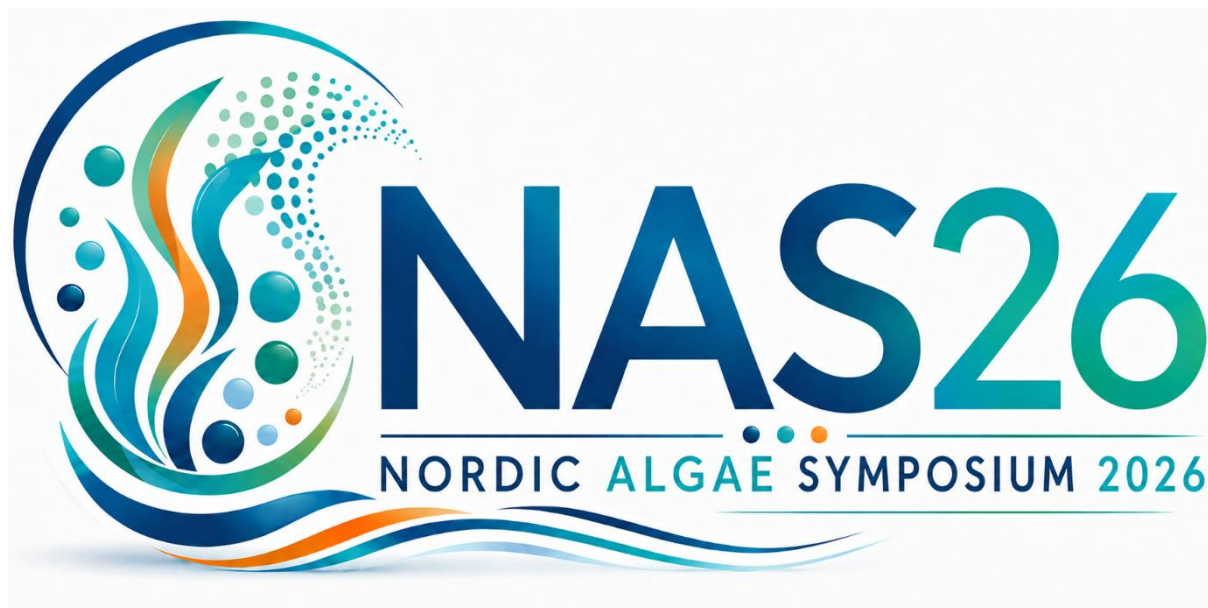




NORDIC ALGAE SYMPOSIUM 2026

BOOK OF ABSTRACTS

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Chlorophyte Cell Walls: Unlocking Their Potential for Sustainable Bioremediation.

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Abstract

Cell walls play essential roles in maintaining cellular integrity and regulating interactions with the surrounding environment. Chlorophytes inhabit marine, freshwater and terrestrial environments and their cell walls are highly diverse, not only between species, but differences may occur even within the same species depending on culture conditions, reproductive phase or stress. Often, Chlorophyte cell walls consist of a cellulose microfibrils framework inserted in an amorphous mold of glycoproteins, hemicelluloses and pectin-like substances, similar to the higher plants primary cell walls. In some Chlorophyte species, additional layers or specialized polymers such as algaenan or sporopollenin-like compounds provide enhanced mechanical robustness and resistance to chemical and enzymatic degradation, but their composition greatly varies among taxa¹. The structural components contain abundant functional groups, including hydroxyl-, carboxyl-, amino-, and sulfate-groups, which provide binding sites for a wide range of pollutants. Consequently, microalgae can adsorb and/or absorb various pollutants from wastewater and contaminated environments ranging from nutrients (nitrogen and phosphorus) via pharmaceuticals to heavy metals. Heavy metals can bind to cell-wall components through ion exchange, electrostatic attraction, complexation, and surface adsorption². Cell-wall-mediated biosorption is particularly advantageous because it can occur rapidly and does not necessarily require metabolically active cells.

Chlorophyta cell walls also can interact with micro- and nanoplastic particles (MNPs). We investigated the bioremediation potential of a natural Nordic microalgal polyculture isolated from an open raceway pond reactor treating municipal wastewater³. Analysis of MNP concentrations in the media after polyculture treatment showed removal efficiencies of approximately 78–90%, at initial MNP concentrations of 100 ppm. Overall, chlorophytes represent a sustainable, renewable, and potentially cost-effective resource for bioremediation.

Keywords: *Chlorophyta, Cell wall, Bioremediation, Heavy metals, Micro-and Nanoplastics*

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The microbiome of bioreactors containing mass-cultivated marine diatoms for industrial carbon capture and utilization

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Abstract

Industrial-scale cultivation of marine microalgae for carbon capture and utilization (CCU) occurs in non-axenic, semi-open photobioreactors that function as highly selective microbial ecosystems. Diverse microbial communities spontaneously assemble through taxonomic migration, originating from adjacent industrial inputs like filtered seawater in the algal mass cultivation systems. This time series study investigates the dynamics of complex microbial communities during cultivation of the cold-adapted marine diatom, *Porosira glacialis* UiT201, on industrial CO₂ in the ever-changing seasons of the northern Norway.

The cultivation system represents a distinctive industrial marine microbial ecosystem, showcasing both prokaryotic and microeukaryotic community succession driven by species replacement. Despite taxonomic turnover, a consistent and abundant core microbiome endures, shaped by microalgae-specific traits and dynamic environmental conditions. Instances of the focal strain (*P. glacialis*) experiencing collapse coincide with shifts in the core microbiome and environmental conditions, unlike the stability observed in successful bioreactor runs. These findings highlight the potential importance of coexisting microbial taxa in industrial microalgae cultivation and their association with process stability. Changes in community structure may provide useful indicators of process stability, highlighting the dynamic relationship between microalgae and their associated microbiome. This research contributes to advancing CCU technologies, drawing inspiration from the resilience of natural Arctic marine ecosystems and establishing them as viable biotechnological solutions.

Keywords: Community succession, Cold-water diatoms, Mass cultivation, Phycosphere

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<https://doi.org/10.1016/j.algal.2024.103701>

Dynamics of Glacier Blood: Cryogen-free meta-omics of highly pigmented extremophile algae from the Swiss Alps

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Abstract

Psychrophilic algal blooms "Glacier Blood" significantly accelerate snow and ice melt in the cryosphere by producing massive concentrations of astaxanthin¹. Despite climatic importance and biotechnological potential, these communities remain poorly understood. Metaproteomics offers unique functional insight compared to DNA/RNA characterisation, capturing past and present protein expression. Challenging field sites, low density, unculturability and logistical challenges preserving samples, combined with lysis-resistant cysts² make proteomic analyses difficult. Cryogenic flash-freezing is often impractical, expensive and/or hazardous in remote environments. We developed a cryogen-free workflow designed to enable meta-omic investigations of psychrophilic algal communities.

We combine in-situ biomass concentration with fixation via broad-spectrum enzyme inhibitors, avoiding cryogens during fieldwork. Compared to cryogens, our method is cheaper, safer, and needs no cold-chain. DNA and protein of sufficient quality for metagenomic/proteomic analysis was obtained, and two stages of the bloom life-cycle were compared. We present preliminary meta-omic data from communities collected in the Swiss Alps in synthesis with metagenomic and barcoding to provide insights into the ecology of psychrophilic algal ecosystems highlighting the algal transition from a photosynthetic reproductive stage to a cystic overwintering form. We also present metagenomic insights into metabolic deficiencies that may impede culturing and highlight novel enzymes with biosynthetic potential. This approach expands opportunities to investigate the ecology of snow algae across remote alpine and polar regions.

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Decoding TOR kinase inhibition: Unraveling autophagic mechanisms and metabolic rewiring in *Parachlorella kessleri*

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Abstract

Introduction: Autophagy is an essential eukaryotic degradation pathway for nutrient recycling and stress adaptation, regulated by the Target of Rapamycin (TOR) kinase. However, the molecular pathways linking TOR suppression to autophagic activity and metabolic shifts in the oleaginous marine microalga *Parachlorella kessleri* iCABeR21 remain undefined.

