS/MS analyses revealed the presence of oligopeptides, including MC variants such as [Asp^3]MC-RR, [Asp^3]MC-YR, and [Asp^3]MC-LR. A surface scum sample collected in November was particularly rich in oligopeptides. Substantial numbers of aeruginosins (AERs) and anabaenopeptins (APs) were identified, indicating complex cyanobacterial metabolite profiles during bloom peaks. MCs were also detected in phytoperiphyton collected from macrophytes *Ceratophyllum demersum* L. and *Phragmites australis* (Cav.) Trin. ex Steud., as well as in gastropods, demonstrating the incorporation of cyanobacterial toxins into periphyton- and benthic-associated communities. The presence of MCs in gastropods suggests trophic transfer and potential ecological and toxicological implications.

Cyanobacterial blooms in Lake Syczyńskie are associated with the production of diverse bioactive oligopeptides. Their detection in water, phytoperiphyton, and gastropods highlights multiple exposure pathways within the ecosystem. This underscores the ecological significance of cyanobacterial blooms and the need for integrated monitoring of planktonic, periphytic, and benthic compartments in hypertrophic lakes.

Physicochemical background of water and its influence on phytoplankton community modeling under high mineralization and temperature stress

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Physicochemical parameters of water critically influence the structure and functioning of aquatic biota, thereby regulating community assemblages and trophic dynamics in lotic systems. This study assessed the spatial variability of physicochemical properties in the Adra, Amadorio, and Argos rivers (SE Iberian Peninsula) across three sections (upper, middle, and lower courses), with particular emphasis on factors determining phytoplankton development. Analysed parameters included temperature, nitrate (NO_3^-), total nitrogen (N_{tot}), electrolytic conductivity (EC), and ionic composition. All parameters showed considerable spatial variability. Water temperature reached up to 28.8°C in the lower sections of the Adra and Amadorio rivers. EC was highest in the Argos River (up to 1898 μS/cm), indicating strong mineralisation, accompanied by elevated concentrations of chlorides, sulphates, and sodium. These conditions, combined with high temperatures, may impose stress on aquatic organisms while promoting metabolic processes and phytoplankton growth. Nitrate concentrations varied widely (0.16–33.20 mg L^{-1}), with the highest values observed in the Argos River and increasing downstream in all rivers, suggesting both nonpoint- and point-source pollution. Si concentrations (3.9–9.32 mg L^{-1}) decreased in more eutrophic and conductive sections.

Phytoplankton abundance in the studied rivers remained relatively low, ranging from 24–44 × 10^3 to 652–699 × 10^3 indiv. L^{-1}, with the highest values recorded in the Argos River. Fresh biomass (0.64–5.48 mg L^{-1}) and chlorophyll-*a* concentrations (1.61–8.99 μg L^{-1}) followed a similar pattern. Communities were strongly dominated by pennate diatoms, primarily from the genera *Ulnaria, Achnanthidium, Navicula, Cymbella, Amphora, Gomphonema,* and *Nitzschia*. Larger forms (e.g., *Rhopalodia*, *Surirella*) contributed substantially to total biomass. The results indicate the co-occurrence of multiple environmental pressures, particularly in downstream sections. Their combined effects may promote ecological instability and alter trophic structure. These findings highlight the need for integrated water quality monitoring and effective management strategies to mitigate nutrient inputs and salinisation in river ecosystems.

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Metabolic changes in *Chlamydomonas reinhardtii* induced by gadolinium present in the aquatic environment

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Gadolinium is commonly used as a contrast agent in magnetic resonance imaging (MRI). The increasing concentration of this element in aquatic environments raises concerns regarding its impact on resident organisms. The aim of this study was to evaluate the effects of various gadolinium compounds on selected parameters of the microalga *Chlamydomonas reinhardtii*. This species was selected as a model organism due to its well-defined metabolism and proven utility in assessing cellular responses to environmental stress.

The experiment was conducted using concentrations ranging from 0.1 nM to 500 µM of gadolinium(III) chloride and commercial contrast agents (i.e., MultiHance, ProHance, and Dotarem), which differ in their gadolinium-chelating ligand structures. The results were compared with a control group. Additionally, various time points between days 1 and 17 were examined to evaluate both short- and long-term exposure. Changes in cell count and biomass were analyzed as primary growth indicators, while sugar and protein levels served as markers of the cells' metabolic state.

