



AQUABIOTECH 2026

4th INTERNATIONAL AQUATIC BIOTECHNOLOGY
SYMPOSIUM

Naples, Italy | September 9–11, 2026

AULA MAGNA – Centro Congressi Federico II, Via Partenope, 36

ABSTRACT BOOK

Naples
where science
meets the sea





4th International Aquatic Biotechnology Symposium

ORGANIZER

4th INTERNATIONAL AQUATIC BIOTECHNOLOGY SYMPOSIUM

Naples, Italy | September 9-11, 2026

AULA MAGNA – Centro Congressi Federico II, Via Partenope, 36

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09-11 September 2026

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FOREWORD

It is our great pleasure to present the Book of Abstracts of the 4th International Aquatic Biotechnology Symposium – AquaBioTech 2026, held in Naples, Italy, from 9 to 11 September 2026, with the support of the University of Naples Federico II. Building on the success of the previous editions, AquaBioTech 2026 brought together an international community of scientists, young researchers, professionals and stakeholders working across the many disciplines that contribute to aquatic biotechnology, including marine biology, chemistry, molecular biology, environmental sciences and biotechnology. At a time when climate change, pollution, biodiversity loss and the increasing demand for sustainable food, health and energy solutions represent major global challenges, aquatic environments offer an extraordinary source of biodiversity, knowledge and innovation. The Symposium was conceived as a platform to explore this potential across the entire value chain, from bioprospecting and aquatic omics to the development, testing and application of innovative products and technologies. The scientific programme reflected the broad and interdisciplinary nature of the field, addressing applications of aquatic biotechnology in health, food, environment and energy. Keynote and invited lectures, oral communications and poster presentations provided opportunities to share new findings, discuss emerging approaches and promote interactions among established scientists and the next generation of researchers. Beyond the scientific programme, AquaBioTech 2026 aimed to strengthen connections across disciplines, institutions and countries. We believe that meaningful scientific progress increasingly relies on our ability to create bridges between fundamental research and technological innovation, and between academia, industry and society. We are deeply grateful to our keynote and invited speakers, session chairs, members of the Scientific and Organizing Committees, sponsors and all those who contributed to the organisation of the Symposium. A special acknowledgement goes to the students and young researchers of the Local Organizing Committee, whose enthusiasm, dedication and invaluable support greatly contributed to the success of the meeting. Finally, our warmest thanks go to all participants who joined us in Naples, the city of Parthenope, bringing their science, ideas and enthusiasm to AquaBioTech 2026. We hope that the discussions, collaborations and connections initiated during these days will continue well beyond the Symposium and inspire new scientific developments and future joint initiatives in aquatic biotechnology. We are delighted to share this collection of abstracts as a record of the science presented in Naples and, above all, as a starting point for the collaborations still to come.

Sincerely,
The Organizing Committees
4th International Aquatic Biotechnology Symposium – AquaBioTech 2026

**4th International
Aquatic Biotechnology Symposium**

INVITED SPEAKERS



Prof. Luisa M. P. Valente
University of Porto



Prof. Spyros Gkelis
Aristotle University of Thessaloniki



Prof. Claire Hellio
Université Bretagne
Occidentale

KEYNOTE SPEAKERS



Prof. Gregory L. Rorrer
Oregon State University



Prof. Michele Fabris
Stazione Zoologica Anton Dohrn
University of Southern Denmark

DAY 1 • Wednesday, September 9, 2026

08:00 Registration & Welcome

09:00 Opening Ceremony
Greetings from the director of the Dept. of Pharmacy (UniNA) Prof. Angelo Antonio Izzo and the former Italian Minister of the Environment Sergio Costa

10:00 Plenary Lecture 01| Luisa Valente – From waste to feed: Biotechnology and the circular bioeconomy in aquaculture

10:45 COFFEE BREAK

SESSION 1

Biotechnology of Aquatic Sustainable Aquaculture

Chairs: C. Messina (Italy) and L. Botana (Spain)

11:13 O-01 C. Messina – Blue skills, living labs and stakeholder engagement for a sustainable blue transformation

11:26 O-02 M. G. Antoniou – Turning toxic cyanobacterial biomass into energy and biofertilizers: The CYANOTECH approach

11:39 O-03 D. Jerry – Born male, destined female: The biology and biotechnology of sex change in barramundi (*Lates calcarifer*)

11:52 O-04 F. Abdi – Evaluation and valorization of shrimp shell waste for astaxanthin recovery: Effect of drying and extraction methods

12:05 O-05 C. Piccini – Microbiome role in restoration and conservation in the freshwater mussel *Unio elongatulus*

12:18 O-06 I. Buttino – Marine copepods and associated microbiome for sustainable aquaculture and biotechnological innovation

12:31 O-07 M. Dormousoglou – Evaluating novel plant extracts as promising phytobiotics for aquaculture

12:44 O-08 E. Della Ceca – From waste to value: Eco-friendly astaxanthin extraction from blue crab shell

12:57 LUNCH BREAK

SESSION 2

Bioprospecting Aquatic Organisms for Novel Metabolites

Chairs: L. Pezzolesi (Italy) and T. Kaloudis (Greece)

14:00 O-09 E. Yeşilada – Conversion of waste seagrass into carbon dots: Synthesis and characterization

14:13 O-10 S. Federico – Extraction and potential biotechnological applications of sulphated polysaccharides derived from four Mediterranean marine sponge species

DAY 1 • Wednesday, September 9, 2026

SESSION 2

Bioprospecting Aquatic Organisms for Novel Metabolites (Continued)

- 14:26** O-11 F. Palma Esposito - *New brominated alterochromides from coral-associated Pseudoalteromonas*
- 14:39** O-12 R. Giaccari - *The omega-3 biosynthetic pathway in the Antarctic diatom Fragilariopsis cylindrus*
- 14:52** O-13 R. Konkel - *From the sea to cancer therapy: Discovery of a new family of chlorinated metabolites*
- 15:05** O-14 R. Li - *Preparation and bioactivities of polysaccharides and peptides from Sea cucumber*
- 15:18** O-15 C. Louati - *Valorization of Daphnia magna and microalgae for high-value biomolecules production*
- 15:31** O-16 A. Oguz - *Assessment of the biodiesel potential of microalgal blooms: Lipid and FAME yields from freshwater ecosystems in Türkiye*
- 15:44** O-17 M. Simonazzi - *Carbon nanomaterials meet algae: Boosting photosynthesis and valuable products*
- 15:57** Free time before the cultural visit to the Madre Museum
- 17:30** CULTURAL AND SOCIAL EVENT: Ice breaker & Music

DAY 2 • Thursday, September 10, 2026

09:00 Plenary Lecture 02|Claire Hellio – Marine biotechnology for a sustainable future: marine organisms bioprospecting and the development of eco-friendly products

SESSION 3

Bioremediation, Biomonitoring and Biosensing in Aquatic Environments

Chairs: A. De Marco (Italy) and J. Diogène (Spain)

- 09:45** O-18 A. Gangwar - *Development of a continuous two-stage system for the remediation of offshore produced water*
- 09:58** O-19 B. Kaya - *Aerobic granular sludge technology for sustainable treatment of high-strength mixed industrial wastewater*
- 10:11** O-20 D. M. Monti - *Microalgae as a biotechnological tool for bio-CCU*
- 10:24** O-21 M. Piscopo - *The impact of microplastics on the properties of protamine-like proteins. A case of gamete plasticity or a risk to reproduction in *Mytilus galloprovincialis*?*
- 10:37** O-22 A. Postiglione - *Biomonitoring of metal(loid) pollution in freshwater ecosystems: An Integrated study of bioaccumulation, oxidative stress, and detoxification mechanisms in *Leptodictyum riparium**
- 10:50** O-23 S. Spatharis - *Towards a data-driven biofouling forecast system for the seaweed biotechnology sector*
- 11:03** COFFEE BREAK

SESSION 4

Bioremediation, Biomonitoring and Biosensing in Aquatic Environments

Chairs: A. Leone (Italy) and D. Jerry (Australia)

- 11:30** O-24 N. G. Apostolopoulou - *Red microalgae *Porphyridium purpureum* under different light colours: Uncovering growth mechanisms*
- 11:43** O-25 M. Dentato - *When bioremediation meets stress: Arsenic in moss-snail aquatic system*
- 11:56** O-26 T. Greca - *Interactive effects of cadmium and nitrogen depletion on resting spore dynamics in *Chaetoceros* spp.*
- 12:09** O-27 L. Harutyunyan - *The diversity of cyanophages in Lake Sevan, Armenia and their potential impact on harmful cyanobacterial blooms*
- 12:22** O-28 C. Marinaro - *Molecular effects of chromium on the sperm chromatin of *Mytilus galloprovincialis**
- 12:35** O-29 I. Ostrovsky - *Acoustic and satellite techniques for quantification and monitoring of gas-bearing cyanobacteria*

DAY 2 • Thursday, September 10, 2026

SESSION 4

Bioremediation, Biomonitoring and Biosensing in Aquatic Environments (Continued)

12:50 O-30 F.A. Ozdemir Olgun - *Adsorptive removal of amoxicillin by Ulva lactuca from aqueous medium*

13:03 LUNCH BREAK

SESSION 5

Omics in Aquatic Biotechnology

Chairs: L. Tartaglione (Italy) and M. Albay (Türkiye)

14:00 Keynote Lecture 01| M. Fabris - *Domestication of algal bio-factories: metabolic mapping and engineering of diatoms*

14:15 O-31 I. Bilgin - *Metagenomic analysis of bacterial pathogens associated with microplastics in the coastal marine environments of Izmir and Istanbul*

14:28 O-32 M.E. Collaro - *Mass spectrometry query language (MassQL)-assisted detection of microcystin variants*

14:41 O-33 D. Giordano - *Antarctic UV-resistant marine bacteria: An untapped carotenoid source*

14:54 O-34 G. Ozbayram - *Bacterial diversity and biotechnological prospects of Antarctic epibenthic biofilms from Horseshoe Island*

15:07 O-35 N. Salmaso - *Genome-resolved taxonomic and functional characterisation of the genus Limnospira*

15:20 O-36 E. Asimakis - *Isolation and phylogenomic characterization of Aeromonas veronii strains associated with outbreaks in commercial Mediterranean aquaculture facilities*

15:33 COFFEE BREAK

16:00 A. Marrano - ERC Workshop

17:00 POSTER SESSION 1

20:30 Social Dinner Experience at A'MBASCIATA Palazzo Venezia

DAY 3 • Friday, September 11, 2026

09:00 Plenary Lecture 03| Spyros Gkelis - *Metabologenomics: Bridging habitat adaptation and biodiscovery in photosynthetic microorganisms*

SESSION 6

Photosynthetic Microorganism Biotechnology

Chairs: R. Akçaalan (Türkiye) and N. Salmaso (Italy)

09:45 Keynote Lecture 02| G.L. Rorrer - Controlled extrusion of N-acetyl glucosamine nanofibers by diatom microalgae

10:00 O-37 L. M. Botana - *Recent findings to update and understand the mode of action of diarrheic and ciguatera toxins*

10:13 O-38 S. Carfagna - *Galdieria phlegrea physiology drives biotechnologically relevant metabolites*

10:26 O-39 L. Cerasino - *Tracking Lake Garda's cyanotoxins: Trend analysis over a fifteen years of monitoring*

10:39 O-40 J. Diogène - *Biotechnology and ecology of harmful marine microalgae involved in Ciguatera, an indispensable partnership*

10:52 O-41 E. Vitale - *Ecological variables modulate bioactive compounds in Mediterranean algal community*

11:05 COFFEE BREAK

SESSION 7

Aquatic Biotechnologies in European and International Projects: The Experience of BIOBASED Project

Chairs: G. Romano (Italy) and H. D. Laughinghouse IV (USA)

11:30 O-42 M. Stulgis - *EU Support for algae sector: So far and what's next*

11:45 O-43 S. Fatica - *Welcome note and Presentation of the Interreg VI-A Italy - Croatia programme 2021/2027*

11:55 O-44 M. Francavilla - *Advancing blue biorefinery development in the Adriatic Sea (BIOBASED Project)*

12:10 O-45 A. Miccoli - *Regulatory framework and market analysis for macroalgae-based value chains in the Adriatic: A cross-border action plan*

12:20 O-46 E. Dobroslavic - *Seasonal cultivation of Ulva spp. in an IMTA system in Mali Ston Bay*

12:30 O-47 E. Rambaldi - *The strategic role of shellfish farmers in ecological transition and IMTA systems*

12:45 POSTER SESSION 2

13:30 LUNCH BREAK

DAY 3 • Friday, September 11, 2026

SESSION 8

Aquatic Bioresources and Biotechnology: From Photosynthetic Microbes to Aquatic Fauna for Sustainable Aquaculture

Chairs: A. Hiskia (Greece) and P. Napoletano (Italy)

- 14:30** O-48 C. Buonocore - *From invasive biomass to bioactive peptides: Pufferfish collagen hydrolyzates*
- 14:43** O-49 C. Spetea - *Screening North Sea and mediterranean microalgae for salmon RAS water valorisation*
- 14:56** O-50 M. Cariglia - *Redesigning the blue economy: Regenerative integrated aquaculture and regional food heritage toward a replicable model of resilience*
- 15:09** O-51 H. D. Laughinghouse IV - *Benthic Cyanobacterial mats on Curaçao reefs: Abundance, nitrogen fixation, and toxicity on changing reefs*
- 15:22** O-52 F. Guidi - *ATL.A.HUB: Accelerating marine algae biotechnology in the Atlantic Area*
- 15:35** COFFEE BREAK
- 16:05** O-53 E. Maresca - *Valorization of fish processing by-products through collagen extraction for biomedical and high-value applications*
- 16:18** O-54 L. Marra - *Exhausted culture media reuse in autotrophic microalgae production: optimization and modelling of Pseudococcomyxa simplex cultures*
- 16:31** O-55 K. Veliz - *Effect of spore encapsulation on the development of the microscopic phase of the South Pacific kelp Lessonia berteroana*
- 16:44** O-56 S. Vergetzi - *Characterization of photosynthetic microorganisms associated with Mentha spp. plants*
- 16:57** O-57 V. Villanova - *Functional screening of halophilic microorganisms in retentate wastewater*
- 17:10** Awards and Closing Ceremony

Poster List

POSTER SESSION 1

- P-01 R. Akcaalan - *Linking lipid accumulation to microbial community dynamics in *Botryococcus sudeticus* under nitrogen stress*
- P-02 M. Albay - *Cross-domain microbial insights into ecosystem resilience and restoration potential in a hypereutrophic coastal lagoon*
- P-03 A. Alfonso - *Pharmacological potential of compounds isolated from *Dictyota* spp. Seaweeds*
- P-04 A. Bagnato - *Production and characterization of marine-based 3D scaffolds: A comparative study of bioreactor and static culture systems*
- P-05 D. Blagojević - *The impact of red and green light on the growth and phycobiliproteins in *Nostoc* strains*
- P-06 G. Borsetta - *From invasive species to economic resource: Valorization and market perspectives of the atlantic blue crab (*Callinectes sapidus*)*
- P-07 P. Davidović - *Microfluidic PLP-RCA detection of the microcystin biosynthesis gene *mcyE**
- P-08 I. Can-Tunçelli - *Emerging contaminants in seafood safety: A one health perspective from biomonitoring to consumer risk assessment*
- P-09 I. Can-Tunçelli - *Marine bioindicator species as sentinels of microplastic contamination: An integrated framework for aquatic food supply safety*
- P-10 V. Ceccherini - *Genomic and metabolic profiling of *Microcystis aeruginosa* blooms in lake Serraia*
- P-11 B. Çelik - *Marine ecosystem assessment of a student-designed offshore wind farm in the aegean sea: The Bozcaada YEKA Cas*
- P-12 A. Coppola - *Bioactivity antiproliferative screening of Antarctic cold-adapted bacteria*
- P-13 H. D. Laughinghouse IV - *From genes to molecules: Connecting biosynthetic gene clusters and specialized metabolism in the Cyanobacterial genus *Floridanema**
- P-14 H. D. Laughinghouse IV - *BCCM/ULC: A public culture collection for ex situ conservation of cyanobacterial diversity and support of biotechnological applications*
- P-15 A. De Felice - *Biosynthetic potential and carotenoids in an Antarctic marine *Arthrobacter* strain*
- P-16 V. Ghionna - *Occurrence of saxitoxins in marine invertebrates from Apulian lagoons*
- P-17 N. T. Papadopoulos - *Isolation and characterization of cyanobacteria from diverse habitats in Naples*

Poster List

POSTER SESSION 1

(Continued)

- P-18 G. Kopp - *Identifying chemical epigenetic modifiers concentration for diatom cultures*
- P-19 I. Hmani - *From regenerative IMTA biomass to blue biorefinery products: Cascade valorisation of Gracilaria and Ulva in the Adriatic*
- P-20 Z. Zengin - *Species level characterisation of Cyanobacterial blooms by nanopore sequencing approach*
- P-21 D. Özyurt - *Green synthesis of CeO₂-x nanoparticles for oxidative removal of geosmin and 2-MIB*
- P-22 A. Leone - *Purple bacteria as novel foods and feeds: Antioxidant and cytotoxic properties*

POSTER SESSION 2

- P-23 D. Memiş - *Bioproduct potential of aquacultured sturgeons*
- P-24 A. Inam - *Phenolic, flavonoid and antibacterial properties of green microalgae and diatoms*
- P-25 N. T. Popović - *Fish-based models for multilevel assessment of aquatic environmental stressors*
- P-26 N. T. Popović - *Novel invasive tunicate species affecting mussels in the northern Adriatic Sea*
- P-27 J. Simeunović - *Exploring the biosynthetic potential of Nostoc 2S3B strain by genome mining*
- P-28 G. Tunçelli - *Effects of experimental microplastic exposure on swimming performance in rainbow trout and russian sturgeon*
- P-29 V. Vedi - *Long-term toxicity of polyethylene (PE) microplastics on the green photosynthetic microalga Chlamydomonas reinhardtii*
- P-30 C. Lauritano - *Antiproliferative activity from Antarctic phytoplankton*
- P-31 V. M. Vivenzio - *Characterization and chitosan immobilization of a marine carbonic anhydrase for CO₂ enrichment in microalgal cultures*
- P-32 A. Yildirim - *Biotechnological valorisation of biomass from recombinant xylanase-secreting Chlamydomonas reinhardtii*

Poster List

POSTER SESSION 2

(Continued)

- P-33 R. Ofano - *AQUASERV: Research services for sustainable aquaculture, fisheries and blue economy*
- P-34 T. Poletti - *Development of a floating monitoring device for water quality assessment in the Piracicaba River, Brazil*
- P-35 L. Pezzolesi - *Re-thinking the role of the microalgal-bacterial association in polyhydroxybutyrate (PHB) accumulating cultures of *Desmodesmus communis**
- P-36 A. Pica - *Assessing the impact of marine protected areas on microbiome dynamics along the Sardinian coast*
- P-37 A. Paraian - *Powerful of mass spectrometry approaches for analysis of toxins*
- P-38 K. I. B. Çetin- *Sustainable cherry waste-derived biochars for methylene blue removal: A promising approach for wastewater treatment*
- P-39 G. Romano- *BIOVAL: Microalgal biomass valorisation for sustainable production of functional food and feed ingredients*
- P-40 B. Bessadok - *Bioprospecting Tunisian aquatic yeasts for blue biotechnology applications*
- P-41 C. Messina - *Blue biotechnology: From aquaculture side streams to cellular agriculture*
- P-42 C. Messina - *Valorizing aquaculture halophyte biomass: A green biorefinery perspective*
- P-43 L. Köker - *Nitrogen and phosphorus removal potential of the aquatic plant *Egeria densa**
- P-44 C. Carbonara - *Chamelea gallina as a sentinel species for microplastic biomonitoring along the Adriatic Apulian coast*
- P-45 S. Rosati - *Alginate as a marine biopolymer for bioactive edible coatings*
- P-46 S. Rosati - *Microbiological quality of sea bass and sea bream from an IMTA system*
- P-47 F.Z. Guellati - *Emergence of *Cylindrospermopsis raciborskii* as the dominant cyanobacterium in lake Oubeira: Insights from community shifts and toxin dynamics*
- P-48 A. Montalbano - *Proteomic analysis and biochemical characterization of the nematocyst extract from *Pelagia noctiluca* (Forsskål, 1775)*

PL-01**From Waste to Feed: Biotechnology and the Circular Bioeconomy in Aquaculture**L.M.P. Valente¹

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¹Interdisciplinary Centre of Marine and Environmental Research (CIIMAR) and School of Medicine and Biomedical Sciences (ICBAS), University of Porto, Portugal.

Aquaculture growth depends increasingly on the availability of sustainable protein and lipid sources for aquafeeds. Within a circular bioeconomy framework, biotechnology offers powerful tools to recover nutrients from underutilized marine and terrestrial biomass, converting sidestreams from agriculture, fisheries, aquaculture, and food processing into high-value feed ingredients.

Unlike conventional linear production systems, circular approaches promote resource reuse, recycling, and regeneration, thereby reducing waste, limiting dependence on finite resources, and retaining nutrients within food-production systems. Technologies such as insect bioconversion, microalgae cultivation, enzymatic processing, and precision fermentation can transform organic side streams into nutrient-rich protein and lipid sources with tailored nutritional and functional properties.

Integrating these technologies into closed-loop production systems can improve resource efficiency, diversify aquafeed raw materials, and reduce the environmental pressures associated with feed production. Increasing technological maturity and industrial scale-up are accelerating the availability of novel ingredients with the potential to support nutritionally balanced aquafeeds.

However, their successful implementation requires more than technological innovation. Regulatory approval, economic competitiveness, consistent ingredient quality, market integration, consumer perception, and the energy requirements of production processes remain important challenges. Addressing these constraints will be essential to fully realise the contribution of biotechnology to a circular and resilient aquaculture food system.

Acknowledgments: This work has been supported by the Blue Bioeconomy Innovation Pact (C644915664-00000026) and InsectERA Mobilising Agenda (PRR - InsectERA - The ERA of the insect industry), funded by Portugal and the European Union - NextGenerationEU, with the identifier C644917393-00000032.

Keywords: Sustainable aquaculture, by-products valorization, processed-animal-protein (PAP); insect meal and oil; single-cell-protein (SCP), environmental impact



PL-02

Marine biotechnology for a sustainable future: marine organisms bioprospecting and the development of eco-friendly products

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The growing demand for sustainable materials, products and processes is driving the search for innovative solutions that combine environmental responsibility with industrial performance. Bioinspiration offers a promising approach by translating nature's strategies and mechanisms into solutions to address contemporary technological and societal challenges. In this context, marine biotechnology represents a largely untapped source of innovation, drawing on the extraordinary diversity of marine organisms and their unique structural, physiological and chemical adaptations, many of which have no direct equivalent in terrestrial environments.

Recognised by policymakers and industry as a strategic driver of the bioeconomy, marine biotechnology holds considerable potential to address unmet market needs and support the development of novel, sustainable products and applications. However, unlocking this potential requires a deeper understanding of the biological mechanisms underlying the ecological functions and adaptive strategies of marine organisms, alongside the development of innovative approaches to identify, assess and validate environmentally responsible solutions.

This plenary lecture will explore how insights from marine chemical ecology can inspire the development of innovative bio-based solutions. Key topics will include the role of chemical defences in ecological interactions, the contribution of associated microorganisms to the production of bioactive compounds, the seasonal dynamics of defence mechanisms, and the synergistic effects of multiple defensive strategies. Particular attention will also be given to the development of innovative bioassays and testing methodologies to identify and evaluate effective, low-impact alternatives to conventional products and processes, while assessing their biological performance and environmental compatibility. Through selected examples from collaborative research projects with industry, the lecture will illustrate how fundamental knowledge of marine biological systems, combined with innovative testing strategies, can be translated into practical applications. It will highlight the importance of bridging marine ecological research, biotechnology and industrial collaboration to accelerate the development of sustainable, nature-inspired solutions that meet both market needs and environmental challenges.

Keywords: Marine biotechnology; Bioinspiration; Marine chemical ecology; Bioactive compounds; Sustainable bio-based solutions.



PL-03

Metabologenomics: Bridging Habitat Adaptation and Biodiscovery in photosynthetic microorganisms

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Cyanobacteria and eukaryotic microalgae are among the most ecologically diverse and biotechnologically promising microorganisms on Earth. Their photosynthetic lifestyles and remarkable physiological plasticity enable them to colonize environments ranging from freshwater and marine ecosystems to hypersaline habitats, hot springs, deserts, polar regions, and other ecological extremes. Adaptation to such contrasting conditions has generated substantial taxonomic, genomic, and metabolic diversity, much of which remains unexplored.

Environmental stressors and biological interactions can shape the production of specialized metabolites involved in defense, competition, communication, and stress tolerance. These compounds may also possess valuable pharmaceutical, nutraceutical, agricultural, or industrial properties. Consequently, underexplored microorganisms from unusual or highly selective ecological niches represent promising targets for the discovery of novel taxa, biosynthetic pathways, enzymes, and natural products.

Nevertheless, connecting environmental adaptation, genomic potential, and observed chemical diversity remains a major challenge. Metabologenomics—the integration of comparative genomics, genome mining, and metabolomic profiling—provides a powerful framework for establishing these connections. By correlating biosynthetic gene clusters and other metabolic genes with mass-spectrometry-derived molecular features, metabologenomics can facilitate the prioritization of strains, link metabolites to their genetic origins, and support the identification of previously unknown compounds.

This presentation will follow the biodiscovery workflow from environmental sampling and strain isolation to polyphasic taxonomic characterization, genome sequencing, untargeted metabolomics, and integrated metabologenomic analysis. Examples from cyanobacteria and eukaryotic microalgae inhabiting underexplored and environmentally challenging habitats will illustrate how ecological context can guide bioprospecting. Particular emphasis will be placed on how combining taxonomy, ecology, genomics, and metabolomics can reveal the molecular basis of habitat adaptation while accelerating the discovery of new biological and chemical diversity with biotechnological potential.

Keywords: metabologenomics; cyanobacteria; microalgae; genome mining; untargeted metabolomics



KL-01

Domestication of algal bio-factories: metabolic mapping and engineering of diatoms

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Diatoms have colonized every aquatic habitat on Earth, largely owing to their unique metabolic traits. This versatility makes them attractive candidates for biotechnological applications, yet they remain underexploited because industrial cultivation is poorly optimized and product yields are low. Our research accelerates the domestication of photosynthetic diatoms through metabolic engineering and synthetic biology, using the biosynthesis of terpenoid-based high-value compounds as a model. We mapped isoprenoid metabolism in the model diatom *Phaeodactylum tricornutum*, and identified and functionally characterized five distinct prenyltransferases, defining their specificity and subcellular localization. We then explored the capacity of *P. tricornutum* to produce terpenoids in different subcellular compartments, particularly the periplastidial compartment (PPC), the minimal endosymbiotic cytoplasm surrounding the plastid in secondary endosymbionts. We show that prenyl phosphate precursors accumulate in the PPC, and that heterologous terpenoid synthases function effectively when targeted to this compartment. We systematically explored the production of mono-, sesqui-, tri-, and tetraterpenoids, including geraniol, squalene, zizaene, and carotenoids, across cellular compartments. By combining modular DNA assembly, rapid high-throughput workflows, and compartment-specific targeting strategies, we established proof of concept for engineering complex biosynthetic routes. This approach positions diatoms as promising synthetic biology platforms for solar-driven, compartmentalized production of industrially relevant compounds and opens new opportunities for sustainable biomanufacturing.

Keywords: diatoms; synthetic biology; terpenoids; isoprenoids, compartmentalized biosynthesis



KL-02

Controlled Extrusion of *N*-Acetyl Glucosamine Nanofibers by Diatom Microalgae

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Photosynthetic diatom algae possess diverse and unique biosynthetic pathways that produce a variety of materials, including nanostructured metal oxides, energy-dense lipids, bioactive compounds, and biopolymers. Diatoms possess a nanostructured, porous biosilica cell wall, and so require dissolved silicate (silicic acid) as a required substrate for cell division. A few species of diatom algae within order Thalassiosirales biosynthesize and extrude *N*-acetyl glucosamine (NAGlc) biopolymer nanofibers of 50 nm diameter and unprecedented length exceeding 100 microns through specialized ports (fultoportula) lining the rim of its nanostructured silica cell wall. The poly *N*-acetyl glucosamine chains hydrogen bond in parallel array to form a rare β -allomorph of chitin. The β -chitin allomorph is much more readily functionalized and biodegradable than α -chitin sourced from the shells of invertebrate organisms. β -chitin is finding many applications, particularly for biomedical materials, as it is strongly hemostatic (promotes blood clotting), and can be blended with other biomaterials to make engineered tissue scaffolds.