Methods: *P. kessleri* cultures were exposed to nutrient-replete, nitrogen-depleted, and AZD8055-induced TOR-inhibited regimes. Cellular responses were monitored using growth profiling, photosynthetic efficiency (Fv/Fm), confocal imaging, integrated omics, qRT-PCR, and ATG8 protein immunoblotting.

Results: TOR inhibition via AZD8055 activated a specific regulatory cascade that included conserved autophagy markers (e.g., ATG8), VPS-driven vesicular transport, and SNF1 signaling, while suppressing PKA pathways. Molecular assays and fluorescent microscopy verified autophagic vesicle formation. Omics analyses showed that TOR attenuation causes distinct metabolic shifts, including reduced Fv/Fm, increased amino acid breakdown, and lipid restructuring, distinct from classical nitrogen starvation responses.

Conclusion: TOR inhibition orchestrates autophagy as a core node balancing energy management and metabolic adaptation in *P. kessleri* iCABeR21. These insights deepen our understanding of microalgal stress biology and highlight potential targets for metabolic engineering.

Keywords: Microalgae, Autophagy, TOR signaling, Omics, Metabolic reprogramming

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Engineering synthetic phycospheres for paracetamol mineralisation using microalgae as a biosensor

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Abstract

Pharmaceuticals such as paracetamol are detected at ecotoxicologically relevant concentrations in wastewater worldwide, yet conventional treatment systems achieve inconsistent removal. Synthetic microbial communities offer a promising detoxification route, with microalgae serving as both a carbon sink for mineralisation-derived CO₂ and a real-time indicator of community performance via chlorophyll *a* fluorescence. The CO₂ dependence of photoautotrophs can be exploited in gas-tight cultivation systems to enable high-throughput screening of bacterial pollutant mineralisers, identifying co-culture members that effectively convert pollutant carbon to biomass under varied conditions. Importantly, this sensor differentiates pollutant mineralisation from incomplete degradation, which yields toxic intermediates.

Using this approach, 59 bacterial isolates enriched from activated sludge were screened alongside the green alga, *Coelastrella terrestris*, with paracetamol and its toxic degradation intermediates as selective carbon sources. After linking algal growth with bacterial paracetamol degradation using HPLC, growth-promoting bacterial candidates were combined into 63 unique synthetic phycospheres and grown in paracetamol at concentrations ranging from 200 to 700 mg L⁻¹ to evaluate consortium mineralisation performance under substrate stress. A global concentration-dependent effect was identified, with mean algal growth scores declining by over 50% above 300 mg L⁻¹, indicating reduced mineralisation performance in these conditions. A *Pseudomonas* isolate showed the sharpest response, shifting from strongly growth-promoting to inhibitory above this concentration threshold.

Scale-up experiments revealed that aeration and paracetamol concentration correlated with accumulation of humic-like, non-extractable brown residues implicated in algal growth inhibition, highlighting the need to control intermediate persistence as a key design criterion for synthetic phycospheres targeting pharmaceutical-contaminated wastewater.

Keywords: Phycosphere, consortia, mineralisation, screening

Solar butanol production by solid-state photosynthetic cell factories

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Abstract

Biomass, a byproduct of natural photosynthesis, has been explored for its potential conversion into energy carriers, particularly biofuels. However, acknowledging the long-term limitations in biomass supply, as highlighted by the European Commission in the EU Bioeconomy Strategy Progress Report (2022), there is an urgent need for the development of advanced bioinspired technologies that mimic nature but exhibit higher efficiency. The Solar to Butanol (S2B) project aims to unlock the potential of photosynthetic microbes for the direct conversion of solar energy and CO₂ into butanol by employing innovative concepts and approaches. Specifically, S2B will transfer the microbial production from conventional suspension cultivation to a tailored solid-state biocatalytic platform, as previously demonstrated for other production platform (1,2). In this platform, engineered thin-layer assemblies of cyanobacteria and bio-based matrix materials will synergistically enable the redistribution of cell resources, such as energy and carbon flows, towards butanol formation. Simultaneously, S2B will improve photosynthetic efficiency by engineering the light reactions, optimizing light management and CO₂ capture. Consequently, the primary technological innovation of S2B will be the continuous, long-term direct solar butanol production by photosynthetic cell factories acting as biocatalysts. The process will be integrated with waste effluent and direct air capture, covering the entire value chain from light harvesting and CO₂ capture to product separation through the circular economy concept. Acting as a multidisciplinary consortium, S2B will construct a TRL4-level prototype, paving the way for a smooth upscaling process.

Keywords: *photosynthesis, synthetic biology, bioproduction, cyanobacteria*

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Discover, understand, engineer: Integrating random mutagenesis and genome editing for industrial microalgal strain development

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Abstract

Microalgae are promising platforms for biobased fuel and high-value lipid production, yet developing strains with robust, industrially relevant performance remains a key bottleneck. While genome editing enables precise metabolic engineering of microalgae, the industrial use of the resulting strains may entail additional regulatory and biosafety considerations. In this context, random mutagenesis remains a relevant strategy to explore genetic diversity and generate strains with complex industrially relevant traits.

This talk will present research from two projects showing how random mutagenesis can contribute to both strain development and a deeper understanding of microalgal lipid metabolism. In the EU project ALGAESOL, random mutagenesis coupled with high-throughput screening generated *Chlorella sorokiniana* mutants for lipid-based sustainable aviation fuel. Candidate strains were evaluated for neutral lipid productivity under trophic conditions relevant to pilot-scale cultivation, highlighting the importance of optimizing strain performance under application-relevant conditions.

Building on this pipeline, the RCN project SafePhaeO3 integrates random mutagenesis with targeted gene editing to enhance omega-3 fatty acid production in *Phaeodactylum tricornutum* and *Nannochloropsis oculata*. Beyond generating promising non-GMO strains ready for validation under industrial settings, mutant libraries provide multi-omics data for AI-driven analysis of regulatory networks underlying omega-3 metabolism and for identifying potential targets for precision engineering. Together, these approaches connect genetic diversity, biological understanding, and precision engineering to accelerate the development of industrially relevant microalgal strains.

Keywords: *Random mutagenesis, microalgal genome editing, lipid production*

Developing microfluidic screening of algal-bacterial consortia & other tools towards making soil bioremediation a reality

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Abstract

Environmental organic pollutants are often biodegraded by co-located bacterial strains. Utilising microbial consortia¹ rather than single strain systems to carry out this process: spreads the metabolic burden of the breakdown pathway; increases resistance of the system to perturbations; and increases the efficiency of biodegradation by cycling other key nutrients². Including algae in these consortia has further advantages², including: conversion of CO₂ produced by biodegradation into valuable algae biomass; provision of O₂ and organic carbon to the bacterial strains; providing an easy detection method for the mineralisation of the target compound to CO₂. However, traditional environmental microbial isolation methods miss potentially useful strains that are “unculturable”, or inseparable from dependent cooperative relationships with other strains.

We are developing a microfluidic droplet-based³ screening pipeline for isolating functional microbial consortia capable of bioremediation of a range of test compounds (VOCs, PAHs, triazines), including combinations that would likely be missed by traditional isolation/screening methods. We are also developing microfluidic, aero-aquatic, and solid substrate test systems for investigating the bioremediation process in environments closer to those found in soil or water.

We have identified a number of interesting individual strains and consortia which show evidence of breaking down some of our target chemicals (melamine, naphthalene) and have made good progress towards developing the microfluidic screening pipeline, as well as using our other techniques in conjunction with a plant germination experiment, to demonstrate the ability of one of our consortia to breakdown phytotoxic chemicals (phenol, melamine).