The results demonstrate the varying impacts of the analyzed compounds and their concentrations on the development of *Chlamydomonas reinhardtii*. Exposure to higher concentrations resulted in inhibited growth and altered biochemical parameters, which may be indicative of stress induction. Conversely, certain forms had a negligible impact on the tested metabolic pathways, suggesting lower bioavailability and a limited metabolic effect.

This research provides crucial insights into the potential environmental consequences of gadolinium, particularly its accumulation in microalgae. As primary producers, these organisms play a key role in organic matter production and form the basis of the aquatic food web. These findings may serve as a foundation for further studies on the environmental fate of this element and its impact on aquatic organisms.

Assessment of the ecological status of Międzyodrze canals based on diatoms (phytobenthos)

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The canals of the Międzyodrze area constitute a significant component of the hydrological system of the lower Oder Valley. However, long-term restrictions in water flow have contributed to their ecological degradation. In connection with the planned investment aimed at restoring canal flow, a comprehensive ecological assessment framework was developed, encompassing biological, physicochemical, and expert-based evaluations of aquatic habitats.

The aim of this study was to assess the ecological condition of canals in the Gryfiński and Widuchowski Polders as a baseline prior to the implementation of planned hydrotechnical works, and to identify the main drivers of aquatic environmental degradation.

The study was conducted in August and early September 2025 at 18 sampling sites (nine in each polder). Diatom phytobenthos samples were collected from submerged macrophytes and reed beds. Microscopic analysis was performed according to standard methodologies, with over 400 valves counted per sample and taxa identified to the lowest possible taxonomic level. Species were classified according to their ecological preferences using the OMNIDIA database. Diatom indices (IPS and IO) as well as biodiversity indices (H′, J′) were calculated.

Parallel measurements of water physicochemical parameters (oxygen, temperature, pH, conductivity, and transparency) were conducted, along with an expert-based habitat assessment, including the characterization of bottom sediments and the degree of canal overgrowth.

A total of 142 diatom taxa were identified, dominated by species typical of eutrophic and moderately polluted waters. Better ecological conditions were observed in the Widuchowski Polder. Overall ecological status ranged from moderate to poor, with poor status recorded exclusively in the Gryfiński Polder.

The ecological condition of the Międzyodrze canals is highly spatially variable and primarily determined by oxygen deficits, water stagnation, and the accumulation of organic matter. The results provide a reference point for evaluating the effectiveness of planned restoration measures and for future environmental monitoring.

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Phytoplankton communities and factors shaping them in two connected urban ponds

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Urban ponds have a positive impact on biodiversity and human wellbeing. However, they usually face multiple anthropogenic pressures that negatively affect their ecosystems. Ponds in Sołacz Park in Poznań (W Poland) have been created on a course of a small river (Bogdanka River). They are also fed by urban rainwater. In January and February 2025, bottom sediments of the pond were dredged, due to their high accumulation.

The aim of this study was to assess the differences between the ecosystems of the two ponds in the year of sediment removal and to explore main environmental drivers of their biotic community. Phytoplankton was used as the object of the study, as this group reflects well ecosystem functioning.

The biomass of the phytoplankton of the ponds fluctuated from 0.2 to 55.2 mg L^{-1}. The community in the first pond was shaped strongly by the phytoplankton inflowing with the river from an upstream dam reservoir, as reflected in the low Bray-Curtis dissimilarity index between the pond and the inflow. Whether the phytoplankton community of the second pond was shaped by the first one and by the river, or whether it differed significantly, depended on hydrology (intensity of water flow through the ponds). In periods of heavy rainfall, the dissimilarity index of the communities was low, and the phytoplankton biomass tended to be low due to dilution effect. With lower precipitation and longer retention time, the phytoplankton community of the second pond would shift considerably from the community of the first pond, despite no significant difference in concentration of total phosphorus, soluble reactive phosphorus, total nitrogen or ammonium nitrogen between the ponds. Among nutrients, only nitrate concentration differentiated between the ponds at $p<0.05$, with higher values in the first pond, but no correlation of this nutrient with phytoplankton biomass or community structure was found.

