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European Conference on Marine Natural Products

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Book of Abstracts

XIV ECMNP
EUROPEAN CONFERENCE ON
MARINE NATURAL PRODUCTS

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XIV ECMNP – CONFERENCE 2025

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2B-BLUE - Boosting the Blue Biotechnology community in the Mediterranean, Projet n°Euro-MED0200514.

PROGRAMME

DAY 0, Monday 29.9.2025	
18:30 – 21:00	Welcome reception *Location*
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10:00 – 10:45	Looking Back - Looking Ahead in Marine Natural Products Research *Bill Fenical, USA, Keynote speaker*
10:45 – 11:15	**COFFEE BREAK and blue economy networking**
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11:15 – 11:45	The New UN Ocean Biodiversity (BBNJ) Agreement: A Scientists Guide To Policy Developments *Federica Casolari, UK, Invited speaker*
11:45 – 12:00	The Nagoya Protocol: Does it Offer a Solution Or Does it Create More Confusion? *Ernesta Grigalionyte-Bembič, Slovenia*
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12:30 – 12:45	Evaluation of Cosmetic Products With *Dunaliella* Extracts and Water Brine From Sečovlje Soline, Slovenia *Alenka Zvonar Pobirk, Slovenia*
12:45 – 13:00	Marine Cyanobacterial Pigments as Sustainable Alternatives for Textile Dyeing *Mariana Reimão, Portugal*
13:00 – 14:30	**LUNCH and blue economy exchange of good practices**
14:30 – 15:30	**Interactive discussion on marine biotechnology** Chair: Ana Rotter
Drug discovery and development Chairs: Efstathia Ioannou and William Gerwick	
15:30 – 16:00	Development of lurbinectedin for the treatment of SCLC *Carmen Cuevas, Spain, Invited speaker*
16:00 – 16:15	Marine Natural Product-Derived Pharmaceutical Pipeline in 2025 *Alejandro M.S. Mayer, USA*
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Day 1, Tuesday 30.9.2025	
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17:00 – 17:15	Therapeutic Potential Of Furanoditerpenes Obtained From *Spongia tubulifera* *Luis M Botana, Spain*
17:15 – 17:30	A Natural Compound From a Marine Sponge and The Use of Its Synthetic Analogues in the Treatment of Pain *Silvia Lino, Portugal*
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Day 2, Wednesday 1.10.2025	
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09:45 – 10:00	From Activity to Molecule: Integrated Omics Approaches for Natural Product Discovery *Sarolt Magyari, Canada*
10:00 – 10:15	Discovering New Antiobiotics: The Power of Marine Fungi Revealed by New Eco-Inspired Cultures *Clémence Marivain, France*
10:15 – 10:30	Marine Acidobacteriota as Halogenation Reservoirs: Discovery of Novel Biosynthetic Gene Clusters *Pavlo Hrab, the Netherlands*
10:30 – 10:45	Marine Cyanobacteria as a Natural Source of Kahalalide F-Like Depsipeptides *William H. Gerwick, USA*
10:45 – 11:00	Monitoring Cyanobacterial Blooms and Application of the FDS Strategy in the Lucrino Sea *Germana Esposito, Italy*
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15:30 – 18:00	Group 2 *Koper*
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09:30 – 09:45	Chemical Ecology of Parasite (*Parvilucifera* sp.) Induced Metabolic Adaptations in the Toxic Dinoflagellate *Alexandrium minumtum* *Ruchicka O'Niel, Germany*
09:45 – 10:00	Do Seaweeds From High UV-Exposure Areas Offer Natural UV Protection? Insight Into Bioactive Properties of Mycosporine Like Amino Acids (MAAs) and Isolation of Novel MAAs From *Chondria cornuta* *Sabeena Farvin Koduvayur Habeebullah, Kuwait*
10:00 – 10:15	Exometabolomics to Illuminate the Waterborne Pathogen Suppression Effect of Seagrasses in Water Column *Deniz Tasdemir, Germany*
10:15 – 10:30	Metabolomic Changes in Antarctic Marine Invertebrates in a Warming Ocean *Andrea Prófumo, Spain*
10:30 – 10:45	Chemodiversity of Marine Invertebrates in Highly Anthropized Environments *Alexandre Le Loarer, France*
10:45 – 11:00	Chemical Interactions of *Carijoa* (*Telesto*) *riisei* on Fish and Benthic Reef Communities on Artificial Reefs in South-East Queensland, Australia *Pauline E. Lindholm, Australia*
11:00 – 11:30	**COFFEE BREAK**
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11:30 – 11:45	Chemo-Taxonomical Markers of Phyllidiidae Species (Heterobranchia) From Koh Tao Island (Thailand) *Giulia Quaini, Italy*
11:45 – 12:00	New Tetrahydrofuran Containing Lipid as First Chemical Evidence of the Kleptopredation in *Cratena peregrina* (Aeolidioidea: Facelinidae) Nudibranch *Genoveffa Nuzzo, Italy*
12:00 – 12:15	Crossing Ecosystems: How Ocean4Biotech Bridged Microbial Research in Extreme Habitats *Lada Lukić Bilela, Bosnia and Herzegovina*
Synthesis of MNP and medicinal chemistry Chairs: Fernando Reyes and Carmen Cuevas	
12:15 – 12:45	The Chemistry And Biology Of The Marine Macrolides Zampanolide And Dactylolide *Karl-Heinz Altmann, Switzerland, Invited speaker*
12:45 – 13:00	A SAR Study of Tetrahydro-β-Carboline and β-Carboline Containing Natural Products *Melissa M. Cadelis, New Zeland*
13:00 – 13:15	Synthesis and Antimicrobial Activities of Acarnidine C12:0 and Analogues *Tim Liu, New Zealand*

Day 3, Thursday 2.10.2025	
13:15 – 14:30	**LUNCH**
Natural products isolation and downstream processing Chairs: Filipa A. Vicente and Federica Casolari	
14:30 – 15:00	Promoting Interdisciplinary Conversations for Advancing Sustainable Research on Marine Natural Products *Valeria Costantino, Italy, Invited speaker*
15:00 – 15:15	Bioassays for Natural Resources: Use With Caution *Jerica Sabotič, Slovenia*
15:15 – 15:30	Unveiling the Metabolic Potential of the Deep-Sea-Derived *Streptomyces profundus* Through the OSMAC Approach *Sofia Correia, Portugal*
15:30 – 15:45	Isolation and Characterization of Bioactive New Chlorinated Secondary Metabolites from the Deep-Sea *Streptomyces acrimycini* B188M101 *Emmanuel T. Oluwabusola, UK*
15:45 – 16:00	From Algal Cells To Self-Assembled Vesicles: Unlocking Drug Delivery Potential *Nadica Ivošević DeNardis, Croatia*
16:00 – 16:30	**COFFEE BREAK**
Natural products isolation and downstream processing, continued Chairs: Filipa A. Vicente and Federica Casolari	
16:30 – 16:45	Chlorophyll Derivatives From *Arthrospira platensis* for Novel Nutraceutical Applications *C. Filipe Henriques, Portugal*
16:45 – 17:00	Valorization of the Blue Crab (*Callinectes sapidus*) Shell Wastes *Elena Bellini, Italy*
17:00 – 17:15	In-Vitro Wound Healing Activities of Chitosan Based Films Containing Astaxanthin Extract (*Aristeaomorpha foliacea* and *Aristeus antennatus*) *Cigdem Dikel, Turkey*
18:30 – 23:00	**CONFERENCE DINNER**

Day 4, Friday 3.10.2025

COMBINED USE OF SPECTROSCOPIC METHODS AND BGC ANALYSIS IN THE STRUCTURAL DETERMINATION OF COMPLEX NATURAL PRODUCTS

Workshop organized by the EU funded project EUREMAP with contributions from Bill Fenical (SIO/UC-San Diego, USA), Bill Gerwick (SIO/UC-San Diego, USA), Daniel Oves (Fundación MEDINA, Spain) and Javier Ortiz (Fundación MEDINA, Spain).

9.30-9.45	Introduction to EUREMAP and the workshop. *Fernando Reyes, Fundación MEDINA*
9.45-10.30	Introduction to Bioinformatics-Based Structural Prediction in Bacterial PKS/NRPS Systems. *Daniel Oves-Costales, Fundación MEDINA*
10.30-11.00	Structure and Stereochemistry Elucidation of Complex Microbial Natural Products by Combining NMR and BGC Analysis: Three Case Studies. Francisco *Javier Ortiz-López, Fundación MEDINA*
11:00 – 11:30	**COFFEE BREAK**
11:30 – 12:30	Stereochemical Assignments using NMR data from Linear Type 1 Polyketides can be Dangerous. *Bill Fenical, Scripps Institution of Oceanography/ University of California San Diego*
12.00-12.30	Integration of Artificial Intelligence and Genomic Information to Efficiently Solve Natural Product Structures. *William H. Gerwick, Scripps Institution of Oceanography/ University of California San Diego*
CLOSING SESSION	
12:30 – 13:00	Group photo (Everybody) Closing speeches, XV ECMNP and other invitations (Ana Rotter, XIV ECMNP chair)
13:00 – 14:30	**LUNCH**
COMBO project meeting **(limited to project partners)**	
14:30 – 16:15	COMBO project meeting (limited to project partners)
16:15 – 16:45	**COFFEE BREAK**
16:45 – 17:30	COMBO project meeting (limited to project partners)

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Invited lectures

IL 1 LOOKING BACK - LOOKING AHEAD IN MARINE NATURAL PRODUCTS RESEARCH

William Fenical[a]

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Marine natural products chemistry began in the late 1960s with some studies in Japan on toxins. This was natural since teh Japanese were heavily involved in diverse seafood. In the 1970s a international academic researchers with a level of marine competence, invested heavily in defining the new structures they isolated from "obvious" marine plants and animals. There was no real goal but to explore new structures, and the more complex the better. This work was funded because it was showing that the oceans were a new source of often unique metabolites. These explorations lasted for about 20 years, when it was realized that marine metabolites could be developed into effective drugs. By that time, thousands of highly bioactive molecules had been published, but none had been developed. Unfortunately, because of patentability issues these fabulous molecules did not form the foundation for novel marine drug development. Around 1985, public health organizations, such as the NIH, and especially the US National Cancer Institute, saw the potential and funding became available to do rigorous drug development.

I participated in all of these decades, first doing structure elucidation and little else. But in the early 1900s my lab developed the Pseudopterosins as an anti-inflammatory additive for skin care. This activity opened the world of drug development that changed my work and the field of marine natural products soon followed.

So, what's in the future? As far as the US is concerned, new research almost exclusively requires the involvement of the medical establishment, with the chemist playing a supplier role. My personal experiences developing marizomib, plinibulin and seriniquinone will be discussed.

IL 2 THE NEW UN OCEAN BIODIVERSITY (BBNJ) AGREEMENT: A SCIENTIST'S GUIDE TO POLICY DEVELOPMENTS

Federica Casolari[a]

[a]Marine Biodiscovery Centre, Department of Chemistry, University of Aberdeen, Old Aberdeen, UK

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The research, development and commercialisation pipeline for accessing, using and sharing marine genetic resources (MGR) of areas beyond national jurisdiction (ABNJ) is highly varied and complex. Equally complex is the governance framework under the 2023 agreement on the conservation and sustainable use of marine biological diversity of ABNJ (the 'BBNJ' Agreement), for which many practical details, including procedures, are yet to be decided by treaty Parties.

In general terms, all actors involved in acquiring, storing and utilizing MGR or associated Digital Sequence Information (DSI) and Traditional Knowledge (TK), including academia, government and industry, need to understand BBNJ Agreement obligations and comply with the laws of the Parties that implement them. Given that there are practical aspects of the framework that are yet to be determined by the Conference of the Parties (CoP), this will require proactive development of procedures and systems to compile, curate and provide necessary information to Parties, including data management plans and the BBNJ Identifier, when undertaking activities regulated under Part II. It is likely that this information will be provided at the first instance to the Party that has jurisdiction or control over the relevant activity, but there may be opportunities for directly sharing information with the Clearing House mechanism (CHM).

This presentation draws from real world examples to analyse ways in which current scientific practice is supported or challenged by framework elements, including notification, monitoring and benefit sharing systems and associated infrastructure such as the BBNJ Standardised Batch Identifier and data management plans. It compares how the elements and infrastructure may work in practice using realistic research and development (R&D) scenarios ranging from an idealised linear pathway to more complex pathways involving automation, sequence information and traditional knowledge associated with MGR in different geographical and temporal scales. For an efficient and 'future proofed' framework that supports innovation and fulfils treaty objectives, it is proposed that treaty bodies and policy makers need to look beyond the idealised R&D pathways envisaged in the treaty and engage directly with scientists and commercial end users when designing the practical details of implementation.

The BBNJ Agreement presents a linear vision of science which belies many inherent complexities. It is crucial that the R&D process for MGR is not imagined as a linear progression where such work would automatically result in commercialisation. Most R&D pathways are non-linear with many side branches that may be abandoned or pursued, iterative loops and long breaks in the process. Often several research threads are pursued in parallel, and the intended application is completely changed between the start and end of the process. Although many existing research practices are consistent with the notification and information sharing requirements, many challenges arise for non-linear scenarios, including utilizing MGR and DSI from collections prior to the BBNJ Agreement, complex uses of multiple DSI, automation in collection and use, change of use from harvest fisheries to R&D and access and use of TK associated with MGR of ABNJ.

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[2] Casolari, F., Westmoreland, A., Vanagt, T., Jaspars, M. (**2025**) Unpacking policy developments in marine natural product research: a scientist's guide to DSI and BBNJ, *Natural Product Reports*. doi.org/10.1039/D4NP00070F

IL 3 DEVELOPMENT OF LURBINECTEDIN FOR THE TREATMENT OF SCLC

Carmen Cuevas[a]

[a]PharmaMar. S.A. Research and Development, Spain

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Small cell lung cancer (SCLC) is a highly aggressive malignancy with a poor prognosis, accounting for approximately 15% of all lung cancer cases. Despite advances in initial treatments, recurrence and chemotherapy resistance remain significant challenges in the clinical management of SCLC. Lurbinectedin, a promising chemotherapeutic agent, has demonstrated potent antitumor activity across several cancer types, including solid tumors. Its mechanism of action involves the inhibition of DNA transcription and the promotion of apoptosis in tumor cells, positioning it as an attractive therapeutic option for SCLC.

Recent clinical trials have shown substantial efficacy of lurbinectedin, both as a monotherapy and in combination with other agents. This presentation will explore the discovery and development of lurbinectedin, its unique mechanism of action, the most recent clinical evidence supporting its use, and its potential to significantly improve outcomes for patients with SCLC.