The rate and yield of *N*-acetyl glucosamine (β -chitin) nanofiber formation is externally controlled by photobioreactor cultivation of the diatom *Cyclotella* with perfusion delivery of dissolved silicon and nutrient solutions. We demonstrate that silicon-limited cultivation stimulates β -chitin nanofiber formation whereas nitrate limitation limits β -chitin nanofiber formation. Increasing the phosphate delivery rate increases the selectivity of β -chitin nanofiber formation over competing lipid production. Overall, the research demonstrates the potential for controlled extrusion of *N*-acetyl glucosamine nanofibers by diatom microalgae in engineered photobioreactor systems.

Keywords: β -chitin; Diatom; Nanofibers; Nanostructured silica; *N*-acetyl glucosamine biosynthesis; Photobioreactor cultivation.



O-01**Blue Skills, Living Labs and Stakeholder Engagement for a Sustainable Blue Transformation**

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Climate change and biodiversity loss are increasingly threatening aquatic systems, exacerbating pressures on food production. Small fishers and producers play a crucial role in maintaining local ecosystems and ensuring food supply resilience; however, they often face significant challenges due to limited access to resources and complex regulatory frameworks. The blue economy sector needs to promote the sustainable use of marine resources to support economic growth, job creation, and ecosystem protection. These challenges are further compounded by fragmented interactions among science, policy, and society, which limit stakeholder participation and hinder the transition towards sustainable and equitable food systems. Capacity-building, knowledge transfer, and training initiatives aligned with the SDGs are key in the transition towards a sustainable Blue Economy. The Quadruple Helix model brings together academia, industry, government, and civil society within a governance framework that fosters blue skills, blue careers, and employment opportunities. In this context, interdisciplinary competencies in marine biotechnology, aquaculture, and marine resource management are increasingly needed to foster innovation and sustainability across marine sectors. Consequently, the development of blue skills through targeted education and lifelong learning has become a key pillar of European policy frameworks, including the European Green Deal, the Blue Growth Strategy, and the EU Strategy for a Sustainable Blue Economy. These approaches have been successfully applied by our group in several European initiatives, particularly projects funded under Horizon Europe, supporting stakeholder engagement, blue skills development, and the implementation of sustainable innovation pathways within the blue bioeconomy at regional and local levels. We demonstrated how Living Lab methodologies provide an operational and collaborative environment for stakeholder engagement and the co-design of social innovation addressing real-world challenges. Ultimately, the integration of blue skills development and stakeholder engagement is essential to address persistent skills gaps across marine sectors and support a sustainable, inclusive, and resilient Blue Economy transition.

Keywords: Blue economy; Stakeholder engagement; Blue skills; Living Labs.



O-02

Turning Toxic Cyanobacterial Biomass into Energy and Biofertilizers: The CYANOTECH Approach

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Cyanobacteria, commonly known as blue-green algae, remain a significant concern due to their persistence in aquatic environments and their ability to produce toxic metabolites (cyanotoxins). Nutrient enrichment of water resources from human activities (such as agriculture, urbanization, and sewage runoffs), along with global warming and water scarcity, drives the global blooming of cyanobacteria. Besides the aesthetic (undesirable taste, color, and odor) and environmental effects of harmful cyanobacterial blooms (cyano-HABs), a few economic sectors, including tourism, fisheries, food, health, and water industries, experience annual losses in the range of millions of USD. With so many diverse sectors of modern living being affected by the same problem, it is crucial to develop and apply innovative and sustainable management systems for toxic cyanobacteria that can be easily integrated into existing infrastructure. In order to address water availability, quality, and scarcity caused by anthropogenic activities (such as intensive agriculture and livestock activities) we have developed and applied an innovative approach to safeguard surface water quality from further deterioration, while utilizing harmful waste as raw materials for the production of fertilizers, food, and energy. The CYANOTECH approach comprises the removal of the excess aquatic biomass (cyanobacteria cells and algae) from water with a low-energy non-mechanical separation technology (tangential flow separator), the treatment of the aquatic biomass for the production of energy and biofertilizers (struvite), and the application of treated and untreated surface water in hydroponic cultures producing crops safe for consumption (cyanotoxin-free crops). Finally, an Environmental Life-Cycle Analysis was conducted for the chemical oxidation and the anaerobic co-digestion processes.

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Keywords: Anaerobic co-digestion; Biogas; Biofertilizers; Cyanobacteria; cyanotoxins.



O-03

**Born Male, Destined Female: The Biology and Biotechnology of Sex Change in Barramundi
(*Lates calcarifer*)**

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Barramundi (*Lates calcarifer*) is a protandrous hermaphroditic fish that matures first as a male before undergoing sex change to female. This sex reversal presents significant challenges to barramundi aquaculture, particularly for the implementation of advanced selective breeding programs aimed at improving production performance. Over the past decade, research conducted by the authors has integrated developmental biology, endocrinology, genomics, transcriptomics, epigenetics, and reproductive biotechnologies to better understand and manipulate sex determination and sex change in this species, thereby enabling greater control of mating and genetic improvement in commercial breeding programs. This presentation synthesizes key discoveries spanning the entire sexual life cycle of barramundi. It describes the timing and molecular regulation of gonadal differentiation, identifying the developmental window during which sex can be manipulated and characterizing the expression dynamics of key sex-related genes, including *dmrt1*, *cyp11b*, and *cyp19a1a*. Building on this foundation, the presentation outlines how precocious male-to female sex change can be induced in juvenile males through hormonal implantation, and examines the extensive gonadal remodelling, altered gene expression, and DNA methylation changes associated with this process. Recent transcriptomic and epigenetic studies are also presented, providing new insights into the natural process of sex change and revealing coordinated shifts in classical sex-regulatory pathways, isoform switching of key genes, and evidence of epigenetic destabilisation and re-stabilisation during the transition from male to female. Collectively, these findings provide unprecedented insight into the mechanisms governing sexual development and sex change in barramundi while establishing practical tools for sex control in aquaculture. The presentation concludes by outlining future directions, including genome editing, germ-cell transplantation, cryopreservation, and investigations into the fundamental triggers that initiate natural sex change.

Keywords: barramundi; sex-change; biotechnology.



O-04

Evaluation and Valorization of Shrimp Shell Waste for Astaxanthin Recovery: Effect of Drying and Extraction Methods

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Shrimp shell waste is an abundant seafood by-product that represents a promising source of high-value carotenoids, particularly astaxanthin. Valorizing this waste stream can contribute to more sustainable seafood processing while providing natural antioxidant pigments for potential food, feed, and nutraceutical applications. This study aimed to evaluate the effects of drying pretreatment and extraction method on astaxanthin recovery from shrimp shell waste. Shrimp shells were dried using freeze drying as a reference method and hot-air drying at 40 °C and 50 °C. The dried samples were extracted using acetone-based extraction and ultrasound-assisted extraction, and pigment recovery was assessed by spectrophotometric analysis at 470 nm and astaxanthin quantification with HPLC-DAD. Freeze drying combined with acetone extraction produced the highest absorbance value (0.4545) and the highest astaxanthin content (50.06 µg/g dry sample), indicating superior preservation and recovery of the carotenoid fraction. Among the air-dried treatments, drying at 40 °C followed by acetone extraction showed the best performance, with an absorbance of 0.3553 and an astaxanthin content of 39.91 µg/g dry sample. In comparison, the 50 °C air-dried sample extracted with acetone showed lower absorbance (0.3177) and astaxanthin content (30.76 µg/g dry sample), suggesting that higher drying temperature may reduce pigment retention or extractability. Acetone extraction consistently outperformed ultrasound-assisted extraction under the tested conditions, probably due to better solubilization of astaxanthin-rich lipid fractions from the shrimp shell matrix. Overall, freeze drying with acetone extraction was the most effective analytical condition; however, 40 °C air drying combined with acetone extraction appears to be the most practical and scalable strategy for shrimp shell valorization.

Keywords: Astaxanthin Recovery; Seafood; Food Waste; Shrimp Shells.



O-05

Microbiome Role in Restoration and Conservation in the Freshwater Mussel *Unio elongatulus*

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Following severe industrial pollution caused by copper- and ammonium-rich effluents discharged between the 1920s and the 1980s, Lake Orta (Piedmont, Italy) has undergone a remarkable ecological recovery since the late 1980s. Among the most notable outcomes has been the re-establishment of the freshwater mussel *Unio elongatulus* Pfeiffer, achieved through the gradual natural recovery of the autochthonous population starting from the early 2000s, followed by the introduction of an allochthonous population from nearby Lake Maggiore in 2018. To investigate the role of the microbiome in the restoration and conservation of *U. elongatulus* Pfeiffer, we compared the digestive gland microbiome across three *U. elongatulus* populations: (i) the donor population from Lake Maggiore; (ii) the translocated population established in Lake Orta using individuals originating from Lake Maggiore; and (iii) the naturally re-established autochthonous population of Lake Orta. Digestive gland samples were collected from mussels belonging to the three populations, together with sediment and water samples from their corresponding habitats. Bacterial communities were characterized through 16S rRNA gene amplicon sequencing.

Preliminary results revealed clear differences in microbiome composition among the three populations. Beta-diversity analyses showed a distinct separation of microbial communities according to population origin, with the translocated mussels displaying an intermediate microbiome profile between the donor (Lake Maggiore) and the native Lake Orta populations. This gradient suggests that both environmental conditions and population history contribute to shaping the mussel-associated microbiome.

These preliminary findings suggest that host-associated microbiomes may contribute to the adaptation of freshwater mussels to local environmental conditions, providing new insights into the role of microbial communities in conservation and restoration programs.

Keywords: Freshwater mussels; Host-associated microbiome; Ecological recovery; 16S rRNA gene.



O-06

Marine Copepods and Associated Microbiome for Sustainable Aquaculture and Biotechnological Innovation

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Zooplankton plays a crucial ecological and functional role in aquatic ecosystems. In particular, copepods represent the most abundant zooplanktonic organisms, supporting the marine food chain. The AQUaBioS project, an Interreg Italy–France Maritime initiative, aims to promote a more sustainable, innovative, and resilient aquaculture, using copepods as an alternative and biologically appropriate feed source, rich in essential unsaturated fatty acids. In fact, current aquaculture systems rely heavily on fish-derived ingredients such as fish meal and fish oil, creating a paradox between economic benefits and environmental costs.

Marine copepods also represent a valuable source of microbial diversity with significant biotechnological potential, supporting natural antimicrobial activities. Bacterial isolates were obtained from wild zooplankton collected in Livorno (North Tyrrhenian Sea) coastal area using a WP2 mesh net. Among them, *Peribacillus* sp. displayed strong antimicrobial activity against multiple strains of *Enterococcus* and *Staphylococcus* spp., including multidrug-resistant variants.

Copepod microbiome is naturally adapted to degrade complex macromolecules, such as chitin and polysaccharides, and may contribute to the breakdown of recalcitrant compounds. Therefore, our research also focused on hydrolytic activities potentially involved in the degradation of bioplastics, such as poly(butylene succinate-co-adipate) (PBSA), using both culture-dependent and culture-independent approaches. Copepod microbiomes, derived from *Acartia tonsa* cultures reared in ISPRA facilities, showed significant bioplastic-degrading activities. Among bacterial isolates, *Vibrio* sp. demonstrated the ability to hydrolyse ester bonds in PBSA, leading to a significant reduction in polymer crystallinity. Additionally, the fungal strain *Cladosporium psychrotolerans* showed remarkable depolymerisation efficiency, achieving a near-complete mass loss of PBSA granules within a few days of incubation.

Overall, these findings highlight the potential of copepod-associated microbiomes as a source of antimicrobial and biodegradative activities, which could reduce the use of antibiotics in aquaculture and facilitate the degradation of environmentally recalcitrant macromolecules.

Keywords: Antibacterial activity; Bioplastics; Microbial degradation; PBSA; Fungi.



O-07

Evaluating Novel Plant Extracts as Promising Phytobiotics for Aquaculture

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Global aquaculture is increasingly challenged by outbreaks of bacterial infections and the rising incidence of antimicrobial resistance (AMR), which threatens both aquatic ecosystems and public health. To align with the One Health framework, there is a critical need to discover natural and effective alternatives to conventional antibiotics. Consequently, phytobiotics are gaining traction as sustainable aquafeed additives. This study investigates the potential of extracts from two distinct plants, *Myrtus communis* and *Equisetum arvense* L., as novel phytobiotic agents for aquaculture health management. Distinct extraction methods were optimized for each plant: *M. communis* leaves were processed using an ultrasound-assisted technique across four solvents (aqueous, ethanolic, methanolic, and ethyl acetate), whereas *E. arvense* was prepared via supercritical CO₂ extraction. Both extracts were comprehensively analyzed for their phytochemical profiles using Gas Chromatography-Mass Spectrometry (GC-MS). Their antimicrobial efficacy was evaluated against significant fish pathogenic bacteria, including *Vibrio harveyi*, *Vibrio alginolyticus*, *Aeromonas veronii*, and *Photobacterium damsela*, utilizing Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) assays. Furthermore, *in vitro* cytotoxicity and safety profiles were assessed to evaluate their potential for application. The results revealed that both plant extracts possess rich bioactive compositions and exhibit potent antimicrobial activity. *E. arvense* was also noted to be rich in phenolic compounds and flavonoids. Specifically, *M. communis* methanolic and ethanolic extracts showed pronounced antibacterial effects, with MIC values reaching 0.19 mg mL⁻¹ against *A. veronii*. Similarly, the *E. arvense* extract demonstrated strong antioxidant capacity and significant bactericidal effects, yielding MIC values between 0.78 and 6.25 mg mL⁻¹. Both extracts exhibited favorable safety profiles. In conclusion, *M. communis* and *E. arvense* extracts act as highly promising and safe phytobiotic alternatives, offering a holistic approach to disease management in aquaculture while minimizing reliance on traditional antibiotics.

Keywords: Phytobiotics; Aquaculture; Antimicrobial; *Myrtus communis*; *Equisetum arvense*.



O-08**From Waste to Value: Eco-Friendly Astaxanthin Extraction from Blue Crab Shell**E. Della Ceca¹, C. Pasqualini¹, C. Mannozi¹, G. Borsetta¹, M. Tiecco¹, S. Vittori¹

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The Atlantic blue crab (*Callinectes sapidus*), native to the western Atlantic, has rapidly become one of the most massive invasive species in the Mediterranean, driven by its high ecological plasticity and resistance. Its growing abundance demands effective management strategies. Crab culinary processing produces 70-80 % waste, whose improper disposal raises serious environmental problems. Astaxanthin is a prominent member of the carotenoid family and exhibits various biological activities, including, among others, antioxidant effects; lipid peroxidation; anti-inflammatory properties; cardiovascular disease prevention and so on. This work focused on the application of Switchable Deep Eutectic Solvents (DESs) that can enable the separation and recovery of astaxanthin while avoiding the use of toxic organic solvents. The tested DESs were composed of edible molecules, making them potentially safer alternatives even when not switchable. Extracting valuable compounds like astaxanthin from these residues offers a sustainable, circular economy-based solution with both environmental and economic benefits. Blue crab is desiccated, ground, collected in vacuum-sealed food bags and stored at -20 °C. Blue crab powder is put in contact with DESs under magnetic stirring and the astaxanthin enriched extract was analyzed through HPLC-DAD. The extract was tested for its own stability after light, air and heat exposure. The final step was the separation of DES from the extracted astaxanthin. In this work, astaxanthin was successfully extracted from blue crab carapace using SDESs that can be separated by switching or, after further analysis, could be used as edible component.

Keywords: Blue crab; Circular economy; SDESs; astaxanthin.

O-09

Conversion of Waste Seagrass into Carbon Dots: Synthesis and Characterization

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Seagrasses are ecologically important marine plants found in the Mediterranean Sea, increasing oxygen levels and providing habitat for various organisms. Due to both natural processes and environmental pollution, the leaves of these plants detach from their roots and accumulate along the coast. This biomass, which is seen as a waste problem especially on tourist beaches, has the potential to be transformed into different products due to its content. Carbon dots (CDs), a product of nanotechnology, find applications in many fields thanks to their high hydrophilicity, biodegradability, stability and unique optical properties. In this study, CDs were synthesized from waste seagrass biomass using a hydrothermal method and characterized optically, morphologically, and structurally using UV-Vis and fluorescence spectroscopy, TEM, and FTIR. Antioxidant activities of these CDs were determined using the DPPH method, while antibacterial activities were determined via disc diffusion and MIC methods. According to the results, an absorbance peak was observed at a wavelength of 270 nm in UV-VIS spectroscopy. The excitation wavelength at 340 nm and the maximum emission at 427 nm were obtained based on the fluorescence spectroscopy. The average size of the CDs is 3.897 ± 1.3 nm according to TEM analysis. According to the antibacterial activity results, CDs showed antibacterial activity against both *Escherichia coli* and *Staphylococcus aureus* with inhibition zones of 15.26 ± 1.4 mm and 13.77 ± 0.3 mm, respectively. Additionally, the MIC value of 4.169 mg/mL in both strains confirmed its antibacterial activity. Regarding antioxidant activity, it exhibited strong antioxidant capacity with 74.75% DPPH radical scavenging activity, demonstrating its potential application as a source of biologically active compounds. Characterization studies have shown that CDs obtained from seagrass are promising nanomaterials that can be used in many environmentally friendly and sustainable application areas. This study was supported by the Scientific Research Projects Coordination Unit of Manisa Celal Bayar University (BAP) under Project No: FLO-2026-3356.

Keywords: seagrass waste; carbon dots; characterization; antioxidant activity; antibacterial activity.



O-10

Extraction and Potential Biotechnological Applications of Sulphated Polysaccharides Derived from Four Mediterranean Marine Sponge Species

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Marine sponges are a goldmine of bioactive compounds that belong to several different chemical classes. Sulphated polysaccharides are endogenous macromolecules involved in key biological processes such as cell-cell recognition, adhesion and interaction with the extracellular matrix. Previous scientific studies have highlighted their ability to block harmful agents from attaching to human cells, thereby preventing infections. In this study, we tested the potential anti-adhesive properties of sulphated polysaccharides extracted from four different Mediterranean sponges. Samples of sponges belonging to the species *Chondrosia reniformis*, *Chondrilla nucula*, *Petrosia* (*Petrosia*) *ficiformis* and *Geodia cydonium* tissues were cut in small pieces and sulphated polysaccharides were extracted by precipitation with cetylpyridinium chloride (CPC). The powder was then desiccated and weighed to determine the yield, which was different depending on the sponge species. The powder was then resuspended in Milli-Q water and analyzed by agarose-gel electrophoresis and for quantification of sulphate group content. Ultimately, the sulphated polysaccharides were tested for their ability to prevent the adhesion of opportunistic bacterial pathogens to the surface of human keratinocytes (HaCaT cells) in vitro. The obtained results showed that the extraction of the sulphated polysaccharides from each sponge species produced different yields and sulphate contents, with *C. nucula* being the one with the highest yield (23.4 mg/g of animal – dry weight) and sulphate content (11.736 µg/g of sulphated polysaccharides). This underlines the species-specific composition of sulphated polysaccharides of each sponge species.

Furthermore, all extracts exerted significant activity inhibiting the attachment of *E. coli* on HaCaT cells showing their potential as anti-attachment molecules.

Keywords: Sponges; Sulphated polysaccharides; Biotechnological applications.



O-11

New Brominated Alterochromides from Coral-Associated *Pseudoalteromonas*

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Coral reefs are essential for socio-ecological stability, particularly in the Republic of the Maldives, but they face severe degradation due to escalating environmental stressors. While coral-associated microorganisms (CAMs) support reef resilience, their specific functional roles and secondary metabolites remain largely unexplored. This study aimed to isolate CAMs from the scleractinian corals *Porites lobata* and *Acropora gemmifera* to evaluate their biotechnological potential for biomedical and environmental applications. From an initial library of 198 isolates, priority strains, including members of the genera *Pseudoalteromonas*, *Streptomyces*, *Microbacterium*, *Micromonospora*, *Saccharopolyspora*, and *Rubrobacter*, were selected based on preliminary antimicrobial, antioxidant, and UV-protectant screening. Genome mining of *Pseudoalteromonas* sp. 39 using the antiSMASH platform revealed cryptic halogenase-encoding genes. To activate this pathway, lab-scale cultivation was performed in KBr-supplemented media, successfully triggering the production of brominated secondary metabolite. Untargeted LC-MS/MS coupled with molecular networking via GNPS unveiled a highly diverse chemical space, leading to the discovery of a novel subfamily and new analogues of brominated alterochromides (modified lipopeptides). Tandem mass spectrometry fragmentation analysis identified structural variations in the aryl-polyene chain length, bromination patterns, and peptide moieties. Utilizing a metabologenomic approach, we established a direct correlation between these newly identified molecular families and their corresponding biosynthetic gene clusters (BGCs). The enriched bioactive fractions demonstrated potent antimicrobial activity against *Vibrio anguillarum* and drug-resistant *Staphylococcus aureus*. Furthermore, these fractions exhibited significant photoprotective properties, safeguarding human keratinocytes (HaCaT) against UV radiation without inducing cytotoxicity. These findings underscore the immense metabolic diversity of marine pigmented *Pseudoalteromonas* and highlight CAMs as a prolific, untapped source of bioactive secondary metabolites for pharmaceutical discovery and coral reef restoration strategies.

Keywords: Coral-associated microorganisms; *Pseudoalteromonas*; Alterochromides; Metabologenomics; Bioactive secondary metabolite.



O-12

The Omega-3 Biosynthetic Pathway in the Antarctic diatom *Fragilariopsis cylindrus*

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Fragilariopsis cylindrus, one of the most abundant Antarctic diatoms and the only cold-adapted diatom with a fully sequenced genome, is a primary source of omega-3 fatty acids in polar marine food webs. Despite its ecological and biotechnological relevance, its omega-3 fatty acid biosynthetic pathway remains poorly characterized. Here, we report the comprehensive reconstruction of the cold-adapted omega-3 fatty acid biosynthetic pathway in *F. cylindrus* by integrating gene sequencing, heterologous expression, gene expression analysis, and targeted lipidomics. To characterize this biosynthetic pathway, we identified *in silico* the genes encoding the membrane-bound enzymes involved in the pathway, recombinantly expressed these enzymes in *Komagataella phaffii*. Their catalytic activity was assessed by whole-cell enzyme assays. *F. cylindrus* was then cultivated in photobioreactors at 1 °C and 7 °C, simulating both a typical Antarctic summer and a potential warming scenario; the resulting biomass was used to analyze differential expression of omega-3 pathway genes and to quantify omega-3 fatty acid concentrations under both temperature conditions. We identified four desaturases and two elongases responsible for the conversion of linoleic acid to docosahexaenoic acid and experimentally confirmed the catalytic activity of one elongase and one desaturase. Genes encoding key pathway enzymes displayed multiple genetic variants, consistent with the polyploid nature of *F. cylindrus*. Gene expression analysis revealed downregulation of three out of the six pathway genes in cells grown at 7 °C; however, omega-3 fatty acid concentrations remained stable under both conditions, indicating robust maintenance of biosynthetic output. The thermal resilience of *F. cylindrus* potentially underscores its adaptability to environmental change and establishes it as a valuable model organism for studying lipid biosynthesis in polar ecosystems. Furthermore, our findings lay the groundwork for the biotechnological application of cold-adapted enzymes capable of synthesizing nutritionally important omega-3 fatty acids.

Keywords: Cold-adapted diatom; Desaturases; Elongases; Omega-3 fatty acids.



O-13

From the Sea to Cancer Therapy: Discovery of a New Family of Chlorinated MetabolitesR. Konkel¹, Ł. Grabowski², M. Cegłowska³, G. Węgrzyn², H. Mazur-Marzec¹

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Marine cyanobacteria are prolific producers of structurally diverse secondary metabolites with a wide range of biological activities. Their remarkable biosynthetic capacity makes them a rich source of novel natural products with significant potential for drug discovery. During a chemical investigation of the Baltic Sea cyanobacterium *Nostoc edaphicum* CCNP1411, LC-MS/MS-guided analysis led to the discovery of a previously undescribed family of chlorinated metabolites. The newly identified metabolites, with molecular masses of approximately 670 Da, comprise several closely related analogues. Preliminary MS/MS analyses revealed the presence of two chlorine atoms and a thiazole moiety, while also indicating that some members of the family are glycosylated. The major metabolite was isolated for biological evaluation. Cell viability assays demonstrated potent antiproliferative activity against the human neuroblastoma cell lines SH-SY5Y and IMR-32. Notably, normal human dermal fibroblasts (HDFc) were considerably less sensitive, suggesting selective cytotoxicity toward malignant cells and underscoring the therapeutic promise of these compounds. Ongoing work focuses on the repeated isolation and comprehensive structural characterization of the metabolites using NMR spectroscopy together with complementary analytical techniques. The discovery of this new family of chlorinated metabolites further highlights Baltic cyanobacteria as an underexplored source of chemically unique natural products with promising anticancer potential.

Keywords: *Nostoc edaphicum*; Cyanobacteria; Neuroblastoma; Chlorinated metabolites; Marine natural products.



O-14

Preparation and Bioactivities of Polysaccharides and Peptides from Sea CucumberR. Li^{1,2}, Y. Liu¹, H. Yu^{1,2}, S. Liu^{1,2}, R. Xing^{1,2}

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Sea cucumbers are widely distributed throughout all oceans worldwide, ranging from tropical, subtropical, and temperate waters to polar regions. There are approximately 1,000 species in total, of which about 40 are edible. Their body walls contain a variety of bioactive compounds, offering significant nutritional and medicinal benefits. Herein, we prepared bioactive polysaccharides and peptides from the sea cucumber *Cucumaria frondosa* by enzymatic digestion and chromatographic separation and then evaluated their anticoagulant and antioxidant activities. Fucosylated chondroitin sulfate (FCScf) was successfully isolated from the digest using DEAE-52 and Sephadex G-100 column chromatography. Structural analysis revealed that FCScf is a unique branched glycosaminoglycan, comprising a chondroitin sulfate backbone with sulfated fucose branches. FCScf exhibits extraordinary anticoagulant activity, which is greatly affected by its molecular weight. The 10 kDa FCScf exhibited greater intrinsic anticoagulant activity than the clinical drug low molecular weight heparin (LMWH), with no bleeding risk, making it a promising candidate for novel anticoagulant drug development. Mechanistically, FCScf-10K specifically inhibits Xase complex formation by binding its negatively charged sulfate groups to the positively charged arginine side chains on the surface of factor IXa. In addition, the peptides derived from sea cucumber also exhibit potent antioxidant activity and have been developed into health foods. Therefore, biotechnology can be employed to achieve the high-value processing and utilization of sea cucumbers and to develop marine-derived drugs or health foods beneficial to human health.

Keywords: Sea cucumber; *Cucumaria frondosa*; Bioactive polysaccharides; Bioactive peptides; High-value processing and utilization.



O-15

Valorisation of *Daphnia magna* and Microalgae for High-Value Biomolecules Production

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Environmental changes and overfishing are increasingly exerting significant pressure on ecosystems, contributing to biodiversity loss and threatening the sustainability of conventional biological resources. In this context, alternative aquatic biomasses offer promising opportunities for the sustainable production of high-value biomolecules with applications in food, biotechnology, and nutraceutical sectors.

This study investigated an integrated culture system based on *Daphnia magna* fed with two microalgal species, *Tetraselmis* sp. and *Scenedesmus dimorphus*, supplied at different proportions. The objective was to optimize biomass production while enhancing nutritional quality and generating valuable bioactive compounds. Growth performance, reproductive output, and biochemical composition (proteins, lipids, carbohydrates, ash, and fatty acid profiles) of *D. magna* were evaluated. In parallel, high-value biomolecules were extracted and characterized from both microalgae and *D. magna* biomass. Results revealed a clear diet-dependent response in *D. magna*. Feeding *Tetraselmis* sp. significantly enhanced growth and reproductive performance compared with *S. dimorphus*. Moreover, the biochemical composition of *D. magna* was markedly affected by the dietary treatments. Both microalgal diets promoted a significant accumulation of proteins and carbohydrates accompanied by a reduction in lipid levels, suggesting a metabolic reallocation of energy toward growth and reproduction rather than lipid storage. This response is likely associated with the nutritional quality and digestibility of the microalgal diets. In addition, polyphenolic extracts obtained from both microalgal species exhibited antioxidant activity, while chitin was successfully recovered from *D. magna* biomass.