Keywords: *Consortia, Bacteria, Microfluidics, Bioremediation, Biodegradation*

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Exploring *Nannochloropsis oceanica* as a host for the expression of olivetolic acid biosynthetic pathway

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Abstract

Cannabinoids are meroterpenoids found in *Cannabis sativa* that have gained significant attention over the last decades, with several compounds, including CBG, THC, and CBD, being extensively studied as potential therapeutics for treating symptoms associated with conditions such as multiple sclerosis, refractory epilepsy, and chronic pain. On the other hand, the marine microalga *Nannochloropsis* has shown potential for metabolic engineering and scale-up due to its mild growth requirements, high productivity, episome receptivity, and strong capacity for foreign gene expression. Moreover, its naturally oleogenic metabolism could be repurposed to enhance recombinant cannabinoids production, while its marine nature can help reduce freshwater use in industrial applications. In this study we evaluate *Nannochloropsis oceanica* as a host for the expression of olivetolic acid synthase (OLS) and olivetolic acid cyclase (OAC), key enzymes in the biosynthesis of olivetolic acid, a cannabinoid precursor with antimicrobial properties. To establish this pathway, OLS and OAC were introduced into the genome individually and as a fused chimeric construct (OLS–OAC) through random integration via non-homologous end joining. Transformed strains were successfully selected and gene integration was verified by colony PCR. Protein expression was detected by Western blot and further confirmed by mass spectrometry for both expression strategies. Then, *in vivo* and *in vitro* functionality of the enzymes was assessed by HPLC-UV using direct ethanolic extracts and enzymatic assays, respectively. With this work, we aim to highlight the potential of *Nannochloropsis* as a host for the sustainable production of plant-derived enzymes, with broader applications in cannabinoid biosynthesis and environmentally friendly industrial processes.

Keywords: Synthetic Biology, Cannabinoids, *Nannochloropsis*, Olivetolic acid

Development of acid-tolerant *Chlorella* spp. and cold-tolerant *Limnospira* spp. (Spirulina) for resilient industrial cultivation

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Abstract

Industrial microalgal cultivation is highly constrained by factors such as biological contamination and seasonal temperature variation, and strain traits and tolerances strongly influence cultivation success. Development of acid-tolerant *Chlorella* spp. could reduce contamination risk during mixotrophic cultivation, while cold-tolerant *Limnospira* spp. (Spirulina) could extend the cultivation season in outdoor raceway ponds. Two strain-development pipelines are being established to select and adapt strains that address these challenges and are more robust for industrial cultivation.

Five *Chlorella* strains were screened across a range of acidic conditions and showed strain-level variation in low-pH performance. Strain NIVA-CHL 108 (*Chlorella vulgaris*) grew faster than the other strains at pH 4.4–4.5 and was advanced through stepwise laboratory adaptation and colony selection on agar prepared at pH 3.9. Colony-derived candidate lines were recovered in liquid medium at pH 5.1 and continued to accumulate biomass as the ammonium-based medium acidified below pH 4.0. The growth kinetics of these laboratory-adapted cell lines are being compared with those of the parental strain as part of ongoing work aimed at developing low-pH mixotrophic *Chlorella* cultivation.

A panel of 14 *Limnospira* strains is being evaluated for growth at low temperature by comparing maximum specific growth rates at 12°C and 20°C. Preliminary experiments indicate strain-level variation. Growth data are being integrated with biochemical, morphological, and genetic characterization to understand variation in low-temperature tolerance and other industrially relevant traits, including protein and phycocyanin content, within the genus *Limnospira*.

Together, this work is establishing laboratory pipelines for selecting and developing microalgal strains with enhanced industrial potential, including acid-tolerant *Chlorella* spp. and cold-tolerant *Limnospira* spp.

Keywords: *Chlorella*, *Limnospira*, *Spirulina*, strain development, industrial applications

INNOAQUA: Integrating salmon and microalgae cultivation at pilot scale

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Abstract

The European Green Deal has recognized aquaculture and algae as promising solutions to achieving the goals of the Farm-to-Fork Strategy. However, despite its potential, the growth of aquaculture in Europe has been limited compared to the significant expansion observed in Asia. The EU-funded INNOAQUA project aims to pave the path towards the upcoming sustainable and diversified EU land-based aquaculture industry. The project will demonstrate the benefits of algae, from the production in combination with fish aquaculture in a circular approach, to the formulation and production of innovative seafood products.

In this context, we developed an integrated Salmon-microalgae production unit at pilot-scale, by connecting a 25 L tubular photobioreactor to a 2500 L RAS (recirculating aquaculture system). Microalgae were cultivated in perfusion mode alongside the fish, by continuously feeding filtered RAS water into the bioreactor, while nutrient depleted water was continuously removed and the microalgal cells were retained in the reactor through membrane filtration. We could show that by altering the process design and conditions, both high microalgal productivities and full removal of nitrate and phosphate from the RAS water could be achieved. Furthermore, bacterial abundances and community composition as well as full elemental composition and concentrations were analyzed from the RAS water, the microalgal culture broth and the microalgal effluent water, and the microalgal biomass composition was analyzed to further evaluate the impact of RAS water on the microalgae.

Keywords: *Aquaculture, RAS (recirculating aquaculture system), microalgae, perfusion cultivation, nutrient removal*

LOCALITY: Coupling waste-stream valorization with microalgae cultivation for nature-positive, circular products

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Abstract

LOCALITY is a Horizon Europe project turning waste streams from greenhouse, fish, and textile industries around the North and Baltic Seas into feedstocks for nature-positive, circular algae-based products. These waste streams were characterized and screened as cultivation media for a diverse panel of NORCCA microalgae strains, and the most promising strain-waste combinations are now being upscaled from laboratory to pilot scale. Seaweed producers were engaged as an added ecosystem service, harvesting 123 kg of biomass in North and Baltic Sea waters for downstream valorization. Biorefinery pipelines were established for both microalgae and seaweed biomass, and the resulting ingredients were tested for their nutritional, functional, and structural properties, leading to prototype products successfully developed and validated across the food, aquafeed, agriculture, and textile sectors. Cultivation was demonstrated across every waste stream tested, with set-ups progressing steadily through upscaling, and industrial synergies among R&D partners, industry, and SMEs proved central to building these resource-circulating production ecosystems. With a market-oriented approach, the project is now addressing consumer perception, regulatory compliance, and technological barriers, and recommendations are being drafted to support successful European market entry. Together, these results show that coupling waste valorization with algae biotechnology offers a robust route to nature-positive, circular products, positioning LOCALITY to help accelerate Europe's transition toward a sustainable bioeconomy.

Keywords: *microalgae, circular economy, waste valorization, nature-positive products*

Microalgal biomanufacturing for defence and resilience: from the International Space Station to a strategic logistics capability for the NATO alliance

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Abstract

Microalgae are emerging as a strategic dual-use biotechnology capable of producing fuels, nutrition, and bio-materials in decentralized, resource-limited environments. Unlike conventional supply chains, which remain vulnerable to disruption, interdiction, and adversarial interference, microalgal production systems require only sunlight, CO₂, and minimal nutrient inputs, enabling self-sufficient, on-demand bioproduction independent of long, fragile logistics networks. This makes microalgae a unique powerful platform for building operational resilience and strategic autonomy in remote, contested, or resource-constrained environments. Having demonstrated successful microalgal cultivation aboard the International Space Station using a compact, deployable bioreactor, this flight-proven capability is directly transferable to forward operating bases, Arctic installations, naval platforms, and other austere military settings where resupply is limited or contested. As Europe and NATO increasingly identify biotechnology as a critical enabler of strategic autonomy, microalgal bioproduction offers a concrete pathway toward biotechnological sovereignty, reducing dependence on geographically concentrated and potentially adversarial supply chains for fuels, nutrition, precursors, pharmaceuticals, and specialty materials. This talk presents the scientific and technological foundations of microalgal biomanufacturing as a self-sufficient, defence relevant capability, covering strain physiology, robust cultivation strategies, and target compound classes most applicable to sustained military operations, including field nutrition, performance enhancers, bio-materials, and biosensing. Biosecurity and dual-use considerations inherent to distributed biological production are also discussed. By linking fundamental microalgal biology to the imperatives of self-sufficiency and resilience, this contribution highlights microalgae's untapped potential to strengthen NATO's and the EU's technological autonomy and long-term supply chain security.

Keywords: *Biomanufacturing, Resilience, Biotechnological sovereignty, Defence*

Valorising salmon RAS water through laboratory screening of marine microalgae

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Abstract

Introduction: Land-based recirculating aquaculture systems (RAS) generate nutrient-rich effluents requiring costly management before discharge. Marine microalgae can convert dissolved nutrients into valuable biomass, supporting circular valorisation of aquaculture waste streams.