In this study, we have demonstrated the predominant role of both rainwater inflows and the river for the phytoplankton community of two urban ponds, with rainfall intensity shaping the scale of impact of the river. Altered precipitation patterns related to climate change, with intensified and more common extreme events, may further increase these effetcs in the future.

Phytoplankton community in a strongly transformed, heated lake system a decade after reduction of main anthropogenic pressures

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Heated lakes provide valuable objects for studies of the impact of climate change and extreme anthropogenic pressures on freshwater ecosystems. The system of Konin lakes, located in central Poland, has served the purpose of cooling a power plant since 1958. Extreme human modification of these ecosystems included not only the release of heated waters, but also chemical pollution and altered hydrology. In the period of 2008-2015, the overall pressure was relaxed, with a lower amount of released heated water and an increase in retention time of the lakes.

The aim of this study was to analyze the state of an extremely modified ecosystem, in which pressures have been relaxed, using the example of the heated Konin lakes and their phytoplankton community as the proxy. The study was conducted in 2024. We hypothesized that the lowered pressure has not resulted in recovery of the lakes, after decades of extreme human pressures, and thus the phytoplankton biomass is high, cyanobacteria-dominated, with strong blooms in summer.

Contrary to our hypothesis, the phytoplankton community was not overwhelmingly dominated by cyanobacteria, and even in summer eukaryotic algae (mostly diatoms, Dinoflagellata and green algae) prevailed over cyanobacteria in all sampling stations except one. Despite high nutrient concentration, phytoplankton biomass reached medium levels. Strong past modifications of the ecosystems were somehow reflected in the presence of thermophilic cyanobacterial species considered invasive, but their biomass was very low. The biomass of the phytoplankton was lowered by abundant alien thermophilic macrophyte species, which still dwelled in the lakes, despite lowered temperatures.

In conclusion, we emphasize the possibility of limiting the growth of phytoplankton by alien macrophyte species, apart from their well-known negative impacts on aquatic ecosystems.

Oxidative stress and antioxidant responses of the green microalga *Chlorella vulgaris* exposed to polystyrene microplastics

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The increasing accumulation of microplastics in aquatic environments poses a growing threat to primary producers and ecosystem stability. Polystyrene (PS) is among the most common types of microplastics and is characterised by high persistence and resistance to degradation, which enhances its potential to interact with aquatic microorganisms. Therefore, assessing the effects of such micropollutants on green algae, key primary producers in aquatic ecosystems, is essential.

The aim of this study was to investigate the effects of polystyrene microplastics on physiological and biochemical parameters in the unicellular green microalga *Chlorella vulgaris.* Due to its unicellular nature, this species enables direct assessment of cellular responses to environmental stressors.

The analysis included cell number, lipid peroxidation (measured as malondialdehyde, MDA), hydrogen peroxide concentration, ascorbate content, antioxidant enzyme activities, and photosynthetic pigment levels.

Exposure to polystyrene microplastics induced oxidative stress, as demonstrated by increased hydrogen peroxide levels and enhanced lipid peroxidation. This was accompanied by changes in antioxidant enzyme activity, alterations in ascorbate content, and disturbances in pigment composition.

These results indicate that polystyrene microplastics adversely affect the physiological state of *Chlorella vulgaris*, triggering oxidative stress and activating antioxidant defense mechanisms. The observed responses highlight the sensitivity of unicellular microalgae to microplastic pollution and their potential role as indicators of environmental stress.

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Are springs truly stable habitats year-round? Physical and chemical water parameters vs. diatoms