In conclusion, the integrated cultivation of microalgae and *D. magna* represents a promising and sustainable platform to produce value-added aquatic biomass. By enhancing the growth and nutritional quality of *D. magna*, particularly through *Tetraselmis* sp.-based diets, this system combines biomass production with the recovery of bioactive compounds of industrial interest. The dual valorisation of microalgae and zooplankton highlights the potential of this approach to support innovative biotechnological applications and sustainable blue bioeconomy development.

Keywords: Alternative aquatic biomass; Integrated culture system; Biochemical composition; Valuable biomolecules; Sustainable approach.



O-16

Assessment of the Biodiesel Potential of Microalgal Blooms: Lipid and FAME Yields from Freshwater Ecosystems in Türkiye

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Eutrophication, particularly cyanobacterial blooms accompanied by microalgal proliferation, severely impacts aquatic ecosystems, however, the biomass generated during these events represents a promising feedstock for economically valuable products such as biodiesel and bioactive compounds. This study evaluated the biodiesel potential of bloom biomass collected in summer 2025 from two artificial ponds (Gümüşyaka and Çakıl, İstanbul) and a natural wetland (Manyas Lake, Balıkesir, Türkiye). Dominant algal groups were determined in situ using a FluoroProbe, and species were identified by light microscopy. According to FluoroProbe analyses, cyanobacteria accounted for more than 70% of the total biomass across all stations throughout the sampling period. Microscopic analysis revealed that *Planktothrix agardhii* and *Aphanizomenon* sp. dominated Gümüşyaka Pond, whereas *Microcystis* species particularly *M. wesenbergii* and *M. aeruginosa* were prevalent together with *Woronichinia* sp. in Çakıl Pond and Manyas Lake exhibited greater taxonomic diversity, including *Microcystis*, *Aphanizomenon*, *Cuspidothrix issatschenkoi* and *Dolichospermum spiroides* alongside diatoms and green algae contributing substantially to total biomass. Based on monthly analytical measurements, lipid contents ranged from 10.6–28.3% in Gümüşyaka, 14.5–16.1% in Çakıl, and 11.8–16.4% in Manyas, while FAME yields varied between 4.2–9.7%, with the highest value recorded in Gümüşyaka in July. Mid-summer samples (July–August) showed enhanced lipid and FAME production. The yields were higher than those reported for laboratory-scale monocultures, suggesting that environmental stress conditions during natural bloom events may stimulate lipid accumulation and FAME production. These findings highlight the potential of bloom biomass for sustainable biodiesel production, supporting its environmental and economic valorization.

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Keywords: Cyanobacteria; Algal Bloom; Biodiesel; Bioactive compounds.



O-17

Carbon Nanomaterials Meet Algae: Boosting Photosynthesis and Valuable Products

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Microalgae can serve as sustainable sun-driven cell factories for producing valuable metabolites (e.g., pigments, fatty acids), enabling applications in food and feed and cosmetics. However, low solar-to-product efficiency, suboptimal use of light, poor selectivity in the carbon flux for high-value compounds, and limited biomass productivity can hamper the development of future algae-based industry. Hybrid systems integrating algal culturing with carbon nanomaterials, including single-walled carbon nanotubes (SWCNTs) and carbon dots (C-Dots), offer a promising solution to boost light harvesting and photosynthesis, and to trigger targeted compound accumulation in algae and cyanobacteria via hormetic responses. Nonetheless, phototrophs-nanomaterials interactions remain poorly explored and further research is needed to elucidate species-specific responses to diverse materials. Here, a series of experiments investigating the effects of SWCNTs functionalized with proteins (e.g., lysozyme) and C-Dots derived from peanut shells on multiple microalgae and cyanobacteria are presented, combining acute toxicity assays and cultivation. Short-term exposure of algae to low-dose SWCNTs ($<1 \text{ mg L}^{-1}$) showed negligible toxicity across most algal species, while responses to C-Dots were more variable in terms of dose-dependent ($1\text{-}50 \text{ mg L}^{-1}$) and species-specific effects. The three most promising candidate phototrophs, exhibiting enhanced photosynthesis or growth performance in preliminary tests, were selected to assess nanomaterial-mediated effects on growth and biochemical composition after long-term exposure. Cultivation with SWCNTs@lysozyme enhanced the production of valuable metabolites, increasing C-phyococyanin in the cyanobacterium *Limnospira platensis* after 14 days (+38%), and polyunsaturated fatty acids (PUFAs) in the marine diatom *Thalassiosira* sp. after 7 days (DHA +92%, EPA +63%) compared to controls. Similarly, PUFAs increased relative to controls (44 vs 41 %/TFAs) following 7-day exposure to C-Dots (5 mg L^{-1}) in *Phaeodactylum tricornutum*. Overall, carbon nanomaterials show potential to enhance photosynthesis and promote valuable metabolite production in phototrophs, paving the way for further investigation.

Keywords: Single-walled carbon nanotubes; Carbon dots; Phycocyanin; Polyunsaturated fatty acids; Blue growth.



O-18

Development of a Continuous Two-Stage System for the Remediation of Offshore Produced Water

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Produced water, a major byproduct of oil and gas extraction, contains high concentrations of oil and grease (O&G), chemical oxygen demand (COD), and other recalcitrant pollutants, posing significant environmental and disposal challenges. Conventional treatment methods often struggle with variable composition, high organic loads, and high operational costs, necessitating the development of sustainable, efficient treatment strategies. In this study, an integrated two-stage biological continuous treatment process was developed for the remediation of produced water. The raw produced water, characterized by 96.0 ± 11.94 mg/L O&G and 940 ± 23.32 mg/L COD, was initially pretreated using the hydrocarbon-degrading bacterium *Rhodococcus opacus*, resulting in a substantial reduction of oil fractions and improved biodegradability. The pretreated effluent was subsequently subjected to phyco-mycoremediation using a co-culture of the filamentous fungus *Aspergillus oryzae* and microalga *Chlorella vulgaris* under continuous operation. After the pretreatment phase, O&G concentrations and COD in pretreated PW ranged from

25 to 33 mg/L and 450-600 mg/l, respectively, and were consistently reduced to 2-5 mg/L and 150-220 mg/L, respectively, corresponding to removal efficiencies of approximately 85-92% for O&G and 60-70% for COD. Overall, two-stage systems achieved 94.79-97.91% O&G and 76.59-87.23% COD reduction. The system exhibited an initial acclimatization phase, followed by stable performance with minimal fluctuations in effluent quality despite influent loading variability. The enhanced performance can be attributed to synergistic interactions within the fungal-algal co-culture, which facilitate hydrocarbon degradation, organic matter assimilation, and nutrient uptake. The process demonstrated robustness and adaptability under continuous operation, highlighting its potential for large-scale application. Overall, integrated bacterial pretreatment with phyco-mycoremediation provides an effective, eco-friendly, and scalable solution for produced water treatment, significantly improving effluent quality and addressing the limitations of conventional approaches.

Keywords: Co-culture; Petroleum hydrocarbon; Phyco-mycoremediation; Pretreatment; Produced water.

This contribution was not presented during the symposium



O-19**Aerobic Granular Sludge Technology for Sustainable Treatment of High-Strength Mixed Industrial Wastewater****B. Kaya¹, A. Konuklar¹, G.E.Z. Balç¹, G. İnsel¹, E. Çokgör¹**

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Population growth and industrialization have intensified environmental pollution, threatened limited natural resources and increased the demand for sustainable wastewater treatment technologies. Conventional activated sludge (CAS) systems require large footprints and high energy consumption, making them less suitable for treating high-strength industrial wastewater with complex characteristics. Aerobic granular sludge (AGS) technology has recently emerged as a promising environmental biotechnology due to its compact configuration, superior treatment efficiency, lower energy demand, and reduced greenhouse gas emissions. The unique layered structure of AGS granules enables the coexistence of aerobic, anoxic, and anaerobic microenvironments, allowing simultaneous organic matter and nutrient removal within a single reactor. Despite its successful application to municipal wastewater, studies on AGS for high-strength mixed industrial wastewater remain limited. In this study, a simulation was conducted using experimental data obtained from a full-scale wastewater treatment plant serving a mixed industrial Organized Industrial Zone in Türkiye. The existing CAS process and a proposed AGS configuration were modelled and evaluated using the SUMO simulation platform (Dynamita). Simulation results demonstrated that the AGS system achieved lower effluent total nitrogen concentrations than the conventional process. The improved nitrogen removal performance was attributed to simultaneous nitrification and denitrification within the granules, where dissolved oxygen gradients create anoxic microzones. Furthermore, the AGS system reduced the required biological reactor volume by approximately 70% and aeration demand by 35% compared with the existing CAS system. Owing to its significantly smaller footprint, the estimated initial civil construction cost was reduced by approximately 65%. These findings demonstrate that AGS technology is a sustainable and resource-efficient alternative for the treatment of high-strength mixed industrial wastewater, providing significant reductions in energy consumption, reactor volume, and capital investment while maintaining superior treatment performance. Results further support the potential of AGS as an innovative environmental biotechnology contributing to low-carbon and circular bioeconomy-oriented wastewater management.

Keywords: Aerobic granular sludge; Industrial wastewater; Wastewater treatment; Nitrogen removal; Process simulation.



O-20

Microalgae as a biotechnological tool for bio-CCU

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The increasing concentration of atmospheric carbon dioxide (CO₂) has intensified the search for sustainable technologies capable of improving carbon capture and utilization (CCU). Microalgae are promising biological platforms for CO₂ fixation and biomass production; however, their efficiency is often limited by the low transfer rate of CO₂ from the gas phase to the culture medium. Carbonic anhydrases (CAs), which catalyze the rapid interconversion of CO₂ and bicarbonate, offer a potential solution by enhancing inorganic carbon availability. Here, a recombinant CA immobilized on silica-coated magnetic nanoparticles (CA-NPs) was evaluated as a strategy to improve CO₂ hydration and support microalgal growth.

CA-NPs were synthesized, functionalized for covalent enzyme immobilization, and characterized to determine immobilization efficiency and catalytic activity. The effect of CA-NPs on biomass production was investigated using a Chlorophyta strain cultivated in a photobioreactor under controlled conditions. Three experimental setups were compared: microalgae cultured without nanoparticles, with enzyme-free nanoparticles, and with CA-NPs. The immobilized enzyme retained approximately 60% of the activity of the free enzyme, while enzyme-free nanoparticles showed no detectable catalytic activity. Growth experiments demonstrated that cultures supplemented with CA-NPs achieved higher carbon fixation rate than the other cultures, indicating that the immobilized enzyme effectively enhanced carbon availability and mitigated the negative effects associated with nanoparticle addition.

These findings demonstrate the potential of CAs immobilized on silica-coated magnetic nanoparticles to enhance microalgal cultivation by improving CO₂ hydration and utilization. This approach represents a promising strategy for integrating biocatalysis and microalgal biotechnology in sustainable CCU systems, although further optimization of enzyme loading and nanoparticle concentration is required to maximize process performance.

Keywords: Microalgae; Carbon capture and utilization; Carbonic anhydrases.



O-21

The Impact of Microplastics on The Properties of Protamine-Like Proteins. A Case of Gamete Plasticity or a Risk to Reproduction in *Mytilus galloprovincialis*?

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At present, plastic pollution has become a pervasive problem in all ecosystems, exerting a particularly deleterious effect on marine ecosystems and external fertilisers such as the mussel *Mytilus galloprovincialis*. This study aims to evaluate the toxicological effects on the reproductive health of this organism following exposure to two concentrations of polystyrene microplastics (PS-MPs) (0.5 and 1 µg/L), which are representative of conditions in the Mediterranean Sea. Following exposure, the electrophoretic pattern of protamine-like (PL) proteins — the primary nuclear basic proteins in the sperm chromatin of *M. galloprovincialis* — was analyzed. Differences were observed by SDS-PAGE for PL of mussels exposed to the higher dose of microplastics compared to unexposed mussels. These proteins also exhibited an increased ability to bind to DNA, as determined by Electrophoretic Mobility Shift Assay (EMSA), as well as a higher capacity to protect DNA from oxidative damage. At this PS-MP concentration, reduced release of all PLs from sperm nuclei was also observed. However, digestion by micrococcal nuclease did not reveal any significant differences between exposed and unexposed conditions. Finally, the potential poly(ADP)-ribosylation of the PLs was investigated. PL-II exhibited an augmentation in poly(ADP)-ribosylation following PS-MPs exposure, a phenomenon that may elucidate the varied capacity of the PLs to bind DNA. In conclusion, while the results suggest a molecular mechanism of gametic plasticity upon exposure to 1 µg/L PS-MPs, they also indicate that this exposure level could severely impact the reproductive health of *M. galloprovincialis* by preventing the release of nuclear basic proteins from sperm DNA at fertilization.

Keywords: Polystyrene Microplastics; *Mytilus galloprovincialis*; Poly(ADP)-Ribosylation; Protamine-like; Reproduction.



O-22

Biomonitoring of Metal(loid) Pollution in Freshwater Ecosystems: An Integrated Study of Bioaccumulation, Oxidative Stress, and Detoxification Mechanisms in *Leptodictyum riparium*

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Metal(loid) contamination poses significant risks to freshwater ecosystems. This study investigates the bioaccumulation capacity and biological responses of the aquatic moss *Leptodictyum riparium* exposed to environmentally relevant concentrations of cadmium (Cd) and arsenic (As), detected in the Regi Lagni basin, to validate its use as a bioindicator.

L. riparium gametophytes were exposed in vitro to increasing concentrations of Cd and As. Bioaccumulation was quantified via ICP-MS. Physiological and biochemical responses were assessed by measuring Reactive Oxygen Species (ROS), the activity of antioxidant enzymes (SOD, CAT, GST, POD), photosynthetic pigment content, and stress markers. Advanced techniques were employed to investigate detoxification pathways: targeted proteomic to analyze phytochelatin synthesis and confocal microscopy with monochlorobimane (MCB) to visualize and quantify thiolic compounds. Both Cd and As accumulated in a dose-dependent manner, with As showing higher bioaccumulation. Exposure triggered oxidative stress and modulated antioxidant enzyme activities. Distinct responses were observed in photosynthetic pigment content and ultrastructure. Proteomic analysis confirmed the induction of phytochelatin synthesis, while MCB staining revealed a significant increase in thiolic compounds, particularly in As-treated samples, indicating a strong detoxification response.

L. riparium is a highly sensitive bioindicator. The results of bioaccumulation, oxidative stress, and the activation of specific detoxification pathways provide a robust mechanistic framework for environmental risk assessment in contaminated freshwater systems.

Keywords: *Leptodictyum riparium*; Bioaccumulation; Oxidative Stress; Phytochelatins; Biomonitoring.



O-23

Towards a Data Driven Biofouling Forecast System for the Seaweed Biotechnology Sector

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The rapid expansion of kelp cultivation across the Northeast Atlantic is opening new opportunities for sustainable bioproducts and blue biotech innovation, yet the sector remains heavily constrained by biofouling, which rapidly reduces biomass quality and limits downstream processing potential. Late season colonization by hydrozoans, bryozoans, bivalves and tunicates persists as a major biological bottleneck. Although these assemblages originate from meroplanktonic larvae, the lack of coordinated, largescale monitoring has prevented early detection and reliable prediction for both researchers and industry. To drive the development of a scalable biotech-ready solution for managing biofouling risk, we established a harmonized observation network across 50 stations situated within ten commercial kelp farms from Norway to southern England. From December 2024 to June 2025, we conducted monthly sampling of nutrient concentrations, chlorophyll, water chemistry, hydrodynamic conditions, plankton community composition and kelp-associated biofouling. This integrated dataset underpins the construction of a causal predictive modelling framework designed to forecast fouling pressure using a reduced set of easily obtainable variables, with the long-term goal of embedding predictions into farm management tools and emerging digital biotechnology systems.

Initial analyses reveal substantial spatial variation in environmental baselines across farms, particularly in winter nutrient regimes. Local deviations in NO₃, NO₂ and PO₄ suggest strong influence from freshwater inputs and catchment-specific dynamics.

Plankton communities exhibited pronounced seasonal shifts, yet the abundance of key biofouling meroplankton—such as bryozoan and hydrozoan larvae—differed markedly between farms even within the same month. These patterns highlight the importance of fine-scale oceanographic and ecological processes operating at the farm level as drivers of biofouling risk. By integrating environmental, hydrodynamic and biological data across this transatlantic network, the project is establishing the foundation for a practical, biotech-oriented predictive tool capable of informing farm design, crop scheduling and spatial planning for fouling-resilient kelp harvest.

Keywords: Biofouling; Sugar kelp; AI tool; Risk prediction; farm aquaculture.



O-24

Red Microalgae *Porphyridium purpureum* Under Different Light Colours: Uncovering Growth Mechanisms

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Narrow-spectrum Light Emitting Diode (LED) technology is a promising method for optimizing microalgal bioactive compounds. Certain wavebands enable distinct physiological responses; for instance, red light often promotes biomass accumulation, while blue light enhances lipid and pigment synthesis. However, these responses are often inconsistent across different studies and species, even within the same taxa. Understanding the underlying mechanisms allows for sophisticated manipulation of molecular pathways to increase growth and clarifies how light colour affects photophysiological processes, e.g. efficiency of light-to-chemical energy conversion. This control relies on light perception through light-harvesting complexes (antennae), which capture light for photosynthesis within the chloroplast.

This study investigates the effects of different light colors (green, blue, white, and red) on the red microalgal species *Porphyridium purpureum*, with all color treatments standardized for the same light intensity. The objectives are to assess differences in growth, pigment composition (phycoerythrin and chlorophyll-a) and photosynthetic performance. Growth was monitored via cell density, and pigment concentrations were measured spectrophotometrically. Phycoerythrin and chlorophyll-a were selected as they reflect the primary light-harvesting and reaction center components in PSII, focusing on light capture rather than excess light stress-related pigment responses. Photosynthetic parameters were evaluated using Pulse-Amplitude-Modulated fluorometry, focusing on the operating quantum efficiency of PSII (Φ PSII) and non-photochemical quenching (NPQ), which reflects heat dissipation. Preliminary results indicate that blue light is associated with a higher phycoerythrin concentration, but it also shows the lowest cell density. In contrast, white light appears to produce the highest cell density overall, while green and red fall in between. For all light conditions other than blue, there do not seem to be differences in phycoerythrin content, and they are all lower than in blue light. Further insights from photochemical analysis, regarding differences in photosynthesis, will help explain the underlying mechanisms behind these observations.

Keywords: Phytoplankton; Wavelength; Light quality; Pigments; Photosynthesis.



O-25

When bioremediation meets stress: Arsenic in moss-snail aquatic system

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Arsenic (As) is a widespread environmental contaminant with well-documented toxic, teratogenic, and carcinogenic effects, posing a serious risk to aquatic ecosystems and human health due to its persistence, mobility, and ability to bioaccumulate along the food chain. Bioremediation, particularly using aquatic plants or gastropods with high accumulation capacity, has emerged as a sustainable strategy to mitigate metal contamination. This study aimed to investigate the bioremediation potential of the aquatic moss *Leptodictyum riparium* and gastropod *Lymnaea stagnalis* and to assess arsenic bioavailability and toxicity. Experiments were conducted under controlled conditions, exposing organisms individually and in a microcosm system to environmentally relevant As concentrations. As accumulation was quantified in water and biological tissues. Oxidative stress responses were assessed through measurements of reactive oxygen species (ROS) levels, antioxidant enzyme activities (catalase, CAT; superoxide dismutase, SOD), and the expression of stress-related proteins (HSP70 and p53). Both species showed a significant capacity to accumulate As, contributing to a reduction of its concentration in water. However, contrary to expectations, their co-presence reduced overall bioaccumulation efficiency and altered arsenic distribution among biological compartments. Arsenic exposure induced oxidative stress in both organisms, as evidenced by modulation of ROS levels, antioxidant defenses, and stress protein expression. Notably, the interaction between moss and snails acted as an additional stressor, amplifying physiological responses rather than mitigating toxicity. These findings highlight the complexity of biotic interactions in remediation systems and suggest that species coexistence can influence contaminant dynamics and stress responses. This has important implications for the application of nature-based solutions in contaminated freshwater environments, indicating that careful consideration of interspecific interactions is essential when designing bioremediation strategies.

Keywords: arsenic; *L. stagnalis*; *L. riparium*; oxidative stress; phytoremediation.



O-26

Interactive Effects of Cadmium and Nitrogen Depletion on Resting Spore Dynamics in *Chaetoceros* spp.

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Diatoms of the genus *Chaetoceros* are well known for their ability to adapt to changing environmental conditions through the formation of resting spores, an adaptive strategy that enhances survival under adverse conditions (Ellegaard & Ribeiro, 2018). Nitrogen depletion and high cell density are recognized as key triggers of resting spore formation in *Chaetoceros socialis* (Pelusi et al., 2020; Pelusi et al., 2023), while the influence of toxic metals and their interaction with nutrient stress remains poorly understood.

In this study, we investigate how cadmium (Cd) exposure and nitrogen depletion affect the growth and resting spore formation in different *Chaetoceros* species. Our experimental design included both Cd-only exposure tests, with concentrations ranging from 0 to >30 µM, and combined Cd and N-depletion treatments aimed at evaluating the interaction between metal toxicity and nutrient limitation. Preliminary observations in *C. socialis* indicate that Cd affects diatom physiology and growth and may modulate life cycle transitions.

These preliminary findings suggest that metal may act primarily as metabolic stressor rather than a direct trigger of spore formation. This hypothesis is consistent with studies showing that Cd exposure can alter the physiology and morphology of marine diatoms (Mišić Radić et al., 2021) and may indirectly suppress sporulation processes (Sanders & Cibik, 1985). Ongoing experiments are extending this approach to *Chaetoceros costatus* and *Chaetoceros didymus*, previously examined under nitrogen depletion and high cell density, to assess whether Cd response is conserved across the genus. Given the widespread use of *Chaetoceros* as live feed in aquaculture hatcheries, where its high PUFA content, including EPA, makes it a key nutritional resource for bivalve and crustacean larvae (Siddik et al., 2023; Ma et al., 2024) a deeper understanding of the biology and survival strategies of this genus is essential to ensure culture reliability and sustainability.

Keywords: *Chaetoceros*; Resting spores; Cadmium toxicity; Nitrogen depletion; Live feed.



O-27

The Diversity of Cyanophages in Lake Sevan, Armenia and Their Potential Impact on Harmful Cyanobacterial Blooms

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In recent years, eutrophication-driven harmful cyanobacterial blooms have become a serious ecological problem in Lake Sevan, Armenia. Cyanophages, viruses infecting cyanobacteria, are considered one of the factors that may influence cyanobacterial population dynamics and bloom development. The aim of this study was to investigate the diversity of cyanophages in Lake Sevan and evaluate their possible role in the regulation of toxic cyanobacterial blooms.

Water samples were collected from coastal areas of the Big and Small Sevan basins before, during and after the bloom period.

Microbial and viral communities were analyzed using shotgun metagenomic sequencing (Illumina Sequencing), complemented by laboratory isolation and host–phage interaction experiments. Metagenomic data were analyzed using the Kbase platform.

The data obtained showed that during the spring-summer period the cyanobacterial community was dominated by representatives of the genera *Synechococcus*, *Cyanobium*, *Nostoc*, *Prochlorococcus* and *Leptolyngbya*, which are associated with bloom formation. Metagenomic analysis also revealed the presence of several cyanophages, including Cyanophage KBS-S-2A, P-RSM6, PSS2 and phages infecting *Synechococcus*. In both basins, an increase in viral diversity was observed during the decline of cyanobacterial blooms, suggesting active interactions between cyanophages and their hosts.

Laboratory experiments confirmed the presence of viable lytic cyanophages capable of infecting an isolated *Leptolyngbya* sp. strain. The increase in cyanophage diversity during cyanobacterial decline supports their role in bloom termination through host lysis and modulation of microbial community structure.

The results of preliminary laboratory experiments support the assumption that cyanophages may contribute to the natural regulation of cyanobacterial populations. These findings provide new information on the viral diversity of Lake Sevan and highlight the potential ecological significance of cyanophages in bloom dynamics and freshwater ecosystem management.

Acknowledgment: This research was funded by the Higher Education and Science Committee of MESCS RA within the framework of research project 25SRNSF-1F020.

Keywords: Lake Sevan; Cyanophage; Cyanobacteria; Toxic cyanobacterial bloom; Ecosystem management.



O-28

Molecular effects of chromium on the sperm chromatin of *Mytilus galloprovincialis*

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Hexavalent chromium (Cr (VI)) is a widespread environmental contaminant with well-documented genotoxic properties, detectable in Mediterranean coastal waters at biologically relevant concentrations. *Mytilus galloprovincialis*, a sessile filter-feeding bivalve, represents an ideal bioindicator for investigating the effects of heavy metals on the reproductive system of marine invertebrates. Studies on the molecular mechanisms underlying heavy metal toxicity in invertebrate reproduction remain limited, and the role of poly(ADP-ribosylation) (PARylation) in sperm chromatin is still poorly understood. This study investigated the effects of environmentally relevant doses of Cr (VI) (1, 10 and 100 nM, 24h exposure) on the male reproductive system of the mussel. Gonadal chromium accumulation was measured by ICP-MS, testicular morphology was assessed by HE and PAS staining, and PARP expression, activity and automodification were evaluated by western blotting and biochemical assays. γ H2A.X phosphorylation was measured as a marker of double-strand DNA damage. For the first time, possible poly (ADP-ribosylation) of protamine-like (PL) proteins was investigated by immunoblotting with anti-PAR antibody. Changes in PL-DNA binding were assessed by absorption spectroscopy and micrococcal nuclease (MNase) digestion assays. Cr (VI) exposure induced dose-dependent chromium accumulation in the gonads, accompanied by progressive morphological damage, including haemocyte infiltrates, germ cell disconnection and lipofuscin granule deposition. γ H2A.X expression increased dose-dependently, while maximum PARP activity was detected at 10 nM Cr (VI). Notably, endogenous poly (ADP-ribosylation) of PL-II was demonstrated under all exposure conditions. This post-translational modification impaired PL-DNA binding, as shown by reduced absorbance at 260 nm in PL/DNA complexes and increased sperm chromatin accessibility to MNase digestion. These findings propose a novel molecular mechanism by which Cr (VI) activates PARP-mediated PARylation of PL-II, compromising sperm chromatin compaction and providing new insights into the ecotoxicological risk of chromium in marine environments.

Keywords: Chromium (VI); *Mytilus galloprovincialis*; Poly (ADP-ribosylation); PARP; Protamine-like proteins.



O-29

Acoustic and Satellite Techniques for Quantification and Monitoring of Gas-Bearing Cyanobacteria

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Bloom-forming toxic cyanobacteria pose a serious threat to environmental safety and public health in eutrophic lakes and reservoirs worldwide. Efficient *in situ* monitoring methods are essential for tracking cyanobacterial dynamics and predicting bloom development. In this study, we developed an acoustic approach to quantify the abundance of gas-containing *Microcystis* colonies using a high-frequency scientific echo sounder in both enclosure experiments and natural lake conditions. Strong correlations were found between volume backscattering strength (Sv) and chlorophyll *a* (Chl *a*) concentration, as well as between Sv and colony biovolume. The approach was applied for *in situ* monitoring of *Microcystis* blooms in Lake Kinneret, where temporal variations in the Sv–biomass relationship likely reflected changes in the proportion of free gas within colonies under different light intensities. Continuous acoustic observations revealed pronounced vertical migrations of *Microcystis* biomass in response to environmental factors such as water column stratification, vertical mixing, wind, and light conditions. In addition, hyperspectral remote sensing of phycocyanin (PC) and Chl *a* concentration enabled the estimation of cyanobacterial contributions to total phytoplankton biomass and the assessment of environmental drivers shaping complex planktonic communities. The integration of acoustic and satellite-based methods provided comprehensive insights into the vertical and horizontal variability of cyanobacterial biomass and bloom patchiness. Overall, our results demonstrate that remote-sensing monitoring is a highly effective, real-time tool for detecting, quantifying, and understanding the spatiotemporal dynamics of *Microcystis* blooms, even at early developmental stages.

Keywords: *Microcystis*; remote sensing; *in-situ* monitoring; cyanoHAB, spatiotemporal dynamics.