IL 4 NAVIGATING THE NATURAL PRODUCT LANDSCAPE: EFFECTIVE STRATEGIES TO PRIORITIZE METABOLITE FEATURES IN METABOLOMICS PROFILES

Justin J.J. van der Hooft[a]

[a]Bioinformatics Group, Wageningen University & Research, the Netherlands

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Nature has always been a rich resource of diverse chemistry. Fortunately, in recent years, technological advances in the omics fields have increased our capacity in measuring them. For example, modern mass spectrometers generate information-rich chemical profiles used for untargeted metabolomics studies. Such studies are typical examples of exploratory data analysis, as one does not *a priory* know what one will discover in the data. Typically, researchers do have a *goal* with the study: whether it is finding out differences in plant tissue metabolic content or associating antimicrobial activity to metabolites in bacterial extracts. However, the current information-rich metabolomics profiles leave researchers with the daunting task to separate valuable signals from everything else.

In this talk, I will highlight the importance of effective visualization strategies linked to computational metabolomics strategies that together allow researchers to make justified, reliable, and reproducible choices in their exploratory analyses[1]. For example, I will highlight recently developed tools such as msFeaST[2] and FERMO[3,4] that allow researchers to use statistics and phenotype information such as bioactivity to filter and select for relevant metabolite features. Besides, I will explain several key computational metabolomics concepts that underpin these priotirization strategies, including mass spectral organization and annotation. I will show examples using case studies from various natural origins.

I will finish the talk with highlighting the important role of Open Science and Software in stimulating community-based science. Altogether, I expect that the presented progress in computational metabolomics tools will empower metabolomics researchers navigating their increasingly complex datasets to find and annotate relevant and novel chemistry in nature.

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[1] K. Mildau et al., "Effective data visualization strategies in untargeted metabolomics". *Natural Product Reports*, **2025**, advanced article.

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IL 5 CONTRIBUTION OF MARINE INVERTEBRATES TO THE CHEMICAL DIVERSITY OF BENTHIC SEAWATER

***Charlotte Simmler*[a], Marie Derrien[a], Morgane Mauduit[b], Titouan Biré[a], Stéphane Greff[a], Pierre Chevaldonné[a], Thierry Pérez[a]**

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Marine sponges and other benthic sessile invertebrates produce a vast array of structurally diverse specialized metabolites, mostly studied for their bioactive properties in the context of drug discovery[1]. Beyond their pharmaceutical potential, these metabolites likely play critical ecological roles, mediating interactions between species[2,3]. Sponges, in particular, are known to release organic molecules into their surroudings, including their specialized metabolites, referred to as exometabolites (EMs). Once released, these EMs are rapidly diluted, possibly bio-transformed, and merged to a pool of other waterborne organic molecules to shape the benthic chemical seascape[4-8]. Part of our research at the marine station in Marseille focuses on characterizing the chemical diversity of EMs released by sponge species, both individually and within benthic communities[4-8]. Our overarching goals are to (1) access new chemical entities with limited impacts on marine biodiversity and (2) progressively decipher molecular signatures involved in species interactions. For that purposes, we designed I-SMEL instruments (*In Situ* Marine moleculE Loggers) to rapidly capture released molecules in different marine ecosystems[4]. The presentation will focus on the results obtained from MS-based metabolomic analyses of EM extracts obtained after the deployments of I-SMEL in Mediterranean, sponge-dominated ecosystems. This presentation will address the challenges of characterizing specialized EMs within the complex matrix of seawater organic molecules. By examining these EMs, our findings also provide new insights into the well-studied chemical composition of Mediterranean sponges while opening research perspectives in marine chemical ecology.

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IL 6 THE CHEMICAL LANGUAGE OF MARINE FORESTS

Ernesto Mollo[a]

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Marine forests, encompassing the intricate structures formed by sessile animals (e.g., sponges, corals, gorgonians) and the canopies of marine plants (e.g., seagrasses, macroalgae), are vital components of coastal ecosystems. They significantly influence the recruitment and distribution of numerous marine organisms, enhance biodiversity at multiple levels, and underpin crucial ecological functions. Understanding the complex interactions within these underwater landscapes is essential, particularly in the face of increasing environmental changes and biological invasions. Marine chemical ecology offers a powerful lens through which to decipher the chemical signals that mediate these interactions, impacting processes ranging from individual behavior to community-level dynamics. Notably, the inherent heterogeneity of these ecosystems is inextricably linked to the spatial distribution and physicochemical properties of chemical cues, giving rise to characteristic "chemo-scapes" and habitats that mirror the diverse lifestyles of marine organisms, and their chemosensory systems[1,2,3]. With a special focus on the Mediterranean biota, this talk will provide insights supporting a natural product-based approach to understanding ecological processes within both animal- and plant-dominated marine forests, including defense from predators and biofoulers, competition for resources, and the establishment and impact of non-native invasive species. Overall, this will provide an overview of the various ways in which chemical ecology can contribute to a better understanding of the dynamics characterizing key marine ecosystems, at the same time as paving the way for the development of novel technologies for environmental protection and sustainable development.

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IL 7 THE CHEMISTRY AND BIOLOGY OF THE MARINE MACROLIDES ZAMPANOLIDE AND DACTYLOLIDE

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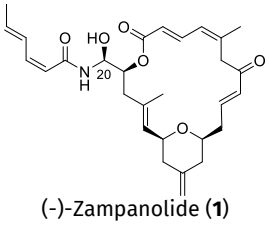
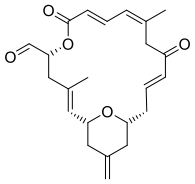
Zampanolide (**1**) is a marine natural product that was first reported in 1996 by Tanaka and Higa[1] and shown to be a potent inhibitor of tumor cell proliferation *in vitro*. In 2009, it was re-extracted from the Togan sponge *Cacospongia mycofijiensis* by Northcote, Miller, and co-workers, who confirmed its antiproliferative activity and uncovered its microtubule-stabilizing and tubulin-polymerizing effects[2]. In 2001, the group of Riccio reported a macrolactone structurally related to zampanolide (**1**) that had been isolated from the sponge *Dactylospongia sp*. and that was termed dactylolide (**2**)[3].



(-)-Zampanolide (**1**)



(+)-Dactylolide (**2**)

In contrast to **1**, dactylolide (**2**) is only a moderately potent antiproliferative agent, with IC_{50}'s in the low µM range and the absolute configuration of **2** is opposite to the configuration of the macrolactone core in **1**;[4] in fact, *ent*-**2**, whose configuration corresponds with that of the macrolactone core in zampanolide (**1**), was first isolated from natural sources only very recently.[5]

Before this background, we have developed convergent total syntheses of **1** and **2**, which have enabled a range of biochemical and structural studies. At the same time, the total synthesis work has established a platform for the synthesis of analogs for SAR studies. After a summary of the total synthesis work and the biological and structural studies with **1** and **2**, this contribution will discuss the synthesis and biological activity of a series of zampanolide and dactylolide analogs.

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IL 8 PROMOTING INTERDISCIPLINARY CONVERSATIONS FOR ADVANCING SUSTAINABLE RESEARCH ON MARINE NATURAL PRODUCTS

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This communication promotes interdisciplinary conversations for sustainable science and emphasizes the idea that scientific progress, especially in fields like marine natural product research, is most effective when scientists from various disciplines collaborate. By encouraging open and collaborative discussions, we can create more innovative, holistic, and sustainable solutions to the complex challenges facing our planet. This approach ensures that scientific advancements benefit both people and the environment in a balanced and lasting manner.

In this discussion, we will explore *TheBlueChemistryLab*'s[1] comprehensive strategy to leverage the abundant potential of cyanobacterial biomass. This approach not only aims to foster sustainable innovation but also seeks to effectively confront the challenges associated with cyanobacterial blooms, which have become a pressing environmental concern. By harnessing the unique properties of this biomass, we can pave the way for innovative solutions that promote ecological balance and sustainability. Cyanobacterial blooms are a growing concern that is closely linked to the impacts of climate change. Rising temperatures, altered precipitation patterns, nutrient enrichment, and ocean acidification are all factors that contribute to the expansion and intensification of these blooms. The consequences of increased cyanobacterial activity include ecosystem disruptions with loss of biodiversity, public health risks, and economic losses. Addressing this challenge requires interdisciplinary, coordinated efforts to mitigate climate change, reduce nutrient pollution, and manage aquatic ecosystems sustainably.

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1. Horizontal aspects in MNP discovery and good practice examples

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OC 1 THE NAGOYA PROTOCOL: DOES IT OFFER A SOLUTION OR DOES IT CREATE MORE CONFUSION?

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The ocean is home to a great diversity of living organisms. According to the World Register of Marine Species (WoRMS), around 242 000 valid marine species are currently known in the world's oceans, with discoveries and taxonomic designations of new marine biota continuing at a rate of approximately 2332 species per year [1].

The exploration of marine biodiversity is highly dependent on access to marine organisms, also known as marine genetic resources (MGRs). In addition to access to MGRs, the fair and equitable sharing of the benefits arising from their use are essential for research and development. Scientists are well aware of the logistical difficulties in collecting MGRs from the marine environment, but they are often less familiar with the legal framework that applies to MGRs sharing among different countries [2,3].

The main international legal document governing access and sharing of MGRs is the "*Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization*" (Nagoya Protocol). However, the Nagoya Protocol is only binding on those countries that have ratified it, and its implementation is left to their national jurisdictions, leading to confusion and inconsistent regulations across countries. This has resulted in the misinterpretation of the provisions of the Nagoya Protocol, poor implementation, and complex bureaucratic and administrative procedures for the country providing the MGRs.

This presentation will address the limitations of the Nagoya Protocol, highlight the most common implementation errors and outline the practical difficulties encountered by scientists attempting to follow its provisions.

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OC 2 COMPARATIVE ENVIRONMENTAL ASSESSMENT OF WATER-FREE POWDER SHAMPOO AS A LITTER PREVENTION SOLUTION

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Plastic packaging from personal care products contributes significantly to post-consumer litter, particularly in high-density public events, where waste management systems are often overwhelmed. As single-use plastics persist in the environment and degrade into microplastics, reducing plastic at the source is a key preventive strategy.

This study presents a comparative life cycle assessment (LCA) of a water-free powder shampoo packaged in paper, evaluated in comparison to conventional liquid shampoo in plastic packaging. The analysis covers all life cycle stages—raw material extraction, production, distribution, use, and end-of-life, focusing on both environmental impacts and resource efficiency. The use of this shampoo by camp attendees at a large festival setting is proposed. Using a functional unit of one 100 kg batch of 123zero shampoo, which is sufficient for 27,714 hair washes and comparing it against conventional shampoo requiring 10.48 g of shampoo per hair wash[1], the results show a 21% reduction in total global warming potential, with an 86% decrease in emissions in the raw material acquisition stage as a result of lower product mass and reduced consumption of fossil fuels.

These findings demonstrate that reformulating consumer products and redesigning packaging can provide substantial environmental benefits and support litter prevention efforts, avoiding both end-of-life impacts of plastic waste as well as upstream burdens of plastic and liquid shampoo production. The case study illustrates a viable intervention point for reducing event-based plastic waste and highlights the importance of upstream innovation in addressing plastic pollution.

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OC 3 MATURATION OF SALINE PELOID FROM SEČOVLJE SALINA: INTERACTIONS WITH BRINE AND PETOLA MICROBIAL MAT

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Saline peloids are multifunctional marine-derived materials whose therapeutic properties are critically influenced by their natural maturation. At the Sečovlje Salina Nature Park (Slovenia), this process involves prolonged interaction between marine sediments and hypersaline brine from crystallization pans, whose bottoms are overgrown with a cyanobacteria-rich microbial mat known as Petola.

Recent research[1] has confirmed and expanded upon earlier findings[2,3,4] by characterizing the elemental and geochemical transformations occurring during maturation, with a particular focus on microbial contributions and brine chemistry. Elemental analysis revealed a significant increase in total sulfur (S) in matured peloids, attributed to microbial sulfate-reducing activity and possible gypsum precipitation. Notable increases in calcium (Ca), magnesium (Mg), and strontium (Sr) concentrations indicate mineral reorganization and ion exchange with the brine. Conversely, levels of potentially toxic elements such as arsenic (As), selenium (Se), and nickel (Ni) were reduced or stabilized below regulatory thresholds for cosmetic and dermatological use, suggesting effective natural attenuation mechanisms during the maturation period.

These findings emphasize the complex interplay between microbiology, geochemistry, and environmental conditions in shaping the properties of saline peloids. The maturation process enhances therapeutic quality by improving elemental safety profiles and introducing potentially bioactive microbial metabolites. As such, the Sečovlje saline peloid represents a valuable, naturally evolving marine-derived material with high potential for use in dermatological, cosmetic, and wellness applications.

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OC 4 EVALUATION OF COSMETIC PRODUCTS WITH *DUNALIELLA* EXTRACTS AND WATER BRINE FROM SEČOVLJE SOLINE, SLOVENIA

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Extracts from the genus *Dunaliella* exhibit antioxidant, moisturizing, and anti-inflammatory effects on the skin, promote skin cell regeneration, and positively impact skin elasticity. *Dunaliella salina* extracts, in particular, are known for their high content of colorless carotenoids (e.g., phytoene, phytofluene) and essential fatty acids. In addition, they serve as a source of glycerol, making them a valuable ingredient in skin care products[1,2,3].

Conventional creams are most commonly used for topical applications. These semisolid emulsions are suitable for the incorporation of both hydrophilic and lipophilic ingredients, and are known for their consistency and sensorial characteristics. Lamellar liquid crystals (LLCs) have emerged as a novel delivery system, particularly suited for topical applications, as they resemble the intercellular lipid matrix of the stratum corneum. As a result, they exhibit excellent skin hydration properties along with potential for controlled drug release[4].

In the present study, we aimed to compare the stability and efficacy of conventional hydrophilic creams (HC) and formulations based on LLCs, both containing *Dunaliella* extracts isolated in the Sečovlje salt pans in Slovenia. The cosmetic products were tested on the lower forearm skin of healthy volunteers — both alone and following the application of brine-mother water (*Lepa Vida*) from the Sečovlje salt pans, known for its high content of dissolved minerals, particularly magnesium, which is used as skin tonic.

The moisturizing activity of the tested products was confirmed by measuring transepidermal water loss (TEWL), stratum corneum hydration, skin pH, and erythema index before and after two weeks of product use. Formulations based on LLCs showed lower TEWL values, indicating superior barrier protection. Furthermore, the use of *Lepa Vida* as a tonic further improved the skin's barrier function, as evidenced by a significant decrease in TEWL values among all volunteers after 7 and 14 days of product application. As the present clinical study did not specifically focus on the UV-protective properties of cosmetic products containing *Dunaliella* extracts, additional in vivo testing would be necessary to confirm this effect.

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OC 5 MARINE CYANOBACTERIAL PIGMENTS AS SUSTAINABLE ALTERNATIVES FOR TEXTILE DYEING

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As concerns grow over the environmental and health risks of synthetic colorants, the search for natural alternatives is gaining renewed interest. Cyanobacteria are known to produce vibrant natural pigments like chlorophylls, carotenoids and phycobiliproteins, which have demonstrated potential for large-scale industrial applications[1,2,3], paving the way for a more sustainable future. This study evaluates the feasibility of using pigments from marine cyanobacteria as sustainable colourants for the textile industry.