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Springs are regarded as very stable habitats with low annual water temperature dynamics. Therefore, current knowledge of the seasonal variability of diatom assemblages is very limited especially in those located in the lowlands. Seasonal analyses of physicochemical water parameters are performed much more often than analyses of diatom variability during the year . The aims of our study were to identify and compare seasonal diversity of diatom assemblages and water quality in five lowland reocrene springs with varying degrees of anthropogenic pressure located in Białystok and the surrounding the Knyszyn Forest (Northeast Poland). Diatom material was collected from three microhabitats present at the following sites: epilithon, epipelon, and epixylon from October 2024 to July 2025. Taxa were divided into ecological guilds – low-profile (nutrient-poor/high disturbance), high-profile (nutrient-rich/low flow), and mobile (sediment dwellers). The following analyses were used: IndVal index (preferred microhabitat for diatoms); the Principal Component Analysis (PCA) (main gradients in hydrochemical parameters and similarity among samples); the Redundancy Analysis (RDA) (relationships among diatoms and hydrochemical variables). Water temperature ranged from 4.0 (winter) to 14.9°C (summer). Statistically significant differences between springs were observed for Ca^{2+}, Mg^{2+}, HCO_3^-, Na^+, Cl^- and SO_4^{2-} ions ($p < 0.05$).

Our results revealed differences in diatom assemblages between microhabitats and seasons. A total of 168 diatom taxa were identified in all springs. The lowest species richness was observed in summer. Among all dominant species (>2%), 22 taxa were found in all studied microhabitats. The RDA diagram revealed significant relationships between diatom assemblages and environmental gradients, especially in the case of *Achnanthidium minutissimum* var. *minutissimum*, *Cocconeis neodiminuta*, *Amphora pediculus*, *Planothidium frequentissimum*, and *P. lanceolatum*.

Contrasting effects of hot and rainy summers on phytoplankton structure in a shallow Lake Oporzyńskie

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Freshwater ecosystems are increasingly exposed to climate-driven variability, with extreme summer conditions, such as prolonged heatwaves and periods of intense precipitation, playing a key role in shaping phytoplankton dynamics. Shallow lakes are particularly sensitive to such fluctuations due to their limited water volume, strong sediment-water interactions, and rapid response to external nutrient inputs. This study examines interannual changes in phytoplankton structure in Lake Oporzynskie, with a focus on contrasting hot and rainy summer conditions and their ecological consequences.

Lake Oporzynskie is a shallow, eutrophic system that has experienced recurring mass development of filamentous green algae, particularly *Cladophora glomerata*, from which several tons of biomass have been harvested over multiple years. These large-scale accumulations represent both a symptom of eutrophication and a potentially important factor influencing nutrient cycling and phytoplankton community composition. The periodic removal of Cladophora biomass may act as a form of nutrient export, thereby modifying internal loading processes and altering competitive interactions within the phytoplankton assemblage.

Phytoplankton and environmental parameters were monitored over multiple growing seasons characterized by markedly different meteorological conditions. Hot summers were associated with elevated water temperatures, reduced mixing, promoting the dominance of green algae and some cyanobacteria, particularly buoyant and filamentous taxa. In contrast, rainy summers were characterized by increased inflow, enhanced mixing, and episodic nutrient pulses, which favoured more diverse phytoplankton communities, including diatoms and cryptohytes.

Our results indicate that extreme summer conditions significantly influence both the taxonomic composition and biomass distribution of phytoplankton. During hot summers, green algal blooms were more persistent and structurally simplified the community, often leading to reduced biodiversity. Conversely, rainy summers promoted greater variability and coexistence of multiple functional groups, resulting in more balanced community structures. The presence and repeated removal of *Cladophora glomerata* biomass appeared to modulate these patterns by influencing nutrient availability and light conditions, potentially buffering or amplifying the effects of climatic extremes depending on timing and intensity.

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Seasonal (dis-)connectivity in functional structure of phytoplankton communities of shallow eutrophic waterbodies - preliminary results

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The consequences of climate change are pronounced not only as summer heat waves and extreme weather events, but also as mild winters with shortened ice cover on freshwater systems. Ice cover is an integral part of the seasonal cycle in periodically freezing lakes and the consequences of its' loss might pose a significant threat for these ecosystems.

The objective of this study is to expand the existing knowledge on functional structure of phytoplankton communities (trait-based approach) of small permanent freshwater systems during the cross-seasonal (Fall/Winter and Winter/Spring) transitions. The study system includes 8 shallow eutrophic water bodies located within two divergent (agricultural vs. forested) catchments.