Methods: Within SEAlgaePower (www.sealgaepower.eu) eleven microalgal and cyanobacterial strains from the North Sea and Mediterranean Sea were screened in brackish salmon RAS water from SmögenLax. Initial screening in 13 psu RAS water identified the six strongest growers: *Nannochloropsis granulata*, *Chlorella* sp., *Chlorella ovalis*, *Phaeodactylum tricornutum*, *Quadricoccus euryhalinus*, and *Dunaliella tertiolecta*. These species were scaled up to benchtop multicultivator photobioreactors to monitor growth, nutrient uptake, biomass production, and accumulation of compounds of interest under optimized conditions.

Results: The selected species were robust in RAS water and achieved complete nitrate and phosphate removal under the tested conditions. Amino acid and fatty acid profiles determined during exponential growth and nutrient-limited phases led to the identification of two high-performing strains for protein- and lipid-rich biomass production.

Conclusion: These results demonstrate the potential of North Sea and Mediterranean microalgae to combine RAS effluent bioremediation with biomass production for future algae-based ingredients. The best-performing strains will be further optimized for pilot-scale cultivation within SEAlgaePower.

Keywords: seafood aquaculture, bioremediation, marine microalgae, microalgae ingredients, waste streams.

Leveraging industrial symbiosis for microalgae production: strain selection and upscaled growth on Norwegian seafood-processing side streams

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Introduction. Norway is Europe's largest aquaculture producer, generating nutrient-rich wastewater from land-based farming and seafood processing. Microalgae cultivation offers a sustainable approach for nutrient recovery and biomass production.

Methods. Two side streams from the local seafood processing industry were characterized physicochemically at different stages of the production process, from processing residues to the final wastewater discharge; Aqua-2024-06 was selected for its higher nutrient content. Twenty-four *Chlorella* sp. strains from the NORCCA collection were screened, and the three best performers were scaled up in 1 L, with one advancing to 5 L flasks, before validation in a 25 L tubular photobioreactor (PBR) under continuous pH control (pH 8) and LED illumination (~200 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$).

Results. *Chlorella vulgaris* NIVA-CHL 123, NIVA-CHL 108, and *Tetrademus* sp. NIVA-CHL 81 showed the highest and most consistent growth in Aqua-2024-06 during screening, achieving μ_{max} of 0.30–0.38 day^{-1} , exceeding Z8 controls (0.20–0.28 day^{-1}). Among them, NIVA-CHL 123 reached the highest final OD_{750} (~1.75) in Aqua-2024-06 during 1 L flask scale-up and was selected for cultivation in the 25 L PBR, where biomass concentration increased from approximately 0.15 to 1.20 $\text{g}\cdot\text{L}^{-1}$, reaching a maximum productivity of 0.55 $\text{g}\cdot\text{L}^{-1}\cdot\text{day}^{-1}$. Cultivation of NIVA-CHL 123 in Aqua-2024-06 reduced total nitrogen by 94% and total phosphorus by 96%, while the harvested biomass contained 42.3% protein, 21.9% carbohydrates, and 24.8% lipids.

Conclusion. These findings demonstrate that seafood processing side streams can support robust microalgae cultivation, wastewater treatment, and protein-rich biomass production, highlighting potential for circular bioeconomy applications.

Keywords: microalgae; aquaculture side streams; circular bioeconomy; *Chlorella vulgaris*

Future Materials from Large-scale Processing of Sustainable Brown Algae Resources

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Abstract

Brown algae is an abundant biomass worldwide and can contribute greatly to the current and future need for more sustainable feedstocks due to their high productivity and low environmental impact. Whereas wild brown algae are highly valued resources for a variety of applications, there are still challenges in fully utilizing all parts of the biomass. At the same time, seaweed cultivation is still at an early stage in Europe due to high production costs and a lack of developed markets requesting large biomass volumes – highlighting a large, unrealized potential.

The presentation provides an overview of brown algal resources in Europe and their uses, before addressing current research challenges tied to expanded biomass production, processing, and utilization. Ongoing research at SINTEF provides examples of novel large-volume applications of underutilized algal biomasses that can contribute to reduced use of today's non-sustainable fossil- and bio-based resources and to increased value creation in the European Blue Bioeconomy, including uses in packaging materials, textile fibres, and biostimulants for agriculture. The research shows key hurdles and bottlenecks to be addressed along the value chain, as well as the opportunities through transnational and cross-disciplinary collaboration.

Keywords: *brown algae, seaweed, biorefinery, alginate*

Beyond extraction: From algal biorefinery to fish performance

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Abstract

Microalgae offer proteins, lipids and bioactive compounds with potential to diversify aquafeed raw materials. Yet their value is often constrained by cellular structures that limit nutrient accessibility. Effective valorisation therefore requires linking biomass-specific processing with ingredient functionality and, ultimately, biological performance in fish.

A series of studies evaluated physical processing strategies for different microalgal biomasses and their subsequent application in Atlantic salmon nutrition. Processing of different microalgal biomasses included pulsed electric fields (PEF), and optimisation of bead milling using central composite design. Selected processed biomasses were subsequently evaluated through digestibility and feeding trials.

Disruption efficiency was strongly biomass dependent, with no single combination of bead-milling parameters optimal across species. Cell disruption enhanced the accessibility of intracellular compounds and affected downstream properties. However, improved disruption did not consistently translate into improved nutritional performance. Feeding studies with different algal biomasses showed responses ranging from reduced feed intake and nutrient utilisation to successful replacement of marine lipid sources without impaired growth. Effects on tissue nutrient deposition, sensory characteristics and immune responses further demonstrated that the nutritional value of algae-derived ingredients extends beyond their gross nutrient composition.

Together, these studies demonstrate that cell-disruption or extraction efficiency alone is not a sufficient indicator of the nutritional value of an algal ingredient. Processing strategies need to be adapted to the characteristics of each biomass and, importantly, to its intended application. Integrating process optimisation, feed functionality and fish responses can help identify when biorefinery improves the value of microalgae for aquafeeds, and when it does not.

Keywords: *microalgae, biorefinery, cell disruption, aquafeed, Atlantic salmon*

Integrating diatom valorisation: sequential deep eutectic solvent recovery of frustules and bioactive compounds

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Abstract

Diatoms package an extraordinary range of high-value products inside a single cell: omega-3 lipids, pigments, proteins, carbohydrates, and an intricate silica shell, the frustule. Conventional processing captures only one of these and sacrifices the rest, discarding most of the biomass and clashing with circular bioeconomy principles. We present a sequential deep eutectic solvent (DES) biorefinery that recovers the frustule alongside the organic fractions in a single integrated workflow, with each step preserving the value of the next. While DES have been shown to separate individual diatom products such as pigments and biosilica [1], a unified cascade that sequentially recovers carbohydrates, proteins, lipids, and intact frustules from the same biomass has not been demonstrated. The cascade begins with a mild aqueous pre-extraction for soluble carbohydrates, followed by a hydrophilic DES (choline chloride with glycerol or ethylene glycol, 70 °C, 1.5 to 3 h) that opens the cell and releases polar lipids, proteins, and pigments without harsh pretreatment. A hydrophobic DES or hexane partition then recovers neutral lipids and remaining pigments, with the aim of leaving the silica frustule structurally intact. Initial screening across a range of DES types, extraction times, and partition solvents is underway to identify the conditions that best balance fraction yield against frustule preservation. By treating every fraction as a product rather than a trade-off, the approach reframes diatom processing from a zero-sum extraction problem into the parallel recovery of complementary, high-value materials.