Cyanobacteria strains were obtained from LEGE-Culture Collection and cultivated in Z8 TM 25 medium, supplemented with Vitamin B_{12}. Textile dyeing experiments were conducted on both semi-synthetic (viscose) and natural (cotton) fibres, considering the pigment content in the aqueous extracts of each strain. Dyeing was performed with a 1:10 bath ratio, using NaCl as an exhausting agent, under a 120-minute cycle at 40°C. A post-dyeing fixation process was applied to enhance colour retention. The dyed fabrics underwent quality control assessments for colour reproduction and fastness to rubbing, washing, water, and perspiration, following European Standards (UNE-EN ISO) for textiles.

The results suggest that the studied pigments are not resistant to alkaline treatments, as both alkaline perspiration and washing ISO tests led to colour loss, with lower fastness observed at pH levels above 10. In contrast, dyed fabrics exhibited satisfactory fastness to acidic perspiration and water. Similar results were observed for dry and wet rubbing fastness; however, the pale pantone obtained from dyeing may have influenced these outcomes. Notably, the semi-synthetic fibre displayed superior dye uptake compared to the natural fibre.

In conclusion, marine cyanobacteria pigments demonstrate significant potential as sustainable alternatives for synthetic dyeing agents in the textile industry, under specific conditions. The current procedure already represents a more environmentally friendly approach to textile dyeing. Nevertheless, further optimization, particularly through the integration of alternative dyeing auxiliaries, could enhance the efficiency of this application.

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POSTER SESSION 1

PP 1 SEARCHING FOR FUTURE BLUE BIOTECHNOLOGIST DEVELOPERS

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Blue Bioeconomy promotes a decarbonized circular economy by using renewable biological resources from the sea, helping to modernize and strengthen the EU's industrial structure, creating new and greener value chains, improving industrial processes in terms of energy and raw material use, while protecting biodiversity and the environment. Marine Biotechnology high education and research contribute to generating know-how and disruptive innovation to boost the green and digital transition to achieve the goals of Green Deal and Sustainable Development Goals. The transition towards a sustainable Bioeconomy requires entrepreneurial thinking that concerns all stakeholders: from business, with a vision of developing new products and processes, to Public Administrations, with entrepreneurs in innovative governance, and Educational institutions, with academic coordinators and educators who promote the change of study plans towards sustainability, circularity and holistic thinking; civil society organizations, with social entrepreneurs who introduce non-profit solutions to resolve situations that cannot be solved with commercial means [1,2,3,4].

With this vision and the funding of Blue Careers call for proposals 2016 from Executive Agency for Small and Medium-sized Enterprises (EASME), the project a Blue Biotechnology Master for a Blue Career (BBMBC), designed and delivered a Master program (1 year, 60 ECTS) during 2017-2022 in both Universities at France and Spain. This experience was the basement for the European University for Smart Urban Coastal Sustainability (EU-CONEXUS), in the context of the European Universities alliances as part of a flagship initiative of the European strategy for universities. The first outcome of this European Universities alliance was the joint Master program in Marine Biotechnology (JMPMB) (2 years, 120 ECTS) awarded by 6 European Universities located in all European marine basins; this JMP has been funded within Erasmus Mundus program during 4 intakes (2022-2027).

This communication focuses on the significance of understanding the current interest of undergraduates in blue biotechnology master level education in Europe as a roadmap for linking higher education, research and industry. A survey on educational background and geographical origin of applicants to both European Master programs in blue Biotechnology has been conducted for the period 2017-2025.

A moderate but steady interest of European undergraduates in a blue Biotechnology career is analyzed.

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PP 2 SUSTAINABLE WATER REMEDIATION AND NATURAL PRODUCT EXTRACTION FROM MACROALGAE THROUGH ICT: A PILOT STUDY IN PORT OF ALICANTE (SPAIN)

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The removal of heavy metals and excess nutrients from port waters poses a significant environmental challenge[1]. *Ulva sp.* macroalgae offer a nature-based solution by enabling water bioremediation while also serving as a sustainable source of high-value bioactive compounds[2]. This pilot study, carried out at the Port of Alicante in collaboration with Mediterranean Algae, the University of Murcia, and the Naval and Marine Technology Centre, explores the integration of macroalgae cultivation with digital technologies to enhance water quality and generate sustainable marine natural products.

The system consists of two 2000-liter tanks where *Ulva sp*. is cultivated using continuously circulating port water. The algae absorb pollutants and nutrients, resulting in cleaner water. IoT sensors monitor key parameters in real time, including nitrates, phosphates, dissolved oxygen, temperature and energy consumption. An ICT platform processes this data to optimize system performance, while blockchain tools track CO_2 capture for blue carbon credit generation in compliance with Spanish regulations.

After each cultivation cycle, the *Ulva sp*. biomass is analyzed to evaluate nutrient removal efficiency. Extraction methods are used to obtain valuable natural products with potential applications in cosmetics, nutraceuticals and animal feed and residual biomass is assessed for secondary uses, promoting circular economy.

The pilot aims to: (1) assess the bioremediation potential of native *Ulva sp*., (2) explore new algae-based products, (3) promote circular economy strategies and carbon credit use and (4) develop a replicable protocol for other port areas. This integrated model demonstrates the synergy between environmental restoration, digital innovation and sustainable marine products development.

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2. Drug discovery and development

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OC 6 MARINE NATURAL PRODUCT-DERIVED PHARMACEUTICAL PIPELINE IN 2025

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Marine natural products continue to deliver novel mechanisms of action benefiting the global marine natural product-derived (MNPD) pharmaceutical pipeline. The website (https://www.marinepharmacology.org/), tracks approval, development (Phases 1, 2 and 3) and withdrawal of MNPD pharmaceuticals. Significant progress in the clinical development of MNPD pharmaceuticals has continued since our last report in 2022 (https://doi.org/10.1124/jpet.122.527010).

Advances in Phases 1 to 3 or withdrawals were researched: (A) for *preclinical* pharmacology: MarinLit, PubMed, PubChem, ScienceDirect, and Google Scholar; (B) for global *clinical* trials registers: United States, European Union, Japan, and China.

Early 2025 the MNPD pipeline included: **Approved**:15 MNPD pharmaceuticals, and 2 withdrawn: Panobinostat (histone deacetylase inhibitor) and the antibody-drug conjugate (ADC) Belantamab mafadotin (targeting B-cell maturation antigen (BCMA)); **Phase 3**: 7 MNPD pharmaceuticals, 5 ADCs with a monomethylauristatin E (MMAE) warhead: MGR003 (targeting epidermal growth factor receptor), SGN-B6A (targeting integrin beta-6), zelenectide pevedotin (BT8009) targeting nectin 4, telisotuzumab vedotin (ABBV-399) targeting c-Met, zilovertamab vedotin (MK2140) targeting ROR1, and ARX-788 (targeting HER-2 with an amberstatin-269 warhead). **Phase 2**: 15 MNPD pharmaceuticals: 12 ADCs with different auristatin warheads, as well as a largazole analog Bocodepsin (OKI-179) targeting histone deacetylases, an alkaloid Ecubectedin (PM14) targeting RNA polymerase II, and a guanidine alkaloid tetrodotoxin targeting sodium channels. **Phase 1**: 10 MNPD pharmaceuticals, including 2 ADCs with a MMAE warhead, EBC-129 targeting N-glycosylated CEACAM5/CEACAM6 and XB010 targeting ST4 trophoblast glycoprotein, and AARX-517 targeting prostate-specific membrane antigen with a PEG4-aminooxy MMAF warhead, and additionally 7 MNPD small molecules. Thus in early 2025 the MNPD pharmaceutical pipeline remains very active.

OC 7 BLUECHEM<ON> A CHEMOINFORMATICS EXPLORATION OF SPECTRAL PATTERNS FOR THE DISCOVERY OF NEW DRUG LEADS FROM NATURAL PRODUCTS – PD-1/PD-L1 MODELLING

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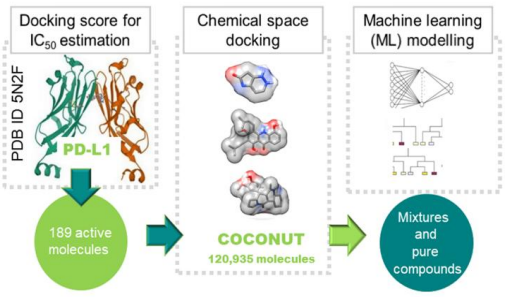
The PD-1/PD-L1 immune checkpoint axis plays a pivotal role in modulating the immune response. PD-1, expressed on the surface of specific immune cells, binds to its ligand PD-L1, initiating an inhibitory signal that suppresses T cell activity against target cells. PD-L1 is frequently overexpressed on the surface of cancer cells, enabling them to evade immune destruction. Consequently, therapeutic agents targeting the PD-1/PD-L1 interaction can block this mechanism, restoring immune cell activity against cancer cells[1]. Recently, our group has reported the application of Spectrometric Data-Activity Relationships (QSDAR) models to identify novel inhibitors targeting the HCT116 cancer cell line[2] and MRSA infection[3]. Furthermore, we have developed an integrated computer-aided drug design (CADD) approach that combines QSAR modeling, drug repurposing, and molecular docking, offering a promising strategy for inhibiting the PD-1/PD-L1 axis[4].

In this study, we explored large datasets of natural products (NPs) using computational tools to automatically identify anti-PD-L1 compounds in complex extracts based on their NMR spectra (Scheme 1). This process involved simulating NMR spectra for a wide range of NPs from the COCONUT database (https://coconut.naturalproducts.net), calculating free binding energies via molecular docking, generating spectral mixtures, and training machine learning (ML) models to classify these mixtures by the presence of anti-PD-L1 compounds. Spectral simulations for the mixtures were performed automatically by combining the spectra of individual compounds in random proportions, using two approaches: (a) random compound combinations, and (b) mixtures limited to compounds with similar predicted LogP values (logarithm of the partition coefficient between octanol and water).



Scheme 1. General blueChEM<ON> workflow used for the PD-1/PD-L1 modelling.

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OC 8 THERAPEUTIC POTENTIAL OF FURANODITERPENES OBTAINED FROM *SPONGIA TUBULIFERA*

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Five furanoditerpenes, isolated from *Spongia (Spongia) tubulifera*, were evaluated in an in vitro neuroblastoma cell line to check for their anti-inflammatory effect. Dose-response treatments revealed that they improved cell survival at nanomolar concentrations through the restoration of mitochondrial membrane potential and the reduction of reactive oxygen species. Their ability to prevent the mitochondrial permeability transition pore opening was also assessed, finding that two of them inhibited the channel at a low concentration of 1 nM. This inhibition was accompanied by a decrease in the expression of cyclophilin D, the main regulator of the pore, which was also reduced by two compounds. However, the activation of ERK and GSK3beta, upstream modulators of the channel, was not affected by compounds. Therefore, their ability to bind cyclophilin D was evaluated by surface plasmon resonance, and the compounds did show equilibrium dissociation constants in the micromolar range. All compounds also had high affinity for cyclophilin A, and some of them with also high selectivity for cyclophilin D. When the effects on the intracellular expression of cyclophilins A-C were determined, it was found that only one decreased cyclophilin A, while cyclophilins B and C were diminished by most compounds, displaying enhanced effects under oxidative stress conditions. Results indicate that the furanoditerpenes studies have mitochondrial-mediated neuroprotective properties through direct interaction with cyclophilin D. Due to the important role of this protein in oxidative stress and inflammation, compounds are promising drugs for new therapeutic strategies against inflammatory-based diseases.

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OC 9 A NATURAL COMPOUND FROM A MARINE SPONGE AND THE USE OF ITS SYNTHETIC ANALOGUES IN THE TREATMENT OF PAIN

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Pain is one of the leading causes of disability worldwide. Current therapies offer limited efficacy, with serious side effects such as risk of addiction (opioids). This highlights the urgent need for safer, more effective, and targeted pain treatments.

Sea4Us is a biotech company whose innovation focuses on targeting ion channels, using marine-derived natural products as pharmaceutical agents for the treatment, prevention, or reduction of both acute and chronic pain.

Nitenin, a C21 furanoterpene isolated firstly from *Spongia nitens*[1], has been proven to be a promising candidate for pain therapeutics, attributed to its ability to modulate K^+ currents[2].

It´s potential was validated in pre-clinical animal models of pain, where its analgesic effect was compared to several standards of care (morphine and carbamazepine). Results showed that Nitenin in addition to having an effect matching or surpassing the standards of care, did not exhibit the negative side effects typically associated with opioid drugs.

Based on the chemical structure of Nitenin, over 100 synthetic analogues were designed and synthetized, aiming to replicate its therapeutic effects with improved properties (physical chemistry or pharmacokinetic profile).

New synthetic molecules for treatment of pain and other illnesses were identified, based on Nitenin's structure and it's innovative mechanism of action[3]. One of the analogues is going through the pre-clinical stages leading to clinical trials (phase I).

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OC 10 INTERROGATING STONEFISH VENOM: SMALL MOLECULES PRESENT IN ENVENOMATION CAUSED BY *Synanceia spp.*

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The stonefish *Synanceia verrucosa* and *Synanceia horrida* are arguably the most venomous fish species on earth and the culprits of severe stings in humans globally. Investigation into the venoms of these two species has mainly focused on protein composition, in an attempt to identify the most medically relevant proteins, such as the lethal verrucotoxin and stonustoxin components.

This study, however, focused on medically relevant small molecules, and through nuclear magnetic resonance, mass spectroscopy, and fractionation techniques, we discovered and identified the presence of three molecules new to stonefish venom, namely γ-aminobutyric acid (GABA), choline and 0-acetylcholine, and provide the first report of GABA identified in a fish venom. Analysis of the crude venoms on human nicotinic acetylcholine receptors (nAChRs) and a $GABA_A$ receptor ($GABA_AR$) showed that *S. horrida* venom could activate neuronal (α7) and adult muscle-type (α1β1δε) nAChRs, while both crude *S. horrida* and *S. verrucosa* venoms activated the $GABA_AR$ (α1β2δ2). Cytotoxicity studies in immunologically relevant cells (human PBMCs) indicated the venoms possess cell-specific cytotoxicity and analysis of the venom fractions on Na^+ channel subtypes involved in pain showed no activity.

This work highlights the need to further investigate the small molecules found in venoms to help understand the mechanistic pathways of clinical symptoms for improved treatment of sting victims, in addition to the discovery of potential drug leads.

OC 11 VILLOSANE A: AN ALLENE-CONTAINING BISABOLANE WITH POTENT ANTIPLASMODIAL ACTIVITY PRODUCED BY THE MARINE-DERIVED BASIDIOMYCETE *Halocyphina villosa*

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The chemotherapeutic armamentarium to fight parasitic diseases such as malaria and Chagas disease needs novel bioactive molecules with potential for development into effective drugs. Sustained efforts in antiparasitic high throughput screening of a collection of microbial extracts[1,2] coupled with bioassay-guided compound isolation led to the discovery of a new family of potent antiparasitic bisabolane sesquiterpenoids containing a hydroxamide functionality, villosanes A-C, from an extract of the marine derived basidiomycete *Halocyphina villosa* CF-090066. (+)-ESI-TOF mass spectrometry, nuclear magnetic resonance spectroscopy and X-ray diffraction were used to establish their structures and absolute configurations.