NMDS revealed a clear separation of phytoplankton communities between the two catchment types, with greater within-group variability in community composition among agricultural systems. Water bodies with agricultural catchments were richer in total nitrogen and total phosphorus, but surprisingly developed lower phytoplankton biomass compared to water bodies with forest catchment. In waterbodies located in agricultural catchments, functional richness (FRic) exhibited pronounced seasonal variability, with a marked decline of the index values in winter. In contrast, reservoirs with forested catchments showed stable FRic values across seasons. The variability of FRic was an outcome of seasonal fluctuations of functional traits of phytoplankton taxa constituting studied communities. The functional traits considered in the analyses were: size as a particle (continuous trait), motility, potential toxicity, siliceous exoskeletal armor and spines possession (binary traits).

Overall, nutrient-enriched water bodies located in agricultural catchments underwent stronger seasonal turnover than less enriched water bodies located in forest catchments. This lead to palpable 'functional bottleneck' effect in water bodies with agricultural catchments. Under future climate change scenarios where altered winter duration is followed by increasing nutrient loading, enriched aquatic ecosystems may experience sharp cross-seasonal instability.

Phytoplankton changes due to the restoration measures in Lake Strzeszyńskie in Poznań

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Lake Strzeszyńskie was a charophyte lake bordering meso- and eutrophic levels. For several years, since 2011, it had been burdened with pollutants from inflows from the expanding suburban area. This was due to sewage system overcharge during storms and sewage leakage into surface waters. This led to intensive phytoplankton growth in the lake, primarily cyanobacteria, which resulted in the closure of the public municipal swimming area. It also led to the disappearance of stoneworts in the lake. Restoration measures included phosphorus inactivation starting from 2012 and oxygenation of the bottom waters using a pulverizing aerator starting from 2013. Additionally, a retention reservoir was created at the lake's tributary to reduce the nutrient load. A new stormwater collector was also constructed in 2018, draining rainwater outside the catchment area. These measures improved water quality and allowed the functioning of swimming area. The stoneworts appeared after several years of restoration in 2019. A significant decrease in phytoplankton abundance and biomass was observed. The greatest changes were observed in the abundance of cyanobacteria, which decreased from approximately 800,000 in 2011 to 225,000-291,000 cells per ml in the surface water layer between 2018 and 2022. They were dominated by species with very small cell sizes of the genera *Aphanocapsa, Cyanodictyon* and *Radiocystis*. Although picocyanobacteria still continued to dominate the phytoplankton abundance during restoration, nanoplanktonic and microplanktonic green algae, diatoms, and dinoflagellates accounted for a larger share of the biomass. As a result, the Phytoplankton Multimetriks for Polish Lakes (PMPL index), calculated based on the mean chlorophyll-a concentration, total phytoplankton biomass, and cyanobacterial biomass, indicated very good ecological status of the lake.

Restoring, protecting and monitoring algal communities in polluted waters

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This study presents an innovative solution for the restoration of industrial waterways and degraded river channels. It is implemented using Rock-Based Algal Niches (RAN) and an autonomous water parameters monitoring system.

RANs are parabolic structures composed of at least 95% natural rock materials, primarily basalt, granite, and greywacke. The composition of the stones can be selected individually for specific water courses, considering water parameters and the preferences of aquatic organisms.

The algae selected for introduction into watercourses are organisms derived from populations native to the local ecosystem. The mix of species is chosen to support biodiversity and maintain balance in the aquatic environment, thereby preventing the dominance of a single species and the collapse of the ecosystem.

The effects of renaturation are continuously monitored by a system of autonomous measuring probes (buoys), which enable the measurement of selected water parameters and quantitative analysis. The system transmits all collected data to a central server, where it can be further processed using machine learning algorithms. This makes it possible to predict changes in the aquatic environment and take proactive measures in the event of unfavorable forecasts.