Keywords: *diatoms, biorefinery, deep eutectic solvents, frustules, multi-stream products*

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Catalytic membrane technology to convert microalgae in growth medium into biofuels

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Abstract

Microalgae are promising renewable feedstocks for sustainable fuels, but conventional harvesting and dewatering substantially increase process energy demand and cost. This study presents a plate catalytic membrane reactor technology (PCMR) for direct conversion of *Nannochloropsis Oculata* in its growth medium under mild conditions, integrating catalytic reaction and in-situ separation within a compact membrane-based system. The catalyst was first synthesized in powder form by a modified single-step sol-gel method and showed 96% algae conversion performance at 80°C and 1 atm. For the three-cell PCMR configuration, 5×5 cm membranes coated with 5 mg catalyst per membrane were operated in series at 80 °C and 1 atm using microalgae paste containing 6-7 wt% dry biomass. The experimentally determined dry-weight-based conversion reached 21.1%>, whereas blank experiments without catalyst gave <4% conversion. LC analysis of the permeate confirmed selective transfer of polar products, including glucose (1088.33 ppm), glycerol (421.48 ppm), succinic acid (380.98 ppm), acetic acid (169.41 ppm), D-fructose (158.15 ppm), formic acid (44.83 ppm), and sucrose (36.49 ppm). GC-MS analysis of the retentate identified predominantly non-polar fuel-range compounds, including branched and linear hydrocarbons and fatty-acid derivatives. Major quantified products included 2,6,10-trimethyltetradecane (21.62%), heptadecane (20.10%), isopropyl myristate (17.24%), 10-methyleicosane (11.84%), 7-hexyleicosane (10.58%) and tetradecane (8.76%). These results demonstrate simultaneous microalgal conversion and fractionation of polar and non-polar products, supporting PCMR as a promising route toward continuous biofuel production without energy-intensive harvesting and dewatering. The modular design enables scale-out operation and provides a pathway for further optimization through increased catalytic membrane surface area.

Keywords: Biofuel, Microalgae, SAF, Oculata, Biorefinery

Feeding the bloom: photophysiological responses of plankton to changing nutrient supply in Mediterranean and Norwegian coastal mesocosms

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Abstract

Human activities are altering coastal and ocean nutrient supply in both quantity and stoichiometry, from aquaculture waste inputs to projected shifts towards lower N:P ratios in a future Atlantic Ocean. Detecting how phytoplankton respond physiologically, and separating stress from community turnover, requires measurements at high temporal resolution. We used daily LabSTAF(single turnover activated fluorometry), alongside chlorophyll and nutrient measurements, to follow plankton communities in two mesocosm experiments. In an Eastern Mediterranean (Crete) experiment, nutrient addition mimicking aquaculture waste was combined with zooplankton predator removal and alkalinity enhancement treatments. Following enrichment, F_v/F_m , light-limited efficiency (α) and electron transport (JVPIIm) rose together into a bloom-like peak around days 3-4, then declined as nutrients were drawn down, while the saturation irradiance (E_k) fell, consistent with increasing self-shading. Alkalinity had little effect, whereas the zooplankton removal later maintained higher efficiency and a lower functional absorption cross-section (σ_{PSII}), suggesting a grazing-mediated community change. We will compare these responses with a factorial mesocosm experiment in Bergen manipulating N:P ratios and temperature, asking which photophysiological parameters respond consistently to the quantity and stoichiometry of nutrient supply across different ecosystems. We discuss how FRRf can complement chlorophyll and nutrient data as a rapid indicator of phytoplankton responses to nutrient change.

Sustainable production and valorisation of *Porphyridium cruentum* for functional food and agricultural applications

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Abstract

The marine microalga *Porphyridium cruentum* holds substantial biotechnological potential for functional applications. This study establishes an integrated framework optimizing upstream culture conditions alongside comprehensive downstream biorefinery strategies to ensure sustainable production and full biomass valorization. Upstream optimization revealed that using sodium nitrate as a nitrogen source improved culture performance by 25–65%, while an N:P molar ratio of 20:1 increased biomass productivity by 24%. Respirometry assays determined the optimal cultivation parameters to be 31.2 °C and pH 7.7. Attempted medium recirculation for water conservation led to bacterial proliferation and accumulated extracellular organic matter, indicating a need for targeted pre-treatment due to increased viscosity and turbidity. To demonstrate food applications, the distinct mineral profile of the biomass was successfully utilized to formulate iron-enriched functional crackers.

For downstream processing, ultrasound-assisted cell disruption followed by pH-driven isoelectric solubilization and precipitation yielded a reagent-grade B-phycoerythrin-rich fraction for food coloring. The remaining insoluble fraction was valorized through two alternative routes: (i) a second isoelectric cycle produced a stable protein-rich emulsifier (pH 8) and a residual plant biostimulant that improved the seedling vigor index of *Cucumis sativus* by up to 58%, outperforming gibberellic acid; or (ii) enzymatic hydrolysis produced an antioxidant peptide-rich fraction, followed by pellet extraction to recover a chlorophyll-rich fraction with reducing capacity for liquid food matrices. Together, these strategies provide a scalable blueprint for a zero-waste *P. cruentum* biorefinery.

Keywords: biomass production, bioactive ingredients, functional foods, pigments, plant biostimulants.

Microalgae-assisted resource recovery and biomass production from Finnish dairy side-streams

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Abstract

Microalgae offer a sustainable feedstock for biotechnological applications, yet their cultivation requires substantial freshwater and nutrients. Utilizing nutrient-rich industrial effluents for microalgal production can reduce these inputs while simultaneously contributing to bioremediation, resource recovery and advancing the circular economy¹.

This study evaluates microalgal strains using side-streams from different production lines – including fresh milk, yogurt and cheese whey, supplied by Finland’s leading dairy producer. Preliminary screening using synthetic dairy wastewater demonstrated 3 candidates: *Scenedesmus* sp., *Tetradesmus* sp., and *Chlorella* sp. Although pre-treatment (e.g. filtration and heat) significantly reduced initial bacterial loads and enhanced nutrient availability, growth was higher in raw effluents. In raw effluent trials, strains demonstrated high removal efficiencies, achieving over 80% removal of chemical oxygen demand (COD), total nitrogen (TN) and phosphorus (TP) (~82% COD, ~92% TN, ~94% TP).

Tetradesmus sp. was selected as the most promising candidate for superior phosphorus removal and lower bacterial load. In semi-continuous cultivation, *Tetradesmus* sp. maintained stable growth and high nutrient removal across two hydraulic retention times (HRTs). However, growth declined during extended operation due to the continuous accumulation of fats, oils and grease (FOG), proteins, and background bacteria. To address this, enzymatic pre-treatment targeting FOG/protein was applied, which effectively broke down these complex organic fractions without compromising microalgal growth. Future studies will focus on microalgal–microbial consortia trials to sustain long-term cultivation under high FOG loads. Overall, these findings demonstrate both the feasibility and the bottlenecks of utilizing raw dairy side-streams for sustained microalgae production, with strategies needed to overcome operational limitations.

Keywords: *Microalgae, Industrial Side-Streams, Resource Recovery, Biomass Production, Dairy side-streams*

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Sustainable pilot-scale cultivation and valorisation of seawater-adapted *Chlorella sorokiniana* for functional food applications

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Abstract

The microalga *Chlorella sorokiniana* is a highly nutritious candidate for functional food production; however, conventional cultivation methods impose a heavy burden on freshwater resources. This study evaluates a comprehensive, sustainable production strategy spanning from seawater adaptation to final biomass valorization. Initially, laboratory-scale optimization successfully reduced nutrient requirements by 85%. While the reutilization of exhausted culture medium (30–70%) led to decreased productivity, adaptive laboratory evolution was effectively deployed to gradually transition *C. sorokiniana* to seawater. This adaptation triggered distinct morphological and biochemical shifts, altering amino acid, fatty acid, and volatile profiles while enhancing pigment accumulation.

At a pilot scale utilizing 3.5 m³ tubular photobioreactors, seawater cultivation demonstrated superior robustness, significantly delaying biofouling formation from 17 to 37 days. Metagenomic analyses confirmed a favorable shift in microbial communities and a notable reduction in contaminants. To ensure culture purity, an AI-based system utilizing deep learning models was trained to distinguish *C. sorokiniana* from biological contaminants, achieving an outstanding classification accuracy (R²=0.98). Downstream processing was further improved by optimizing mechanical cell disruption to minimize specific energy consumption. Finally, the resulting biomass extracts exhibited potent antioxidant and antimicrobial activities, alongside strong biostimulant activity in agricultural applications, where they favorably modulated rhizosphere microbial populations. Overall, these findings establish a robust, circular, and sustainable framework for utilizing seawater-grown *C. sorokiniana* in high-value commercial sectors.