Villosane A, featuring a rare allene moiety in its structure, was the most potent and most selective of the three compounds, exhibiting EC_{50} values of 0.0055 and 6.2 µM against *Plasmodium falciparum* 3D7 and *Trypanosoma cruzi* Tulahuen C4 parasites, respectively. Villosanes B and C exhibited weaker activity against P. falciparum and were both inactive against T. cruzi at 25 µM. Preclinical profiling of villosane A revealed non-inhibition of hERG, Nav 1.4 and Cav 1.5 ion channels at 50 µM, adequate in vitro metabolic stability, weak potential for drug-drug interaction and no in vivo toxicity at a dosage of 50 mg/kg in mice. Hence, villosane A, the major component of the extract, presents a promising potential for development into an effective antimalaria drug.

Data on the production from the fungal source, isolation, structure elucidation and antiparasitic properties of the villosane family of natural products will be presented in this communication.

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OC 12 NEUROPROTECTIVE POTENTIAL OF SPHAEROCOCCENOL A-DERIVED ANALOGUES IN MITIGATING PARKINSON'S DISEASE PATHOLOGY VIA MULTI-PATHWAY MECHANISMS

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Marine-organisms represent a prolific source of bioactive molecules with potential therapeutic applications in neurodegenerative disorders[1]. Parkinson's disease (PD), the second most common neurodegenerative disorder, is characterized by the progressive degeneration of dopaminergic neurons. Previous studies have implicated oxidative stress, mitochondrial dysfunction, neuroinflammation, and increased monoamine oxidase B (MAO-B) activity in the pathophysiology of PD[2]. Currently, there is no cure for PD, and available treatments only alleviate symptoms without halting disease progression[3]. This highlights the urgent need to discover and develop novel neuroprotective agents. This study aimed to evaluate the neuroprotective effects of sphaerococcenol A and its analogues (SPA1 - SPA4) in differentiated SH-SY5Y human neuroblastoma cells exposed to 6-hydroxydopamine (6-OHDA), a well-established in vitro model of PD. The anti-neuroinflammatory activity of the compounds was further investigated in BV-2 microglial cells stimulated with lipopolysaccharide (LPS; 0.5 µg/mL). Complementary in silico analyzes were performed to predict the binding affinity of the tested analogues towards monoamine oxidase B (MAO-B), a key therapeutic target in neurodegeneration, using molecular docking approaches. SPA2 and SPA3 analogues demonstrated significant neuroprotection by improving cell viability in SH-SY5Y cells and attenuating inflammatory responses in BV-2 cells. In silico results also suggested favorable interactions with the MAO-B active site, supporting a potential multitarget mechanism of action.
These findings highlight the relevance of marine-derived analogues as promising leads for the development of neuroprotective and anti-neuroinflammatory agents.

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POSTER SESSION 1

PP 3 A NEW SYNTHETIC CHOLINESTERASE INHIBITOR INSPIRED BY THE ACTIVITY OF THE DISCORHABDIN G ALKALOID FROM ANTARCTIC *LATRUNCULIA* SPONGES

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Sponges from the genus *Latrunculia* produce several discorhabdins, brominated pyrroloiminoquinone alkaloids that exhibit many biological effects. We showed for the first time that selected discorhabdin members also act as potent reversible competitive inhibitors of acetylcholinesterase (AChE) and butyrylcholinesterase (BChE) enzymes. The most potent compound, discorhabdin G, inhibited electric eel and human AChE in a low micromolar range (K_i values: 1.6 µM and 56.2 µM, respectively) and horse serum BChE (K_i = 5.0 µM). An additional muscle twitch study showed no adverse effects of this metabolite on neuromuscular transmission and skeletal muscle function[1]. The result is auspicious as the compound has no side effects that can occur in patients with Alzheimer's disease treated with some currently used drugs acting as AChE inhibitors.

Recently, the hypothesis on the pharmacophore moiety in the discorhabdin G structure suggested by molecular docking calculations has allowed us to reduce the molecular complexity of the metabolite. We have selected 5-methyl-2H-benzo[h]imidazo[1,5,4-de]quinoxalin-7(3H) as the most effective anti-cholinesterase candidate by a computational analysis including molecular docking, ADME prediction, and drug-likeness consideration on a series of potential lead compounds as cholinesterase inhibitors. The molecule has been synthesized by a four-step sequence and tested *in vitro*, showing better inhibition than discorhabdin G against human AChE (K_i = 5.8 µM)[2].

Our results demonstrate the efficacy of the approach to use discorhabdin G as a hit towards a simplified synthetic structure useful for further lead optimization, which will have to include studies on undesirable cytotoxicity and neuromuscular transmission effects.

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PP 4 AN UNPRECEDENTED REPORT ON OCCURRENCE AND BIOTECHNOLOGICAL POTENTIAL OF MYXOBACTERIA FROM A BRAZILIAN MANGROVE

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Myxobacteria are deltaproteobacteria characterized by remarkable social behaviors and a complex life cycle. These bacteria further stand out for producing a wide range of bioactive compounds, including those with antibacterial, antifungal, anticancer, and antiparasitic activities. Traditionally linked to terrestrial habitats like organic-rich soils, myxobacteria have recently been found in marine and coastal environments. In this scenario, mangroves are unique environments featuring variations in salinity, nutrients, oxygen, and organic matter, which directly influence the microbial community, distinguished for having the highest relative abundance of myxobacteria among saline environments. Therefore, this study presents the first report of the occurrence of myxobacteria in Brazilian mangroves, highlighting the species richness and potential of these ecosystems for bioprospecting bioactive compounds. Myxobacteria were isolated using the baiting method, where soil samples collected at the *Portinho* Mangrove (Praia Grande, São Paulo, Brazil), were distributed on nutrient-poor agar dishes spotted with *Escherichia coli* BL21(DE3) as bait to attract predatory myxobacteria. Eighteen swarming colonies or fruiting bodies, typical behaviors of myxobacteria, were collected and transferred to new Petri dishes until completely purified. 16S rDNA sequencing for taxonomical identification revealed most strains belong to the genus *Myxococcus*, with higher homologies to *M. xanthus*, *M. fulvus* and *M. virescens*. Still, the isolates formed three specific clades when compared to type sequences, indicating the existence of potentially novel lineages within the *Myxococcus* genus among Brazilian strains. Acetone:methanol extracts were obtained from liquid cultures of isolated strains added with XAD-16 resin and cytotoxicity of these extracts was assessed based on their ability to inhibit proliferation of tumor and non-tumor cell lines. While none of the extracts were cytotoxic to the non-tumor fibroblast NIH/3T3 at 50 µg/mL, the fibrosarcoma HT-1080 cells and, even more so, the colorectal carcinoma HCT-116 cells, were sensitive to selected extracts. Indeed, strains BRX-002 and BRX-014 were highly cytotoxic against tumor cell lines, with IC_{50} below 1µg/mL. Furthermore, BRX-010 and BRX-015 showed IC_{50} below 1µg/mL against HCT-116 and below 10µg/mL against HT-1080. Extracts were further compared by their chemical profile using HPLC, which allowed clustering extracts into three main groups according to chromatogram similarities. In fact, chemical clusters correlated to the phylogenetic data obtained, so one extract from each chemical group was analyzed using HRMS. Spectral similarity network based on HPLC-MS/MS data allowed to observe the distribution of compounds within the samples and annotations of cytotoxic metabolites. A large cluster including myxothiazol A, an antifungal and mitochondrial uncoupler, was annotated for BRX-002 and BRX-014. This compound has been previously isolated from *M. fulvus*. Myxalamide B, another mitochondrial uncoupler with antibiotic properties, was found exclusively in BRX-008, while microbeMASST showed that myxalamide B and other exclusive nodes of BRX-008 were previously described only for *M. xanthus*. The results presented herein reveal that Brazilian mangroves host a singular and putatively undescribed diversity of myxobacteria that, moreover, hold noteworthy pharmacological potential. Therefore, this work contributes to expanding knowledge on myxobacteria in tropical environments and their potential applications in medicine and industry.

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PP 5 ANTICANCER ACTIVITY OF ANTARCTIC MARINE BACTERIA

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Marine organisms represent an excellent source of natural products with bioactivities useful for the treatment and prevention of human pathologies, such as cancer, inflammation, and infections. Extreme environments, such as the poles, represent an almost untapped source of marine natural products which is still largely unexplored compared to more accessible sites. Antarctic marine microorganisms, exposed to extreme conditions of temperature, UV radiation and ice have developed unique strategies to cope with extreme conditions and, therefore, are capable of producing potentially valuable compounds for pharmacological and biotechnological applications[1]. They have evolved photoprotective defense mechanisms to counteract UV-damage due to the solar UV-B radiation. In this study, we have performed a bioassay-guided fractionation on UV-resistant bacteria isolated by UV-C assay[2] and identified by 16S rRNA[3] to find bioactive bacteria extracts with anticancer activity. In particular, screenings have been performed on melanoma, leukemia, liver and lung human cancerous cells, as well as a normal cell line. Raw extracts and fractions were tested for each bacterium at three different concentrations[4]. Promising results have been found for some of the tested bacteria which resulted active against malignant melanoma human cells with a dose-dependent response without negative effects on normal cells. Successive chemical analyses will clarify the chemical composition of the active fractions.

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PP 6 ANTI-INFLAMMATORY PROPERTIES OF PSAMMAPLIN A AND ITS ANALOGS IN RAW 264.7 CELLS

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Psammaplins are bromotyrosine alkaloids that have been described as antitumoral compounds, an activity that is mediated by their ability to inhibit class I histone deacetylases (HDACs). One of the consequences of HDAC inhibition is the nuclear translocation of peroxisome proliferator-activated receptor gamma (PPARγ), which regulates genes involved in lipid metabolism, antioxidant defence and anti-inflammatory signalling. We recently reported that psammaplin A, along with its analogs psammaplin K and bisaprasin, are able to induce the activation of PPARγ. In this context, the objective of this work was to test the anti-inflammatory potential of these compounds in RAW 264.7 macrophages. With this purpose, cells were treated with psammaplin A, psammaplin K and bisaprasin, isolated from the sponge *Aplysinella rhax*, and stimulated with lypopolisaccharide (LPS) for 24 and 48 h. Then, the effects of compounds on the release of inflammatory mediators was assessed. The three psammaplins produced a decrease in NO release after 24 and 48 h of LPS activation. In addition, IL-6 levels were diminished in cell supernatant when macrophages were treated with psammaplin K and bisaprasin. Interestingly, the release of the anti-inflammatory cytokine IL-10 was increased almost two times by the three *A. Rhax* metabolites, suggesting that they are able to modulate the inflammatory phenotype of macrophages. These results suggest that psammaplins have potential as anti-inflammatory compounds, not only by inhibiting the release of pro-inflammatory mediators, but also by inducing an anti-inflammatory and protective phenotype of inflammatory cells.

PP 7 CHEMICAL DIVERSITY OF THE BROWN ALGA Ericaria selaginoides

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Ericaria selaginoides (Linnaeus) Molinari & Guiry 2020, formerly known as *Carpodesmia tamariscifolia* and previously as *Cystoseira tamariscifolia*[1] is a perennial fucoid alga (Fucales, Phaeophyceae). This brown seaweed is a widespread Atlantic species, commonly found on rocky substrata in the lower intertidal and upper subtidal zones along the north coast of Spain.

Regarding the chemical content of this species, it has been described as high in phlorotannins, usually associated with the antioxidant activity of its extracts, but it is also a rich source of terpenes and terpenoids of mixed biogenesis[2,3,4]. Extracts of *E. selaginoides* have shown significant antimicrobial activity against food pathogens such as *L. monocytogenes*, *S. aureus* and *B. cereus*, as well as against *G. stearothermophilus* and *S. haemolyticus*, positioning it as a promising source of natural preservatives for the food industry[5,6]. In a previous work we studied the effects of *Ericaria selaginoides* extracts on the antioxidant status of Caco-2 cells and the results of the biomarkers analyzed show that treatment of Caco-2 cells with *Ericaria selaginoides* extracts enhances antioxidant defences, implying an improved cell response to an oxidative challenge. The phenolic content/mg extract was also correlated with the antioxidant effect.[7]

The aim of the present study was to evaluate the chemical content of selected antimicrobial organic extracts of *E. selaginoides* collected from Cantabria (Spain), to compare different extraction methods and to purify and identify the secondary metabolites produced by this species. These results provided a set of compounds whose antimicrobial and antioxidant activities will be tested in the future.

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PP 8 EXPLORING MARINE MICROORGANISMS AS SOURCE OF BONE MORPHOGENETIC PROTEIN (BMP) ACTIVATORS

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Bone Morphogenetic Proteins (BMPs) are cytokines that play crucial roles in embryonic development, tissue homeostasis, and regeneration[1]. As the most potent osteoinductive factors identified, their therapeutic value for bone tissue regeneration across various etiologies is well established. However, the currently available recombinant BMPs are costly and often associated with numerous side effects[2], highlighting the urgent need for small-molecule BMP stimulators as alternatives. Marine natural products present a unique chemical landscape and serve as a valuable source for discovering new drug candidates with distinct mechanisms of action and biological targets. The integration of modern technologies -including genomics, metabolomics, high-throughput bioactivity screen platforms, mass spectrometry-based molecular networks, and machine learning approaches- enhances the discovery rate of marine natural products. Marine microbial metabolites, such as largazole derived from a marine cyanobacterium, have shown significant BMP-mediated alkaline phosphatase activity[3]. This emphasizes the high potential of marine microorganisms for the discovery of novel BMP activators.

We established a new, stem-cell-based phenotypic drug discovery platform for high-throughput screening of BMP activators[4,5]. Herein, we merged the discovery platform with the unique chemical space of marine microorganisms. To improve the likelihood of finding new classes of active compounds, we developed state-of-the-art computer-assisted methods to identify biologically interesting and chemically novel ingredients from these extracts at an early stage. Using this technology, we successfully screened a marine microbial extract library composed of 1,059 bacterial and fungal extracts. This was followed by the selection of 92 extracts for hit verification, and they were ultimately narrowed down to 18 extracts for further validation. The validation involved quantifying multiple osteogenic marker gene expressions and assessing cell morphological variations, leading to the identification of four fungal strains as promising candidates for BMP activator discovery. These strains have now been fermented on a large scale and are undergoing chromatographic separations towards targeted isolation of the bioactive compounds, guided by computational untargeted metabolomic approaches, alongside the findings from phenotypic high-throughput screening. Subsequently, the bioactivity, mechanism of action, and translation potential into human models will be investigated following the purification of these metabolites.