This contribution was not presented during the symposium



O-30

Adsorptive Removal of Amoxicillin by *Ulva lactuca* from Aqueous MediumD. Cerşit¹, D. Ozyurt², F.A. Ozdemir Olgun¹

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As antibiotics are widely used in veterinary care, human healthcare, and agricultural uses, pharmaceutical waste is constantly discharged into marine environments. Due to its high consumption and inability to be eliminated by conventional wastewater treatment methods, amoxicillin trihydrate (AMX) is one of these antibiotics that is commonly found in wastewater systems. The presence of AMX in aquatic habitats may result in the emergence of antibiotic-resistant bacteria, detrimental effects on aquatic life, and environmental contamination. Therefore, developing ecologically acceptable and sustainable AMX removal treatment methods is more important than ever. The adsorption potential of *Ulva lactuca* macroalgae biomass for the removal of amoxicillin trihydrate from aqueous solutions was investigated within the scope of this study. *Ulva lactuca* species were selected as biosorbent materials due to their natural abundance, rapid growth, low cost, and high concentration of functional groups such as hydroxyl, carboxyl, sulfate, and amino groups. Adsorption studies were carried out under a variety of operational conditions, including pH, contact time, and adsorbent dosage, to determine the optimal adsorption parameters, with the aid of experimental design software. Adsorption performance was further investigated using Freundlich and Langmuir isotherm models. The higher correlation coefficient of the Freundlich model suggested heterogeneous adsorption activity on the adsorbent surface. Thermodynamic study revealed a negative Gibbs free energy value under the investigated conditions, suggesting a spontaneous process. To the best of our knowledge, based on an extensive review of the literature, this is the first study to evaluate the adsorption potential of *U. lactuca* specifically for the removal of AMX.

Keywords: Amoxicillin trihydrate; *Ulva lactuca*; Adsorption; Antibiotic removal.



O-31

Metagenomic Analysis of Bacterial Pathogens Associated with Microplastics in the Coastal Marine Environments of Izmir and Istanbul**I. Bilgin¹, M. Dagdeviren², E. Bozcal³**

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Plastic pollution in marine environments is of considerable significant in terms of its impact on ecosystems and biodiversity. Microplastics constitute a significant source of anthropogenic pollution in marine environments. The increase in microplastic pollution could lead to alarming levels of microplastics acting as vectors for pathogen transmission. The surfaces of microplastics can serve as an important environmental substrate for the colonization of different microbial community members, including bacteria. Ecological processes could shape microbial formation on the microplastic surface. The ecological niche that forms a biofilm on the microplastic surface, called the plastisphere, can contain bacterial pathogens that would affect the marine ecosystem and human health. In this context, microplastic and coastal seawater sampling was carried out from coastal seawater stations in Izmir (n=2) and Istanbul (n=2) of Türkiye. Microplastic samples were grouped, and surface and elemental analyses of microplastic samples were performed using SEM/EDX. To determine the microplastic-associated and water column planktonic bacterial community composition, 16S rRNA amplicon metagenomic sequencing analysis was performed. A total of 159 microplastic particles with fragment and film morphology were identified at all sampling stations. According to SEM/EDX analysis, the elemental distribution of microplastics was determined to consist of C, O, and N. In addition to local marine bacteria capable of forming biofilms and observable planktonic in the water column, the distribution of *Vibrio* and *Acinetobacter* genera, which may pose risks to the environment and public health, was observed on the surface of microplastic samples from the Haliç and Bakırköy stations. Our findings suggest that microplastics may cause the transmission of plastispheres, including bacterial pathogens, to previously unaffected marine ecosystems, potentially impacting marine biodiversity and human health.

Acknowledgment: This study was supported by Istanbul University Scientific Research Projects Coordination Unit with project number FYL-2024-41158

Keywords: Microplastic; metagenomic; biofilm; pathogen; sea water

This contribution was not presented during the symposium



O-32

Mass Spectrometry Query Language (MassQL)-Assisted Detection of Microcystin Variants

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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 determination of these hepatotoxins in complex environmental and biological matrices is essential for hazard assessment and environmental monitoring. Liquid chromatography coupled with high-resolution mass spectrometry (LC-HRMS) is the method of choice for this purpose, with compound identification commonly relying on matching experimental LC-HRMS/MS spectra against reference spectral libraries. However, the remarkable structural diversity of microcystins, with more than 300 congeners described to date, together with the continuous discovery of new variants, limits the coverage of existing spectral libraries, often resulting in missed or uncertain annotations, underscoring the need for improved detection strategies. To address this analytical gap, we developed a novel computational workflow for targeted screening of microcystin variants using Feature-Based Molecular Networking (FBMN) and microcystin-specific Mass Spectrometry Query Language (MassQL) queries implemented in the Global Natural Products Social Molecular Networking (GNPS2) platform. Microcystins were systematically classified into structurally related groups according to the identity and positional distribution of conserved amino acid residues within the cyclic peptide scaffold. Group-specific MS/MS fragmentation patterns were then used to design dedicated MassQL queries using a minimal set of highly informative diagnostic features, including characteristic fragment ions, immonium ions, and neutral losses, defined as required or excluded criteria. The workflow was designed to maximize sensitivity while maintaining high specificity, thereby minimizing both false negatives and false positives. The resulting collection of microcystin-specific MassQL queries provides a robust, complementary, and transferable strategy for screening proprietary libraries and large public metabolomics repositories. By complementing conventional spectral library matching, this approach enables detection of both known microcystins and structurally related analogs that are absent from current reference libraries, offering a powerful tool for environmental monitoring, cyanotoxin research, and public health surveillance.

Keywords: Microcystins; MassQL; LC-HRMS.



O-33

Antarctic UV-Resistant Marine Bacteria: An Untapped Carotenoid Source

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Antarctic marine microorganisms thrive under extreme environmental conditions, including low temperatures, high ultraviolet (UV) radiation, and persistent ice, which have driven the evolution of specialized adaptive strategies. Among these, photoprotective defense mechanisms are essential to mitigate UV-induced damage, particularly from solar UV-B radiation, and involve both enzymatic and non-enzymatic antioxidant systems. This study aims to investigate the diversity of UV-resistant Antarctic bacteria and to explore their potential to produce photoprotective and biotechnologically relevant compounds. Thirty-one UV-resistant bacterial strains were isolated from Antarctic aquatic environments (surface seawater, ice, and shallow lake sediments) using a UV-C exposure assay and identified through 16S rRNA gene sequencing. The isolates were affiliated with Proteobacteria, Actinobacteria and Firmicutes phyla and clustered into 15 bacterial genera, 5 Gram negative (*Brevundimonas*, *Qipengyuania*, *Sphingorhabdus*, *Sphingobium*, *Psychrobacter*) and 10 Gram positive (*Staphylococcus*, *Bacillus*, *Mesobacillus*, *Kocuria*, *Gordonia*, *Rhodococcus*, *Micrococcus*, *Arthrobacter*, *Agrococcus*, *Salinibacterium*). To investigate adaptive traits at the molecular level, whole-genome sequencing and annotation were performed on three representative strains: *Arthrobacter* sp. R5, *Brevundimonas* sp. RA4, and *Sphingorhabdus* sp. G5G. A large proportion of the isolates exhibited distinct pigmentation, suggesting a central role for carotenoid-type compounds in protection against UV radiation and cold stress. Genomic analyses revealed the presence of genes involved in stress response, antioxidant defense, and metabolic pathways supporting survival under extreme conditions. Importantly, carotenoid biosynthetic gene clusters were identified in the three sequenced strains, supporting their ability to produce structurally diverse pigments. These findings highlight Antarctica as an underexplored reservoir of pigmented microbial diversity. UV-resistant Antarctic bacteria represent promising sources of sustainable carotenoid-based bioactive compounds and potential platforms for bio-pigment production, with applications in cosmetics, food, pharmaceuticals, and other industrial sectors.

Keywords: Antarctica; Bacteria; Cold adaptation; UV-resistance; Carotenoids.



O-34

Bacterial Diversity and Biotechnological Prospects of Antarctic Epibenthic Biofilms from Horseshoe Island

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Antarctic microorganisms are increasingly recognised as valuable sources of bioactive metabolites, pigments, and cold-active enzymes with potential biotechnology applications. Despite the growing interest in Antarctic habitats, much of their diversity and functional potential remains unexplored.

This study aims to evaluate the prokaryotic diversity of poorly characterised epibenthic biofilms from Horseshoe Island and to identify bacterial taxa with potential biotechnological relevance. For this purpose, samples were collected from Horseshoe Island, located in the southwestern Antarctic Peninsula, across hard substrates during the austral summer (February–March) of 2025 as part of the Turkish Antarctic Expedition (TAE-IX). Following DNA extraction from 12 samples, 16S rRNA amplicon sequencing was performed by an Oxford Nanopore Mk1C platform with an R9.4 flowcell for a 48-hour sequencing run. The bacterial community was represented by 18 prokaryotic phyla. Actinomycetota emerged as the predominant bacterial phylum, a group widely recognised for its capacity to synthesise diverse secondary metabolites. Notably, the genus *Corynebacterium* was dominant (62.7%) in the bacterial community, and it is reported here for the first time in Horseshoe Island, potentially associated with nearby local penguin colonies as a possible environmental source. Pseudomonadota (19%) and Cyanobacteriota (15%) were the next most abundant phyla. Within the western sampling sites, *Limnospira* exhibited the highest relative abundance, a genus known for its metabolic versatility and adaptation to extreme habitats. The phylum Pseudomonadota was represented by diverse genera, including *Aliivibrio*, which comprises psychrotolerant species adapted to cold environments through cold-active enzymatic systems. In conclusion, these preliminary findings demonstrate distinct bacterial assemblages in Horseshoe Island epibenthic biofilms and identify taxa with known associations to biotechnologically relevant traits, highlighting their potential as a source for future functional and applied investigations.

Acknowledgments: This study was carried out in the 9th (TAE-IX) National Turkish Antarctic Science Expedition, which was under the auspices of the Presidency of the Republic of Türkiye, supported by the Ministry of Industry and Technology, and coordinated by TÜBİTAK MAM Polar Research Institute (KARE). This work was supported by the Scientific and Technological Research Council of Türkiye (TÜBİTAK) under grant 123G044.

Keywords: 16S rRNA amplicon sequencing; MinION; Polar biology; Prokaryotes; Biotechnology.



O-35

Genome-Resolved Taxonomic and Functional Characterisation of the Genus *Limnospira*

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The cyanobacterial genus *Limnospira* comprises economically important species that are cultivated under the commercial name “Spirulina”. Despite being based on both single-marker gene and recent whole-genome analyses, the clear delineation of species and functions within the genus remains a matter of debate. This study presents the results of a taxonomic assessment and metabolic annotation of two new *L. platensis* and *L. maxima* genomes, compared to a selection of high-quality genomes obtained from the Genome Taxonomy Database and GenBank. Average nucleotide and amino acid identities (ANI and AAI) and digital DNA–DNA hybridisation values (dDDH) revealed distinct differences between the two species, which were further confirmed by phylogenomic and pangenomic analyses. While the two species shared a broadly similar core cyanobacterial metabolism, striking differences were related to the exclusive enrichment of dispensable genes associated, among others, with defence mechanisms, transposons, prophage-derived genes, and signal transduction systems, indicating different evolutionary pathways. Analyses carried out using liquid chromatography–mass spectrometry (LC-MS) on the two *Limnospira* strains confirmed the absence of the main legacy cyanotoxins, including several microcystin congeners, nodularin-R, anabaenopeptin-A, anatoxin-a, homoanatoxin-a, dihydroanatoxin-a, cylindrospermopsins and saxitoxins. Annotation of all the *Limnospira* species included in the analysis confirmed the absence of biosynthetic gene clusters (BGCs) encoding legacy cyanotoxins. Conversely, a few other classes of BGCs, including cyanobactins, were identified across the entire genome set. Furthermore, annotation revealed the presence of metabolic pathways associated with the biosynthesis of many bioactive compounds and nutraceuticals, including several vitamins, antioxidants, photosynthetic pigments (such as phycocyanin) and quinones, among others. Comparative genomics supports *L. platensis* and *L. maxima* as distinct species with conserved core metabolism, while species-specific enrichments in defence, mobile elements and signalling indicate divergent evolution. The absence of cyanotoxins, combined with the presence of widespread vitamin, antioxidant and pigment biosynthetic pathways, underscores their high nutraceutical potential and safety.

Keywords: *Limnospira*; Metagenomics; Metabolomics; Phylogenomics; Pangenomics.



O-36

Isolation And Phylogenomic Characterization of *Aeromonas veronii* Strains Associated with Outbreaks in Commercial Mediterranean Aquaculture Facilities

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Aeromonas veronii is an emerging pathogen causing severe disease outbreaks and substantial economic losses in marine aquaculture. Since 2021, recurrent outbreaks have affected European seabass (*Dicentrarchus labrax*) in commercial facilities across Greece. To investigate the diversity and pathogenic potential of the causative strains, we characterised ten *A. veronii* isolates by phenotypic assays, whole-genome sequencing, and *in vitro* virulence analysis. API20E profiling confirmed a conserved species phenotype with strain-specific variation in beta-galactosidase, gelatinase, and arginine dihydrolase. All isolates formed biofilms with distinct kinetics, strain BDA2 showing the strongest capacity, indicating differences in persistence potential. Genomic sequencing confirmed all strains as *A. veronii* and identified 207 virulence-associated genes plus resistance determinants against beta-lactams, carbapenems, streptogramins, and aminoglycosides. Comparative phylogenomics resolved distinct lineages that correlated with secretion-system distribution. All strains encoded a type III secretion system (T3SS), whereas only six carried a complete type VI secretion system (T6SS). T6SS-positive strains harboured two auxiliary VgrG-associated effector clusters, while T6SS-negative strains contained four auxiliary loci encoding candidate antibacterial effectors targeting peptidoglycan, including Tle1 phospholipases mediating membrane phospholipid hydrolysis. T6SS-positive strains also retained an intact aerolysin gene, whereas T6SS-negative strains showed a fragmented aerolysin locus linked to putative genome rearrangements. Functional assays mirrored genomic data: strains carrying both T3SS and T6SS induced rapid cytotoxicity in BF-2 fish cells, reducing viability to 49.5% within 4 hours, whereas T3SS-only strains caused delayed cytotoxicity, with viability at 73% after 7 hours. These findings indicate that the combination of T3SS, T6SS, and an intact aerolysin gene is associated with enhanced virulence, while strain-specific biofilm formation may further support environmental persistence and disease transmission. The study clarifies the pathogenic mechanisms of *A. veronii* circulating in Mediterranean aquaculture and supports improved surveillance and disease-management strategies.

Keywords: *Aeromonas veronii*; European seabass; Whole-genome sequencing; Secretion systems; Virulence.



O-37

Recent Findings to Update and Understand the Mode of Action of Diarrheic and Ciguatera Toxins

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The mode of action (MoA) of the classical marine toxins was considered understood many years ago. Although some groups, such as the azaspiracids have a yet unknown target, the oldest known groups, such as paralytic toxins (PST) and diarrheic toxins (DST) were supposed to be well understood. This is important because the MoA is the basis for the definition of toxicity equivalency factors (TEF), and the monitoring system is based on an instrumental method which results are translated with TEF. In this presentation we show that the MoA of ciguatoxins (CTXs) and DST is far from being understood, and that today's TEF for these groups are biased. We show evidence that DST trigger a strong inflammatory response in intestinal cells, as evidenced by many mediators to be shown, this response being 5 times stronger in humans than in rodents. Current knowledge about the MoA of these toxins does not support the rationale behind the current use of TEF for DST. Also, allodynia caused by ciguatoxins can be explained by our recent findings about the effect of these toxins in TRPV1 channels.

Keywords: Okadaic acid; Mode of action.



O-38

***Galdieria phlegrea* Physiology Drives Biotechnologically Relevant Metabolites**

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The extremophilic red microalga *Galdieria phlegrea* has recently attracted increasing scientific interest due to its remarkable metabolic flexibility and biotechnological potential.

This unicellular alga thrives in harsh environments characterized by high temperatures and low pH values, displaying a unique ability to adapt its metabolism to changing environmental conditions. Unlike many microalgae, *G. phlegrea* can grow under both autotrophic and heterotrophic regimes. In the presence of light and carbon dioxide, it performs photosynthesis and accumulates biomass through autotrophic growth. Conversely, in the absence of light, it can efficiently utilize a wide range of organic substrates, including sugars, amino acids, organic acids, and alcohols, sustaining heterotrophic growth. Importantly, *G. phlegrea* can readily switch between these trophic states in response to changes in cultivation conditions, such as light availability and carbon source composition. The transition between these trophic modes triggers significant metabolic reprogramming, leading to the production and accumulation of compounds of high biotechnological value. Among these, C-phycocyanin (C-PC), a phycobiliprotein widely used in the food, cosmetic, pharmaceutical, and nutraceutical industries, represents one of the most promising metabolites due to its antioxidant, anti-inflammatory, and natural coloring properties. In addition, *G. phlegrea* is able to synthesize and accumulate high intracellular concentrations of glutathione, recognized as one of the most important cellular antioxidants. Glutathione plays a crucial role in protecting cells against oxidative stress and has numerous applications in health-related and industrial sectors.

Understanding how different cultivation conditions influence trophic switching and metabolite production in *G. phlegrea* may provide valuable insights for optimizing biomass productivity and enhancing the sustainable production of high-value compounds for biotechnological applications.

Keywords: *Galdieria phlegrea*; Metabolic flexibility; C-phycocyanin; Glutathione; High-value metabolites.



O-39

Tracking Lake Garda's Cyanotoxins: Trend Analysis Over a Fifteen Years - Monitoring

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Cyanobacterial proliferations in freshwater pose significant risks to human and animal health due to the production of toxic metabolites (cyanotoxins). In Lake Garda, the long-term distribution and dynamics of these cyanotoxins have been systematically monitored since 2009. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) technique has been utilized to monitor cyanotoxins within the lake's pelagic zone monthly. The high sensitivity of this analysis allowed the detection of very low toxin concentrations (a few ng/L), enabling the tracking of their presence even at low cyanobacterial abundances, which is typical for an oligo-mesotrophic lake.

The study identified distinct toxigenic profiles among the lake's dominant cyanobacterial species. While *Dolichospermum lemmermannii* forms sporadic surface blooms but produces no toxins, *Planktothrix rubescens* and *Tychonema bourrellyi* actively proliferate in the euphotic zone, producing hepatotoxic microcystins and neurotoxic anatoxins, respectively. Long-term data show that the chemotypes associated with these toxic cyanobacteria are remarkably constant: *P. rubescens* produces demethylated variants of microcystins (mainly [D-Asp3]MC-RR), while *T. bourrellyi* primarily produces anatoxin-a. In general, anatoxins and microcystins co-occurred in the samples, with anatoxin concentrations being one order of magnitude higher than microcystins. Peak concentrations were typically recorded during the summer and autumn periods, with maximum values reaching µg/L levels only in specific years.

Despite reassuring results regarding the baseline levels of toxic compounds normally found in the lake, this research highlights the critical need for continued monitoring to cope with local and global stressors, such as nutrient loads and global warming, which could favor future cyanobacterial proliferation.

Keywords: Cyanobacteria; Cyanotoxins; LC-MS; Lake Garda.



O-40

Biotechnology and Ecology of Harmful Marine Microalgae involved in Ciguatera, an indispensable partnership

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Ciguatera is a type of seafood poisoning caused by consumption of marine food, mainly toxic fish, carrying ciguatoxins (CTXs). Benthic marine microalgae of the genera *Gambierdiscus* and *Fukuyoa* (dinoflagellates) are responsible for the production of CTXs and precursors. Understanding the population dynamics of these dinoflagellates is crucial to characterize and predict the risks of ciguatera. We have carried out studies of these populations in the Balearic Islands since 2016. The use of optical microscopy, scanning electron microscopy (SEM) and molecular genetics has allowed us to identify the species present in the area. The use of calcofluor staining facilitates the recognition of these thecate dinoflagellates while systematically processing samples for counting. SEM allows to improve species recognition. The use of molecular genetic techniques (Sanger sequencing, biosensors, and metabarcoding) are essential for species level confirmation. Evaluation of their toxicity and toxin content was conducted with the Neuro2a cytotoxicity assay and with LC-MS/MS and LC-HRMS respectively. The evaluation of their abundance in macroalgal substrates was carried out to study their temporal and spatial distribution in the Balearic Islands archipelago. The recording of environmental variables during samplings, the continuous monitoring of environmental conditions using submerged HOBO data loggers, and the use of Copernicus satellite data enabled us to identify the main drivers that determine their population dynamics. These environmental datasets also support the identification of ciguatera-related dinoflagellate coldspots and hotspots, and the development of predictive models to forecast the potential hazards posed by ciguatera under different climate change scenarios. The complementary use of several technological and biotechnological approaches, from a multidisciplinary perspective, is an essential strategy for advancing the study of the ecology of these hazardous species.

Keywords: Ciguatera; Dinoflagellates; Biotechnology; Ecology; Prediction.



O-41

Ecological Variables Modulate Bioactive Compounds in Mediterranean Algal CommunityE. Vitale¹, R. Donadio², G. Battaglia³, C. Fontanarosa³, A. Amoresano³, C. Arena¹

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Macroalgae are a repository of bioactive compounds involved in a wide range of ecological and physiological functions, including resistance to environmental stress and herbivory. The production of these secondary metabolites is finely regulated by environmental drivers, contributing to macroalgal acclimation, adaptation, and survival. We investigated the annual dynamics of a rocky shore macroalgal community along the Bacoli coast (Gulf of Pozzuoli, Italy) to assess species-specific patterns of bioactive compound production in three co-occurring dominant species: *Dictyota spiralis*, *Cladophora prolifera*, and *Jania pedunculata*. Over one year, we monitored species composition the modulation of pigments carbohydrates, and antioxidant production, emphasizing differences in polyphenol composition profile. Our results evidenced that *D. spiralis* dominated the community in spring, whereas *C. prolifera* and *J. pedunculata* were more representative in summer and autumn. Among species, *C. prolifera* and *D. spiralis* showed the highest photosynthetic performance, while *D. spiralis* exhibited the highest accumulation of antioxidant compounds, suggesting a higher allocation of resources to secondary metabolism. Peaks in concentration of target metabolites coincided with periods of maximal species abundance, emphasizing the role of bioactive molecules in enhancing species under different seasons. The variability in the phenolic profiles, especially the up regulation of compounds involved in human health, supports the close relationship between environmental drivers and metabolic regulation. Stressful conditions, such as elevated temperatures and irradiances in summer, were associated with a reduction in polyphenols and antioxidant pool across all species, likely reflecting acclimatory adjustments aimed at mitigating potential photo-oxidative damage. From a biotechnological perspective, maximizing the yield of bioactive compound required sampling during the period in which the target metabolites reach the highest amount. Furthermore, utilizing green extraction methods is essential to guarantee the integrity of bioactive molecules and reduce environmental impacts. Overall, this study provides insights into the sustainable valorization of marine natural products from the Phlegrean coastal ecosystem.

Keywords: Bioactive compounds; Environmental stressors; Macroalgae; Polyphenols.



O-42

EU Support for algae sector: So far and what's next

M. Stulgis

Abstract not available for inclusion in the Book of Abstracts.

O-43

Welcome note and Presentation of Interreg VI-A Italy-Croatia programme 2021/2027

S. Fatica

Abstract not available for inclusion in the Book of Abstracts.



O-44

Advancing Blue Biorefinery Development in the Adriatic Sea (BIOBASED Project)

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The Blue Economy offers substantial opportunities for the sustainable use of marine resources by fostering synergies among fisheries, aquaculture, energy, tourism, environmental conservation and local development. However, important knowledge gaps remain regarding the interactions between ocean health, resource exploitation and Blue Economy activities. Addressing these gaps is essential for achieving a sustainably harvested and productive ocean, one of the ambitions of the United Nations Decade of Ocean Science for Sustainable Development.

Within this framework, the BIOBASED project, funded by the Interreg Italy–Croatia Programme 2021–2027, aims to strengthen research and innovation capacities in the Adriatic Blue Economy by integrating regenerative aquaculture with advanced biorefinery processes. Coordinated by the University of Foggia, BIOBASED develops regenerative Integrated Multi-Trophic Aquaculture (IMTA) systems combining mussels, oysters and seaweeds to support sustainable marine biomass production, nutrient recovery and resource-efficient utilisation. The project includes four demonstration sites: two in Italy, located in the Gargano area and Emilia-Romagna, and two in Croatia, in the Dubrovnik area and Mali Ston Bay. Native seaweeds, including *Gracilaria* spp. and *Ulva* spp., were cultivated in lantern nets with two mesh sizes and under three mussel-rope-to-seaweed-lantern configurations. During the cultivation period, macroalgal specific growth rate, biomass productivity and biochemical composition were monitored to assess the effects of farming conditions and identify the most suitable biomass valorisation pathways.

The resulting seaweed biomass and aquaculture side-streams were subsequently evaluated through integrated chemical and biochemical conversion processes following a cascade blue biorefinery approach based on green chemistry principles. The project results demonstrate how regenerative IMTA and blue-biotechnology solutions can support circular value chains, reduce waste and enhance the economic and environmental sustainability of aquaculture in the Adriatic region.

Acknowledgments: This contribution is presented in the framework of the BIOBASED project, funded by the Interreg Italy–Croatia 2021–2027 Programme.

Keywords: Regenerative IMTA; Blue biorefinery; Macroalgae.



O-45

Regulatory Framework and Market Analysis for Macroalgae-Based Value Chains in the Adriatic: A Cross-Border Action Plan

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Despite growing interest in macroalgae as a strategic resource for the European blue bioeconomy, the development of competitive macroalgae-based value chains in Europe remains constrained by fragmented regulatory landscapes and uncertain market entry pathways for small and medium-sized enterprises (SMEs). This contribution presents the integrated regulatory analysis and market assessment conducted within the BIOBASED project, focusing on the Adriatic cross-border context and on two target macroalgae genera, i.e. *Ulva* (green) and *Gracilaria* (red), cultivated in Regenerative Integrated Multi-Trophic Aquaculture (IMTA) settings at pilot sites in Italy and Croatia. The regulatory analysis demonstrates that blue biotechnologies in aquaculture, including algae cultivation, biorefinery processing and by-product valorization, are governed at EU and national level by a layered, multi-instrument framework rather than a dedicated vertical law. In Italy, governance is distributed across national ministries, regional authorities and local maritime administrations, creating administrative complexity and legal uncertainty for SMEs. In Croatia, a more centralized aquaculture licensing regime applies. A comparative assessment of the two regulatory frameworks reveals both synergies and divergences, particularly with respect to permitting algae cultivation, food and feed product classification, and by-product valorization pathways. The market analysis identifies biostimulants, food and nutraceuticals, and functional feed additives as the most accessible and commercially relevant value chain segments for Adriatic SMEs, particularly when supported by circular and integrated IMTA-based business models. Commodity biomass production is not a viable standalone strategy; competitiveness depends on functional differentiation, species-specific positioning, and circular integration. *Ulva* is particularly suited for ulvan-based biostimulant and nutraceutical applications, while *Gracilaria* supports agar and pigment-oriented pathways. These findings fed into a Joint Action Plan (JAP) for the development of product marketing phases, structured in three sequential phases, i.e. Production, Conversion, and Commercialisation, each with explicit regulatory compliance steps built in. The BIOBASED IMTA approach is shown to provide a streamlined regulatory pathway compared to standalone algae operations, avoiding the need for new maritime concessions, bypassing Novel Food pre-authorization for both target species, and qualifying under Regulation (EU) 2019/1009 for CE-marked biostimulants.

Acknowledgments: This contribution is presented in the framework of the BIOBASED project, funded by the Interreg Italy–Croatia 2021–2027 Programme.

Keywords: Macroalgae; Regulatory framework; Market analysis; IMTA; Blue bioeconomy.