Keywords: *biomass production, contamination control, bioactive ingredients, functional foods, plant biostimulants.*

Environmental Drivers of Phlorotannin Variability in the Macroalga *Alaria esculenta* (Phaeophyceae)

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Abstract

Brown macroalgae contain a great variety of unique polyphenolic compounds, the phlorotannins, which are based on phloroglucinol subunits. The polyphenolic compounds possess numerous biological functions, ranging from eco-physiological response to environmental stress and structural cell integrity to novel biotechnological applications.

While algae of the taxonomic order Fucales are characterised by high phlorotannin contents, Laminariales are generally known for their low concentrations. However, *Alaria esculenta* from Northern Norway, a member of the Laminariales, seems to be an exemption. It demonstrated a significant variability in its phlorotannin contents and associated antioxidant performance. This presentation compiles results from several integrated projects. First, we examine the spatial and temporal differences in phlorotannin levels and antioxidant capacities across wild-grown populations and seasons in Northern Norway. Second, given the commercial importance of *A. esculenta* to the Norwegian aquaculture industry, we present data from professional cultivation sites near Bodø to understand eco-physiological stress responses and optimize harvest timing. Finally, laboratory stress experiments were conducted to identify the primary environmental drivers such as irradiance, UV radiation, salinity, and temperature that trigger phlorotannin accumulation.

This research provides a better understanding of the previously unexpected variability of phlorotannins in *A. esculenta*. These insights are not only of ecological interest regarding the alga's stress management in its natural habitat but also play a critical role in the commercial production of phlorotannins and the blue economic development of Northern Norway.

Keywords: Brown Macroalgae, Marine Polyphenols, Abiotic Stress, Kelp Cultivation, Bioactive Compounds

Environmental and Carbon Performance of Sargassum-based Bio-construction Materials: A Screening Life Cycle Assessment of Alternative Valorization Pathways

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Abstract

The increasing occurrence of large-scale Sargassum beaching events has become a significant environmental and waste management challenge along the Tropical Atlantic and the Caribbean coastline. Although removing stranded Sargassum is necessary to protect coastal ecosystems, tourism, and local communities, the subsequent management of the collected biomass remains a major challenge. This study evaluates the environmental and carbon performance of three alternative Sargassum management pathways using a screening Life Cycle Assessment (LCA). Three selected scenarios can be identify as landfill disposal, compost production, and the manufacture of Sargassum-based bio-bricks. A functional unit of 1000 kg of wet Sargassum collected from the beach and a cradle-to-gate system boundary were applied. The assessment was conducted using openLCA with the ecoinvent 3.12 database and the ReCiPe 2016 Hierarchist midpoint method. Due to limited Sargassum-specific inventory data, literature-based assumptions and suitable proxy datasets were used to develop the foreground inventory. The results indicate clear environmental trade-offs between the three pathways. Landfill disposal showed the highest climate change impact (494.8 kg CO₂-eq), primarily due to methane emissions, while the bio-brick pathway recorded the lowest climate change impact (197.8 kg CO₂-eq) with drying electricity, Portland cement production, and collection and transport contributing in roughly comparable measure. Composting pathway showed intermediate climate change (294.2 kg CO₂-eq) and highest acidification (4.17 kg SO₂-eq) and ozone depletion impact. The findings demonstrate that Sargassum valorization does not inherently guarantee lower environmental impacts across all categories, and highlight the importance of multi-category, life cycle-based assessment when developing sustainable management strategies for Sargassum.

Keywords: *Sargassum, Algae Biomass Valorization, Life Cycle Assessment, Circular Economy, Climate Change*

Cyanobacterial carbon capture at inhibitory high CO₂ concentrations

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Abstract

Photosynthetic microbes are often cultivated under CO₂ concentrations elevated above air level to promote growth. Very high CO₂ levels, however, inhibit growth, which limits the usability of cyanobacteria for carbon capture from industrial CO₂ point sources and biotechnological applications. To better understand why cyanobacteria cannot utilize the elevated CO₂ intake we cultivated the cyanobacterium *Synechococcus* sp. PCC 7002 at varying growth rates governed by different gas-phase CO₂ levels. Compared to optimal growth (4-8%), we observed large differences of the transcriptome in growth-inhibiting 30% CO₂ [1], including strong down-regulation of genes encoding CO₂ uptake mechanisms, photosynthetic electron transfer, and light-harvesting antennae proteins. The most strongly up-regulated genes were associated with stress responses but did not closely resemble any of the previously studied stresses. A number of RNA regulators, such as 6S RNA and PsrR1, were markedly higher expressed under 30% CO₂, and might be involved in the adaptation to very high CO₂. Genetic knockdown of CO₂ uptake or overexpression of a heterologous Na⁺/H⁺ antiporter improved tolerance to high CO₂ [2]. In a complementary study, we identified genes that directly impact cell growth at very high CO₂ by a CRISPR interference mutant library in the related *Synechocystis* sp. PCC 6803 [3]. Based on our data at high CO₂-stress, I will discuss how its integration with publicly available data at other physiological stresses will improve the analysis of gene regulation and carbon fluxes to support sophisticated design of cyanobacterial cell factories.

Keywords: cyanobacteria, carbon capture, transcriptomics, CRISPR, environmental stress

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The power of Dynamical Darwinian Selection to enhance strain performance

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Abstract:

The natural production of astaxanthin by *Haematococcus pluvialis* represents a dynamic and promising market. Unfortunately, current production technologies are hampered by the physiological limits of wild-type strains, which are ill-suited for intensive cultivation, resulting in too high sales costs. While severe environmental stress can push certain *H. pluvialis* strains to accumulate astaxanthin up to 5% of their dry weight, it is therefore essential to go further and to develop a strain with significant higher astaxanthine content for productivity improvements.

To overcome these barriers, DareWin Evolution, supported by a decade of academic research in collaboration with Inria, CNRS, and Sorbonne University, has developed advanced strain selection methodologies. Enhancing Darwinian selection theory by integrating mathematical modelling to trigger dynamic stresses, DareWin Evolution optimizes microalgal performance using advanced closed-loop control directly within photobioreactors. In this setup, individuals capable of better adaptation, typically those exhibiting enhanced traits of interest, gradually emerge, dominate, and persist.

DareWin Evolution has successfully implemented this protocol across various microalgal species, achieving substantial biochemical improvements: +24% DHA in heterotrophic algae, +57% EPA in autotrophic algae, or a 31% productivity increase in Cyanobacteria. Recently, our selection toolbox was applied to a wild-type *H. pluvialis* strain. Within approximately six months, the astaxanthin content significantly increased during the maturation phase (+37%) reaching 6.3% of dry weight. Given that astaxanthin accumulation is intimately linked to lipid storage during stress adaptation these results, achieved without prior optimization of the culturing and maturation method, demonstrate the immense potential of dynamic directed evolution.

Keywords: Strain selection, Strain improvement, Astaxanthin, Dynamic Darwinian selection

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Use of the volatile organic compound 2,3-butanediol as an inducer of biomolecules in the microalgae *Neochloris oleoabundans*

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Abstract

Microalgae such as *Neochloris oleoabundans* represent key biotechnological platforms due to their capability to accumulate high-value compounds, including proteins and carbohydrates, essential for cellular growth, structure and energy storage¹. Volatile organic compounds (VOCs), such as 2,3-butanediol, are promising tools for modulating cellular metabolism². This study evaluated the effect of different 2,3-butanediol concentrations on the growth kinetics and biomolecule content of *N. oleoabundans*.

Cultures were established in batch bioreactors under controlled conditions. Growth was monitored by optical density at 540 nm and chlorophyll measurements to identify the exponential phase. During this phase, cultures were assigned to non-induced controls (a basal control with Bold medium alone and a 0.05% v/v polysorbate 80 solution control) and three induction treatments with 2,3-butanediol 100, 150, and 200 ng/mL dissolved in polysorbate 80 solution. At 0, 24, 48 and 72 h after induction, protein and carbohydrate contents were determined using the Lowry and Dubois methods, respectively.