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PP 9 EXPLORING THE NATURAL PRODUCT BIOSYNTHETIC POTENTIAL OF ANTARCTIC ACTINOMYCETES

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Despite advancements in natural product (NP) discovery, high rediscovery rates continue to hinder progress in combating antimicrobial resistance[1]. As a result, recent efforts have focused on exploring extreme ecological niches to discover novel NPs[2]. Actinomycetes are promising sources of novel NPs, contributing to nearly two-thirds of clinically used antibiotics[3]. The Antarctic ecosystem diversity represents a valuable bioprospecting target; however, it has largely remained underexplored for NP discovery[4]. This project aims to investigate the biosynthetic potential of Antarctic actinomycetes for bioactive compounds production. Marine sediment samples were collected from six Antarctic locations (140-1150 m depth), and isolation protocols were optimized to selectively recover filamentous actinomycetes. Sixteen strains were selected for further investigation, with a representative subset subjected to PacBio long-read genome sequencing. Among them, strains from different genera were identified, including *Streptomyces*, *Nocardiopsis*, *Micromonospora*, *Pseudonocardia,* and *Actinacidiphila*. The strains were cultivated in ten different media and analysed for antimicrobial activity against a panel of microbial test organisms. Thirteen strains exhibited antimicrobial activity, with *Actinacidiphila* sp. DSM 41987, *Streptomyces diacarni* DSM 109305 and *Streptomyces* sp. DB7_152, as the most bioactive strains. A combinatory genome mining and metabolomics analysis approach was employed to correlate gene cluster predictions with compounds production. *Actinacidiphila* sp. DSM 41987 produced a potential new depsipeptide-like compound, which was correlated with an actinomycin BGC sharing 89% cluster similarity. *S. diacarni* DSM 109305 produced the compounds tartrolon, griseusin, and dudomycin, in addition to a compound with an *m/z* of 903, which could not be linked to any known compound, indicating that it may represent a novel compound. *Streptomyces* sp. DB7_152 produced surugamide and antimycin, both of which could be linked to their BGCs, with cluster similarity values of 95% and 100%, respectively. The latter two compounds are known to have antifungal activities and were tested against the fungal Antarctic co-isolate *Metschnikowia australis.* Thereby it was found that antimycin shows bioactivity against *M. australis* but also against the clinically relevant pathogen *Candida auris,* underscoring the importance of understanding the ecological roles of natural compounds in their native environments for future applications.

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PP 10 HARNESSING RIPP DIVERSITY: DIPAC CLONING AND FUNCTIONAL EXPRESSION

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Ribosomally synthesized and post-translationally modified peptides (RiPPs) are a diverse group of natural products produced across Archaea, bacteria, fungi and plants. Their biosynthesis starts with simple expression of a precursor peptide from a genome, but they further undergo wide range of modifications such as cyclization, methylation, acetylation, dehydration etc. that generate complex chemical architectures and confer potent biological activities. Due to this simplicity of the biosynthesis and the fact that the genes are usually organised in close vicinity in biosynthetic gene clusters (BGCs), the search for novel RiPP families and their associated biosynthetic pathways can be efficiently performed using genome—and metagenome—mining approaches.

Nostatin A is a recently reported RiPP, which belongs to nitrile hydratase-like leader peptide RiPPs (proteusins), isolated from a terrestrial cyanobacterium *Nostoc* sp. It is unique in possessing anti-proliferative effects in cancer cells. In parallel, microviridins are among the most recognized class of ribosomal peptides produced by cyanobacteria. These oligopeptides are potent inhibitors of proteases.

Here we report the use of the DiPAC (Direct Pathway Cloning) method to capture the BGCs of these compounds and their heterologous expression in *Escherichia coli*. Furthermore, we applied a combinatorial biosynthetic approach to dissect the roles of individual tailoring enzymes by systematically assembling subsets of biosynthetic genes. This allowed us to explore pathway modularity, clarify enzyme function, and enhance the structural diversity of the produced RiPPs. Further, variants of the compounds will enable us to study the importance of particular modifications for bioactivity. Our work demonstrates the power of DiPAC for RiPP discovery and engineering, and provides new tools for the production of bioactive compounds with therapeutic potential.

PP 11 *IN SILICO* ANALYSIS OF PSEUDOMONADOTA PHYLUM ISOLATED FROM MARINE SAMPLES AT PHARMAMAR. A TOOL TO IDENTIFY PRODUCERS OF POTENTIAL ANTITUMORAL COMPOUNDS

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Pseudomonadota (also known as Proteobacteria) is a widely diverse major phylum of Gram-negative bacteria. Along PharmaMar's history, hundreds of thousands of bacteria have been isolated from marine samples. Part of our bacteria collection has also been identified and characterized through 16S ribosomal gene DNA sequencing and more than 40% belong to Pseudomonadota phylum.

Due to the importance of this phylum, we decided to conduct a more in-depth analysis of its four classes: Alpha-proteobacteria, Beta-proteobacteria, Epsilon-proteobacteria and Gamma-proteobacteria. For that, an *in silico* strategy was carried out in order to identify and explore the most promising genera in our collection able to produce secondary metabolites with biological activity.

The genetic potential to produce secondary metabolites was determined by the BLAST algorithm using the prokaryotic RefSeq genomes from NCBI, based on a highly conserved amino acid sequence from the polyketide synthase gene cluster. These *in silico* analyses were complemented with experimental antitumoral screening results of the PharmaMar's isolated strains fermentation extracts.

Analysis results showed the best genera of Pseudomonadota to be deeply explored with the aim to identify the best candidates able to produce bioactive compounds through different approaches. Whole Genome Sequencing (WGS) as well as optimization of fermentation process (elicitors, media nutrients, aeration, etc.) among others, are key techniques to identify, promote and/or increase the production of these compounds.

PP 12 INVESTIGATION OF SMALL MOLECULES IN CANCER IMMUNOTHERAPY

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The interaction between programmed cell death protein 1 (PD-1) and its ligand PD-L1 plays a critical role in immune checkpoint regulation, and disrupting this binding has proven to be an effective strategy in cancer immunotherapy. Current therapeutics targeting the PD-1/PD-L1 bindings are primarily monoclonal antibodies, which present limitations in terms of cost, delivery, and immune-related adverse effects[1]. Therefore, an effort to discover novel small molecules has been made in recent years[2][3]. In this study, we explore the potential of marine bacterial secondary metabolites as a source of small-molecule inhibitors capable of modulating PD-1/PD-L1 binding.

Marine bacteria, with their rich biosynthetic diversity, offer an untapped reservoir of bioactive compounds. We provided fractionated extracts from marine bacterial culture to our collaborators for high-throughput bioassay screening against the PD-1/PD-L1 interface. While the hit rate is very low, a few fractions out of 9,500 samples demonstrated promising inhibitory activity. This leads to the identification and structural characterization of small molecules with potential checkpoint blockade properties. These findings represent a step toward developing novel small-molecule immunomodulators that may overcome limitations of antibody-based therapies.

On the poster, we present data on key candidate compounds, detailing their origin, structural features, and bioactivity profiles. Our results suggest that marine microbial secondary metabolites can serve as a foundation for the development of new immunotherapeutic agents, expanding the toolbox for cancer treatment.

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PP 13 MARINE BACTERIA FROM THE ASCIDIAN *Tridemnum maragogi*, COLLECTED AT SAINT PETER AND SAINT PAUL'S ARCHIPELAGO, BRAZIL, AS A PROMISING SOURCE OF BIOACTIVE COMPOUNDS

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Ascidians are a staple host to bioactive marine natural products, sourcing a myriad of compounds with pharmacological potential. In fact, trabectedin, lurbinectedin, and plitidepsin represent natural molecules, or derived thereof, isolated from ascidians that are clinically approved drugs for anticancer treatments. *Tridemnum* is a notable ascidian genus in the pharmacological realm. Indeed, Tridemnum solidum, a species from the Caribbean, is the source of didemnins, a series of cyclic depsipeptides with anticancer properties described in the early 1980s. During the last decades, evidence has linked the production of didemnins, trabectedin and other notable compounds initially isolated from ascidian to their associated bacteria, revealing the importance of the host microbiome in the search for new drugs. Herein, we assessed *T. maragogi*, collected at the Saint Peter and Saint Paul's Archipelago (SPSPA), a collection of islets located on the Equatorial Atlantic Ocean, 590 nmi off the coast of Brazil, for the anticancer potential of its culturable associated bacteria, which were described for taxonomy, cytotoxicity and metabolomics. *T. maragogi* was collected at SPSPA during four different expeditions, from which a total of 45 strains were isolated. 16S rDNA analysis indicate the recovery of diverse bacteria organized within 8 genera: *Micromonospora*, *Serratia*, *Bacillus*, *Rhodococcus*, *Streptomyces*, *Microbacterium*, *Brucella* and *Salinispora*. Crude extracts were obtained from all the isolated strains and tested for cytotoxicity against colorectal cancer (HCT-116) and melanoma (501Mel) cell lines using the MTT assay. Six extracts, mostly derived from actinobacteria strains, displayed remarkable inhibition of cancer cell proliferation, with IC_{50} as low as 3.97 µg/mL, and then they were analyzed using metabolomic tools. A molecular network based on LC-MS/MS data notably indicated the presence of rifamycins, staurosporines, indole derivatives and N-acyl-tyramines. Furthermore, searches of MS/MS spectra in microbeMASST tool showed that rifamycin S and staurosporine, well known compounds for their anticancer effects, were associated to *Salinospora* strains, mostly in *S. arenicola*. These results support the integrations of bioactivity assays with metabolomics approaches in prioritizing extracts for further pharmacological investigations, and highlight the chemo and biodiversity level founds in Brazilian oceanic islands.

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PP 14 MARINE FUNGAL BIOTECHNOLOGY FOR THE EARLY CONTROL OF METASTATIC MELANOMA

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Metastatic melanoma is a highly aggressive and therapy-resistant form of skin cancer, with rising incidence and limited long-term treatment success, particularly in advanced stages[1]. Marine-associated fungi represent a valuable resource for the discovery and development of novel anticancer agents with high efficacy and low toxicity. For example, plinabulin, the synthetic tert-butyl analog of diketopiperazine halimide that derives from a seaweed-derived fungus *Aspergillus* sp., has progressed through Phase 3 clinical trials. Its clinical efficacy was validated in the DUBLIN-3 trial (NCT02504489), where its combination with docetaxel, significantly improved overall survival in patients with non-small cell lung cancer (NSCLC)[2]. Plinabulin exhibited high efficacy in preventing chemotherapy-induced neutropenia (CIN) in patients with solid tumors, while demonstrating a more favorable safety and immunosuppressive profile[3].

In a previous pilot study, we isolated two decalinoyltetramic acid derivatives, pyrenosetin A and B with high activity against human malignant melanoma A375 cells from the seaweed endophytic fungus, *Pyrenochaetopsis* sp[4]. In this study, we aimed to optimize culture conditions further for large-scale fermentation, in order to isolate and characterize target compounds (and their novel derivatives) in sufficient quantities to investigate their mechanism of action via proteomic profiling, and evaluate their in vivo efficacy in early prevention of metastatic melanoma in a mouse model. *Pyrenochaetopsis* sp. was cultured in varying conditions (different culture regimes, aeration, duration, salinity, and more) as part of a detailed OSMAC (One-Strain-Many-Compounds) approach. Crude extracts were assessed for extract yield, anticancer activity against melanoma (A375) cells and cytotoxicity against non-cancerous HaCaT cells, and chemically profiled by LC-MS/MS using Feature-Based Molecular Networking (FBMN) workflow. Bioactivity predictions performed by the FERMO (Formulation of mEtrics from Reproducible Molecular feature Objects) tool[5] identified 15 molecular features linked to anti-melanoma activity. Based on the extract yield, in vitro efficacy and prevalence of target compounds as well as their derivatives, optimal culture conditions have been determined. *Pyrenochaetopsis* sp. is currrently undergoing a large-scale fermentation (up to 250 L) for downstream compound isolation, characterization and bioactivity evaluations.

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PP 15 OPTIMIZATION ASSAYS TO TRIGGER THE PRODUCTION OF ANTITUMORAL COMPOUNDS FROM RARE MARINE ACTINOMYCETES

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The evaluation of Actinomycetota phylum in drug discovery identified *Streptomyces* genera as one of the main producers of active metabolites, becoming target of several research studies. However, the increasing availability of whole-sequenced genomes have revealed the potential of other genera of the phylum as a source of new chemical entities[1]. Among them, *Gordonia* seems to be one of the most promising genera of the group[2]. With the aim of unlocking all this potential, an optimization project focused on *Gordonia sp*. strains with residual cytotoxic activity but with genomic interest, was developed by our department.

Through OSMAC (One Strain Many Compounds) approaches and Box-Behnken and Plackett-Burman designs, this work has shown a consistent response of some of the *Gordonia sp.* strains to media composition, and physical factors such as agitation and aeration. Also, the WGS (whole Genome Sequence) analysis of the most responsive strain deciphered its potential BGC (Biosynthetic Gene Cluster) responsible of the biological activity observed. The fermentation optimization process conducted on the selected strain, achieved a significant cytotoxic activity in tumoral cell lines, which together with the genomic data analysis, allowed us to continue the antitumoral compound(s) purification and identification.

These results show the relevance of continue studying rare Actinomycetes genera as producers of metabolites of interest, combining both, optimization of fermentation processes as well as WGS analysis to unlock and/or induce secondary metabolites production by these less explored genera.

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PP 16 PHARMACOLOGICAL ACTIVITY OF CONTIGANASTEROL AND TWO CONTIGNASTERINES ISOLATED FROM A BISMARCK SEA SPONGE

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Inflammation is a key process for body's repair and defense. However, persistent inflammation produces tissue damage and is the basis of many diseases such as cancer, cardiovascular diseases or neurodegenerative processes. Several studies have shown that the neutralization of inflammation markers stabilizes atherosclerotic disease and improves the prognosis of patients after a heart attack. Therefore, the identification of natural compounds that modulate the inflammatory cascade may be a useful tool to allow strategies for drug development. In this context, the pharmacological activity of contignasterol and two contignasterines (1 and 2) isolated from a sponge of the order *Leucosolenida* was checked in an inflammatory model of macrophages. RAW 264.7 cells were pre-incubated in the presence of compounds and the production of pro- and anti-inflammatory markers was studied after the addition of lipopolysaccharide (LPS), a potent inflammatory stimulus. Contignasterol and derivatives decrease the release of NO and the production of reactive oxygen species (ROS) as well as the release of IL6 and IL2 while IL10 levels and the ability to modify the cellular phenotype were not modified. In addition, intracellular calcium fluxes were reduced in the presence of the sponge compounds. Therefore, contignasterol and contignasterines modulate the inflammatory cascade and have an interesting anti-inflammatory effect.