Physicochemical properties of exopolysaccharides (EPS) isolated from autotrophically grown green algae

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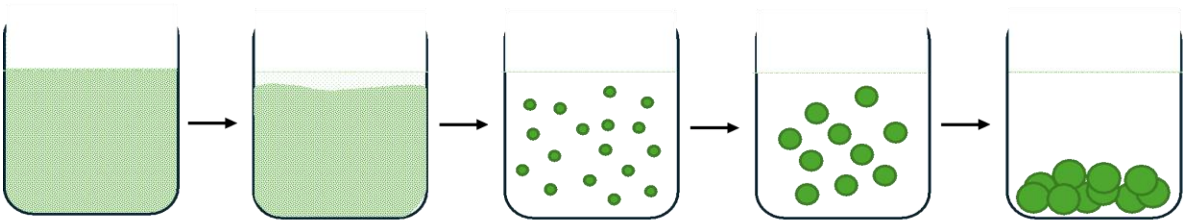
Exopolysaccharides are secondary metabolites secreted outside the cell. Their main function is to protect cells against adverse environmental conditions. Therefore they exhibit a number of physicochemical properties that enable them to do so. These include stabilizing, sorption, rheological, biofilm-forming, aggregation, destabilization and flocculation properties.

Flocculation is considered one of the methods of microalgal biomass harvesting. The first stage is the destabilization of the tested suspension, followed by the aggregation of particles/cells. EPS initially contribute to the formation of aggregates, and then stabilizes them.

To determine the flocculation properties of EPS, turbidity changes were measured as an indicator of their destabilization properties. Kaolin was used as a model material in the research. The properties of EPS were then tested in an algae cell suspension.



Flocculation stages: 1-suspension, 2-destabilization, 3-aggregation, 4-flocculation, 5-flocs.

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Assessment of antioxidant potential of natural cyanobacteria biomass from Lithuanian freshwaters

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Cyanobacteria are recognised as valuable natural resources in biotechnology due to their ability to produce a wide range of bioactive compounds. These organisms synthesise over 1,100 secondary metabolites, including pigments, phenolic compounds, and vitamins, with potential applications across various industrial and scientific fields (Dittmann et al., 2015). Increasing environmental concerns and the growing demand for natural products have intensified interest in sustainable sources of these compounds. At the same time, anthropogenic activity and climate change promote more frequent and intense cyanobacterial blooms, leading to substantial biomass accumulation that could serve as a promising source of bioactive substances. The study aimed to assess the antioxidant potential of natural cyanobacterial biomass collected from blooming freshwater ecosystems in Lithuania during bloom events dominated by various cyanobacterial species.

The results showed that cyanobacterial biomass contains a diverse range of bioactive compounds with antioxidant properties, and their content varied depending on sampling location and time. Pigments, particularly phycobiliproteins, dominated (up to 90.6% of total pigments). Biomass dominated by *Aphanizomenon flos-aquae* was rich in phycocyanin and allophycocyanin, whereas *Microcystis*-dominated biomass also contained phycoerythrin at low levels. Chlorophyll-a and carotenoids were present in lower amounts (up to 14.5% and 4% of total pigment, respectively). Total phenolic content was relatively low, whereas antioxidant activity reached up to 23.6% and 49.0% (DPPH and ABTS assays, respectively).

These results indicate that natural cyanobacterial biomass is a promising, sustainable source of bioactive compounds with antioxidant potential for biotechnological applications.

The use of PlanktoScope for phytoplankton monitoring

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Among the latest trends in global plankton research, imaging techniques are emerging as the future of rapid, semi-automated quantitative and qualitative solutions. PlanktoScope, as an affordable imaging platform based on open-source software, is one of the devices most highly regarded by the scientific community. Obtaining thousands of high-resolution images of living planktonic organisms in a relatively short time opens up new possibilities for monitoring the pelagic environment as well as for ecological research.

We are conducting our pilot studies by analyzing environmental samples collected from the Baltic Sea, using imaging compatible with the EcoTaxa program. This program enables automatic recognition of organisms in images, based on deep learning algorithms in plankton community analyses, and facilitates collaboration among experts in manual taxon identification

Analysis of samples collected during seasonal research cruises has demonstrated the significant potential of PlanktoScope and EcoTaxa for rapidly detecting environmental changes, such as increases in the abundance of toxin-producing organisms or large-scale seasonal shifts in plankton species composition.