O-46

Seasonal Cultivation of *Ulva* spp. in an IMTA System in Mali Ston Bay

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Integrated Multi-Trophic Aquaculture (IMTA) represents a promising approach to improving resource efficiency and increasing biomass production in sustainable aquaculture. This study evaluated the growth performance of *Ulva* spp. integrated with Mediterranean mussel (*Mytilus galloprovincialis*) farming at two experimental sites in Mali Ston Bay, Croatia. Two cultivation trials were conducted, the first starting in July 2025 and the second in April 2026. Wild *Ulva* spp. biomass was collected from the environment and cultivated in lantern nets with two mesh sizes (2.5 and 9 mm). The experiment evaluated the effects of lantern mesh size, cultivation depth (3.0 m, 3.5 m, 4.0 m), and mussel longline:lantern density (1, 3 or 5:1). Biomass was measured every 15 days and the specific growth rate (SGR) was calculated for each sampling interval. The results showed that the SGR was significantly affected by cultivation depth and lantern mesh size, while growth dynamics differed between the two cultivation sites, reflecting differences in local hydrodynamic conditions. The summer cultivation cycle was characterized by rapid initial biomass accumulation in the first month followed by intense biofouling, predominantly by serpulid polychaetes, which substantially reduced further growth. In contrast, the spring trial maintained growth over a longer period, with biofouling becoming evident only after seawater temperatures increased in early summer, when juvenile mussels became the dominant fouling organisms. Overall, the findings demonstrate that the feasibility of *Ulva* spp. cultivation in IMTA systems is strongly affected by seasonal environmental conditions and biofouling dynamics. While cultivation depth and lantern mesh size significantly influence biomass production, the timing of deployment appears to be the key factor determining cultivation success. These results suggest that short, seasonally targeted production cycles may represent a more feasible strategy for *Ulva* spp. cultivation in the Mali Ston Bay than continuous year-round production.

Acknowledgments: This contribution is presented in the framework of the BIOBASED project, funded by the Interreg Italy–Croatia 2021–2027 Programme.

Keywords: Blue economy; Integrated multitrophic aquaculture; Macroalgae cultivation.



O-47

The Strategic Role of Shellfish Farmers in Ecological Transition and IMTA Systems

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Italian aquaculture is undergoing a deep transformation, oriented towards Blue Growth and environmental sustainability. In this context, shellfish farmers, in addition to being food producers, are becoming true providers of essential ecosystem services, especially when combining shellfish farming with algal cultivation techniques, as demonstrated in the BIOBASED experience.

Therefore, the development of Integrated Multi-Trophic Aquaculture (IMTA) techniques—a system in which molluscs and algae act as natural bioextractors capable of recycling excess nutrients (nitrogen and phosphorus) deriving from fish farming and anthropogenic activities—is transforming potential pollutants into valuable biomass.

Key Points:

- Ecosystem Services and the Carbon Sink: achieved through the creation of carbon and nutrient credits.
- Resilience and Diversification: through the adoption of multi-trophic systems that allow producers to diversify their income and increase economic resilience in the face of climate change.
- The National Strategic Plan (PNSA 2021-2027): places IMTA among the absolute priorities to ensure that production growth occurs in harmony with the protection of biodiversity and sensitive habitats, including Natura 2000 sites.

In conclusion, the modern shellfish farmer emerges as a key entrepreneurial figure for the decarbonisation of marine ecosystems and the promotion of a circular economy that enhances the excellence of the national territory.

Acknowledgments: Contribution in the framework of the BIOBASED project, funded by the Interreg Italy–Croatia 2021–2027 Programme

Keywords: IMTA; Algal cultivation; Ecosystem Services; Carbon sink.



O-48

From Invasive Biomass to Bioactive Peptides: Pufferfish Collagen Hydrolyzates

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Marine collagen and its bioactive peptide derivatives are increasingly investigated as functional ingredients for nutraceutical, cosmeceutical, and pharmaceutical applications. Within a circular bioeconomy framework, collagen-rich invasive and non-indigenous marine species may represent sustainable feedstocks, converting ecological pressure into high-value products. This study evaluated the invasive pufferfish *Lagocephalus sceleratus* as a raw material for collagen recovery and to produce bioactive collagen hydrolyzates with biotechnological applications. Collagen was recovered from *L. sceleratus* skin using sustainable supercritical fluid extraction and subsequently hydrolyzed with two commercial proteases, Alcalase and Flavourzyme, at different enzyme-to-substrate ratios (0.5, 1.0, 2.0, and 5.0% v/w) and hydrolysis times (1, 2, 3, and 4 h). Antioxidant activity was used as a primary screening criterion, followed by further characterization of selected Alcalase-derived hydrolyzates, including degree of hydrolysis, ultrafiltration into > 3 kDa and < 3 kDa fractions, ACE-inhibitory activity, cytotoxicity, and redox status evaluation in human HaCaT keratinocytes. Alcalase-derived hydrolyzates showed stronger antioxidant activity than Flavourzyme-derived samples, with all Alcalase conditions exceeding 60% ABTS radical scavenging at 1 mg/mL. The selected Alcalase hydrolyzates showed time-dependent degrees of hydrolysis, increasing up to about 10% at 4 h. After ultrafiltration, the >3 kDa retentate fractions displayed the highest antioxidant activity, particularly at 4 h, where all retentates exceeded 80%. ACE-inhibitory activity was detected in almost all samples, reaching up to 80% inhibition, while HaCaT cell viability remained above the 70% cytotoxicity threshold across all tested conditions. Redox analyses further showed that selected hydrolysates modulated cellular oxidative homeostasis, reducing susceptibility to oxidants without increasing oxidative damage markers, while the <3 kDa fractions significantly enhanced total antioxidant capacity. Overall, *L. sceleratus* skin collagen hydrolyzates combine antioxidant and antihypertensive potential with good in vitro biocompatibility, supporting the valorization of this invasive biomass as a sustainable source of bioactive marine peptides.

Keywords: Invasive species; *Lagocephalus sceleratus*; Collagen hydrolyzates; Bioactive peptides; Circular bioeconomy.



O-49

Screening North Sea and Mediterranean microalgae for Salmon RAS Water Valorization

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The rapid expansion of land-based seafood aquaculture generates large volumes of nutrient-rich wastewater, which requires costly management before discharge. At the same time, there is an increasing demand for sustainable resources for food, materials, and energy. Marine microalgae offer a promising solution by converting dissolved nutrients into valuable biomass while contributing to wastewater remediation. This study is part of the Horizon Europe Sustainable Blue Economy Partnership project SEAlgaePower (www.sealgaepower.eu) and aims to develop technologies in which marine microalgae clean nutrient-rich effluents from the recirculating aquaculture system (RAS), while simultaneously producing biomass for novel sustainable ingredients.

A diverse collection of eleven microalgae and cyanobacterial strains originating from the North Sea and the Mediterranean Sea was tested for growth in brackish RAS water from a local salmon facility, SmögenLax. Initial laboratory screening to assess performance at low salinity led to the identification of the six strongest growers in 13 psu RAS water: *Nannochloropsis granulata*, *Chlorella* sp. and *Chlorella ovalis*, *Phaeodactylum tricornutum*, *Quadricoccus euryhalinicus*, and *Dunaliella tertiolecta*. Those species were scaled up to benchtop multicultivator photobioreactors to monitor nutrient uptake capacity and accumulation of compounds of interest under optimized growth conditions. The trials highlighted the robustness of the selected species, all of which achieved complete nitrate and phosphate removal under the tested conditions. Promising amino acid and fatty acid profiles observed during exponential growth and nutrient-limited phases led to the identification of two high-performing strains that will be further optimized for pilot-scale cultivation.

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Keywords: Seafood aquaculture; Bioremediation; Marine microalgae; Microalgae ingredients; Waste streams.



O-50

Redesigning the Blue Economy: Regenerative Integrated Aquaculture and Regional Food Heritage toward a replicable model of resilience

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This study proposes a comprehensive redesign of the blue economy by leveraging regenerative integrated aquaculture and regional food heritage as catalysts for systemic coastal resilience. Connecting Pacific ecosystems via the "Callao Model" with the Adriatic basin in Manfredonia Gulf, the research introduces a novel framework based on the paradigm of elliptic economy. This model replaces the static nature of standard circular loops with a dynamic, multi-focal trajectory driven by technological innovation and cultural identity, demonstrating how cross-continental blue skills transfer transforms regional assets into socio-ecological restoration. Methodologically, the paper examines bottom-up training models designed to close the digital gap in small and medium enterprises, alongside advanced integrated multi-trophic aquaculture (IMTA) systems. These regenerative setups are deployed for a dual purpose: high-quality food production and active marine bio-regeneration. Crucially, the approach integrates "Intelligenza Nutrizionale" (Nutritional Intelligence), embedding human well-being into environmental stewardship under a unified One Health paradigm. Key results reveal that linking traditional food heritage with precision IMTA systems dramatically accelerates regional development and climate adaptability. Circular bio-economy loops, wherein monitored marine biomass and aquaculture side-streams are upcycled into functional nutrition, yield quantifiable environmental, social, and governance benefits. These ESG impacts are robustly driven by adopting a resilient model of development through the cross-fertilization of the Adriatic shoreline IMTA applied in Manfredonia with the recovery and leveraging of artisanal fishery in Callao, ensuring environmental protection and a regenerative blue economy through strategic technology AI and cloud-based adoption. All multi-dimensional impacts are validated using the Sustainable Global Return on Investment (SGROI) index. In conclusion, the strategic alignment of the Callao and Manfredonia elliptic frameworks provides a scalable blueprint for coastal zones, establishing that anchoring technological innovation in food heritage allows communities to rebuild marine ecosystems.

Keywords: Regenerative aquaculture; Blue economy; Integrated multi-trophic aquaculture; Coastal resilience; One Health.



O-51

Benthic Cyanobacterial mats on Curaçao reefs: Abundance, nitrogen fixation, and toxicity on changing reefs

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Benthic cyanobacterial mats (BCMs) are expanding across Caribbean reefs as coral mortality from bleaching and SCTLD creates extensive bare substrate rapidly colonised by these groups. These mats are highly active microbial assemblages that can strongly influence reef biogeochemistry through nitrogen fixation, organic matter production, and the release of bioactive secondary metabolites. Yet, their ecological roles and potential risks remain poorly quantified.

We surveyed 28 sites along the leeward coast of Curaçao (10 m depth) to assess BCM distribution, biomass, nitrogen fixation, and toxicity. Average BCM cover was 10%, dominated by red mats. Biomass analyses of the most abundant mat types enabled calculation of ash-free dry weight per m² of reef. Nitrogen fixation rates were quantified using the acetylene-reduction assay (per unit dry weight) and extrapolated to reef-scale estimates. Culturing of dominant cyanobacterial strains revealed substantial variability in N-fixation potential, identifying species most relevant to the reef nitrogen budget.

Most BCM morphotypes exhibited toxic potential in *Thamnocephalus platyurus* bioassays, with LC₅₀ values indicating the presence of bioactive or toxic secondary metabolites. Untargeted metabolomic analyses (LC-MS/MS) confirmed diverse chemical profiles and candidate compounds likely contributing to toxicity.

Together, these results show that BCMS on Curaçao's reefs are abundant, metabolically active, and often toxic. Their capacity for substantial nitrogen input, combined with secondary metabolite production, suggests that BCMS already play a significant role in shaping reef biogeochemistry and may influence benthic community dynamics. Understanding the ecological functions and impacts of BCMS is essential for predicting future reef trajectories in an era of coral decline.

Keywords: Benthic cyanobacterial mats; Nitrogen fixation; Coral reefs; Toxicity; Curaçao.



O-52**ATL.A.HUB: Accelerating Marine Algae Biotechnology in the Atlantic Area**C. Fernandez-Avila¹, M. Venuleo¹, F. Guidi¹, A.M. Barrera², E. Portillo¹

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The Southeast of Gran Canaria is one of Europe's most favorable locations for algae cultivation, benefiting from year-round solar radiation, stable temperatures, low rainfall, high-quality seawater, and rich biodiversity of native strains. However, limitations related to water supply, effluent management, and land-use availability constrain sector growth. To address these bottlenecks, the Experimental Area of Blue Biotechnology, Aquaculture and Water Technologies of ITC-Pozo Izquierdo is being developed as a large-scale hub with a public investment exceeding €25 million to date. It provides shared laboratories, cultivation areas, processing equipment, and co-working facilities dedicated to pre-industrial testing and innovation.

Within this context, ATL.A.HUB (Atlantic Hubs to Boost Marine Algae Land-based Aquaculture and Biotechnology) aims to strengthen the European algae value chain by promoting specialized hubs that provide shared infrastructure and regulatory support. The project leverages two of Europe's largest algae cultivation and processing facilities as launch pads for innovation, fostering the development, scale-up, and commercialization of novel algae-based products. The initiative also explores hub replication opportunities and develops exploitation strategies adapted to both public and private governance models.

To demonstrate the market potential of this hub-based approach, a case study evaluated consumer acceptance of a pineapple juice enriched with full-seawater grown spirulina biomass produced at ITC. The product, developed with a local juice company, exemplifies public-private collaboration as one of the Hub's product acceleration pathways. After sensory evaluation, 171 consumers completed a structured survey. The product achieved a mean acceptance score of 4.71/5.00, with over 94% positive ratings. More than 90% of participants expressed purchase intention, driven by perceived health benefits, sustainability, and local sourcing.

These findings demonstrate how integrated algae innovation hubs can accelerate the transition to market-ready products. Combining advanced infrastructure, pre-industrial testing and validated consumer demand can strengthen the competitiveness of the European algae sector.

Keywords: Atlantic algae hubs; Full-seawater grown Spirulina; Blue biotechnology; Land-based algae aquaculture.



O-53

Valorization of Fish Processing By-Products through Collagen Extraction for Biomedical and High-Value Applications

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The fish processing industry generates substantial amounts of waste, accounting for up to 50–70% of the total biomass depending on the species and processing method. These by-products, including skin, scales, bones, and fins, remain largely underexploited despite being rich sources of bioactive compounds and biomaterials.

Among these, marine collagen has attracted considerable interest in its biocompatibility, biodegradability, low immunogenicity, and broad application potential. Recovering collagen from fish-derived biomass offers an opportunity to transform industrial residues into high-value materials, supporting more sustainable, circular production models and reducing the environmental impact of waste disposal.

Marine collagen represents an attractive alternative to mammalian-derived collagen due to the absence of religious restrictions and the reduced risk of transmitting animal-borne diseases. In the biomedical field, efforts focus on fabricating scaffolds for tissue engineering and developing collagen-based skin substitutes and wound dressings for burn treatment and tissue repair. At the same time, the obtained biomaterial shows potential for exploitation in other sectors, including cosmetics, nutraceuticals, and the formulation of high-value bio-based products. This work aims to optimize collagen extraction from fish by-products by maximizing recovery while preserving the structural and functional properties required for biomedical applications. Different extraction and purification strategies are evaluated to improve process efficiency and ensure the quality of the recovered collagen. Attention is devoted to developing reproducible, scalable procedures to facilitate future industrial implementation and support the production of collagen-based biomaterials. Overall, this work highlights the potential of fish-derived collagen as a versatile and sustainable material, contributing to circular bioeconomy approaches and promoting the valorization of seafood-processing residues into innovative products for healthcare and other industrial sectors.

Keywords: Fish skin; Marine collagen; Circular bioeconomy.



O-54

Exhausted Culture Media Reuse in Autotrophic Microalgae Production: Optimization and Modelling of *Pseudococcomyxa simplex* CulturesL. Marra¹, E. Aurino¹, F. Raganati¹, W. Wukovits², A. Pollio³, A. Marzocchella¹

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The high-water demand associated with autotrophic microalgae cultivation remains one of the main barriers to large-scale implementation. This study investigates the long-term reuse of exhausted culture medium during semi-continuous cultivation of *Pseudococcomyxa simplex*, combining experimental optimization with process modelling to identify sustainable operating conditions. Different purge ratios (0, 30 and 100%) and dilution rates (0.13–0.25 day⁻¹) were evaluated in bubble-column photobioreactors under autotrophic conditions. Partial medium recycling (30% purge ratio) maintained stable biomass production for more than 30 days, achieving biomass productivities comparable to cultivation in fresh medium while substantially reducing freshwater consumption and culture medium costs. An optimal dilution rate of approximately 0.19 day⁻¹ maximized biomass and carbohydrate productivity by balancing nutrient availability and growth kinetics. In contrast, complete medium recycling, despite nitrate replenishment, resulted in progressive growth inhibition, accompanied by chlorophyll depletion, reduced photosystem II efficiency and metabolic redistribution, indicating that the lack of trace elements rather than dissolved organic matter accumulation limited long-term culture stability. An integrated ASPEN Plus® model was developed to describe the overall process, including gas conditioning, cultivation, harvesting and medium recycling, enabling the assessment of water, carbon, nitrogen and phosphorus footprints under different operating conditions. Model predictions were consistent with the experimental trends and identified phosphorus depletion as the main constraint for stable long-term recycling, while accurately estimating water consumption and carbon capture performance. Under the optimal operating conditions, medium recycling reduced the water footprint from approximately 1000 to 320 kg water kg⁻¹ biomass without compromising biomass productivity. These results demonstrate that partial recycling of exhausted culture medium represents an effective strategy for improving the environmental sustainability of autotrophic microalgae cultivation and provides a combined experimental and modelling framework for the design and optimization of circular microalgal production systems.

Keywords: Microalgae; Culture medium reuse; Circular bioeconomy; Water footprint; Carbon capture.



O-55

**Effect of spore encapsulation on the development of the microscopic phase of the
South Pacific kelp *Lessonia berteroana***

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The development of the microscopic phase of kelps (large brown macroalgae of the order Laminariales) is a key stage in sustaining the natural beds formed by these coastal ecosystem engineers. Climate change and overexploitation impose additional pressure on the natural mortality factors affecting these organisms, with local extinction events of some populations being reported worldwide. Encapsulation in hydrogels is a technique used to protect cells, bacteria, and microscopic stages of multicellular terrestrial and aquatic organisms from environmental stressors. However, the optimal conditions for applying hydrogels to marine macroalgae need to be further determined. In this study, the effects of different concentrations of sodium alginate (1%, 1.5%, 2%, and 3%) were evaluated for the encapsulation of spores of the intertidal kelp *Lessonia berteroana* and the subsequent development of the gametophytic phase and fertility. Calcium chloride with the inclusion of NaCl was used to prevent osmotic stress during the hydrogel crosslinking process. Spore survival and germination did not vary significantly among the treatments; however, differences in gametophyte growth and fertility were observed after day 21 of laboratory culture. In general, encapsulation at alginate concentrations less than or equal to 1.5% exhibited a better response in the development of the microscopic phase, with the appearance of juvenile sporophytes observed after 28 days. In contrast, encapsulation in sodium alginate at concentrations above 1.5% induced vegetative growth of gametophytes during the study period (42 days). The results suggest that encapsulation with different hydrogel concentrations modulates the developmental response and fertility of *L. berteroana* gametophytes, which could have various applications in the cultivation of the microscopic phase and restoration of natural populations of this species.

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Keywords: Laminariales; gametophytes; alginate encapsulation; Chile.



O-56

Characterization of Photosynthetic Microorganisms Associated with *Mentha* spp. Plants

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Photosynthetic microorganisms are microscopic eukaryotic (microalgae) and prokaryotic (cyanobacteria) organisms, with considerable genetic diversity, contributing to ecological adaptability and extensive metabolic capabilities. Cyanobacteria are known to form symbiotic relationships with numerous eukaryotic hosts, including plants. On the other hand, plant-microalgae interactions have received less attention in the past, with the focus being on co-cultivation. In plant-associated symbiosis, photosynthetic microorganisms provide fixed nitrogen and a variety of bioactive compounds, such as phytohormones, which can enhance plant growth, productivity, and stress tolerance. In return, host plants offer a protected environment and a stable nutrient supply. Recent advances in microbiome research have revealed that photosynthetic microorganisms, including both cyanobacteria and eukaryotic microalgae, are important yet often overlooked members of the plant microbiome. Despite growing interest in plant-photosynthetic microorganism interactions, the diversity of these symbionts remains poorly explored in many plant species. The present study aims to broaden the knowledge of plant-photosynthetic microorganism symbiosis and characterize the culturable diversity of cyanobacteria and microalgae associated with *Mentha* spp. plants. To this end, seventeen (17) *Mentha* spp. plants were collected from three lakes in the Balkan Botanic Garden of Kroussia (Greece) during two sampling events in spring 2025. Microbial colonies embedded within stems or present on leaves were excised and cultured under laboratory conditions. Eight (8) cyanobacteria and eleven (11) green algae strains were isolated and characterized with molecular markers, including 16S-23S rRNA, 18S rRNA, ITS2 and rbcL regions. The isolated cyanobacteria were preliminary assigned to the orders Nostocales, Oculatellales, Nodosilineales, and Leptolyngbyales, whereas the green algae were preliminary assigned to the orders Chlamydomonadales, Sphaeropleales, and Watanabeales. This study represents the first report of isolated cyanobacterial, and microalgal species exhibiting endophytic or epiphytic associations with *Mentha* spp. plants and provides a foundation for future investigations into their ecological roles, evolution, and potential biotechnological applications.

Keywords: Cyanobacteria; Green algae; *Mentha* spp.; Symbiosis; Phylogenetics.



O-57

Functional Screening of Halophilic Microorganisms in Retentate Waste Water

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Hypersaline ecosystems, such as the Trapani salterns, host unique microorganisms with underexplored biotechnological potential. Traditional upstream processes for halophilic microorganisms' cultivation face high economic and environmental costs due to freshwater and synthetic salt requirements. Concurrently, the valorization of saltern subproducts aligns with circular bioeconomy goals. This study, developed within the Horizon Europe SEAlgaePower project, investigates the reuse of real natural bitter subproducts as a novel, nutrient-dense culture medium. Bittern from solar saltworks was processed through an ultrafiltration unit to separate and recover organic matter, which is concentrated in the retentate up to 50 times. We evaluated this ultrafiltration retentate as a specialized growth substrate for three newly isolated extremophilic strains from the Trapani salterns: the halophilic archaeon *Haloarcula* sp., the cyanobacterium *Eubacterium salina*, and the green alga *Dunaliella salina*. Cultivation trials were conducted in a multicultivator system to monitor growth kinetics, adaptation capacity, and biomass productivity under different concentrations of retentate. The methodology focused on evaluating cellular tolerance to the intense mineral concentrations of the retentate by flow cytometry, pigment analysis and the assessment of the strains' antioxidant activities. Key results confirmed robust growth and acclimation for all three novel isolates in the retentate medium. All strains exploited the concentrated substrate to trigger the metabolic accumulation of high-value pigments, including carotenoids, bacterioruberin, and echinenone, induced by high salinity stress. Finally, antioxidant activity was determined using the DPPH radical scavenging assay, revealing that the *Haloarcula* sp. extracts exhibited the strongest antioxidant activity. In conclusion, ultrafiltration retentate wastewater serves as a highly effective, low-cost medium for cultivating halo-tolerant microorganisms. Our findings expand knowledge of microbial biodiversity in Sicilian hypersaline environments and highlight these halophilic microorganisms as promising platforms for sustainable, circular blue biotechnology.

Keywords: Trapani salterns; Ultrafiltration retentate; Halophilic microorganisms; *Dunaliella*; *Haloarcula*, *Eubacterium*, SEAlgaePower.



P-01

Linking Lipid Accumulation to Microbial Community Dynamics in *Botryococcus sudeticus* Under Nitrogen Stress

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Microalgae are photosynthetic microorganisms producing diverse sustainable bioproducts, while *Botryococcus sudeticus* is a promising high-lipid biofuel feedstock. Although bacteria naturally coexist with microalgae in aquatic environments, they are often regarded as contaminants in laboratory cultures. However, understanding microbiome dynamics in xenic microalgal cultures may provide new opportunities for improving biomass and biofuel production through microbiome engineering. In this study, xenic *B. sudeticus* UTEX B 2629 was cultivated under controlled conditions, and bacterial community dynamics were investigated for the first time together with lipid and fatty acid methyl ester (FAME) production. A two-stage cultivation strategy was applied. During the first stage, cultures were grown in 3N-BBM medium, while in the second stage they were transferred to nitrogen-depleted media to evaluate the effects of nitrogen stress on microbiome composition, lipid accumulation, and FAME production. Growth was monitored by optical density and dry weight measurements, while lipid and FAME yields were determined gravimetrically, and FAME composition was analyzed by GC-FID. Prokaryotic community composition was characterized by 16S rRNA amplicon sequencing using the MinION™. Alphaproteobacteria dominated the bacterial community throughout cultivation. However, in nitrogen-depleted cultures where algal growth had ceased, the relative abundance of Sphingomonadales and Caulobacterales increased. Previous studies have suggested that Sphingomonadales contribute to the degradation of hydrocarbons and extracellular polymeric substances, Hyphomicrobiales facilitate nutrient remineralization by recycling nitrogen and phosphorus, whereas Caulobacterales have been reported to become more abundant during stress-induced metabolite accumulation. The microbiome analysis demonstrates that nitrogen availability shapes the bacterial community associated with *Botryococcus sudeticus*. Ongoing lipid and fatty acid methyl ester (FAME) analyses will be integrated with these findings to evaluate the relationship between microbial community dynamics and lipid accumulation. The combined results will provide new insights into the role of microbiome in optimizing lipid production and advancing microbiome-based strategies for sustainable biofuel applications.

Acknowledgement: This work was supported by the Scientific Research Projects Coordination Unit of Istanbul University under Project No. FYL-2025-42403.

Keywords: *Botryococcus sudeticus*; Microbial community Dynamics; Nitrogen stress; Lipid accumulation; Biofuel.



P-02

Cross-Domain Microbial Insights into Ecosystem Resilience and Restoration Potential in a Hypereutrophic Coastal Lagoon

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Küçükçekmece Lagoon, an urban coastal lagoon in Istanbul, Türkiye, has been subjected to decades of anthropogenic pressures, resulting in persistent hypereutrophic conditions since the 1990s, leading to oxygen depletion, hypoxia, internal nutrient loading and ecosystem degradation. Despite the recent attention to restoration strategies for the lagoon, there is very limited understanding of its microbiome dynamics across temporal scales and environmental gradients by molecular tools. To address this gap, a one-year monitoring study was carried out with a monthly sampling in three sites. In total, 72 water samples and 12 sediment samples were collected. The bacterial, eukaryotic, and archaeal communities were determined by amplicon sequencing using MinION platform (Oxford Nanopore, UK) together with physicochemical analyses, to provide a cross-domain perspective on microbiome dynamics in this degraded ecosystem.

Bacterial communities also exhibited pronounced spatial and temporal variability. Sulfur bacteria were enriched in deeper waters and showed a positive correlation with H₂S concentrations, suggesting an active role of sulfur metabolism under anoxic conditions. Archaeal communities displayed clear habitat specificity, with sediment samples dominated by Methanobacteriota, while surface waters were enriched in Candidatus Woeseearchaeota, Nanobdellota, and Thermoplasmatota. Eukaryotic communities were dominated by Ciliophora, Chlorophyta, and Bacillariophyta, although their relative abundances varied markedly among stations, sample types, and sampling periods.

Overall, the pronounced spatiotemporal heterogeneity and distinct cross-domain microbial assemblages revealed by this high-resolution survey highlight the strong influence of environmental gradients on microbiome structure and underscore the importance of incorporating microbial processes into ecosystem resilience assessment and restoration strategies for hypereutrophic coastal lagoons.

Keywords: 16S rRNA amplicon sequencing; Anoxia; MinION; Water pollution.



P-03

Pharmacological potential of compounds isolated from *Dictyota* spp. seaweeds

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M.P-12

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The sea is a source of molecules with interesting pharmacological activities. Marine organisms produce active secondary metabolites, with advantageous structures and interesting mechanisms of action for pharmacological studies. Persistent or chronic inflammation produces tissue damage and is the basis of many diseases such as cancer, cardiovascular diseases or neurodegenerative processes and plays a pivotal role in the inflammatory response due to ischemia-reperfusion injury. In this context the pharmacological activity of seven diterpenes (1-7 dictyol derivatives) isolated from two species of brown seaweeds of the genus *Dictyota* were tested over microglia cells. Results show that these compounds are as potent as cyclosporin A reducing the impact of ischemia. When cells are reperfused, the compounds avoid cellular damage, showing compounds 4 and 5 the strongest effects. The treatment with 1–7 also reduces ROS levels and restores mitochondrial membrane potential, indicating antioxidant and mitochondrial-protective properties. In addition, compounds 4, 5 and 7 display high affinity by cyclophilins, the cyclosporin A targets, with equilibrium dissociation constants in the micromolar range. Besides, 1-7 downregulate cyclophilins A and D as efficiently as cyclosporin A, suggesting a role in preventing mitochondrial dysfunction and inflammation. Interestingly, compounds modulate the activation of HIF1 α and Nrf2, hallmarks involved in hypoxia adaptation and redox homeostasis, while cyclosporin A has no effect. Compound 1 increases the nuclear translocation of both proteins, 3, 6 and 7 enhance HIF1 α activation, and 2 increases Nrf2 nuclear translocation. This study identifies diterpenes from *Dictyota* spp. as promising protective agents against pro-inflammatory stimulus as ischemia/reperfusion injury through the modulation of cyclophilins and stress-response pathways with better outcomes than cyclosporin A.