PP 17 UNLOCKING THE BIOACTIVE POTENTIAL OF *APOSTICHOPUS JAPONICUS* TO TACKLE ANTIMICROBIAL RESISTANCE AND BIOFILM RELATED INFECTIONS

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Despite the promising bioactive potential of marine invertebrates, *Apostichopus japonicus* (sea cucumber) remains largely underexplored as a source of novel antimicrobial and antibiofilm agents. This study investigates the extraction of bioactive compounds from *A. japonicus*, an underexplored marine invertebrate, as part of discovering novel natural products from Korean marine species with antimicrobial activity against antibiotic resistant bacteria, both in planktonic and biofilm form. A sequential extraction process with methanol (2x) and dichloromethane (DCM, 1x) was employed, followed by solvent evaporation and removal of impurities, including salts. To maximize compound recovery, the dried extract was resuspended in a methanol, acetone, and water mixture (2:2:6). Thin-layer chromatography (TLC) was performed for intial profiling of the crude extract, with silica gel and chloroform: ethanol: water: acetic acid (2:8:2:0.5) as stationary and mobile phase, respectively. Astaxanthin, a well-known bioactive marine natural compound with established antimicrobial properties, was used as a positive control for preliminary profiling[1]. TLC revealed multiple distinct spots using both iodine and vanillin-sulfuric acid stains, suggesting the presence of unsaturated and aromatic compounds including carotenoids and saponins[2,3]. These results support the hypothesis that *A. japonicus* contains a variety of compounds, including astaxanthin-like compounds, that may possess antimicrobial and antibiofilm potential. Although further optimization and characterization are needed, *A. japonicus* appears to be a promising candidate for future efforts in discovering novel antimicrobial and antibiofilm agents.

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PP 18 USING METABOLOMIC TOOLS TO BIOPROSPECT THE ANTIBIOFILM ACTIVITY OF A SEAWEED ENDOPHYTE IN A CO-CULTURE

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This study aims to identify bioactive secondary metabolites from the co-culturing endophytic fungi *Dendryphiella salina* with biofilm forming bacteria *Pseudomonas aeruginosa* (PA). The endophyte was isolated from the Scottish seaweeds *Laminaria hyperborean,* which already has been identified and proven its antimicrobial activity against *methicillin-resistant Staphylococcus aureus* (MRSA) and PA[1]. Principle component analysis along with Nuclear Magnetic Resonance Spectroscopy (NMR), High Performance Liquid Chromatography coupled with High-Resolution Mass Spectrometry (HRMS) and anti-biofilm assay were employed to screen for the optimum co-culturing conditions and revealed that inoculating the bacteria first prior to incubating both microorganisms together in malt extract with sea salt media provided the highest levels of the bioactive metabolites with highest yield. To spot the bioactive compounds in the co-culture, the crude extract was obtained by liquid-liquid partitioning followed by medium pressure liquid chromatography (MPLC) for further purification of the antibiofilm metabolites. Thin layer chromatography was executed to identify fourteen fractions with different chemical profiles and anti-biofilm assay was performed to confirm that nine fractions are biologically active against MRSA. Multivariate analysis and dereplication studies of the HRMS data with 1D and 2D NMR analysis, conveniently annotated linoleic acid (LNA) in one fraction. Recent studied have shown that combination of LNA with many antibiotics assist to reduce the doses and prevent the formation of biofilm as it can act as quorum sensing inhibitor[2]. Moreover, formulating LNA as a nanoemulsion was non-toxic and exhibited a 205-fold greater increase in the antibacterial activity than plain LNA against *S. aureus* and MRSA[3]. Whereas, the other fractions were further fractionated and sub fractions provided metabolites produced by marine derived *Pseudomonas* and chromanone derivatives, which exhibits antibacterial activity.

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3. Omics tools in MNP research and discovery

XIV ECMNP
EUROPEAN CONFERENCE ON
MARINE NATURAL PRODUCTS

ORAL COMMUNICATIONS

OC 13 FROM ACTIVITY TO MOLECULE: INTEGRATED OMICS APPROACHES FOR NATURAL PRODUCT DISCOVERY

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Natural products (NPs) continue to serve as a foundation for drug discovery, but have a tendency for rediscovery[1]. The Linington lab focuses on large-scale analysis and the development of computational tools for optimized and automated active NP discovery[2]. Recently, we acquired liquid chromatography-coupled mass spectrometry (LC-MS) data and image-based screening (Cell Painting (CP)) results on 35,200 plant and sponge prefractionated samples from the US National Cancer Institute. Using the LC-MS data, we have determined compound families through molecular networking. After doing segmentation on the CP images with CellProfiler software[3], we have also determined the phenotypical fingerprints and infer compound modes of action (MOA). Also, by collaborating with the US National Cancer Institute we are determining the structure of compounds with strong or unique MOAs and or interesting structures.

This presentation will focus on the analysis of the segmented CP dataset. This dataset is the largest CP dataset acquired on NPs, enabling us to address several large-scale questions about plant and sponge NP MOAs, including: 'how are biological phenotypes distributed across taxonomic space?', 'does phenotypic behavior correlate with producing organism taxonomy?', and 'are there phenotypes unique to the natural world?'.

To answer these questions, we first identified the extract groups with similar MOAs employing principal component analysis (PCA) and hierarchical clustering. By using PCA we assessed whether the features are active, then grouped active features based on their similarity with hierarchical clustering. Since the phenotypical fingerprint can be highly dependent on compound concentration, we used dilution series of compounds with known MOAs to establish bioactivity parameters and used this data to determine compound MOAs at unknown concentrations.

Using this dataset, we will connect the MOA groups with the putative compound groups to investigate whether the metabolomic space correlates with the phenotypical space and whether similar compounds have different MOAs. This presentation will provide a general picture on the plant and sponge activities on mammalian cells. Our image-based screening interpretation algorithm enables the identification of bioactive molecules with distinct MOAs. This should provide insight on the distinct MOAs of the NP world and the connection of these MOA groups to metabolite groups. This presentation will paint a general picture on the parts of the plant and sponge taxonomical and metabolomic space that are important and interesting to consider for further research on anticancer therapeutic agents.

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OC 14 DISCOVERING NEW ANTIBIOTICS: THE POWER OF MARINE FUNGI REVEALED BY NEW ECO-INSPIRED CULTURES

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Today, the antibiotics overuse led many bacteria to develop resistance to antimicrobial treatments. This constitutes a major public health issue, requiring the development of new therapeutic molecules[1]. Marine fungi and their specialized metabolites (SMs) represent an interesting, underexploited source of potential antibiotics. However, under conventional laboratory conditions the number of observed SMs remains limited relative to the biosynthetic gene clusters (BGCs) present in the genomes[2,3]. To induce the expression of some of these BGCs remaining cryptic, some strategies have been successfully developed, such as the OSMAC approach[4] using different media including host-derived media for strains from holobionts and co-cultures of microbial partners. However, co-culture methods are mainly performed using pairs of microorganisms, which does not reflect what naturally occurs within marine microbiomes.

This project aspires to develop eco-inspired multicultures of different fungal strains sampled from the seaweed *Palmaria palmata*, aiming to highlight metabolic inductions in microbial consortia when cultured on a reconstituted seaweed-based medium.

First experiments have been conducted on four fungal strains belonging to the genera *Penicillium*, *Aspergillus*, *Acremonium*, and *Parengyodontium*. They were cultivated on 12 different culture media including host-derived media in which *P. palmata* powder was added in different amounts. Extracts obtained were tested on 6 bacterial strains, and analyzed by UHPLC-HRMS/MS to construct bioactive molecular networks. This allowed us to find the best host-derived medium for antibacterial and original compounds production.

Co-cultures involving 2 to 4 of the strains have been engaged, and MS-based chemometrics analyses led to the induction of specific signals in some of the microbial consortia. Promising microbial consortia will be up-scaled in order to isolate the most promising compounds. This study lays the foundations for a new concept in fungal NPs discovery combining multicultures rather than co-cultures, together with the use of eco-inspired host-derived media.

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OC 15 MARINE ACIDOBACTERIOTA AS HALOGENATION RESERVOIRS: DISCOVERY OF NOVEL BIOSYNTHETIC GENE CLUSTERS

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Acidobacteriota is an environmentally ubiquitous bacterial phylum, widely detected across terrestrial and aquatic ecosystems, yet largely remains uncultivated. Recent discoveries indicate that Acidobacteriota constitute an emerging hotspot for natural product discovery, harboring biosynthetic gene clusters (BGCs) with novel architectures[1,2]. Moreover, several recent studies highlight that marine host-associated Acidobacteriota, especially from marine sponge microbiomes, harbor substantial and unique biosynthetic potential[3]. However, the full diversity and specificity of these marine symbiotic Acidobacteriota remain underexplored. In this study, we curated a comprehensive dataset of Acidobacteriota genomes from public repositories, followed by quality control, dereplication, and targeted selection of metagenome-assembled genomes (MAGs) derived from marine host-associated samples. Clustering of BGCs revealed several unique gene cluster families (GCFs) specific to symbiotic Acidobacteriota lineages. Notably, we identified a significant enrichment of tryptophan halogenase-containing BGCs in marine host-associated representatives compared to free-living counterparts. Detailed analysis further revealed several hybrid clusters characterized by the embedding of halogenase genes among core biosynthetic domains, suggesting halogenation of the final metabolites. One such example is a Type III polyketide synthase (PKS) BGC from the host-associated UBA8438 family, which shares core biosynthetic gene similarity with the alkylresorcinol BGC of *Streptomyces griseus subsp. griseus* NBRC 13350. However, the halogenase-containing variant appears to be exclusive to UBA8438. These results highlight marine Acidobacteriota as promising reservoirs for discovering unique halogenated natural products, shaped by their symbiotic lifestyle.

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OC 16 MARINE CYANOBACTERIA AS A NATURAL SOURCE OF KAHALALIDE F-LIKE DEPSIPEPTIDES

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Kahalalide F is a cyclic depsipeptide with demonstrated potent anticancer activity, originally isolated from the marine green alga *Bryopsis* sp. and its sacoglossan mollusk predator *Elysia rufescens*. Although biosynthesis was initially attributed to the host organisms, evidence over the past decade has revealed that the true origin is a bacterial endosymbiont, *Candidatus* Endobryopsis kahalalidefaciens[1]. In this study, we report the discovery of a novel kahalalide F-like compound from a marine cyanobacterium collected from the Las Perlas islands, Panama. To prioritize unknown metabolites, we applied a comprehensive metabolomics workflow that integrated high-resolution LC-MS/MS with *in silico* structural annotation, aided by DeepSAT, an AI-based platform trained to predict chemical structures from HSQC NMR data[2]. This revealed the presence of a kahalalide F-like compound in this cyanobacterial extract, and its structure was subsequently elucidated through rigorous analysis of 1D and 2D NMR spectroscopy, HRMS, and chemical degradation sequences. To determine the biosynthetic origin, we performed whole-genome sequencing of the cyanobacterial strain and identified a putative NRPS Biosynthetic Gene Cluster (BGC) entirely consistent with the compound's structural framework. This study provides compelling evidence that marine cyanobacteria are also native producers of kahalalide F-like metabolites. Our findings expand the known phylogenetic diversity of kahalalide F-producing microorganisms and underscore the power of integrating AI-driven metabolomics with genome-resolved biosynthetic analysis. This approach accelerates natural product discovery and highlights cyanobacteria as a sustainable source of complex therapeutic leads.

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OC 17 MONITORING CYANOBACTERIAL BLOOMS AND APPLICATION OF THE FDS STRATEGY IN THE LUCRINO SEA

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Cyanobacteria are ubiquitous microorganisms found in phototrophic aquatic environments, including recreational waters, fisheries, and reservoirs. Under eutrophic conditions, they can proliferate rapidly, forming harmful algal blooms (HABs) and releasing cyanotoxins with significant ecotoxicological effects on human health and ecosystem balance. These toxins can accumulate through the food chain, amplifying their impact via bioaccumulation and biomagnification processes.

To address this issue, an interdisciplinary Fast Detection Strategy (FDS) has been developed[1-3], integrating remote/proximal sensing with advanced mass spectrometry-based molecular networking. FDS enables the timely identification of cyanobacterial blooms and their associated toxins, allowing targeted interventions for environmental and public health risk management.

A notable case study involves the bloom of *Planktothrix rubescens* in Lake Avernus (Campi Flegrei, Italy) in March 2022, which caused a striking red discoloration of the water. Using FDS, researchers tracked the movement of cyanotoxins from the lake to the Sea of Lucrino through a connecting channel, detecting their bioaccumulation in mussels (*Mytilus galloprovincialis*) cultivated along the coast.

By integrating remote sensing techniques with chemical analysis, the study identified a group of anabaenopeptins in both water and bivalve samples, providing the first documented evidence of cyanotoxin transfer from a freshwater bloom to marine organisms. This approach highlights the importance of integrated monitoring strategies for managing HABs and protecting both fishery resources and public health.

In this communication I will present the implementation of FDS that represents an innovative model for controlling toxic blooms in complex coastal systems, enhancing response and prevention capabilities through multispectral and molecular data-driven monitoring.

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POSTER SESSION 1

PP 19 BIOACTIVE METABOLITES DISCOVERY IN CYANOBACTERIA THROUGH OSMAC AND METABOLOMICS

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Over the past few decades, researchers have increasingly explored biodiversity—particularly in marine environments—in the search for novel natural products with well-established bioactive properties[1]. Among the most promising sources are microorganisms, especially cyanobacteria, known for their ability to produce specialized bioactive metabolites[2,3]. Despite their rich biosynthetic potential, many cyanobacterial biosynthetic gene clusters remain silent under standard laboratory conditions, limiting the full exploitation of these organisms. One strategy to overcome this challenge is the "One Strain Many Compounds" (OSMAC) approach, which involves altering specific physical (e.g., type of culture support, growth duration) or chemical parameters (e.g., nutrient composition, pH) to induce differential metabolite production[4]. This can lead to the discovery of new bioactive molecules.

In this study, the OSMAC approach was applied to five cyanobacterial strains isolated from hypersaline environments. These strains were cultivated in Z8 medium at 25 °C under a 14/10 h light/dark cycle, with additional synthetic sea salts supplementation at 15, 25, and 60 g/L, respectively. Lyophilized biomass was extracted using a solvent mixture of CH_2Cl_2:MeOH (2:1 v/v) and fractionated by reverse-phase HPLC using a H_2O:MeCN gradient. A total of 120 fractions (5 strains × 3 salinity conditions × 8 fractions each) were screened for biotechnological potential in both health and environmental applications. To explore potential health benefits, three assays were performed: two to assess lipid reduction - one in zebrafish larvae (Nile Red fat metabolism assay) and another in human HepG2 liver cells (anti-steatosis assay), and a third in zebrafish larvae to evaluate glucose uptake (2-NBDG assay). For environmental applications, two assays were conducted to assess antifouling properties: an anti-settlement assay against *Mytilus galloprovincialis* larvae and an antibacterial assay using five marine bacterial strains.

LC-HR-ESI-MS/MS-based metabolite profiling was performed on the most promising fractions to identify compounds potentially responsible for the observed bioactivities. Preliminary results indicate that a single cyanobacterial strain can produce distinct bioactive metabolites depending on the cultivation conditions, such as variations in salinity. Changes in environmental parameters led to the expression of compounds with different biological activities, including antifouling effects, glucose uptake modulation, and lipid accumulation inhibition. This supports the potential of the OSMAC strategy as a valuable approach for diversifying and uncovering bioactive compounds from cyanobacteria.