Plankton responses to sustainable lake restoration

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The research was carried out on Lake Raczyńskie, a shallow (84.4 ha; max depth 5.8 m) polymictic lake located in western Poland. The total catchment area of the lake covers 9.15 km^2 and is dominated by forest (45%) and agricultural land (35%). The shoreline is adjacent to urban and recreational areas, which increases the pressure on water quality. As a result of high external loading from the catchment area, the lake became heavily polluted and hypertrophic. To improve water quality, restoration measures were implemented, including low-dose chemical phosphorus precipitation from the water column using iron sulphate and magnesium chloride, combined with biomanipulation through increasing the abundance of predatory fish**.**

Field research was conducted during three distinct phases of the restoration process: before, during restoration, and six years after the completion of restoration measures, allowing assessment of both short-term and long-term ecosystem responses. The aim of the study was to assess changes in physicochemical parameters and the quantitative and qualitative composition of plankton over three study periods and to determine whether restoration induced persistent ecosystem changes rather than only short-term responses.

Comparison of the three study periods revealed significant temporal shifts in both abiotic parameters and plankton communities. Several years after the completion of the restoration activities, higher values of conductivity and pH were observed. In turn, the concentration of chlorophyll-a, seston, ammonium nitrogen, nitrite and nitrate, DIN, phophorus concentration and N:P decreased. The positive trend of low phytoplankton abundance continued several years after treatment– particularly cyanonbacteria were significantly less numerous during and after restoration procedure. The abundance of chlorophytes, diatoms, chrysophytes, and conjugatophytes increased. The abundance of zooplankton (cladocerans, copepods and rotifers) decreased after the treatment. A higher number of phytoplankton and zooplankton taxa were also noted. Restoration induced transitional plankton responses and persistent ecosystem changes, indicating long-term ecological improvement of the lake.

Microalgal response to *Rhodococcus opacus* exopolymers

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Interactions between microalgae and bacteria can induce beneficial changes in metabolic processes, which may be used to increase the production of valuable microalgal bioproducts, such as lipids. According to the literature, Rhizobium sp. increases the growth rate of microalgae, but also stimulates fatty acid oxidation, whereas *Mesorhizobium sangaii* enhances lipid production in *Chlorella vulgaris*. In microalgal-bacterial co-cultures, extracellular polymeric substances (EPS) play an important role.

This study aimed to analyse the effect of bacterial exopolymers produced by the *Rhodococcus opacus* strain on growth processes and metabolic profile of unicellular green algae. The EPS isolated from the *Rhodococcus opacus* strain was composed of 64.6% polysaccharides and 9.44% protein. The polysaccharide fraction consisted of mannose, galactose, and glucose in a molar ratio of 2.7:1.3:1. Microalgal growth was assessed by monitoring changes in optical density using UV–Vis spectrophotometry. The effect of EPS on the microalgal cellular biochemical composition was evaluated by quantitatively determining lipids using a modified Bligh and Dyer method, proteins using the Bradford assay, and carbohydrates using a colorimetric anthrone-based approach. The impact on the expression of genes involved in fatty acid and lipid biosynthesis pathways was analyzed using real-time PCR.

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A turning point for phytoplankton? Post-restoration changes in Lake Góreckie (the Wielkopolski National Park, western Poland)

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The study reported was performed in Lake Góreckie, a dimictic postglacial lake located in a strictly protected area of the Wielkopolski National Park (western Poland, central Europe), which has experienced long-term eutrophication driven by historical sewage discharge, agricultural runoff, and internal nutrient loading. To improve the quality of water and combat cyanobacteria blooms, restoration measures, including aeration, phosphorus inactivation, and fish biomanipulation, were implemented from 2009 to 2022.

The aim of the study was to investigate the current state of water quality in Lake Góreckie in the year that the water reclamation was terminated (2022) and three years later (2025) based on biotic indicators and abiotic factors. Interrelationships between the lake's physico-chemical water properties and the communities of water quality indicators, planktonic cyanobacteria and algae, and macrophytes were also analysed. The obtained results were interpreted in light of groundwater properties and the long-term catchment land use changes, additionally included in the study.

Surprisingly, despite similar nutrient concentrations in both study years, clearly related to groundwater properties, water transparency and hypolimnetic oxygen content improved markedly in 2025, along with a decline in phytoplankton abundance and biomass and a recovery of submerged vegetation, particularly charophytes. These changes coincided with increased water levels and prolonged spring mixing in 2025 and were preceded by the long catchment afforestation. Our results highlight the complex and multidimensional interplay between catchment hydrology and long-term land use, and primary producers dynamics. Further study is needed, however, to definitively confirm the results regarding the recovery of Lake Góreckie, which has long been recognised as an example of eutrophic lakes situated in protected areas subject to human pressure.