All VOC treatments exceeded the optical density of both controls at 72 h. A dose-dependent response was observed, with increasing 2,3-butanediol concentrations promoting growth, and protein and carbohydrate accumulation. The highest growth was observed at 200 ng/mL, while the highest protein content was obtained at 150 ng/mL at 24 h.

In conclusion, these findings highlight the potential of 2,3-butanediol as a metabolic inducer for enhancing growth and biomolecule accumulation in *N. oleoabundans*. Furthermore, they provide a basis for future studies on the expression of phytohormone-related genes in this species.

Keywords: *Neochloris oleoabundans*, volatile organic compound, 2,3-butanediol, biomolecules

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Engineering cell aggregation and carotenoid accumulation in *Chlamydomonas reinhardtii* for sustainable food production

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Abstract

Microalgae are packed with essential nutrients and can be grown on waste streams, making them attractive food sources in an increasingly unstable climate with growing global food demand. The model green microalga *Chlamydomonas reinhardtii* is naturally rich in bioactive compounds, including carotenoid pigments and extracellular polysaccharides (EPS) that can support gut health. Its well-characterised genome and growing repertoire of synthetic biology tools make it a useful model for metabolic engineering to boost its nutritional output while optimising its growth characteristics. Moreover, its GRAS status and recent recognition as a novel food product by the European Commission present a promising avenue for commercial applications.

We are applying synthetic biology strategies in *C. reinhardtii* to both improve the production of key metabolites for human health and optimise growth in a custom bioreactor on food waste streams. We have knocked out the DYRKP kinase gene, producing an aggregating phenotype with increased EPS, and are characterising fasciclin-associated (FAS) genes implicated in cell aggregation and carotenoid accumulation. Overexpression lines have been generated, and a FAS3 knockout is pale green, slower-growing, and fails to aggregate under high light unlike its parental strain, suggesting roles in cell aggregation, photoprotection and pigment accumulation. Further work targeting cell adhesion, EPS production, and carotenoid biosynthesis is ongoing to generate a stacked strain for improved bioreactor growth and nutritional value. Resulting strains will be assessed by our collaborators for growth performance, nutrient profiles, and effects on gut health using *in vitro* digestion experiments.

Keywords: *Chlamydomonas reinhardtii*, synthetic biology, functional foods, carotenoids, cell aggregation

Effects of nitrogen and phosphorus stress on nutrient removal and exopolysaccharide production by *Limnospira indica*

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Abstract

Introduction: Microalgae offer a promising approach to wastewater treatment through active assimilation of nitrogen and phosphorus. Inducing nutrient stress to biomass can improve resource recovery by stimulating cellular responses that enhance nutrient uptake and exopolysaccharide (EPS) production. EPS are valuable bioproducts with rheological and biological properties relevant to diverse industrial applications sectors.

Materials and methods: *Limnospira indica* (PCC8005) was cultivated in Zarrouk's medium under controlled batch conditions. Medium variants with graded nitrogen and phosphorus limitation and a standard control were tested. Biomass and nutrient concentrations were monitored daily. Released and biomass-bound EPS were quantified initially and at the end of exponential growth phase.

Results: Under standard conditions, nutrient removal was limited, with 17% nitrate and 5% phosphate removed after 14 days. Nitrogen stress improved nitrate depletion, reaching 99% under moderate and strong N limitations within 14 and 7 days, respectively. Similarly, phosphate removal increased with phosphorus limitation, reaching 70% under the strongest P stress conditions.

Nitrogen-stressed cultures produced more EPS than phosphorus-stressed and standard cultures. Moderate nitrogen stress yielded the highest EPS concentration (91.88 mg/L), significantly exceeding phosphorus-stressed and standard samples. The EPS fraction bound to cells remained stable, indicating that increased EPS under nitrogen stress resulted primarily from EPS fraction released by the cells.

Conclusions: Nutrient stress can improve nutrient removal and promote EPS accumulation, particularly under nitrogen limitation. Complete phosphorus removal is challenging and requires stronger or longer biomass exposure to phosphorus deficiency. Controlled nutrient stress offers possible strategy for wastewater treatment with enhanced cyanobacterial EPS production.

Keywords: cyanobacteria, exopolysaccharides, nutrient stress

Phenotypic diversification in F₁ offspring of laboratory-bred marine Arctic diatom *Cylindrotheca closterium*

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Abstract

Introduction: Diatoms are among the most diverse groups of microalgae, exhibiting immense phenotypic and genetic diversity in nature. However, how this diversity arises and is transmitted across generations remains poorly understood. The overall objective of this project was to examine diatom mating patterns and offspring traits, toward a lab-based experimental breeding program.

Methods: Thirty-eight isolates of the marine diatom *Cylindrotheca closterium* were collected from Arctic Norway and classified into seven distinct clades. Crossing experiments were performed between isolates from different clades and successful mating was identified in multiple clade combinations. The parental strains were identified by sequencing the *rbcl* gene. Based on the initial crossing results, five parental strains were selected to establish three pairs for the breeding experiment. F₁ offspring produced from the three pairs were isolated and phenotyped. Statistical analyses were performed to determine whether phenotype inheritance in the F₁ offspring was primarily influenced by individual parental contribution or specific parental combinations.

Results: F₁ offspring isolated from the three different crosses exhibited phenotypic variation in growth rate, plastid traits and photo-physiological responses to blue and green actinic light. Besides, variations were also observed in the motility of the offspring, with regard to gliding speed and behaviour. The statistical analysis showed that the inheritance of growth rate in F₁ offspring is primarily influenced by individual variation whereas the inheritance of morphological and motility traits was influenced to a greater extent by specific parental combinations.

Conclusion: Experimental diatom breeding provides a unique strategy to understand the evolution and phenotypic diversification in diatoms while facilitating strain improvement for commercial applications.

Keywords: diatom, mating, reproduction, phenotyping, trait

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SEAlgaePower – Sustainable Development of Microalgae-Based Ingredients Using Waste Streams from Aquaculture and Seafood Processing Industry as Feedstock

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Abstract

The rapid expansion of land-based recirculating aquaculture (RAS) and seafood processing industries generates substantial nutrient-rich wastewater, posing high remediation costs and environmental risks. SEAlgaePower addresses this dual challenge by developing microalgae-based technologies that simultaneously treat wastewater and produce valuable biomass for novel bio-based ingredients. The project selects marine microalgae strains, including *Nannochloropsis*, *Phaeodactylum*, *Dunaliella*, and *Chlorella*, from the North Sea (Skagerak, Norwegian coast) and Mediterranean Sea (Sicilian coast), evaluating their growth performance and nutrient removal efficiency across diverse wastewater types from salmon RAS and seafood processing plants. A two-stage laboratory cultivation approach identifies optimal microalgae–wastewater combinations, which are then scaled to pilot cultivation systems, including both conventional RAS and innovative BioPod containers. The resulting biomass undergoes sequential biorefinery processing to recover proteins, omega-3-rich lipids, polysaccharides, and carotenoids, with fractions evaluated for applications in food, fish feed, textile fibers for wound care, fertilizers, and nutra-/pharmaceutical ingredients with anti-tumoral, antioxidant, anti-bacterial, and anti-diabetic properties. Environmental, economic, and social sustainability assessments accompany technology development to ensure viable value-chain circularity. By transforming a costly waste stream into an income-generating resource, SEAlgaePower supports the transition toward a climate-neutral, resilient blue economy, contributing novel carbon-neutral ingredients while advancing EU environmental and circular economy policy goals.