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PP 20 BIO-TRACKING, BIO-MONITORING AND BIO-MAGNIFICATION INTERDISCIPLINARY STUDIES TO ASSESS CYANOBACTERIAL HARMFUL ALGAL BLOOMS (CYANOHABS)' IMPACT

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Cyanobacteria thrive from polar salt marshes to tropical lagoons, adapting quickly to light, salinity and nutrient swings. When nutrient-rich conditions tip the balance, these ancient microbes can erupt into expansive surface blooms whose pigments stain the water and whose secondary metabolites—cyanotoxins—threaten ecosystems, aquaculture and public health[1]. Because the organisms respond so visibly and so fast, they are powerful natural barometers of changing coastal conditions.

To turn that ecological warning system into a management tool we developed the Fast Detection Strategy (FDS)—a multidisciplinary workflow that marries satellite and drone imagery with high-resolution mass-spectrometry metabolomics. In practice the method works like this: space-borne and proximal sensors flag unusual optical signatures on the water; targeted field sampling follows within hours; and molecular-networking algorithms rapidly screen extracts for cyanobacterial chemotypes, all without lengthy chromatographic purification[2]. The result is a same-week picture of "who is blooming, where, and with which toxins," delivered in language that local agencies can act on.

The approach proved its worth during the crimson bloom of *Planktothrix rubescens* in Lake Avernus (Naples). Remote sensing traced the bloom's downstream journey through a short emissary channel to nearby mussel farms, while mass-spectrometric networking revealed the presence of anabaenopeptins—a class of hepatotoxic peptides now attracting international attention. Early warning allowed authorities to issue precautionary harvest closures before the toxins entered the market[3].

Our experience shows that pairing wide-area vision with fast laboratory tools turns cyanobacteria into practical sentinels of water quality. Timely alerts give local authorities room to act—closing shellfish beds or advising swimmers—before toxins pose a significant risk. Continued, integrated monitoring will therefore be essential to safeguard both marine ecosystems and human health as nutrient pressures and climate change intensify.

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PP 21 CAMPYLOBACTEROTA AN UNDEREXPLORED BACTERIAL PHYLUM WITH UNTAPPED BIOSYNTHETIC POTENTIAL

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Today large-scale genome mining or microbial isolation projects often focus on soil-dwelling bacteria from the phylum Actinomycetota or other so-called 'gifted' phyla such as Myxococcota[1-3]. The oceans however, offer the largest untapped potential for specialized metabolites by sheer size and recently the rich biosynthetic potential of the ocean microbiome was described[4]. Still, due to sequencing bias and other factors there are only a small number of large-scale genome mining studies on marine bacteria[5,6]. For the most part, marine natural product research still focuses on individual studies of specific macro- or microorganisms[7,8]. In this study, we analyzed over 1000 publically available and proprietary genomes of the Campylobactertoa phylum, formally Epsilonproteobacteria[9,10], for their potential to produce specialized metabolites. Members of this phylum inhabit a diverse set of habitats, ranging from the human stomach wall to deep-sea thermal vents and anoxic marine sediments[9,10]. We identified over 400 biosynthetic gene clusters (BGCs) belonging to diverse gen cluster families (GCF), and evaluated their characteristics *in-silico*. To validate one of the predicted novel GCF, two *Arcobacter* species encoding the BGC were analyzed for their metabolome in a targeted metabolomics approach. Complementary, one biosynthetic gene cluster was selected for in-depth characterization by heterologous expression and its product elucidated and biological activity evaluated.

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PP 22 FEATURE-BASED MOLECULAR NETWORKING BRIDGES MARINE AND TERRESTRIAL SIDE-STREAMS FOR RAPID BIOACTIVE METABOLITE DISCOVERY

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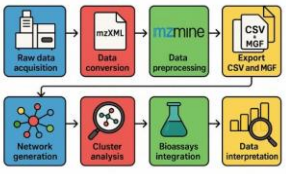
Feature-based molecular networking (FBMN) converts large LC-HRMS/MS datasets into graphs of structurally related features, enabling rapid dereplication, clustering and prioritisation of metabolites in chemically heterogeneous extracts. We applied the same open-source FBMN workflow to three contrasting matrices: Caribbean sponge *Aplysina cauliformis*, brewers' hot trub and Aglianico grape pomace to illustrate its unifying reach across marine and terrestrial sources. In the sponge[1], FBMN highlighted a distinct cluster of brominated tyrosine derivatives; targeted purification from that cluster yielded *N,N,N*-trimethyl-3,5-dibromotyramine, an antiproliferative agent active against HepG2 cells. In hot trub[2], molecular networking grouped prenylated flavonoids with hop-derived α/β-bitter acids into separate families that matched the extract's strongest antioxidant responses . In grape pomace[3], FBMN uncovered stilbenoid ellagitannin conjugates associated with the marc's high radical-scavenging capacity, underscoring the nutraceutical value of this winery by-product. These case studies show that FBMN accelerates the recognition of bioactive chemotypes regardless of biological origin, allowing researchers to link chemical clusters to functional assays before engaging in time- and solvent-intensive purification steps . Such early insight aligns with circular-economy principles by facilitating the valorisation of marine biomass and agri-food side-streams while minimising resource use. We propose FBMN as a versatile platform for streamlining natural-product discovery, bridging marine and terrestrial chemotypes, and guiding sustainable exploitation of underutilised biological materials.



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PP 23 INSIGHT INTO THE GENOMIC AND METABOLIC PROFILE OF A HYDRACTINIA-ASSOCIATED *RHODOCOCCUS* SYMBIONT

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Marine invertebrates harbor a diverse community of predominantly beneficial microbes that contribute significantly to host development, fitness, and defense[1]. To thrive in these often extreme and highly competitive host-specific microenvironments, microorganisms have developed specialized metabolic and physiological adaptations[2]. Notably, marine microbes are renowned for synthesizing structurally diverse secondary metabolites with valuable pharmacological properties, including antibiotic, antifungal and anticancer activities[1]. In this study, a bacterial strain was isolated from the tissue of *Hydractinia echinata*, a colonial marine hydroid found on gastropod shells inhabited by hermit crabs (*Pagurus pollicaris*). The 16S rRNA sequencing identified the strain as a member of the *Rhodococcus* genus. Further whole-genome sequencing and phylogenomic placement using the Type Strain Genome Server and the Gdtbk database search revealed the strain as a new *Rhodococcus* species. Genome mining with antiSMASH revealed a rich repertoire of biosynthetic gene clusters (BGCs; n = 21), with a notable abundance of clusters encoding nonribosomal peptide synthetases. To explore the strain's metabolic potential, it was cultured in minimal media supplemented with various hydrocarbons as sole carbon sources, including hexadecane, olive oil, and sunflower oil. Metabolomic analysis using GNPS molecular networking uncovered two uncharacterized metabolite clusters when the strain was grown in the olive oil-supplemented minimal medium. Subsequently, prominent activity of the extract from this medium was observed against *Bacillus stercoris*, *Pseudomonas monteilii*, and *Candida albicans*. To enhance production of metabolites from these two unknown clusters, an elicitor-based strategy was employed by adding DMSO and valproic acid to the olive oil-supplemented minimal medium. Future work will focus on upscaling selected culture conditions to facilitate metabolite isolation, structural characterization and pharmacological activities.

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PP 24 METABOLOGENOMICS FOR DISCOVERY OF NOVEL ANTIBIOTICS FROM RARE MARINE ACTINOBACTERIA FROM ANTARCTICA

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The rapid increase in resistance development, the rise of new pathogens, and the lack of effective treatments against the most problematic human and environmental pathogens pose an important threat to global health, as well as agriculture and aquaculture sectors[1]. These challenges emphasize the urgent need for novel antibiotics. In this regard, marine extremophilic microorganisms represent excellent reservoirs of new bioactive scaffolds due to their evolution and metabolic adaptation to extreme environments[2]. Actinobacteria, particularly well-studied genera such as *Streptomyces*, have long been recognized as major sources of antibacterial natural products, with approximately two-thirds of clinical antibiotics originating from them[3]. However, rare actinomycetes, such as *Nocardioides* spp. (family Nocardioidaceae), have remained underexplored[4].

In this study, we explored a set of Antarctic marine actinobacteria using synergistic metabolomic and genomic approaches to identify their biosynthetic potential and to facilitate prioritization of the most promising species for further chemical work-up for discovery of new antibiotics. We identified five *Nocardioides* spp. showing differential antimicrobial activity against a panel of human, agriculture, and aquaculture-associated pathogens. We sequenced their genome by Nanopore and Illumina technologies and performed comparative genomics by enabling the identification and analysis of biosynthetic gene clusters (BGCs) across the genomes. By investigating the genomic differences, we distinguished putative novel BGCs that may be responsible for producing previously undescribed antibacterial compounds. Hence, we cultivated *Nocardioides* spp. in two different growth media. The resulting extracts were assessed for broad-spectrum antimicrobial activity and analyzed, comparatively, by an LC-MS/MS based untargeted metabolomics approach using Feature-Based Molecular Networking workflow. The culture medium affected the metabolome composition and bioactivity. Notably, only a few molecular families were annotated, indicating novel chemistry in these bacteria. This integrated approach supported the selection and large-scale cultivation (50 Liters) of strain *Nocardioides* sp. strain AA937B for subsequent isolation and structural characterization of new antibiotic molecules.

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PP 25 SECONDARY METABOLITES OF ENDOPHYTIC *HYPOXYLON RUBIGINOSUM* ISOLATED FROM *FUCUS VESICULOSUS* SEAWEED BY USING SPECTRAL-BASED METABOLOMICS APPROACH

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Bioactive compounds derived from seaweeds were previously assessed to belong to their host macroorganisms while more recently, they are being attributed to microorganisms associated with these seaweeds[1]. Lately, seaweed-associated microorganisms have drawn a lot of attention as a potential source of new antibiotics. Nowadays, 40%-80% of bacterial biofilms lead to antibiotic resistance[2]. There has been evidence that some marine fungal metabolites do possess antibiofilm activity[3,4]. Therefore, we aim to determine antibiofilm metabolites from endophytic *Hypoxylon rubiginosum* associated with a Scottish brown seaweed called *Fucus vesiculosus* against *Staphylococcus aureus* (MRSA) biofilms by using a metabolomic bioassay-guided method. From an OSMAC approach along with metabolomic methods, rice media incubated for 30 days at 27 °C was chosen for scale-up fermentation. Ethyl acetate extracts (10 µg /ml) of *H. rubigonisium* exhibited interesting antibacterial activity and inhibition of biofilm formation in MRSA at more than 50% as compared to the active control ciprofloxacin in the same concentration. Four secondary metabolites were isolated from bioactive fractions of endophytic *H. rubigonisium* and they were identified by using 2D NMR and HRLC-MS methods. Compounds 3-(p-hydroxyphenyl)propionic acid **(1)** and 4-hydroxyphenyl acetic acid **(2)** inhibited growth of MRSA only. While hypoillexidiol **(3)** and 3,4-dihydro-3-methyl-1H-2-benzopyran-6,7,8-triol **(4)** afforded both 70% inhibition of MRSA growth and pre-biofilm formation. Moreover, compounds **(1)**, **(2),** and **(4)** have been isolated for the first time from the genus *Hypoxylon*.

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PP 26 STRUCTURE AND BIOSYNTHESIS OF CAROTENOIDS PRODUCED BY UV-RESISTANT ANTARCTIC MARINE BACTERIA

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Antarctic marine microorganisms are subjected to extreme temperatures, UV radiation, and ice formation. They have evolved unique strategies to survive in these harsh conditions. In particular, photoprotective defense mechanisms are crucial for mitigating damage from solar UV-B radiation, and involve both non-enzymatic and enzymatic antioxidant systems. Thirty-one UV-resistant bacteria, collected from different Antarctic aquatic environments (surface sea waters/ice and shallow lake sediments), were isolated by UV-C assay[1] and identified by 16S rRNA[2]. 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*). Many of these bacteria produce pigments, generally carotenoid-type compounds, representing an important antioxidant defense against exposure to harmful levels of UV and the low temperature in the Antarctic environment. Antarctica, still poorly explored, is a huge reservoir of pigmented bacterial biodiversity and offers promising candidates for novel chemical structures and for cell factories of bio-pigments. In this study, we sequenced and annotated the complete genomes of three UV-resistant bacteria, the red *Arthrobacter* sp. R5, the orange *Brevundimonas* sp. RA4 and the yellow *Sphingorhabdus* sp. G5G. Bioinformatic analyses of their genomes revealed the presence of genes involved in the expression of compounds that facilitate bacterial survival in extreme conditions. We also identified the carotenoid biosynthetic gene clusters and the carotenoid compounds they produce. Bacterial pigments are promising and sustainable bioactive compounds, with potential applications in cosmetics, food, textiles, printing, and pharmaceuticals.

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PP 27 UNLOCKING CHEMICAL PROFILES OF FUSARIUM SOLANI, AN ENDOPHYTE FROM THE MARINE ALGA DICHOTOMARIA MARGINATA: A MULTI-OMIC APPROACH TO CHEMODIVERSITY ENHANCEMENT

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Marine microorganisms are keystones of ecological balance and drivers of green innovation. Many marine species depend on microbes, which are crucial for ecosystems balance. Endophytic fungi associated with marine organisms have emerged as important producers of metabolites with multiple bioactivities and broad chemodiversity. However, the removal of these microorganisms from their natural environment often leads to gene silencing, loss of expression of specific metabolic/biosynthetic pathways, and lower chemodiversity[1]. This study explored the biological potential and chemodiversity of a *Fusarium solani* strain, which was isolated from the marine red alga *Dichotomaria marginata* and is known for its promising potential for the production of bioactive compounds. Growth curves were established in malt extract liquid medium to determine optimal cultivation conditions in terms of time and extract yield. The endophyte was also cultivated in solid media with oat, wheat bran and rice, which resulted in higher biomass yields than liquid cultures. LR and HRMS (ESI-QTOF-MS) were used for extracts analyses and enabled the construction of molecular networks that highlighted similarities and differences among the extracts, as well as the annotation of metabolites from the GNPS database, including fusaridione, N-fructosyl amino acids, peptides, fusaridioic-A and -D acids, NG-391 and cyclosporins D, P, X and Z. Extracts and partition fractions were tested against a HCT116 tumor cell line (colorectal carcinoma) at 5 and 50 µg/mL. Samples from the liquid media cultivation exhibited inhibitory activity higher than 90% at 50 µg/mL and moderate inhibition at 5 µg/mL. Best results were obtained for samples from solid media extracts, with inhibitory activity of MeCN fractions from the oat, wheat and rice extracts at 73%, 87% and 93% against HCT 116 tumor cells. Such results highlight the sustainable exploration of microbes as a keystone for decoding their chemical blueprints, adding value to marine biodiversity and protection of marine ecosystems.

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PP 28 UNTARGETED METABOLOMICS AND MASS SPECTROMETRY IMAGING TO INVESTIGATE THE CHEMICAL IMPACTS OF *CARIJOA (TELESTO) RIISEI* ON ARTIFICIAL REEFS IN SOUTH-EAST QUEENSLAND, AUSTRALIA.