Keywords: marine compounds; seaweeds derivatives; ischemia; inflammation; neuroprotection.



P-04

Production and Characterization of Marine-Based 3D Scaffolds: A Comparative Study of Bioreactor and Static Culture Systems

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Three-dimensional scaffolds represent a cornerstone not only for Tissue Engineering and Regenerative Medicine (TERM) but also for industrial biotechnology, where they are employed to optimize cell culture performance. The pressing need for sustainable, biocompatible materials derived from industrial secondary products has pivoted research toward marine resources. In this context, collagen extracts stand out as the materials of choice for scaffold fabrication, owing to their intrinsic biocompatibility and biodegradability. In this preliminary study, we evaluated the efficacy of 3D scaffolds in both mammalian and invertebrate (Porifera) cell cultures. A comparative analysis was performed between scaffold produced from purified collagen of *Chondrosia reniformis* (Nardo, 1847), a marine sponge renowned for its high collagen content, and scaffolds obtained via the decellularization of tissues from other Porifera species. These two types of marine-derived systems are characterized by unique 3D architectures and biochemical profiles, potentially capable of providing the necessary cues to drive the commitment of diverse cell populations. The biological performance of these scaffolds was evaluated by comparing cell growth kinetics and spatial distribution under two distinct experimental conditions: conventional static culture (multi-well plates) and dynamic culture (BioAxFlow Bioreactor, Cellex S.r.L.). Our findings suggest that integrating marine-based 3D templates with controlled fluid-dynamic stimuli represents a scalable and efficient strategy for advanced cell cultures applications.

Keywords: Bioreactor; Collagen; Scaffolds; Sponges; Biotechnological applications.



P-05

The Impact of Red and Green Light on the Growth and Phycobiliproteins in *Nostoc* Strains

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Cyanobacteria produce phycobiliproteins, valuable commercial pigments that have been found only in a few algal divisions. They are divided into phycoerythrins (PE, red), allophycocyanins (APC, bluish green), and phycocyanins (PC, blue). The present study aimed to investigate the production of biomass and phycobiliproteins under red and green light in four *Nostoc* cyanobacteria strains. Tested parameters were determined by spectrophotometric analysis every 7 days during a 35-day cultivation, using light-emitting diode (LED) lighting tubes emitting cool white light covered with red and green polyethylene foil, with lighting durations of 5 and 10 hours per day. As the control, cultures were illuminated with cool white, fluorescent tubes (12:12 h light:dark regime). The results showed that biomass production under green light was lowered in all strains compared to the control, while the content of all phycobiliproteins was reduced or close to the content in the control. Under red light, the biomass production was inhibited in two strains, but it was increased in strains S8 and 2S1 ~ 2-fold, reaching 1.3 and 1.2 mg mL⁻¹, respectively. Under red light, in these two strains, the highest content of the blue pigment PC, 69.4 µg mL⁻¹ and 37.3 µg mL⁻¹ (12- and 6-fold more compared to the control, respectively) was registered, while the stimulating effect was also observed in the case of the bluish green APC, with the highest content of 29.5 µg mL⁻¹ (22-fold more compared to the control). The influence of red light on the PE was not so pronounced, with the highest content of 14.1 µg mL⁻¹. The results suggest the potential for increasing the production of biomass, PC, and APC in *Nostoc* strains by using red light.

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Keywords: Biomass production; Cyanobacteria; Green and red light; Phycobiliprotein pigments.

This contribution was not presented during the symposium



P-06

From Invasive Species to Economic Resource: Valorization and Market Perspectives of the Atlantic Blue Crab (*Callinectes sapidus*)

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The rapid spread of the Atlantic blue crab (*Callinectes sapidus*) across Mediterranean coastal ecosystems has generated significant ecological and socio-economic impacts, particularly affecting fisheries and aquaculture activities. At the same time, the increasing availability of this invasive species offers opportunities for its valorization within circular economy and blue bioeconomy frameworks. The objective of this study was to evaluate the potential of blue crab exploitation as a sustainable resource by analyzing its socio-economic impacts, food safety aspects, valorization pathways, regulatory framework and market opportunities.

A comprehensive review of scientific literature, institutional reports and regulatory documents was conducted. Particular attention was devoted to the nutritional characteristics of blue crab meat, food safety considerations, commercial applications, and the recovery of high-value compounds from processing by-products. Existing market trends and current management approaches in Mediterranean countries were also examined. The analysis revealed that *C. sapidus* represents a valuable biological resource with considerable potential for both direct human consumption and industrial applications. Blue crab meat is characterized by high nutritional quality and increasing consumer acceptance, while shells and processing residues can be exploited to produce chitin, chitosan and other bioactive compounds suitable for food, feed, pharmaceutical and biomaterial sectors. The growing commercial interest observed in several Mediterranean countries demonstrates the possibility of transforming an invasive species into an economic opportunity. However, effective valorization requires adequate monitoring systems, information among stakeholders, food safety controls and supportive regulatory measures to ensure product quality, traceability and market development.

The findings suggest that the sustainable exploitation of *C. sapidus* biomass can contribute simultaneously to invasive species management, waste reduction and the creation of new value chains, supporting the transition towards a more circular and resilient blue economy.

Keywords: *Callinectes sapidus*; blue economy; invasive species; seafood valorization; circular economy.



P-07

Microfluidic PLP–RCA Detection of the Microcystin Biosynthesis Gene *mcyE*

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Cyanobacteria produce toxic secondary metabolites that threaten human and environmental health through the contamination of drinking water, recreational exposure and bioaccumulation in aquatic food chains. The *mcy* gene cluster is a reliable genetic marker for identifying potential microcystin producers, however, conventional molecular detection methods remain time-consuming and lack the sensitivity required for rapid and reliable environmental monitoring.

To develop and evaluate a sensitive microfluidic Padlock Probe-based Rolling Circle Amplification (PLP-RCA) assay for the detection of the *mcyE* gene, a key genetic marker of microcystin-producing strains.

A PLP targeting the *mcyE* gene and corresponding RCA primers were designed. A PDMS microfluidic chip with 30 streptavidin bead-packed chambers was fabricated by soft lithography. Genomic DNA (gDNA) isolated from *Microcystis aeruginosa* PCC 7806 was used for assay validation. Following target hybridization and PLP ligation, onchip RCA was performed at 37 °C and fluorescence signals were analyzed by fluorescence microscopy.

Results: The microfluidic PLP-RCA platform detected the *mcyE* gene over a 0.1-10 ng/μL gDNA concentration range. Fluorescence intensity increased in the presence of the target, confirming successful amplification. Detectable signals were observed down to 0.1 ng/μL, with the highest fluorescence response at 1 ng/μL. Negative controls showed minimal fluorescence, indicating high assay specificity.

Successful detection of the *mcyE* gene over a 0.1-10 ng/μL gDNA concentration range demonstrates the potential of the proposed microfluidic PLP-RCA platform for rapid and sensitive cyanobacterial monitoring. The assay exhibited high specificity, with the negative control producing a signal comparable to the blank level. The integration of PLP-based target recognition with on-chip isothermal amplification provides a promising approach for simplified molecular detection. Future work will focus on assay optimization, limit of detection determination, and validation using environmental samples.

Keywords: Cyanobacteria; *mcyE*; GenePadlock probe; Rolling circle amplification; Fluorescent biosensor.

This contribution was not presented during the symposium



P-08

Emerging Contaminants in Seafood Safety: A One Health Perspective from Biomonitoring to Consumer Risk Assessment

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Seafood represents a nutritionally valuable source, but it is also highly exposed to environmental contamination due to the direct interaction between aquatic organisms and their surrounding ecosystems. In recent years, emerging contaminants such as microplastics, nanoplastics, plastic additives, per- and polyfluoroalkyl substances, pharmaceutical residues, toxic metals, pesticides, and antimicrobial resistance-related pollutants have become increasingly relevant for seafood safety. These contaminants may enter aquatic food chains through water, sediment, suspended particles, feed, packaging, and post-harvest handling processes, creating complex risks that cannot be evaluated only through conventional food safety approaches. This study aims to present a One Health-based framework linking aquatic biomonitoring, seafood contamination, consumer exposure, and human health risk assessment. Particular attention is given to contamination routes in seafood systems, including environmental exposure, aquaculture inputs, processing practices, packaging-related transfer, and post-harvest handling as key determinants of consumer exposure. Biomonitoring tools, including spectroscopic detection methods, biochemical biomarkers, molecular approaches, and risk assessment models, are considered as complementary components for identifying contamination pathways and evaluating potential hazards. The One Health perspective provides an integrated basis for interpreting seafood safety within the interconnected context of ecosystem health, aquatic organism health, food production, and consumer protection. This perspective highlights that emerging contaminants in seafood should be addressed not only as isolated chemical or physical hazards, but as part of a broader environmental and public health challenge. Strengthening biomonitoring, harmonizing analytical methods, and improving consumer-oriented risk assessment strategies are essential for sustainable seafood safety management.

Keywords: Environmental contaminants; Food Safety; Exposure pathways; One Health; Consumer risk assessment.



P-09

Marine Bioindicator Species as Sentinels of Microplastics Contamination: An Integrated Framework for Aquatic Food Supply Safety

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Microplastic contamination is an emerging threat to aquatic ecosystems, seafood safety, and sustainable food supply. Marine invertebrates are of particular importance since they may act both as seafood resources and as biological indicators of environmental pollution. Beyond their direct role in human nutrition, these aquatic organisms are increasingly regarded as aquatic bioresources with potential relevance for bioactive compounds, biomaterials, and functional ingredients; therefore, their contamination status has implications not only for seafood safety but also for the safe and sustainable use of marine biological resources. This project aims to establish an integrated framework for evaluating microplastic contamination in selected bioindicator species and linking environmental exposure with aquatic food supply safety. The study focuses on edible and ecologically relevant species sampled from the Sea of Marmara and the North Aegean Sea, including the Mediterranean mussel, wedge clam, European flat oyster, sea urchin, and sea cucumber. The methodological approach combines field sampling, microplastic isolation and characterization, biochemical biomarker assessment, controlled laboratory exposure, molecular docking, and consumer-oriented risk evaluation. Microplastics will be isolated using optimized digestion and density-separation procedures, followed by microscopic examination and polymer characterization. In parallel, oxidative stress and cellular damage responses will be evaluated through enzymatic and nonenzymatic biomarkers. Molecular docking will be used to support the interpretation of possible interactions between polymer-related compounds and selected target enzymes. This framework is expected to provide a multi-level perspective on microplastic retention, biological response, and potential consumer exposure in aquatic foods. The project may contribute to evidence-based monitoring strategies for marine pollution, seafood safety, sustainable management of marine resources, and the safe valorization of aquatic bioresources.

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Keywords: Microplastics; Bioindicator species; Seafood safety; Biomonitoring; Risk assessment.



P-10

Genomic and Metabolic Profiling of *Microcystis aeruginosa* Blooms in Lake SerraiaV. Ceccherini^{1,2}, A. Boscaini², L. Cerasino², A. Papini¹, D. Cavalieri¹, N. Salmaso²

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Cyanobacterial blooms are an increasing global threat, driven by eutrophication and climate change. Lake Serraia, a shallow peri-alpine dimictic lake of high natural and touristic value in NE Italy, has experienced anthropogenic eutrophication since the late 1990s. While historical summer cyanobacterial blooms between 2017 and 2020 were dominated by non-toxic *Dolichospermum* species, a massive *Microcystis aeruginosa* (Kützinger, 1846) bloom emerged in summer and autumn 2023. Since then, blooms of *M. aeruginosa* have become a regular occurrence in the lake. In response to this critical shift, a comprehensive, multidisciplinary project has been initiated with the aim of deepening the understanding of the taxonomic and metabolomic characteristics of the *Microcystis* population responsible for the blooms in Lake Serraia. Here, we present the initial findings of metabolic, and metagenomic analyses conducted on an environmental sample collected during the bloom on 31 August 2023, as well as on a unicellular, non-axenic culture of *M. aeruginosa* isolated from the same sample. Metabolomic profiling, performed using Liquid chromatography-tandem mass spectrometry (LC-MS) techniques, confirmed the presence of high microcystin (MC) concentrations in the bloom (up to 200 µg/L of MC-LR and 42 µg/L of MC-RR) and in the isolate. Both assemblies showed close taxonomic correspondence with other *M. aeruginosa* genomes in public repositories (with ANI values greater than 96%). While detecting the presence of the biosynthetic gene cluster (BGC) involved in the biosynthesis of MC, genome annotation using Antismash identified several secondary metabolites not targeted by LC-MS analysis, including functional operons responsible for the potential biosynthesis of micropeptins, microcyclamides and aeruginosins. In conclusion, the integration of metabolomic profiling with advanced genomic analyses represents a robust, multidisciplinary approach for elucidating the factors controlling the development of toxigenic species in freshwater ecosystems.

Keywords: Cyanobacterial blooms; LC-MS; Genome mining.



P-11

Marine Ecosystem Assessment of a Student-Designed Offshore Wind Farm in the Aegean Sea: The Bozcaada YEKA Case

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The expansion of offshore wind energy into ecologically sensitive marine environments demands environmentally integrated planning approaches. This study presents an environmental and marine ecosystem assessment conducted within Türkiye's first student-designed offshore wind farm project, developed for the designated Renewable Energy Resource Area (YEKA) offshore Bozcaada Island in the northern Aegean Sea.

Technical and environmental planning of a utility-scale offshore wind facility was carried out using WASP and WindPRO software, supported by ERA5 reanalysis data and regional meteorological observations. Alongside technical feasibility analyses, an environmental impact assessment framework was developed for the marine ecosystem of the project area.

The Bozcaada coastal waters host biologically productive habitats supporting commercially and ecologically important fish species, crustacean assemblages, and benthic shellfish communities, including mussel and oyster populations that contribute to regional biodiversity and fisheries productivity. Ecological sensitivity screening was conducted to evaluate potential interactions between offshore wind infrastructure and marine habitats.

Drawing on literature regarding the artificial reef effect of offshore wind turbine foundations, the study discusses the potential ecological role of monopile structures as secondary habitat-forming elements capable of supporting marine biodiversity. Climate change projections from CMIP5/6 scenarios were additionally incorporated to assess the long-term sustainability of offshore wind resources in the region.

This study demonstrates that offshore wind development, when supported by ecosystem-based environmental assessment, can be planned in harmony with marine conservation objectives. A multidisciplinary and replicable framework for ecological risk screening is proposed, contributing to the scientific discussion on environmentally responsible offshore energy development in the Aegean and Eastern Mediterranean regions.

Keywords: offshore wind energy; marine ecosystem assessment; environmental impact assessment; artificial reef effect; Aegean Sea



P-12

Bioactivity Antiproliferative Screening of Antarctic Cold-Adapted Bacteria

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Antarctica represents one of the most extreme environments on Earth. These harsh conditions have contributed to the adaptation of a plethora of microorganisms that exhibit unique characteristics to survive at low temperatures, typically below 20 °C, high salinity, and strong ultraviolet (UV) radiation. Cold-adapted bacteria serve as a reservoir of promising bioactive compounds produced in response to environmental stress, often displaying properties distinct from those of their mesophilic counterparts.

This study aims to identify and characterize cytotoxic molecules produced by selected Antarctic bacterial strains, with a focus on peptides, proteins, and enzymes exhibiting potential therapeutic activity against melanoma, acute monocytic leukemia, and acute lymphoblastic leukemia, through *in vitro* evaluation on human cancer cell lines. UV-resistant bacterial strains, isolated through UV-C assay, were collected from various Antarctic aquatic environments (surface seawater, ice, and shallow lake sediments) and included: *Staphylococcus*, *Kocuria*, *Gordonia*, *Rhodococcus*, *Arthrobacter*, *Brevundimonas*, *Sphingorhabdus* and *Salinibacterium* genera. Strains were cultured under optimal growth conditions at 20 °C in marine broth for one week to stimulate metabolite production. The biomass was extracted with both methanol and water. The methanolic extract was further subjected to bioactivity-guided fractionation using solid-phase extraction (SPE) columns whereas the aqueous extract was sonicated. Additionally, the culture supernatant was extracted with ethyl acetate. All extracts and fractions were screened for antiproliferative and cytotoxic activity using standard MTT and WST-8 cell viability assays on melanoma (A2058 and SKEMEL) and leukaemia (THP-1, CCRF-CEM) cell lines.

Preliminary results indicate that some fractions exhibit significant cytotoxic effects, suggesting the presence of bioactive compounds with potential pharmaceutical relevance. Through the isolation and characterization of these bioactive molecules, we aim to support the development of innovative therapeutic strategies and contribute to the discovery of new treatments.

Keywords: Antarctica; Marine bacteria; Anticancer; Bioactive compounds.



P-13

From Genes to Molecules: Connecting Biosynthetic Gene Clusters and Specialized Metabolism in the Cyanobacterial Genus *Floridanema*

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Cyanobacteria generate structurally complex peptides and hybrid polyketide-peptide natural products with diverse biological functions and vast chemical diversity, yet the enzymatic logic that produces their many documented hybrid molecules remains incompletely understood. Here we show that the recently described genus *Floridanema* harbors biosynthetic systems that unify the production of tychonamides and pahayokolide-like peptides, including the assembly of the signature residues 3-amino-2,5,7-trihydroxy-8-phenyloctanoic acid (Atpoa) and 3-amino-2,5,7,8-tetrahydroxy-10-methylundecanoic acid (Athmu). Furthermore, we expand the chemical diversity found in this group by characterizing additional metabolites from many known and new molecule classes.

Using an integrated ‘pathways-to-products’ strategy combining comparative genomics, bioinformatics analyses, and structure elucidation by NMR and MS, we link previously cryptic gene clusters to new metabolites and define shared architectural features across these pathways. Together, our findings reposition *Floridanema* as a central source organism for previously reported peptide families and establish generalizable biosynthetic principles that can be leveraged to predict, discover, and engineer related natural products.

Keywords: Natural products; Genome mining; Polyketide synthases; Nonribosomal peptide synthetases; Comparative genomics.



P-14

BCCM/ULC: A Public Culture Collection for *Ex Situ* Conservation of Cyanobacterial Diversity and Support of Biotechnological Applications

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Cyanobacteria are a cosmopolitan group of oxyphototrophic bacteria that are notoriously difficult to isolate and maintain in living cultures. Nevertheless, their ability to produce a variety of functionally diverse and structurally complex bioactive metabolites with potential biotechnological applications places them in the spotlight of bioprospecting studies. Cyanobacterial culture collections around the world enable screening studies and have already led to the characterization of several new bioactive metabolites. For example, new bioactive compounds such as floridanemamides as well as new variants of known bioactive metabolites (e.g., tychonamides, pahayokolides, anabaenopeptins, scytocyclamides, lassopeptides, apratoxins and guanitoxins) have been identified from strains of the Berthold–Laughinghouse Culture Collection (Florida, USA).

The BCCM/ULC is a young Belgian public collection, currently hosting more than 500 cyanobacterial strains from various habitats (e.g. freshwater, marine, terrestrial) with more than 20 reference (or “type”) strains of newly described taxa, including *Plectolyngbya*, *Shackletoniella*, *Timaviella*, *Parakomarekiella*, *Petrachloros*, *Leptochromothrix*, *Vermifilum*, *Tigrinifilum*, *Affixifilum*, *Sirenicapillaria*, *Ophiophycus*, *Floridanema*, *Dapis* and *Sivoneniella*. The catalogue of all publicly available strains can be found in [https:// bccm.belspo.be/catalogues/catalogue-search?collection=ULC](https://bccm.belspo.be/catalogues/catalogue-search?collection=ULC). Recently, a large number of strains from the Berthold–Laughinghouse Culture Collection have been deposited in the collection. At BCCM/ULC, public deposition and distribution of strains are covered by an ISO 9001 certification, granted as part of the multi-site certification for the Belgian Coordinated Collections of Microorganisms (BCCM) consortium. Our team of experts offers services in cyanobacterial strain isolation, maintenance, preservation, and characterization. Customized, on-demand training courses are also available. All strains are studied by a polyphasic approach integrating morphological, molecular, and ecological data. Yet only a small percentage of these strains have been used in screening studies. With only a small fraction of its strains chemically characterized to date, BCCM/ULC represents a largely untapped, openly available resource for future bioprospecting.

Keywords: Cyanobacteria; Natural products; Bioprospecting; Culture collections; BCCM/ULC



P-15

Biosynthetic Potential and Carotenoids in an Antarctic Marine *Arthrobacter* StrainA. De Felice¹, A. Levante², C. Lazzi², A. Coppola¹, S. Del Prete¹, C. Verde¹, D. Giordano¹

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Polar microorganisms represent a promising source of novel bioactive compounds. Antarctic marine microorganisms have evolved unique adaptive strategies to thrive under harsh environmental conditions, including low temperatures, high ultraviolet (UV) radiation, and elevated oxygen levels. This study aimed to investigate the biosynthetic potential of an Antarctic marine bacterium, with a particular focus on carotenoid production and its antioxidant activity in relation to cold adaptation. The pigmented strain was isolated following UV-C treatment and identified as a member of the genus *Arthrobacter* by 16S rRNA gene sequencing. Whole-genome sequencing and annotation were subsequently performed to assess its biosynthetic capacity. Genome mining revealed several biosynthetic gene clusters associated with secondary metabolite production. Pathways potentially involved in non- α -poly-amino acid biosynthesis and ribosomally synthesized and post-translationally modified peptides (RiPPs) were identified using the antiSMASH platform. Moreover, bioinformatic analyses enabled the reconstruction of the carotenoid biosynthetic pathway responsible to produce bacterioruberin, a rare C50 carotenoid that confers pigmentation to bacterial colonies. The strain was cultivated at different temperatures to evaluate carotenoid production in response to cold conditions. Bacterioruberin levels varied with growth temperature, suggesting a role in cold adaptation. In parallel, antioxidant activity was assessed using the ABTS radical scavenging assay, confirming the antioxidant potential of bacterial extracts. Overall, these findings highlight the biotechnological potential of this Antarctic *Arthrobacter* strain as a source of bioactive metabolites. Bacterioruberin may contribute to both cold adaptation and oxidative stress protection, supporting further investigations into its ecological role and potential applications.

Keywords: *Arthrobacter*; Secondary metabolite; Carotenoid; Bacterioruberin; Cold adaptation.



P-16

Occurrence of Saxitoxins in Marine Invertebrates from Apulian Lagoons

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Saxitoxins (STXs) are neurotoxic compounds produced by certain dinoflagellates during harmful algal blooms (HABs), representing a risk for marine ecosystems and seafood safety. This study investigated the occurrence and distribution of STXs in marine invertebrates collected from two coastal lagoons in southern Italy (Lesina and Varano), characterized by environmental variability typical of transitional systems, over the period May–November 2024. Sampling targeted species representing diverse trophic strategies, including the oyster *Magallana gigas*, the invasive crab *Callinectes sapidus*, and gelatinous zooplankton (ctenophores and jellyfish). Toxin occurrence was assessed and compared among species and sampling sites. Oysters showed the highest frequency of positive samples (40%) although with relatively low mean concentrations (22.08 $\mu\text{g kg}^{-1}$). In contrast, crabs exhibited lower frequencies (16% in Varano and 20% in Lesina) but higher mean toxin levels (31.83 and 45.93 $\mu\text{g kg}^{-1}$, respectively). Gelatinous plankton displayed the lowest prevalence (11%). Tissue-specific analysis in *C. sapidus* revealed STXs accumulation in all organs, with mean concentrations ranging from 16.40 $\mu\text{g kg}^{-1}$ in muscle to 74.35 $\mu\text{g kg}^{-1}$ in the hepatopancreas. Although all detected STXs levels were below regulatory limit (800 $\mu\text{g kg}^{-1}$), the findings highlight the role of non-traditional matrices in STXs transfer within aquatic food webs. The inclusion of multiple taxa beyond bivalve molluscs may improve toxin monitoring strategies and provide a more comprehensive understanding of STXs dynamics in transitional environments.

Keywords: Saxitoxins; Harmful algal blooms; Coastal lagoons; Marine invertebrates; Food safety.



P-17**Isolation and Characterization of Cyanobacteria from Diverse Habitats in Naples**N.T. Papadopoulos¹, S. Gkelis¹

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Cyanobacteria are prokaryotic photoautotrophic microorganisms, renowned for their remarkable diversity and complex survival strategies; they can thrive in almost every environment on Earth. In an expedition to identify biodiversity and isolate cyanobacterial strains, we collected 24 samples from five diverse sites in Naples, Italy: Lakes Lucrino, Fusaro, and Miseno; Stufe di Nerone thermal spas; and from Vesuvio volcano. To isolate cyanobacteria, samples were categorized by temperature requirements and incubated accordingly: high- temperature samples at 40°C and ambient-temperature samples at 23°C. The media used in the cultures are BG-11 and BG-110 and they were placed in 24-well plates with serial dilutions and agar plates. Each culture was regularly monitored for growth using light microscopy. Following isolation, a polyphasic identification approach was undertaken starting with morphological characterization, followed by genetic identification via sequencing of the 16S rRNA and ITS regions and concluded with the comparison of their evolutionary relationships by reconstructing a phylogenetic tree. These efforts led to the successful isolation of several cyanobacterial strains, demonstrating significant taxonomic diversity that encompasses several distinct orders. This study enhances our understanding of the cyanobacterial diversity in extreme and/or underexplored habitats. In the meantime, a well-characterized collection of isolates was acquired enabling future physiological and biotechnological exploration.

Keywords: Cyanobacteria; Isolation; Extreme habitats; Naples; Polyphasic taxonomy.



P-18

Identifying Chemical Epigenetic Modifiers Concentration for Diatom CulturesG. Kopp¹, C.N. Velanis², M. Jaspars³, C. Lauritano¹

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Diatoms are the most diverse group of phytoplankton, offering a vast source of new molecules with possible applications in cosmetic, nutraceutical and pharmaceutical sectors. The use of chemical epigenetic modifiers (CEM) to activate silent biosynthetic pathways in microorganisms has recently emerged as a promising approach in bioactive compounds production. However, their application in microalgae remains poorly explored, resulting in limited data to guide their use without unintended ecophysiological effects (e.g. cells death). In this study, different concentrations of epigenetic modifiers were applied to microalgal cultures to assess their effects on the growth of two diatoms, *Phaeodactylum tricornutum* and *Cylindrotheca closterium*. These two species are well-known producers of bioactive molecules with anti-inflammatory and anti-proliferative activities. Here, we present the results obtained from the screening of CEMs in two diatom species. The objective is to identify treatment conditions that preserve culture growth while inducing epigenetic changes. This study particularly focuses on nicotinamide, an NAD⁺-dependent histone deacetylase inhibitor, for which the lowest concentration exhibited the most suitable growth conditions relative to control. Determining the CEM optimal concentration for diatom growth is essential for subsequent scale-up experiments, including ChIP, Western blotting, and chemical analyses, to evaluate whether the epigenetic modifier affects molecular mechanisms underlying the production of compounds of interest. This study provides foundational knowledge for applying chemical epigenetic modifiers in microalgae biotechnology.

Keywords: Epigenetics; Diatoms; Nicotinamide.



P-19

From Regenerative IMTA Biomass to Blue Biorefinery Products: Cascade Valorisation of *Gracilaria* and *Ulva* in the Adriatic

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The Blue Economy requires integrated strategies combining sustainable marine biomass production with complete resource valorisation. The Interreg Italy–Croatia BIOBASED project develops regenerative Integrated Multi-Trophic Aquaculture (IMTA) systems and blue-biorefinery solutions to strengthen circular value chains across the Adriatic region. This work presents the updated outcomes of Activity 2.1, focused on selecting green conversion pathways for seaweeds and aquaculture side-streams.

Biomass of *Gracilaria gracilis*, *Ulva laetevirens* and *Ulva* sp. was characterised for macromolecular and elemental composition, amino acids, lipids, phenolics, phycobiliproteins and structural carbohydrates. The resulting dataset was used as a decision framework for species-specific cascade processing. *G. gracilis* contained approximately 40–42% sugars and 18–20% proteins on a dry-weight basis, together with measurable R-phycoerythrin, allophycocyanin and phycocyanin. These results support a high-value-first sequence based on mild aqueous recovery of heat-sensitive pigments, followed by hot-water agar extraction and subsequent utilisation of protein- and mineral-rich residues. *Ulva* biomass showed a more carbohydrate-dominant profile, with total sugars reaching 64.24% dry weight and an ulvan-related fraction containing glucose, rhamnose, xylose and uronic-acid-derived components. Accordingly, an ulvan-first pathway was selected, followed by saccharification of residual glucan and cellulosic fractions.