Green microalgae as bioindicators and bioremediators in sedimentary phosphorus-containing waters

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Sedimentary phosphorus-containing waters are waters formed as a result of phosphate rock leaching, discharge of agro-industrial effluents, and biogeochemical redistribution of phosphorus in bottom sediments. The total phosphorus concentration in such waters often exceeds regulatory standards by 10–50 times, triggering eutrophication of water bodies. Green microalgae, being primary producers and active participants in the phosphorus cycle, are of particular interest as subjects of fundamental and applied research in this context. In phosphorus-enriched sedimentary waters, representatives of the genera *Chlorella* Beij., *Scenedesmus* Meyen, *Chlamydomonas* Ehrenb. dominate. High concentrations of orthophosphates stimulate vegetative reproduction of these organisms, forming stable algal communities with cell suspension densities of up to 10^8–10^9 cells/mL. Phosphorus absorption by green microalgal cells is carried out through high-affinity transport systems — phosphate-specific permeases, whose expression increases under phosphorus deficiency and is suppressed under excess conditions via a negative feedback mechanism. Under conditions of luxury uptake, cells are capable of accumulating polyphosphates in intracellular granules in amounts many times exceeding current metabolic requirements. This phenomenon is of key importance for biological phosphorus removal.

Microalgae participate in the formation of authigenic carbonate-apatite sediments: during mass development of phytoplankton, local pH rises due to photosynthetic consumption of CO_2, which leads to chemical precipitation of hydroxylapatite $Ca_5(PO_4)_3(OH)$ from a supersaturated solution. Thus, algal communities indirectly regulate the geochemical fluxes of phosphorus between the water column and bottom sediments. The use of immobilized cultures of *Chlorella vulgaris* and *Scenedesmus obliquus* in High Rate Algal Pond systems allows the total phosphorus concentration in effluents to be reduced by 70–95% under optimal conditions (pH 7.5–8.5; illumination 150–300 μmol photons$\cdot m^{-2}\cdot s^{-1}$; temperature 20–28°C). The biomass recovered during the treatment process is a valuable source of polyphosphate fertilizers and lipid feedstock for biofuels, which aligns with the principles of the circular economy.

Optimization of cultivation and extraction for *Pseudanabaena galeata* CCNP1313 to enhance the discovery of anti-cancer compounds via Activity-Annotated Molecular Networking

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Pseudanabaena galeata CCNP1313 strain isolated from the Baltic Sea has been previously identified as a producer of compounds with promising anti-cancer potential. However, the bioactive agent responsible for this effect has not been identified. This study focuses on maximizing the yield of bioactive metabolites by independently optimizing extraction protocols–through the evaluation of various solvents–and cultivation parameters, including light intensities and nutrient (nitrogen and phosphorus) limitation. To bridge the gap between biological activity and chemical composition, a high-throughput analytical pipeline is employed, utilizing LC-MS/MS profiling combined with Feature-Based Molecular Networking (FBMN). Preliminary *in vitro* bioassays revealed that the 100% acetonitrile (100% ACN) extract exhibited the highest cytotoxicity against the T47D breast cancer cell line, followed by the 75% aqueous methanol (75% MeOH) extract. Chemical profiling demonstrated that 100% ACN selectively extracted a narrow range of lipophilic compounds. In contrast, 75% MeOH maintained strong anti-cancer activity while yielding a substantially broader and chemically diverse metabolic profile. Furthermore, evaluating light-dependent metabolic shifts revealed that varying light intensities and growth phases detectably influenced both the cytotoxic efficacy and the chemical profiles of the extracts. The core of this research involves the application of Activity-Annotated Molecular Networking (AAMN), integrating cytotoxicity data from the T47D breast cancer line and HDF control cells directly into the molecular networks. Supported by statistical analysis, this approach aims to identify specific molecular clusters and bioactivity markers within the extracts responsible for the observed effects. By correlating optimized cultivation conditions with the enrichment of targeted metabolites, this study provides a systematic framework for the efficient discovery of natural anti-cancer compounds and the development of biotechnological strategies for their production.

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