Keywords: *microalgae biorefinery, wastewater remediation, aquaculture waste valorization, blue bioeconomy, bioactive compounds*

From aquaculture side streams to high-value astaxanthin: A circular bioeconomy approach with *Haematococcus lacustris*

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Abstract

Recirculating aquaculture systems (RAS) produce nutrient-rich effluent water and CO₂-rich exhaust air, yet these side streams are commonly treated as waste. This study investigated their potential for cultivating *Haematococcus lacustris* and producing natural astaxanthin under Nordic RAS conditions (18 °C). Cultures were grown in 1.5-L photobioreactors and aerated with either ambient air (~400 ppm CO₂) or RAS exhaust air (1900–2500 ppm CO₂). During the stationary phase, ambient-air cultures were subdivided and aerated with either ambient air or RAS CO₂, whereas RAS-CO₂ cultures continued under the same aeration. All cultures were then exposed to high-light stress to induce astaxanthin synthesis. In a second study, effluents from four Finnish RAS facilities (pilot-to-commercial scale) were characterized and used to cultivate *H. lacustris* after standardizing initial N and P concentrations. The effluents differed in physicochemical properties and in the concentrations of major and trace elements (Ca, Mg, K, S, Fe, Mn, Mo, Co, Cu, Zn). Relative to ambient air, RAS CO₂ increased growth rate by 15%, cell density by 57%, biomass dry weight by 76%, astaxanthin content by 17–19% (up to 11.2 mg g⁻¹). Removal of TN, NO₃-N, and PO₄-P exceeded 95% in all treatments. Across the four RAS effluent treatments, biomass ionomes differed significantly during both the green and red phases, whereas growth rate, dry weight, and astaxanthin content remained comparable, indicating that facility-specific variation in trace elements does not limit *H. lacustris* performance. Overall, integrating RAS with *H. lacustris* cultivation supported high-value astaxanthin production through effluent bioremediation and CO₂ fixation, advancing a circular bioeconomy in RAS.

Keywords: Microalgae, Nordic RAS, Bioremediation, Carotenoid, RAS-CO₂

The AMPLIFY high-throughput algae fermentation platform at UCPH

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Abstract

The AMPLIFY platform at University of Copenhagen provides advanced high-throughput cultivation capabilities for photosynthetic microorganisms such as microalgae and cyanobacteria. Based on the BioLector XT system equipped with Light Array and Microfluidics Modules (BL-LAM), the platform enables parallelized optimization of cultivation conditions under controlled phototrophic, mixotrophic, and heterotrophic growth regimes. The system allows precise control of key process parameters including light intensity, pH, nutrient availability, and gas composition, with CO₂ supplementation of up to 12%. Advanced filter-based fluorescence and scattering detection provides continuous assessment of OD, chlorophyll as well as common fluorescent markers, enabling detailed monitoring of physiological performance throughout cultivation. The platform is suitable for strain screening, cultivation optimization, media development, physiological characterization, and process engineering studies.

Since becoming operational in early 2026, the AMPLIFY platform has supported cultivation of multiple industrially relevant microalgae, including *Nannochloropsis*, *Chlamydomonas*, *Picochlorum*, and *Chlorella*. Cultivation of cyanobacteria is also supported. AMPLIFY currently serves as a collaborative research infrastructure for academic and industrial partners across northern Europe. Access is offered through research collaborations, providing opportunities for joint projects in algal biotechnology, sustainable bioproduction, carbon capture, food ingredients, and bio-based manufacturing. As the platform grows, a fee-for-service model will be introduced to support long-term sustainability. We welcome discussions with researchers, companies, and innovation partners interested in leveraging high-throughput cultivation technologies for algae and cyanobacteria research.

Keywords: Strain screening, optimization, high-throughput fermentation

Engineering dinoflagellate carotenoid pathways in plants

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Abstract

Microalgae contribute to approximately 50% of global CO₂ fixation through photosynthesis. Carotenoids play a crucial role in photosynthesis by assisting in light harvesting and providing photoprotection. Dinoflagellates that live in symbiosis with corals have distinctive carotenoids such as peridinin that enhance the light-harvesting capacity of these microalgae in this unique marine ecosystem. However, the enzymatic pathways for the biosynthesis of these carotenoids are not fully elucidated.

Our research focuses on characterizing candidate algal carotenoid biosynthetic genes using two complementary expression systems: a heterologous plant platform (*Nicotiana benthamiana*) and an evolutionarily related alga (*Nannochloropsis oceanica*). We utilize LC-MS to study changes in pigment composition upon expression of dinoflagellate carotenoid candidate genes. We have furthermore identified a two-domain enzyme that substantially increases the precursors for peridinin. We are currently implementing this gene into our transient expression plant system using *Nicotiana benthamiana*, applying it as a tool to have an algal-like carotenoid profile in plants. This platform will allow us in the future to screen and characterize other carotenoid related genes, potentially generating plants with dinoflagellate carotenoids for improved light harvesting, leading to higher crop yields.

Keywords: *dinoflagellate carotenoids, heterologous gene expression, Nicotiana benthamiana, Nannochloropsis oceanica, LC-MS*

Photosyntech - the Norwegian graduate school on photosynthetic eukaryotes

Photosyntech

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Abstract

The national graduate school Photosyntech is for PhD candidates working on plants or algae, in the ranges from molecules to ecosystems and for basic research to technology and applications. This poster is a presentation of the benefits of joining the network. You will meet the coordinator and two of our student members.

Keywords: *National research school, photosynthesis, network, grants, courses, activities.*

Genetic transformation of hard-to-transform cyanobacteria using BPP Bioportides™ as a gene delivery tool

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Abstract

Cyanobacteria produce a wide range of secondary metabolites that are valuable biorefineries. However, a high percentage of industrially relevant cyanobacteria remains difficult to as they are difficult to genetically modify. BPP Bioportide™ is a multifunctional gene delivery tool for applications in plants and a variety of microorganisms, including many strains of planktonic and filamentous cyanobacteria.

BPP Bioportide™ is a small fusion protein. The substrate of this binding moiety is the sugar-phosphate-backbone of the nucleic acid. The protein binds nucleic acids regardless of their secondary structure and does not discriminate between RNA or DNA, single stranded or double stranded, linear or circular nucleic acid sequences. Circular replicative or linear integrative plasmids and PCR products have been integrated in *Synechocystis* and *Synechococcus* strains successfully.

In April 2026, we published a research contribution with the group of Karl Forchhammer and Sofia Doello-Roman at Eberhard-Karls-Universität in Tübingen, Germany. They adapted the protocol that had been established for *Escherichia coli* transformation in the BPP laboratory in Heidelberg and showed that this protocol had the following positive implications on their workflow. They required a reduced amount of DNA. Instead of 10µg of plasmid per experiment, 10ng material was sufficient. The BPP Bioportide™ mediated transformation fully replaced conjugation as a transformation method. The simplified protocol could without modification be applied for the transformation of a *Synechococcus* UTEX strain that had not been genetically transformed before.

We showed that BPP Bioportide™ mediated transformation expands the population of cyanobacteria that are available for industrial application through optimized strain development.

Keywords: *transformation, synechocystis, synechococcus UTEX* (maximum 5 keywords)

References

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Utilization of wine lees via anaerobic digestion and production of *Chlorella vulgaris*

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Abstract

Wine lees represent a potentially valuable resource due to their content of residual organic matter, nitrogen compounds, phenolic substances, and other nutrients. However, their high organic load, acidic character, and potentially inhibitory compounds may adversely affect microalgal growth. This study evaluated the potential of wine lees for bioenergy production and algal biomass generation through an integrated approach combining anaerobic digestion and cultivation of *Chlorella vulgaris*. Different forms of wine lees utilization, including direct addition, anaerobically treated substrate, and sterilized wine lees, were investigated. Microalgal growth was monitored by light microscopy and cell concentration measurements, while ammonium nitrogen ($\text{NH}_4^+\text{-N}$) concentrations, lipid and protein contents were determined using spectrophotometric methods. During cultivation of *C. vulgaris*, a decrease in ammonium nitrogen concentration was observed, indicating removal of available nitrogen from the cultivation medium. Anaerobic digestion of the wine-lee substrate produced approximately 0.45 m³ of methane per kg COD removed. Gradual addition of sterilized wine lees initially stimulated microalgal growth, with the highest cell concentration observed up to day 7. Subsequently, increasing pH and changes in ammonium nitrogen concentration coincided with a decline in cell concentration and changes in cell size, indicating deterioration of cultivation conditions. These results demonstrate the potential of wine lees for integrated methane and microalgal biomass production, while highlighting the need to optimize substrate concentration, pretreatment, and feeding strategies.

Keywords: *Chlorella vulgaris*; wine lees; anaerobic digestion, biorefinery.