The two core routes are complemented by the recovery of proteins, lipophilic pigments, polyunsaturated fatty acids and phenolics, while final residues and IMTA biowaste are directed towards biostimulants production. This integrated approach links regenerative aquaculture, green extraction, analytical quality control and zero-waste processing, providing a transferable framework for Adriatic SMEs and advancing the transition from marine biomass production to market-oriented blue biorefineries.

Acknowledgement: This contribution is presented in the framework of the BIOBASED project, funded by the Interreg Italy–Croatia 2021–2027 Programme.

Keywords: Regenerative IMTA; Blue biorefinery; Macroalgae.



P-20**Species Level Characterisation of Cyanobacterial Blooms by Nanopore Sequencing Approach****Z. Zengin¹, A. Oğuz¹, L. Köker¹, G. Özbayram¹, M. Albay¹, R. Akçaalan¹**

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Cyanobacteria blooms have become frequent due to eutrophication from anthropogenic activities and global climate change. They also have toxin and odour production potential directly affect public health or perception of water users. Therefore, rapid determination of species composition within cyanobacterial blooms is essential for timely surveillance and risk assessment. In this study, we aimed to characterise cyanobacteria bloom communities in an urban freshwater pond by nanopore sequencing approach to better understand their potential. For this purpose, monthly samples were collected from May to October 2025 in Gümüşyaka Pond. Phytoplankton net samples were filtered using sterile 0.22 µm filter following DNA isolation with the NucleoSpin Soil DNA isolation kit. Concentrations were measured with Qubit and cyanobacterial species were identified under the Oxford Nanopore MinION platform sequencing results after obtaining a 16S rRNA (V1-V9) amplicon. *Planktothrix agardhii* was dominant in bacterial community with a relative abundance reached to 97.8% in October, minimum abundance was 16.64% in June. *Anabaena* was detected in June with 5.9% abundance with mostly *A. cylindrica* (3%) which had a decreasing trend throughout the study period. *Limnospira indica* was detected with maximum abundance in August and September (3.6% and 3.8% respectively). *Nostoc* was detected with maximum abundance in June (2.3%) including mostly *Nostoc punctiforme* (0.93%), with a decreasing trend in study. *Aphanizomenon* was detected with maximum 1.79% abundance in July, *Dolichospermum* 1.05% in September. *Synechocystis* was also detected with stable (0.6-0.7%) abundance. *Woronichinia*, *Pseudanabaena*, *Microcystis*, *Geitlerinema* and *Cyanobium* were also detected with relatively low abundances (0.1%-0.3%). Identified cyanobacteria species are known cyanometabolite (microcystin, anatoxin, geosmin, mycosporine-like amino acids) producers, especially *P. agardhii* has also toxin production potential with the high relative abundance in the pond. Our results demonstrate that Nanopore sequencing is a promising approach for the rapid assessment of cyanobacterial bloom diversity, enabling timely species screening.

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Keywords: Nanopore sequencing; Cyanobacteria; Cyanometabolites.



P-21

Green Synthesis of CeO₂-x Nanoparticles for Oxidative Removal of Geosmin and 2-MIB

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Deterioration in water quality affects human and ecosystem health, and consumption of packaged water is increasing every year due to taste and odor problems in drinking water. In this study, it is aimed to develop a new method based on oxidation and reduction that can be used in advanced oxidation water treatment processes for the removal of Geosmin, 2-Methylisoborneol (2-MIB) compounds causing undesirable taste and odor formation in water. In the current work, we reported a rapid, facile, low-cost, and one-pot fabrication approach for synthesizing cerium oxide nanoparticles (CeO₂-x NPs) by using microwave-assisted synthesis. Here, the effect of varying concentration of reducing agent, along with control over microwave irradiation power, on the physicochemical attributes, size, shape, and morphology of the CeO₂-x NPs was investigated in detail. The CeO₂-x NPs were characterized by the results of analytical techniques such as FTIR, zetasizer/potential, XPS, XRD, and FESEM/EDX. The outcomes of XRD pattern affirmed the crystalline structure of this product with suggested size of about 20-50 nm, while the FESEM pictures presented spherical morphology. Additionally, XPS analysis of CeO₂-x NPs affirmed the presence of a Ce³⁺ and Ce⁴⁺ oxidation state in the sample, as well as Ce³⁺ as the major valence of cerium oxide. Macroalgae (*Cystoseira* sp.) extracts were used as stabilizers and reducing agents in the green synthesis of CeO₂-xNP. Macroalgae were extracted by microwave-assisted extraction method in an aqueous environment, without need for organic solvents, in optimum conditions and in a short time that provides efficient extraction of secondary metabolites with thermal heat. Within the scope of this study, combined use of macroalgae and microwave-assisted synthesis system in the green synthesis of CeO₂-xNPs were done for the first time. Batch process experiments were conducted to evaluate the removal efficiency of geosmin and 2-MIB from aqueous solutions under varying pH conditions, contact times, and initial CeO₂-xNPs dosages. Under the optimized conditions, the developed CeO₂-xNPs system achieved removal efficiencies exceeding 85% for both geosmin and 2-MIB.

Acknowledgments: This study was supported by the Scientific and Technological Research Council of Türkiye (TUBITAK) under Project No. 124Z436.

Keywords: Green synthesis; CeO₂-x nanoparticle; Geosmin; 2-Methylisoborneol; *Cystoseira* sp.



P-22

Purple Bacteria as Novel Foods and Feeds: Antioxidant and Cytotoxic Properties

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Purple non-sulphur bacteria (PNSB) are anoxygenic photosynthetic microorganisms with remarkable metabolic versatility, widely explored for applications in industrial or environmental biotechnology. Their capacity to accumulate high-value bioactive compounds, including carotenoids, coenzyme-Q10 (CoQ10), and high-quality proteins, makes them a promising source of nutraceuticals for more sustainable feed and food supplement sectors. However, biological activity and cytotoxicity must be evaluated before food and feed applications to ensure safety and regulatory compliance. Within the framework of EU-funded Purple4Life project, the present study focuses on characterizing the bioactive potential and safety profile of biomass produced by two PNSB species: *Rhodospirillum rubrum* and *Rhodobacter capsulatus*. Hydroalcoholic extracts (HE) were prepared from freeze-dried biomass, and the pigments' profile was characterized by UV-Vis absorbance spectroscopy. Quinone, carotenoids and fatty acid profiles of the extract were further characterized by LC-MS analysis. Antioxidant activity was evaluated using the Trolox Equivalent Antioxidant Capacity (TEAC) assay. Cytotoxic activity was assessed on human intestinal epithelial (Caco-2) and breast adenocarcinoma (MCF-7) cell lines using MTS assay. UV-Vis absorbance spectra revealed characteristic peaks within the carotenoid absorption range. LC-MS analysis confirmed the presence of unusual omega-7 MUFAs in PNSB as well as the presence of the low-potential rholoquinone in *R. rubrum* extract. Both extracts exhibited considerable antioxidant activity, with *R. rubrum* showing significantly higher activity than *R. capsulatus* (28.13 ± 0.49 vs 19.98 ± 2.92 $\mu\text{mol TE/g}$). Concentrated HE showed no significant dose-dependent reduction in cell viability in either cell line across the tested concentration range (8.6–2205 $\mu\text{g/mL}$ of dried HE). Notably, certain concentrations appeared to stimulate Caco-2 cell viability. These findings constitute a first step towards the comprehensive characterization of PNSB biomass, highlighting its bioactive potential while underscoring the need for more systematic investigations to fully establish its safety profile and suitability as a novel food and feed ingredient.

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Keywords: Cytotoxicity; Antioxidant activity; Carotenoids; Food safety; Purple non-sulphur bacteria.



P-23

Bioproduct Potential of Aquacultured Sturgeons

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Sturgeons are among the most economically valuable species in aquaculture, primarily known for caviar and meat production. However, farmed sturgeons can also serve as a source of diverse bioproducts, making them relevant to food technology, cosmetics, pharmaceuticals, and other industrial sectors.

This study reviews the range of products that can be derived from farmed sturgeons. Caviar remains the flagship product, while sturgeon meat is marketed fresh, frozen, smoked, or processed. Since meat constitutes the bulk of farm output, its commercial development is key to farm viability. Beyond these primary products, several by-products offer additional value. Sturgeon skin can be processed into leather for use in fashion and accessories. The swim bladder yields isinglass and bio adhesive materials. Cartilage, oil, and other tissues have applications in functional foods, nutraceuticals, cosmetics, and biomedical products.

These findings suggest that sturgeon aquaculture holds potential well beyond caviar. Treating the whole fish as a multi-product biological resource supports circular economy principles, reduces waste, and improves economic efficiency. Sturgeon aquaculture can thus serve as a practical model linking high-value fish farming with aquatic biotechnology and sustainable bioeconomy goals.

Keywords: Sturgeon aquaculture; Caviar; bioproducts; Aquatic biotechnology; Value-added products.



P-24

Phenolic, Flavonoid and Antibacterial Properties of Green Microalgae and DiatomsA. Inam¹, F. Ozan Coven¹, Z. Demirel², T. Oncu-Oner¹, M. Conk-Dalay²

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Microalgae are photosynthetic microorganisms that can live in freshwater, marine, brackish water or even wastewater in different shapes and colors. These microorganisms have gained popularity for their valuable and diverse biometabolites, which are now being applied in various fields like food, medicine, agriculture and cosmetics. In addition, the extracts or metabolites of several microalgae species could exhibit antimicrobial, antioxidant and antitumor activities. Increasing bacterial antibiotic resistance has intensified the search for novel and natural antibacterial agents. Microalgae may exhibit antibacterial activities due to their rich phenolic and flavonoid contents. This study aims to compare the phenolic and total flavonoid contents, and antibacterial activities of ethanolic extracts obtained from four green microalgae (*Dunaliella polymorpha*, *Tetraselmis chuii*, *Desmodesmus* (*Scenedesmus*) *protuberans*, *Ettlia* (*Neochloris*) *texensis*) and four diatom species (*Phaeodactylum tricornutum*, *Amphora capitellata*, *Nitzschia thermalis* and *Cylindrotheca closterium*). Total phenolic and flavonoid contents were determined using the Folin-Ciocalteu, aluminum chloride colorimetric methods, respectively. In the antibacterial analysis, minimum inhibitory concentration (MIC) method was performed using Gram-positive *Staphylococcus aureus* and Gram-negative *Escherichia coli* bacteria. The total phenolic contents were generally higher in the green microalgae than in diatom species, with the highest value determined in the *D. polymorpha* extract (10.50 ± 1.34 mg GAE/g). Similarly, the highest total flavonoid content was obtained in the *D. polymorpha* extract (0.905 mg/mL). MIC values ranged between 0.09 and 6.25 mg/mL, with *A. capitellata* and *N. thermalis* showing the highest antibacterial activity against *S. aureus*, while *D. polymorpha* and *D. protuberans* were the most effective against *E. coli*. These results highlight the potential of microalgae as sources of bioactive compounds for biotechnological applications. This study was supported by the Scientific Research Projects Coordination Unit of Manisa Celal Bayar University (BAP) under Project No: 2023-034.

Keywords: Green microalgae; Diatom; Phenolic contents; Flavonoid contents; Antibacterial activity.



P-25

Fish-Based Models for Multilevel Assessment of Aquatic Environmental Stressors

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The impact of treated wastewater discharged from a wastewater treatment plant (WWTP) was investigated through its effects on downstream wild fish populations, specifically Prussian carp (*Carassius gibelio*). The study evaluated fish health by examining microbiological contamination, antimicrobial resistance patterns, tissue histology, blood biochemical parameters, and erythrocyte nuclear abnormalities. Bacterial isolates obtained from both fish and surrounding water predominantly included aeromonads with known zoonotic potential. These isolates exhibited high levels of resistance to several antimicrobial agents, particularly sulfamethoxazole and erythromycin. Histological analyses revealed pronounced alterations in gill structure of fish collected from effluent-impacted sites, including lamellar fusion and decreased interlamellar spaces. Biochemical assessment indicated significantly elevated plasma concentrations of urea, total proteins, albumin, and triglycerides, alongside a reduction in superoxide dismutase activity in fish inhabiting the effluent-receiving canal. Additionally, a higher incidence of erythrocyte nuclear abnormalities was observed in these specimens, suggesting genotoxic stress. Both histological and hematological indicators showed clear differences between fish from effluent-affected and downstream locations. The findings demonstrate that treated wastewater discharge alters environmental conditions in receiving waters and contributes to the spread of antimicrobial resistance. The observed physiological and structural changes in fish are likely linked to multiple environmental stressors, including xenobiotics, microbial burden, reduced water quality, and potential heavy metal exposure. Gill tissue alterations may serve as sensitive biomarkers for distinguishing polluted environments. Furthermore, the presence of antimicrobial-resistant aeromonads raises public health concerns, especially for recreational fishers and WWTP personnel exposed to contaminated water or aerosols. The high prevalence of multidrug-resistant bacteria highlights the need for further investigation into the environmental consequences of antimicrobial use. Expanding such studies across additional WWTPs would improve understanding of these complex ecological and health-related interactions.

Acknowledgments: Center of Research Excellence for Marine Bioprospecting – BioProCro, a project co-financed by the Croatian Government and the European Union through the European Regional Development Fund - the Competitiveness and Cohesion Operational Programme (PK.1.1.02): Sustainable bioprospecting of organisms from the Adriatic Sea for innovative natural products.

Keywords: WWTP; Fish models; Environmental interactions.



P-26

Novel Invasive Tunicate Species Affecting Mussels in the Northern Adriatic Sea

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Clavelina oblonga is a non-native ascidian tunicate introduced into the Adriatic Sea. Its expansion appears linked to human activities and climate change. The species proliferates rapidly in mariculture zones, especially on mussel culture ropes, where it has become a dominant biofouling organism colonizing mussels. This study investigated biological and biochemical characteristics of *C. oblonga* by assessing its fatty acid profile, mineral composition, and trace elements. Specimens were collected from a mussel farm located on the western coast of the Istrian Peninsula, Croatia. A total of 150 colonies were sampled from mussel culture ropes. Fatty acid methyl esters were prepared by transesterification with methanol according to ISO 5509:2000 method. Gas chromatography was conducted on the Agilent Technologies 6890N Network GC system (USA) equipped with flame ionization detector. Multielement analysis was performed by a triple quadrupole inductively coupled plasma mass spectrometer (ICP-QQQ, 8900, Agilent Technologies, USA). All prepared solutions of lyophilized *C. oblonga* were analyzed for total concentration of 32 trace elements and 6 macroelements. The analyses revealed elevated concentrations of toxic metals, including arsenic and lead, which may pose potential risks to marine organisms and seafood safety. The FA composition of *C. oblonga* differs from that of other tunicates. It seems to possess a high proportion of C16:0, despite retaining a smaller amount of MA. Field observations indicate that *C. oblonga* has adapted to the colder waters of the northern Adriatic, suggesting a capacity for further geographic expansion. Its continued spread could disrupt shellfish aquaculture, deplete plankton communities, and alter the structure and functioning of local marine ecosystems. Despite its invasive nature, the species produces substantial biomass, which may have potential for industrial applications. Understanding the physiological composition and ecological behavior of *C. oblonga* is therefore essential for both assessing its environmental impact and exploring possible sustainable uses of its biomass.

Acknowledgments: Center of Research Excellence for Marine Bioprospecting – BioProCro, a project co-financed by the Croatian Government and the European Union through the European Regional Development Fund - the Competitiveness and Cohesion Operational Programme (PK.1.1.02): Sustainable bioprospecting of organisms from the Adriatic Sea for innovative natural products.

Keywords: *Clavelina oblonga*; Mussel farming; Invasive species; Nutrition.



P-27

Exploring the biosynthetic potential of *Nostoc* 2S3B strain by genome miningJ. Simeunović¹, P. Davidović¹, M. Tanurdžić², D. Blagojević¹

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Cyanobacteria are recognized as a remarkable source for biotechnological applications due to their ability to synthesize a diverse range of bioactive compounds. In the present study, we applied a set of genomic and bioinformatics tools to investigate the metabolic potential of the cyanobacterial strain *Nostoc* 2S3B based on the presence of biosynthetic gene clusters (BGCs) responsible for the synthesis of the bioactive compounds. Illumina whole-genome sequencing and assembly were performed to construct the genome map of the strain. Furthermore, comparative genomic analyses were utilized to study the metabolic capacity of the strain, especially pathways derived from thiotemplate modular systems such as non-ribosomal peptide syntheses (NRPS) and polyketide synthetases (PKS). Prokka software was used for detailed annotation and identification of ORFs, while antiSMASH software was used for the detection and analysis of BGCs for the synthesis of secondary metabolites. The results indicated the presence of 14 biosynthetic clusters, among which were clusters involved in the production of muscoride A and nostophycin, which are known to exhibit antimicrobial activity. Importantly, the bioinformatics analysis showed that the strain harbored genes for shinorine, the mycosporine-like amino acid with photoprotective, antioxidant and anti-inflammatory activity. In addition, gene prediction and genome annotation studies identified genes encoding hapalosin, 1-heptedecene, geosmin, microviridin N9, anachelin, scytocyclamide and anacyclamide, which possess diverse biological features and serve as valuable pharmaceutical leads. The elucidation of the whole-genome organization of this microorganism increased our understanding of its biochemical profile by providing valuable information on the essential genes related to the synthesis of biotechnologically valuable secondary metabolites. Our findings pointed out the significant potential of cyanobacterial strain *Nostoc* 2S3B in various biotechnological and industrial applications, considering its capacity to produce valuable pharmaceutical compounds.

Keywords: Bioactive compounds; Cyanobacteria; Genome exploration; *Nostoc*.

This contribution was not presented during the symposium



P-28

Effects of Experimental Microplastic Exposure on Swimming Performance in Rainbow Trout and Russian Sturgeon

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Microplastics are widespread aquatic contaminants, but their functional effects on fish remain insufficiently understood. Swimming performance integrates locomotor capacity and aerobic metabolism and can therefore reveal sublethal physiological responses that may not be apparent from growth measurements alone. This study investigates the effects of experimental microplastic exposure on rainbow trout (*Oncorhynchus mykiss*) and Russian sturgeon (*Acipenser gueldenstaedtii*). Acute and chronic exposure trials are conducted under controlled conditions. Swimming performance is assessed by swim-tunnel respirometry using critical swimming speed and oxygen consumption during stepwise velocity tests. The resulting metabolic measures, including resting and maximum metabolic rates and aerobic scope, are evaluated together with growth, feed utilization, condition indices, biochemical responses, and histopathological observations. Comparing these responses between exposed and control fish will show whether changes in locomotor and metabolic performance correspond with organism- and tissue-level effects.

The study tests whether swimming and metabolic performance respond to sublethal microplastic exposure and whether response magnitude differs between species and exposure durations. By relating functional performance to growth, biochemical, and histopathological responses, it aims to clarify the physiological consequences of microplastic exposure. The findings will establish the experimental sensitivity and biological relevance of swimming-based measures for assessing effects on fish performance and welfare under controlled conditions.

Acknowledgement: This study is supported by the Research Universities Support Program under the project titled “Investigation of the Effects of Microplastic Pollution on Swimming Performance in Rainbow Trout (*Oncorhynchus mykiss*) and Russian Sturgeon (*Acipenser gueldenstaedtii*)” with Project ID: 41260 and Project Code: FBA-2025-41260.

Keywords: Microplastics; Swimming performance; Rainbow trout; Sturgeon; Aquaculture.



P-29

Long-term toxicity of polyethylene (PE) microplastics on the green photosynthetic microalga *Chlamydomonas reinhardtii*

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The ubiquitous presence and persistence of microplastics (MPs) in ecosystems have raised global concerns due to the potential threat to human and environmental health. Academic interest has grown in MPs, particularly in how these polymers affect microorganisms, including microalgae. This study provides a novel assessment of the interaction between the green photosynthetic microalgae *Chlamydomonas reinhardtii* and polyethylene (PE) microplastics. Specifically, the long-term impacts (over a 3-week exposure period) of PE microplastics (ranging in size from 300 µm to 1 mm and at an environmentally relevant concentration of 200 µg/L) on microalgae growth, pigment content, and photosynthetic activity were assessed by absorption and fluorescence spectroscopy. Simultaneously, the microalgae potential to biodegrade PE microplastics was assessed by scanning electron microscopy (SEM), optical microscopy (OM), and Fourier transform infrared spectroscopy (FTIR). Specifically, a 40% growth inhibition was observed after 15 days of exposure to PE and a 70% inhibition after 18 days. Pigment production was shown to be inhibited by 45% for carotenoids and 80% for chlorophylls after 15 days of exposure to PE. Photosynthetic activity decreased by 25% after 14 days of PE exposure and by 85% after 18 days. Extracellular protein production increased by 60% on day 14 in treated cells, while polysaccharide content by 45% in response to PE exposure. The antioxidant capacity of the microalgae (DPPH and FC tests) revealed an increase in oxidative stress on day 14 of treatment, with a 35% increase in free radicals and a 60% increase in polyphenols when treated with PE. Finally, the microalgae showed biodegradation on PE, as evidenced by FTIR and SEM, with rates ranging from 1 to 17% on PE from bottle caps of different colors, demonstrating the potential of algae to affect the polymer differently when produced with diverse pigments.

Keywords: Microalgae; Microplastics; Biodegradation; Environmental pollution.



P-30

Antiproliferative Activity From Antarctic Phytoplankton

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Marine microalgae represent a rich and eco-sustainable source of natural compounds with a high range of bioactivity. These microorganisms are characterized by a remarkable biodiversity in terms of species and metabolite production, as well as their ability to be cultivated in large quantities using eco-sustainable approaches, making them a valuable resource for drug discovery. The search for novel natural products with anticancer properties

remains a priority, given the persistent global burden of cancer. Polar marine ecosystems, particularly Antarctica, are still underexplored reservoirs of unique biodiversity. To cope with extreme environmental conditions, Antarctic microorganisms have developed specialized adaptive mechanisms that may be associated with the production of structurally distinctive metabolites with potential biomedical applications. The aim of this study was to evaluate the biological activity of 15 phytoplankton samples collected in different sites during the XXXIII Italian Antarctic Expedition (Mario Zucchelli Station, 2017–2018). Biomass samples were extracted by soaking the samples in methanol, followed by solvent evaporation. The resulting crude extracts were screened for antiproliferative activity against human cancer cell lines, including malignant melanoma and lymphoma cells and compared with their effects on normal human cell lines. Cells were exposed at three concentrations (1, 10, and 100 µg/mL) of each extract for 24 hours. Among the tested samples, extract 12A exhibited a dose-dependent reduction in malignant melanoma cell proliferation while exerting a lower effect on normal keratinocytes, suggesting a selective effect toward tumor cells. This promising extract will be further investigated through additional chemical and molecular analyses.

Keywords: Extreme environments; Marine phytoplankton; Antiproliferative activity; Melanoma, Leukemia.



P-31

Characterization and Chitosan Immobilization of a Marine Carbonic Anhydrase for CO₂ Enrichment in Microalgal Cultures

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Microalgae are increasingly investigated for sustainable biotechnological applications, including biomass production, aquaculture feed, recovery of bioactive compounds and CO₂ mitigation. Since their growth is strongly influenced by the availability of inorganic carbon in the culture medium, strategies able to improve CO₂ conversion into more accessible carbon forms may support photosynthetic productivity. Carbonic anhydrases (CAs), metalloenzymes that catalyze the reversible hydration of CO₂ to bicarbonate, are therefore attractive biocatalysts for supporting carbon enrichment in microalgal cultures.

In this study, we explored a CA-based system in which CAs are immobilized on chitosan beads, that was selected as support material because it is biocompatible, biodegradable, inexpensive and chemically versatile. The selected enzyme is CDCA1, a CA from the marine diatom *Thalassiosira weissflogii*, whose marine origin makes it particularly relevant for aquatic biotechnology and microalgal cultivation. The work focuses on the biochemical and biophysical characterization of both the full-length protein (CDCA1-FL) and its isolated R3 domain (CDCA1-R3), with the aim of comparing their properties and identifying the most suitable construct for immobilization. Recombinant proteins were analyzed by circular dichroism to evaluate thermal and pH stability, dynamic light scattering to assess size distribution and aggregation state under different conditions, and enzymatic assays to compare catalytic activity. CDCA immobilization conditions on chitosan beads were optimized, and the activity of the immobilized enzyme was evaluated *in vitro* using a calcium carbonate precipitation assay. Overall, this work provides a preliminary characterization of CDCA1-based biocatalysts and lays the groundwork for reusable chitosan-supported systems for CO₂ conversion and inorganic carbon enrichment in microalgal cultures.

Keywords: CO₂ capture; Carbonic anhydrase; Chitosan beads; Enzyme immobilization.



P-32

Biotechnological Valorization of Biomass from Recombinant Xylanase-Secreting *Chlamydomonas reinhardtii*

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This study evaluated a recombinant *Chlamydomonas reinhardtii* strain engineered to secrete xylanase, with the aim of confirming recombinant protein production and assessing the suitability of the residual biomass as a functional animal feed ingredient. The recombinant strain was compared with the wild-type strain to determine whether genetic modification adversely affected its nutritional value.

Successful xylanase production was confirmed by the detection of 0.99 mg of purified enzyme in the culture medium. Recombinant protein expression imposed a moderate metabolic burden on the host cells, resulting in significant reductions in photosynthetic pigment levels. These findings suggest a metabolic trade-off in which cellular resources were redirected from pigment biosynthesis toward recombinant enzyme production. In contrast, total lipid content remained stable, while protein content increased from 15.77 to 18.04 mg/mL, indicating enhanced protein metabolic activity.

Despite the observed decrease in pigment content, the recombinant biomass retained its nutritional quality. Lipid levels were maintained at approximately 18%, and the remaining carotenoid content (3.24 mg/g dry weight) continued to provide a valuable source of natural antioxidants. Furthermore, the presence of xylanase may improve feed digestibility, reduce intestinal viscosity, and enhance animal growth performance. Overall, the engineered *C. reinhardtii* biomass represents a promising multifunctional feed ingredient with potential applications in animal nutrition and other downstream biotechnological processes.

Keywords: *Chlamydomonas reinhardtii*; Recombinant xylanase; Residual biomass.



P-33**AQUASERV: Research Services for Sustainable Aquaculture, Fisheries and Blue Economy****R. Ofano¹, A.G. Caporale¹, A. Maddalon¹, D. Agrelli¹, P. Adamo¹**

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AQUASERV is an international consortium of 32 scientific institutions with 82 scientific installations across 15 European countries. Its mission is to support the sustainable transformation of the blue economy, particularly aquaculture and fisheries, in line with the European Common Fisheries Policy, the Farm to Fork Strategy, the Sustainable Blue Economy framework, and the European Green Deal. The consortium aims to create an integrated research infrastructure network by offering customized transnational and virtual services to stakeholders. AQUASERV promotes open science and knowledge transfer through collaborative research and training. Researchers can access a wide range of infrastructures dedicated to marine and freshwater resources, food traceability and quality, and biotechnology, including the European Marine Biological Resource Centre (EMBRC), Analysis and Experimentation on Ecosystems (ERIC), Aquaexcel, METROFOOD, and the International Council for the Exploration of the Sea.

The Food Authenticity, Safety and Quality (FASQ) laboratory at University of Naples Federico II leads WP28 and provides traceability and authenticity services based on near-infrared spectroscopy, multielement fingerprinting and stable isotope ratios. Analytical platforms include IR spectrometer, ICP-MS, ICP-OES, TQ-ICP-MS and EA-IRMS for solid and liquid samples. FASQ also supports users in sampling design, methodological development, analytical standardization, data pre-treatment, and statistical modelling.

AQUASERV offers free on-site or remote Transnational Access (TA) and Virtual Access (VA) to researchers from academia and industry worldwide, including training opportunities. Access is granted to facilities located outside the applicant's home country through a dedicated online application platform. By strengthening collaboration among partners and developing new service pipelines, AQUASERV will enhance research infrastructure capacities and maximize their availability to users. The project will also implement communication, dissemination, and outreach activities to increase scientific and societal impact. AQUASERV is funded by the European Union under the HORIZON-INFRA-2023-SERV-01 programme and runs from 1 April 2024 to 31 March 2029.

Keywords: Traceability; Multielement fingerprinting; Stable isotopes; Transnational Access.



P-34

Development of a Floating Monitoring Device for Water Quality Assessment in the Piracicaba River, Brazil

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Water quality monitoring plays a fundamental role in assessing environmental conditions and supporting water resources management. However, conventional monitoring strategies are generally based on discrete sampling campaigns, which may fail to capture rapid fluctuations in water quality. In this context, this study presents the development of a prototype floating device for real-time environmental monitoring in the Piracicaba River, São Paulo, Brazil. The device is designed to monitor temperature, pH, turbidity, electrical conductivity, apparent watercolor, and nitrate, with the potential for future incorporation of sensors for the determination of additional nutrients and other environmental quality indicators. The platform is based on an ESP32 microcontroller and integrates low-cost commercial sensors as well as electrochemical sensors containing polyvinyl chloride (PVC)-based selective polymeric membranes. For nitrate determination, sensors were developed using laser-induced graphene (LIG) electrodes configured as solid-contact ion-selective electrodes (SC-ISEs), comprising working and reference electrodes. The selective membrane incorporates the ionophore tetradodecylammonium nitrate (TDMAN), which enables the selective recognition and real-time potentiometric determination of nitrate ions. In parallel, historical and current datasets provided by the Municipal Water and Wastewater Service of Piracicaba (SEMAE) and by the monitoring programs of the Piracicaba, Capivari, and Jundiaí River Basins (PCJ) are being compiled to support the calibration, validation, and interpretation of field data. Future work includes operational validation of the device under real aquatic conditions and the implementation of artificial intelligence tools for pattern identification, correlation of environmental variables, and prediction of events associated with water quality degradation. Furthermore, the continuous availability of environmental data may support the improvement of public policies related to water resources management, environmental monitoring, and the prevention of impacts associated with water quality degradation.

Keywords: Public policies; Sensors; Predictive modeling; Water resources management.



P-35

Re-Thinking The Role of the Microalgal-Bacterial Association In Polyhydroxybutyrate (PHB) Accumulating Cultures of *Desmodesmus communis*

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Microalgae have progressively drawn attention in the frame of the circular economy for their ability to utilize inexpensive substrates and produce high-value biomolecules. Among these, the biopolymer polyhydroxybutyrate (PHB) can be accumulated as a storage compound in several microalgal biomasses under nutrient- and light-limiting conditions. Herein, the Chlorophyta *Desmodesmus communis* was grown under mixotrophic conditions (low light, phosphorus-free medium, 1 g L⁻¹ sodium acetate) in a 1 L semicontinuous system over 25 days. PHB accumulation progressively increased, reaching 57% w/w on day 25. Since mixotrophic conditions also favor bacterial growth, the associated bacterial community was analyzed through 16S rRNA gene metabarcoding at different time points (day 0, 12, 21, 25) to investigate its potential contribution to PHB accumulation. A selection in bacterial genera was observed after prolonged cultivation. Moreover, antibiotic treatments markedly reduced bacterial diversity and PHB content, indicating a central bacterial role in PHB production and highlighting key genera likely involved. Environmental Scanning Electron Microscopy (ESEM) and Transmission Electron Microscopy (TEM) revealed close interactions between algal and bacterial cells, suggesting a potential endophytic presence of PHB-accumulating bacteria within *D. communis* cells. These findings propose a new perspective on microalgae-associated bacterial communities, viewing them not as contaminants but as essential contributors to microalgal growth and valuable metabolites production. The findings of this study suggest that microalgae-associated bacterial communities should not be regarded merely as contaminants, but rather as key contributors to microalgal growth dynamics. They also highlight the importance of investigating bacteria–microalgae consortia in PHB production research, rather than focusing exclusively on photoautotrophic organisms.

Keywords: Microalgal cultivation; Polyhydroxyalkanoates; Bacterial community.



P-36

Assessing the Impact of Marine Protected Areas on Microbiome Dynamics Along the Sardinian Coast

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Marine microbiomes drive essential ecological processes, including oxygen production, primary production, nutrient cycling, and carbon sequestration, thereby sustaining marine food webs and underpinning critical ecosystem services. However, little is known about the extent to which Marine Protected Areas (MPAs) contribute to preserving marine microbiome diversity and functional potential. To address this question, we assessed the impact of MPAs on marine microbiome communities along the Sardinian coast. To this aim, we conducted a comparative metagenomic survey of coastal waters in Sardinia (Italy), focusing on paired MPAs and unprotected control sites. We selected two MPAs classified as no-take marine zones (Spargi Island in the Archipelago of La Maddalena, and Capo Caccia) with their corresponding non protected areas (Palau and Alghero coasts, respectively). The sampling design included spatial replication across the 4 sites, with three sampling stations per site, two sampling areas per station, and three replicates per area, for a total of 18 samplings per site allowing robust assessment of microbial community structure and variability. Seawater samples were filtered and processed for DNA extraction, and microbial community was assessed through 16S rRNA gene metabarcoding. Our findings highlight the important role of MPAs in preserving the diversity and functional potential of marine microbiomes. Our results suggest that MPAs should be considered as an integral component of biodiversity conservation across multiple levels of biological organization, extending beyond macroorganisms to include microbial communities and their essential ecological functions that sustain marine ecosystems. Furthermore, our findings support the implementation of systematic surveys of microbiome community composition and metabolic potential across Mediterranean MPAs. In the framework of the Marine Strategy Framework Directive and the Nature Restoration Regulation, such monitoring would provide valuable insights into the effectiveness of marine conservation strategies and reinforce the ecological importance of MPAs in safeguarding marine microbiomes and the ecosystem services they provide.

Keywords: Marine microbiome; Marine protected areas; 16S rRNA gene; Coastal environments.



P-37**Powerful of Mass Spectrometry Approaches For Analysis of Toxins****A. Paraian¹, M. Rambla-Alegre², M. García-Altares², M. Campàs², J. Diogène², C. Flores¹**

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Detection of toxins is challenging due to the diversity of their molecular structures and a lack of certified standards. A wide range of methods is available for toxin analysis. These include numerous techniques relying on biological and physico-chemical approaches.

Liquid chromatography coupled to mass spectrometry (LC–MS) is a powerful and reference technique, ensuring reliable identification and quantification, to validate biological assays and biosensors. Targeted analysis, suspected and non-targeted screening are the three main strategies used for MS analysis. Quantitative and targeted analysis are mainly performed by tandem mass spectrometry (MS/MS) by monitoring predefined precursor-to-product ion transitions in multiple reaction monitoring (MRM) mode using commercially affordable instruments (triple-quadrupole mass spectrometers). MS/MS is a technique with excellent selectivity, specificity, sensitivity, while minimizing matrix interferences and owing to its wide linear dynamic range. However, this approach is strictly limited to the detection of pre-selected analytes. On the other hand, the use of full scan MS approaches employing high-resolution mass spectrometers and accurate mass measurements (AMM) has also strongly emerged as an attractive alternative for the analysis of toxins. Specifically, the application of Orbitrap high-resolution mass analyzer can support rapid and reliable identification of known toxins even when analytical reference standards are not available. Because high-resolution mass spectrometry (HRMS) acquires full-scan mode, it allows for targeted, suspected and non-targeted analysis, as well as retrospective data analysis. This methodology enables simultaneous detection of target toxins, metabolites, and degradation products, as well as other toxins and pollutants. In this work, some practical examples of powerful mass spectrometry approaches for toxin analysis and the complementarity of toxicity, biological, and mass spectrometry studies will be presented. In conclusion, combining toxicity analysis, biological screening and specific toxin profile determination by LC–MS proved to be a useful approach for toxin analysis.

Keywords: Toxins; Liquid Chromatography; Tandem Mass spectrometry; High-resolution mass spectrometry.



P-38**Sustainable Cherry Waste-Derived Biochars for Methylene Blue Removal: A Promising Approach for Wastewater Treatment**K.I. Berker Çetin¹

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The increasing discharge of dye-containing industrial wastewater has become a major environmental concern due to the persistence and poor biodegradability of synthetic dyes. Adsorption is considered one of the most effective and cost-effective methods for dye removal. In this context, converting agricultural wastes into biochar offers a sustainable approach for wastewater treatment while promoting agricultural waste valorization. This study comparatively evaluated biochars produced from cherry stems, cherry pits, and their mixture for the removal of methylene blue (MB), a model cationic dye widely used to simulate dye-contaminated wastewater. Biochar was produced by slow pyrolysis at 500 °C for 1 h. Batch adsorption experiments were performed using a 24 mg L⁻¹ methylene blue solution. Following adsorption, the suspensions were filtered through 0.45 µm membrane filters before UV–Visible spectrophotometric analysis to minimize interference from suspended biochar particles. Adsorption performance was evaluated using the characteristic absorption band of methylene blue at 664 nm. Preliminary results demonstrated high methylene blue removal efficiencies for all prepared biochars. Cherry pit-derived biochar exhibited the highest methylene blue removal efficiency (approximately 98.9%), whereas cherry stem-derived and mixed biochars achieved removal efficiencies of approximately 92.2% and 92.8%, respectively. The marked decrease in the characteristic absorption band of methylene blue confirmed the high adsorption capability of the prepared biochars.

These findings highlight the potential of cherry waste-derived biochars as sustainable adsorbents for dye-contaminated wastewater treatment and provide a foundation for future studies on adsorption kinetics, equilibrium isotherms, and pH optimization.

Keywords: Biochar; Methylene blue; Cherry waste; Adsorption; Wastewater treatment.



P-39

BIOVAL: Microalgal biomass valorisation for sustainable production of functional food and feed ingredients

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Marine microalgae are a renewable, low-impact bioresource able to supply multiple high-value compounds while minimizing freshwater and arable land use. Among these, polyunsaturated fatty acid (PUFA)-rich monoacylglycerides (MAGs) are of particular nutritional interest due to their superior intestinal absorption compared with other lipid formulations. However, conventional MAG synthesis relies on high-temperature glycerolysis, generating toxic glycidyl fatty acid esters and raising safety and regulatory concerns.

BIOVAL addresses this challenge by developing a scalable, zero-waste biorefinery pipeline based on three marine microalgae species—*Tetraselmis chuii*, *Phaeodactylum tricornutum*, and *Skeletonema marinoi*—to produce naturally biosynthesized (n-MAGs) and enzymatically generated (g-MAGs) PUFA-rich MAGs under mild, non-toxic conditions. The project integrates: (i) optimization of cultivation, combining abiotic stressors, phytohormones, sustainable nutrient sources, genetic engineering and machine learning to enhance lipid and n-MAG productivity; (ii) green cascade extraction technologies (supercritical fluid extraction, ultrasound, pulsed electric fields) coupled with enzymatic hydrolysis/alcoholysis for MAG synthesis and co-recovery of proteins, carotenoids and polysaccharides; (iii) in vitro and in vivo bioactivity and safety assessment of MAGs against metabolic syndrome and cancer cell lines, plus neurotoxicity evaluation; (iv) valorisation of protein- and pigment-rich side streams into novel aquafeeds for sea bream, assessed for growth performance and product quality; and (v) Life Cycle Assessment to guide sustainable scale-up.

Combining innovative modular photobioreactor technology, AI-driven process optimization, and a cascading multiproduct biorefinery model, BIOVAL aims to deliver safe, novel food supplements/additives and functional aquafeeds, supporting the EU Farm to Fork Strategy, the Sustainable Blue Economy, and Sustainable Developmental Goals 3, 12 and 14, while strengthening Europe's leadership in the microalgae-based blue bioeconomy.

Keywords: microalgae biorefinery; monoacylglycerides; PUFA; blue food; sustainable aquafeed.



P-40**Bioprospecting Tunisian Aquatic Yeasts for Blue Biotechnology Applications****B. Bessadok¹, S. Sadok¹**

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Aquatic ecosystems represent a rich yet underexplored source of microbial diversity with significant potential for blue biotechnology. This study focused on the screening and isolation of yeast strains from diverse Tunisian aquatic resources, including sediments, fish, algae, fishery by-products, and dredging by-products. A total collection of isolates was obtained and subjected to molecular identification using ribosomal DNA sequencing (ITS and D1/D2 regions), allowing accurate taxonomic assignment and revealing notable species diversity across the sampled niches. Beyond taxonomy, the isolated strains underwent comprehensive biochemical characterization, including quantification of lipid content and fatty acid profiles, protein content, mineral element composition, and carbohydrate levels. This multi-parameter screening enabled the classification of strains according to their biotechnological potential. In parallel, extraction and preliminary characterization of biomolecules of interest were performed to evaluate the industrial relevance of selected isolates. The results highlighted significant strain-dependent variability and identified several promising candidates for distinct applications. Certain strains, characterized by favorable protein and amino acid profiles, were identified as potential aquafeed supplements for aquaculture. Oleaginous strains exhibiting high lipid accumulation and suitable fatty acid profiles emerged as promising candidates for biodiesel production. Other isolates demonstrated notable capacity for pigment and enzyme production, suggesting applications in the food, cosmetic, and industrial biocatalysts sectors. Additionally, several strains were found to produce biosurfactants, indicating strong potential for environmental biotechnology applications, particularly in bioremediation of hydrocarbon- or pollutant-contaminated aquatic environments. Overall, this work underscores the biotechnological value of indigenous Tunisian aquatic yeasts and provides a foundation for their further exploitation in aquaculture, renewable energy, biocatalysis, and environmental remediation. Future research will focus on optimizing production conditions and scaling up the most promising strains for targeted industrial applications.

Keywords: Marine yeast, Blue biotechnology; Characterization; Application.



P-41

Blue Biotechnology: From Aquaculture Side Streams to Cellular Agriculture

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Aquaculture plays a critical role in global food security, providing an essential source of highquality animal protein for a growing population. Meeting future food demands, reducing the environmental impact of food production requires a transition toward circular, sustainable, ethical, inclusive, and efficient food systems. A key challenge is the valorization of aquaculture by-products and underutilized biomasses by advanced biotechnological strategies, able to convert these resources into high-value products, such as proteins, peptides, lipids, and other bioactive compounds. Within this framework, blue biotechnology is increasingly recognized as a strategic field for the sustainable development of aquatic resources, enabling the establishment of novel value chains that link aquaculture with food, pharmaceutical, and emerging bio-based sectors. Cellular agriculture is recognized as an emerging technology able to produce sustainable alternatives to animal products, including cell-based seafood and among the most promising applications to support the development of sustainable food. However, the large-scale production of cultivated seafood meat presents significant challenges, among these the availability of sustainable and cost-effective cell culture media, able to substitute the conventional animal-derived supplements such as fetal bovine serum. This presentation will show how the integration of blue biotechnology with the domain of cellular agriculture could offer a new perspective for transforming aquaculture from a conventional food-producing sector into a source for future food technologies. Bioactive ingredients derived from marine biomasses demonstrated to be a promising source of functional, serum-free alternatives that can support cell growth and proliferation, improving the sustainability of production systems. By aligning this approach with the principles of the “Blue Transformation strategy” these solutions could promote resource efficiency, waste valorization, and innovative pathways for sustainable food production, ultimately contributing to the reduction of pressure on natural aquatic resources and supporting the transition toward more resilient and sustainable food systems.

Keywords: blue biotechnology; cellular agriculture; sustainable aquaculture; circular bioeconomy.



P-42

Valorizing Aquaculture Halophyte biomass: A Green Biorefinery Perspective

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Salicornia spp., also known as pickleweed, glasswort or sea asparagus, is a halophyte that belongs to the Amaranthaceae family. Due to its physiological and biochemical adaptation this plant can thrive in extreme environments characterized by high salinity and intense UV radiation. It grows along the edges of wetlands, marshes, coastlines, and muddy areas. *Salicornia* spp. can grow in saline aquaculture effluents without the requirement for freshwater, while acting as a biofilter. This integrated recirculating system represents a circular economy approach, in which animal effluents are used as a source of nutrients for the plant.

In this system, the use of *Salicornia* significantly increases plant biomass, representing a valuable resource for food, cosmeceutical, nutraceutical, and feed sectors. This biomass is characterized by secondary metabolites such as phenolic acids, flavonoids and tannins, which exhibit important biological activities such as antioxidants, anti-inflammatory, antidiabetic, and anticancer effects.

In the food sector, *Salicornia* can be consumed directly. Furthermore, its use is important to obtain sustainable extracts for seafood processing and preservation. It is observed that the application of *Salicornia* extracts to fish fillets increases their shelf life due to reduced lipid peroxidation, maintaining their nutritional and sensory properties. Additionally, *Salicornia* extracts have antioxidant properties and reduce oxidative stress, suggesting their potential application in cosmeceuticals and pharmaceuticals. In the context of a green biorefinery, these extracts can be used as functional feed ingredients in aquaculture and terrestrial livestock production.

Overall, the cultivation of *Salicornia* spp. in integrated aquaculture systems represents a sustainable strategy for producing high-value bioactive compounds, promoting circular bioeconomy principles and supporting the development of zero-waste biorefinery models.

Keywords: *Salicornia* spp.; Integrated aquaculture systems; Bioactive compounds; Green biorefinery.



P-43

Nitrogen and Phosphorus Removal Potential of the Aquatic Plant *Egeria densa*

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Nutrient pollution in aquatic ecosystems rapidly increases with population growth and industrialization. Although several effective technologies are available for nutrient removal, their high operational costs and practical limitations often restrict large-scale application. Phytoremediation using invasive macrophytes has emerged as an environmentally sustainable and cost-effective alternative. Due to their opportunistic nature, invasive species possess high pollutant tolerance, a key prerequisite for phytoremediation. Therefore, utilizing established invasive plants represents a realistic approach to managing both nutrient pollution and invasive species.

This study evaluated the nitrogen (N) and phosphorus (P) tolerance and nutrient removal potential of *Egeria densa*. Experimental treatments were established in triplicate using a control (distilled water) and five specific N/P combinations: low-N+P (2 mg L⁻¹ NO₃-N + 1 mg L⁻¹ P), high-N (30 mg L⁻¹ NO₃-N), medium-N+P (15 mg L⁻¹ NO₃-N + 5 mg L⁻¹ P), high-P (10 mg L⁻¹ P), and high-N+P (30 mg L⁻¹ NO₃-N + 10 mg L⁻¹ P). Physiological responses were assessed by monitoring growth, pigment composition via Lichtenthaler (1987), total antioxidant capacity via CUPRAC, water nutrients via APHA (2005), and tissue nutrient content via Temminghoff and Houba (2004).

Plant growth responded positively to nutrient enrichment, peaking in the high-N+P treatment (6.66% relative increase), while the lowest occurred in the control (2.47%). Chlorophyll-a levels rose significantly on days 5 and 22 in the low-N+P treatment, reaching 3.28 mg L⁻¹ on day 22. High nutrient concentrations induced oxidative stress, reducing chlorophyll, while antioxidant activity rose substantially to activate defense mechanisms, peaking in high-N+P and high-P treatments. Regarding purification, the highest P removal efficiency occurred in the low-N+P treatment (94.4%), whereas maximum N removal was recorded in the medium-N+P treatment (30.3%).

Overall, the results demonstrate that *Egeria densa* can maintain growth and physiological activity under nutrient stress. These findings highlight its robust phytoremediation potential and support its evaluation as a biological tool for nutrient management in eutrophic aquatic ecosystems.

Keywords: Phytoremediation; Nutrient removal; Macrophyte; *Egeria densa*.



P-44

***Chamelea gallina* as a Sentinel Species for Microplastic Biomonitoring along the Adriatic Apulian Coast**

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Marine microplastics (MPs) contamination represents an escalating threat to coastal ecosystems. The striped venus clam, *Chamelea gallina* (Cg, Linnaeus, 1758), is a filter-feeding bivalve present at the benthic level, with limited mobility, characteristics that favor the accumulation of microplastics in the edible part, making them effective sentinel species for environmental biomonitoring.

This study investigated MPs occurrence in Cg collected along the Adriatic Apulian coast (between Barletta and Margherita di Savoia) across four seasons (July 2022 – May 2023), at two depths (2 m and 5 m); sampling was conducted at three sites (Cartiera, Mennea, Fiumara), each at a different distance from the mouth of the Ofanto river. A total of 1,200 individuals were analysed using flotation methodology combined with stereomicroscopic characterisation, following strict contamination-prevention protocols. MPs were detected in all sampled individuals, with a mean abundance of 2.3 ± 0.8 MPs/individual (range: 1–6) and a total of 2,780 particles identified. Significantly higher MPs concentrations were recorded at 2 m compared to 5 m depth ($p < 0.01$), attributed to proximity to riverine inputs, increased hydrodynamic energy promoting particle resuspension, and greater anthropogenic pressure in shallow nearshore habitats. The highest contamination was observed at Fiumara (3.78 ± 1.1 MPs/ind.), consistent with riverine transport from the Ofanto river. Seasonal variation was also significant, with peak abundances in summer (3.1 MPs/ind.) versus winter (1.6 MPs/ind.), likely reflecting tourist-related plastic inputs. Morphological characterisation revealed fibres as the dominant MPs type (61–66%), followed by fragments (18–25%) and films (11–21%), with depth- and site-specific variation in the latter two categories suggesting sensitivity to local hydrodynamic conditions. These results demonstrate that Cg represents a reliable bioindicator of MPs contamination in coastal environments, and highlight the critical role of bathymetric gradients, riverine inputs, and seasonality in shaping MPs bioavailability.

Keywords: Filter-feeding bivalves; Coastal pollution; Bioindicator species; Plastic debris accumulation; Riverine input.



P-45

Alginate as a Marine Biopolymer for Bioactive Edible Coatings

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Alginate is a marine-derived polysaccharide obtained from brown algae, including species of the genera *Laminaria*, *Macrocystis*, and *Ascophyllum*, and represents a promising natural biopolymer for sustainable food applications. Its food-grade status, biocompatibility, biodegradability, water solubility, and film-forming ability make it particularly suitable for developing edible coatings to preserve food quality and reduce waste.

We studied alginate, also within the AVATIM project, as a functional polymeric matrix for the protection of ready-to-cook fish products. Alginate-based systems were investigated for properties relevant to coating performance, including surface tension, rheological behavior, film formation, and calcium-mediated gelation. A system containing 1% sodium alginate and 1% Tween 80 was found to be suitable for surface application due to both the reduction of surface tension by Tween 80 and its liquid-like behavior compatible with spraying, confirmed by rheology. The functional contribution of alginate was also evaluated for antimicrobial coating design. At the concentrations used for edible coating formulation, alginate alone did not show antimicrobial activity against foodborne pathogens and spoilage microorganisms. Therefore, its activation was explored through the incorporation of lemongrass, oregano, sweet orange, and lemon essential oils, resulting in antimicrobial activities that varied according to essential oil type and concentration. Among the tested formulations, a 1% alginate-based emulsion containing 1% oregano essential oil was selected for a seafood-oriented application. When applied to ready-to-cook fillets stored at 4 °C, the active coating delayed microbial growth, markedly inhibited *Pseudomonas* spp. during the challenge test, reduced lipid oxidation, and preserved surface appearance. Alginate-based coatings also showed applicability to fruit and vegetables, as demonstrated by delayed ripening and shelf-life extension in fruit. Overall, these findings highlight alginate as a multifunctional marine biopolymer for clean-label, biodegradable, and bioactive edible coating systems.

Keywords: Alginate; Marine biopolymer; Bioactive coatings.



P-46

Microbiological Quality of Sea Bass and Sea Bream from an IMTA System

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Integrated Multi-Trophic Aquaculture (IMTA) represents a promising model to improve the environmental sustainability and productive quality of Mediterranean aquaculture. The data reported here arises from research activities carried out within the recently concluded FishVision project and the newly launched AVATIM project. This study evaluated the microbiological quality and refrigerated storage aptitude of European sea bass (*Dicentrarchus labrax*) and gilthead sea bream (*Sparus aurata*) produced in an IMTA system by an aquaculture company located in Apulia, Italy, and harvested according to the same procedures used for fish intended for commercial distribution. Skin samples from fish harvested during three climatic periods, namely January, March, and June, were analyzed for total mesophilic count, Enterobacteriaceae, *Escherichia coli*, lactic acid bacteria, enterococci, eumycetes, and *Pseudomonas* spp. Scanning electron microscopy was also performed to observe microbial colonization on fish surfaces. In addition, skin-on fillets were subjected to a five-day storage test in air at 4 °C and periodically analyzed for microbial counts, pH, and surface microbial colonization by SEM.

Microbiological analyses showed excellent microbiological quality throughout the study, with only slight variations attributable to seasonal climatic conditions. Most microbial groups remained below the detection limit or at very low levels across the sampling periods, and the limited increase observed in June did not compromise the overall microbiological quality. During the storage test, microbial loads increased progressively on skin-on fillet surfaces, with slight species-related differences becoming evident during refrigerated storage. SEM observations revealed the transition from isolated microbial cells to structured biofilm-like communities, supporting the usefulness of surface imaging for describing microbial colonization during storage.

Overall, these results support the microbiological quality of fish produced in an IMTA system under market-oriented harvesting conditions and provide a basis for developing sustainable post-harvest biotechnological strategies aimed at supporting quality preservation, shelf-life extension, and economic value of Mediterranean aquaculture products.

Keywords: IMTA; Microbiological quality; SEM.



P-47

Emergence of *Cylindrospermopsis raciborskii* as the Dominant Cyanobacterium in Lake Oubeira: Insights from Community Shifts and Toxin Dynamics

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In Mediterranean lakes like Lake Oubeira in Algeria, ongoing warming and eutrophication are expected to promote warm adapted invasive cyanobacteria. This study investigated the recent rise of *Cylindrospermopsis raciborskii* (Raphidiopsis), following a long-term shift away from historical dominance by *Microcystis*. To identify the main drivers and characterize morphology and toxin production, we combined recent field observations from 2021–2022 with earlier community records. Monthly surveys showed that *C. raciborskii* now prevails, accounting for up to 76% of total cyanobacteria with annual densities ranging from 1.13×10^6 to 1.52×10^6 cells/mL. Its abundance peaked from June to December.

Principal component analysis (PCA) indicates that *Raphidiopsis raciborskii* was positively correlated with $\text{NO}_3\text{-N}$ ($r = 0.60$), conductivity ($r = 0.67$), turbidity ($r = 0.64$), *Planktothrix* ($r = 0.32$), and water temperature ($r = 0.30$) ($p < 0.001$). Morphological assessment based on filament shape and apical cell features confirmed the species, with more than 90% of filaments lacking heterocytes and akinetes. Extracellular cylindrospermopsin was detected from October through September at 80–750 ng/L. Four episodes exceeded 500 ng/L but did not coincide with biomass maxima, which points to delayed or conditional toxin release. Intracellular microcystins were also measured year-round at 165–490 ng/L, despite the low presence of *Microcystis* and *Planktothrix*. Overall, the data indicate that *C. raciborskii* is both dominant and actively producing toxins, heightening the risk to the ecosystem and water uses. Given its adaptability and toxic potential under changing conditions, it is urgent to integrate coordinated morphological, ecological, and toxicological monitoring into water management.

Keywords: *Cylindrospermopsis raciborskii*; Cyanobacterial blooms; Cylindrospermopsin; Morphological variability; Toxin dynamics



P-48

Proteomic Analysis and Biochemical Characterization of the Nematocyst Extract from *Pelagia noctiluca* (Forsskål, 1775)

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Cnidarian venoms represent an underexplored source of bioactive compounds with significant biotechnological potential (Jouiaei et al., 2015). The Mediterranean jellyfish *Pelagia noctiluca*, for instance, is well known for its stinging capability (Mariottini et al., 2002; 2008); its venom exhibit hemolytic, cytolytic, and pore-forming activities (Maisano et al., 2013; Marino et al., 2008; Morabito et al., 2012; 2015), although its molecular composition remains only partially characterized. Recent advances in venom research highlight the importance of integrative omics approaches to unravel toxin diversity and function in non-model organisms.

The presented study aimed to provide a comprehensive proteomic and biochemical characterization of the crude nematocyst extract from *P. noctiluca*. Our analysis identified 234 proteins, of which 127 were considered contaminants, excluded from further investigation. Among the remaining proteins, several were considered as putative toxins, characterized by the presence of signal peptides and a broad molecular weight range spanning from 30 to 120 kDa. Notably, some of these candidates exhibited a multidomain architecture, combining metalloprotease and serine protease domains and ShK toxin-like domains, known as inhibitors of potassium channels, within the same molecule.

Biochemical assays corroborated the proteomic findings, revealing significant metalloprotease and serine protease activities, while no phospholipase activity was detected, consistent with the absence of phospholipase proteins in the proteome. These results indicate that *P. noctiluca* venom is predominantly characterized by proteolytic components. Overall, this study advances the characterization of *P. noctiluca* venom through a multi-omics approach, enhancing our understanding of cnidarian venom systems and providing a basis for future investigations into their ecological significance and biotechnological potential.

Keywords: proteomics, venomics, *Pelagia noctiluca*.



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