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Artificial reefs are designed to enhance marine biodiversity, restore habitats, and support fisheries by providing structure for marine life to colonise[1]. However, these structures may inadvertently facilitate the establishment and spread of opportunistic species[2]. This threatens the ecological and economic value of both artificial and natural reef systems[3].

The soft coral *Carijoa (Telesto) riisei* is a prolific coloniser on natural and artificial reefs and has been reported as invasive in several regions worldwide[4]. In Australia, its increasing presence raises concerns about potential impacts on benthic community dynamics. Here, it is not currently classified as invasive, but this may be due to the limited research on its ecological impacts rather than an absence of competitive behaviour. Notably, this species is a known producer of bioactive secondary metabolites[5][6], which may play a role in competitive interactions and colonisation success.

This study examines the metabolomic profile of *C. riisei* on artificial reefs in Southeast Queensland, Australia, using NMR Spectroscopy and Mass Spectrometry (MS). By applying an integrative metabolomics-based approach with Data Independent Acquisition, Molecular Networking, and NMR, we characterise the chemical diversity of *C.riisei* and identify metabolite classes that may be involved in its ecological interactions. Additionally, MS Imaging techniques (DESI and MALDI) are used to investigate the spatial distribution of these metabolites[7] within *C.riisei* tissues, providing insights into their potential roles in shaping community structure.

This integrative approach offers a deeper understanding of the chemical strategies employed by *C. riisei* and their implications for artificial reef ecosystems. By combining chemical analysis with ecological context, this study contributes to the broader discussion on how invasive species interact with their environment and the consequences for reef biodiversity.

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4. MNP chemical biology and biotechnology

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OC 18 ANTI-INFLAMMATORY ACTIVITY OF BROMODITERPENES ISOLATED FROM THE RED SEAWEED *Sphaerococcus Coronopifolius*

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Inflammation is a critical defense mechanism of the human body. However, when it becomes chronic, it can lead to tissue and organ damage, contributing to the development of severe diseases or even death[1]. The development of effective anti-inflammatory therapies remains a challenge due to the complexity of immune responses and the limitations of conventional treatments, which often cause adverse effects[2]. Marine organisms have proved to be a prolific source of novel bioactive compounds. The red seaweed *Sphaerococcus coronopifolius* is known to produce brominated terpenes with reported cytotoxic, antifouling, and antimicrobial properties[3,4]. However, its anti-inflammatory potential remains largely unexplored. This study evaluated the anti-inflammatory activity of four compounds isolated from *S. coronopifolius*, one sesquiterpene (alloaromadendrene) and three bromoditerpenes (sphaerococcenol A, bromosphaerol, and 12*R*-hydroxy-bromosphaerol).

The compounds were isolated using chromatographic techniques, including column chromatography and HPLC, and their structures elucidated by NMR spectroscopy. The cytotoxicity was evaluated in RAW 264.7 macrophages (0.01 – 10 µM; 24h) to determine non-toxic concentrations for further assays. The anti-inflammatory activity was assessed in lipopolysaccharides (LPS; 1 µg/mL)-stimulated RAW 264.7 macrophages, in the presence or absence of compounds at non-toxic concentrations. The levels of key inflammatory mediators (nitric oxide-NO,TNF-α,IL-6,IL-10) were quantified. Alloaromadendrene (1 µM) decreased NO levels by 60%, while bromosphaerol (10 µM) reduced TNF-α levels by 48% compared to the LPS treatment. Sphaerococcenol A (0.1 µM) significantly inhibited IL-6 production by approximately 85%. Notably, 12*R*-hydroxy-bromosphaerol (1 µM) enhanced IL-10, an anti-inflammatory cytokine, to 1301 ± 381.1 pg/mL compared to LPS treatment (154.7 pg/mL ± 98.7 pg/mL).

The compounds isolated from *S. coronopifolius* demonstrated significant anti-inflammatory activity by modulating the production of key inflammatory mediators, highlighting their potential as candidates to inspire the development of novel anti-inflammatory therapies.

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OC 19 UNVEILING INNOVATIVE SIDEROPHORE SYNTHESIS IN PATHOGENIC VIBRIO THROUGH INTERACTIONS BETWEEN DIFFERENT IRON UPTAKE SYSTEMS

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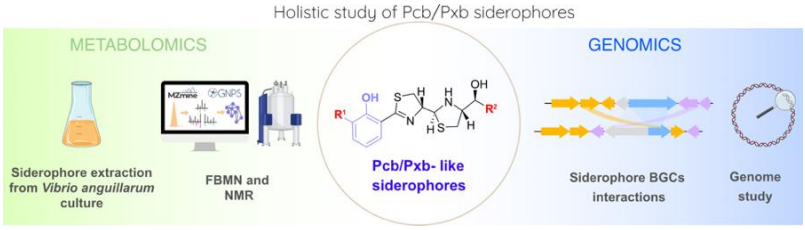
Production of siderophores, organic compounds involved in iron uptake mechanisms, is advantageous to bacterial fitness and a key virulence factor in pathogenic bacteria. Understanding the molecular basis of their biosynthesis, chemical diversity, and transport mechanisms facilitates the design of novel antimicrobial treatments and the search of new therapeutic targets[1]. Piscibactin (Pcb) and photoxenobactins (Pxb) are phenolate siderophores encoded by the High Pathogenicity genomic Island *irp*-HPI, which has a significant impact on the virulence of pathogenic bacteria such as *Vibrio anguillarum*, which affects fish and mollusks[2]. Through genomic analysis, we discovered that *irp*-HPI often coexists with other siderophore systems within recipient genomes, predominantly catecholate-type systems like vanchrobactin (Vb)[3].

The goal of this work was to deepen our understanding of the siderophore metabolome of *V. anguillarum*. We generated mutant strains defective in Pcb or Vb production and used LC-MS/MS and Feature-Based Molecular Networking computational tools. This study led to the identification of two new catechol analogues, 2-hydroxyPcb and 2-hydroxyPxb E, along with the known Vb and Pcb/Pxb-like siderophores, revealing interaction between these two siderophore systems.

We found that the salicylate-activating enzyme Irp5 functions as a versatile aryl acid adenylation enzyme, capable of adenylating 2,3-dihydroxybenzoate (DHBA) and facilitating the production of catecholate-Pcb/Pxb and fluoro-salicylic acid derivatives through precursor-directed biosynthesis. Furthermore, these results indicate that Pxb E is the final product of the piscibactin/photoxenobactin biosynthetic pathway in *V. anguillarum*.



From an ecological perspective, the coexistence and interplay of multiple siderophore systems likely enhance metabolome diversity, enabling bacteria to adapt to a wide range of environmental conditions. This study advances our understanding of virulence factors in *Vibrionaceae* carrying *irp*-HPI and provides meaningful insights for developing targe-ted antimicrobial therapies.

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OC 20 UNLOCKING JELLYFISH MUCUS SECRETS: FROM CHEMICAL COMPOSITION TO BIOTECHNOLOGICAL POTENTIAL

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Jellyfish can release significant quantities of mucus, which is a complex matrix abundant in proteins and glycoproteins. The specific composition of jellyfish mucus at the compound level and its function(s) remain largely unexplored. We conducted chemical analyses on the mucus from four different species of Scyphozoan jellyfish collected from different European waters: *Aurelia aurita s.l.*, *Periphylla periphylla*, *Rhizostoma pulmo*, and *Cotylorhiza tuberculata*. Our analytical techniques included protein and carbohydrate analysis, amino acid and monosaccharide profiling, SDS-PAGE for protein and glycoprotein separation, as well as FTIR, ^{13}C NMR, and LC-MS/MS spectroscopy for structural and protein examinations. The findings confirmed that jellyfish mucus is a highly diverse and complex biomaterial, predominantly consisting of proteins, mucins, and carbohydrates. The absolute concentrations of the analytes varied across species, but their relative proportions were similar. Notably, *C. tuberculata* and *P. periphylla* mucus had half the number of identified proteins as compared to *A. aurita*, attributed to the lack of a jellyfish protein database. Over 70% of the identified proteins and glycoproteins are associated with the binding of calcium and metal ions, indicating a potential functional role of mucus. Furthermore, we identified structural proteins, enzymes with antioxidant properties, and self-protective proteins such as metalloproteinases, serpins, and superoxide dismutase, suggesting diverse physiological roles of mucus as well as some possible applications in cosmetics and medicine.

OC 21 MARINE NATURAL PRODUCTS VALORIZATION: SUSTAINABLE ACTIVE MATERIALS FROM CRUSTACEAN WASTE

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The growing need for renewable materials to reduce dependence on fossil fuels is widely recognized. Chitin, the most abundant nitrogen-containing natural polymer from renewable biomass, has gained significant attention for its unique properties, availability, and environmental benefits. Found in large quantities in underutilized seafood waste, especially crustaceans, chitin offers a valuable opportunity for upcycling into high-value functional materials[1]. Chitosan, the water-soluble form obtained through the partial or complete deacetylation of chitin, is a highly promising material for the development of innovative products, thanks to its low cost, film-forming ability, and intrinsic antimicrobial and antioxidant properties[2]. The broad spectrum of applications of this unique polymer will be presented, emphasizing the properties that make it particularly suitable for the development of sustainable materials. It will also address the main challenges associated with its implementation and discuss the different development approaches, from laboratory research to industrial-scale production[3,4]. Chitosan supports waste reduction and promotes a circular bioeconomy. Its modifiable chemical structure enhances its functionality, making it suitable for a wide range of applications. From the development of active food packaging through its use in bio-based adhesives, to applications in agriculture, chitosan offers a distinctive contribution across multiple sectors. Thanks to its strong antimicrobial properties, chitosan is valuable in food preservation. In the FISH4FISH project*, chitosan was used to create active, sustainable packaging that extends fish shelf life. The biocomposite packaging contains 80% renewable materials, is home-compostable, allergen-free, and offers UV shielding and antimicrobial protection. Chitosan also shows great potential in adhesives. A new chitosan-based adhesive formulation effectively bonds materials like glass, cardboard, and textiles, offering water resistance, high strength, and flame-retardant properties[5]. In agriculture, it promotes plant growth, enhances immunity, and acts as a biopesticide, improving yields with less need for fertilizers and pesticides[6].

*Fish4Fish project - Project co-funded by EU under the program EASME/EMFF/Blue Economy-2018/n.863697

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POSTER SESSION 1

PP 29 ANTIVIRAL ACTIVITY AND STRUCTURAL INSIGHTS OF A CELL WALL SULFATED POLYSACCHARIDE FROM THE MARINE DIATOM *CYCLOTELLA CRYPTICA*

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Sulfated Polysaccharides (SPs) are abundant in marine organisms, where they play an essential role in the mechanisms of adaptation to saline environments[1]. SPs from macro- and microalgae possess unique structural features, which often correlate to taxonomy, and are under active investigation due to their various potential fields of application[2]. We have investigated the structure of the sulfated polysaccharide isolated from the cell wall of the marine diatom Cyclotella cryptica (CcSP), finding that it consisted of a homopolysaccharide with a backbone of (1 → 4)-α-D-Manp carrying, in the most abundant form, sulfation at O-6. CcSP exhibited promising antiviral activity against Herpes Simplex Virus-1 (HSV-1), which was likely associated with a mechanism involving steric hindrance and/or electrostatic repulsion, preventing viral attachment to host cells. In addition, we have also proved the binding of CcSP to the innate human receptor Langerin, a well-known C-type lectin that recognizes sulfated polysaccharides and is involved in virus entry in cells. We attempted to partially reconstruct the biosynthetic pathway of CcSP: analysis of C. cryptica genome revealed the presence of several putative carbohydrate 6-O sulfotransferases (CH-STs) with homology to the human enzymes involved in glycosaminoglycans sulfation. Our results suggest an ancient evolutionary origin for the regioselective specialization of CH-STs, and could pave the way for future research on diatom cell wall biogenesis, as well as for biotechnological applications relying on the manipulation of the sulfation levels in CcSP for enhanced activity[3].

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PP 30 DEVELOPMENT AND APPLICATION OF SUSTAINABLE FRACTIONATION APPROACHES FOR BEACH WRACK BIOMASS

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Beach wrack, a coastal biomass rich in lignin and polymeric sugars such as glucose, presents a promising substrate for biotechnological valorisation. This study investigates enzymatic and chemical hydrolysis methods to produce reducing sugars suitable for microbial fermentation, alongside lignin recovery for potential use as a high-value additive. To enhance biomass accessibility and process efficiency, a comprehensive pre-treatment workflow was investigated, incorporating separation, grinding, sterilisation, steam explosion, and homogenization. Specific fractions, such as neptune balls and rhizomes, were excluded due to their high fibrous content and contamination levels, which hinder processing.

Deep eutectic solvents (DES), particularly choline chloride and urea mixtures, were also explored as a green alternative for biomass fractionation and lignin and cellulose extraction. While preliminary results demonstrated potential, batch-to-batch variability highlighted the need for further optimisation and consistency in DES preparation and application.

Following enzymatic and chemical hydrolysis, laboratory-scale methodologies were developed to produce glucose solutions, cellulose, and lignin. The glucose-rich hydrolysates have promising potential as carbon sources in fermentation-based processes, such as ethanol or other valued compound production. Due to its antioxidant, antimicrobial, and structural properties, lignin may serve as an additive in bioplastics, coatings, or composite materials. Depending on purity and structure, cellulose fractions could be repurposed for paper alternatives, biomedical applications, biocomposites, or further converted into micro- or nano-cellulose.

These results suggest that beach wrack can be valorized into multiple value-added bioproducts through sustainable and scalable methods, supporting a circular bioeconomy approach.

Acknowledgements. The Maritime Seed Award 2023 (Malta) supported the research project.

PP 31 EXOPOLYSACCHARIDES FROM MARINE MICROALGA *Cylindrotheca closterium*: ANTIOXIDANT AND ANTIPROLIFERATIVE ACTIVITY

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Microalgae have emerged as a promising source of novel bioactive compounds with potential applications in biomedicine, food and cosmetics industries. This study investigated the marine diatom *Cylindrotheca closterium* and focused on the antioxidant and antiproliferative properties of its exopolysaccharides (EPS). The EPS extracted from *C. closterium* cultures during the stationary phase yielded 50.6 mg l^{-1} and consisted of 39.0% carbohydrates and 8.1% proteins. Elemental analysis showed the presence of 25.3% carbon, 7.2% hydrogen and 1.8% nitrogen. The antioxidant activity evaluated using ABTS (2,2'-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid)) and H_2O_2 scavenging assays and TAC (total antioxidant capacity) assay showed a dose-dependent response. At an EPS concentration of 4 mg ml^{-1}, ABTS scavenging activity reached 38.8%, while H_2O_2 scavenging activity and TAC were lower than those of ascorbic acid (6% and 20%, respectively). *In vitro*, EPS showed strong antiproliferative effects against human pharyngeal cancer cells (Detroit 562) and human colon cancer cells (SW480, SW620, HCT116). At a concentration of 750 µg ml^{-1}, Detroit 562 cells were completely eliminated and the survival rate of SW480, SW620 and HCT116 cells was reduced to 27%, 37% and 27%, respectively. These results indicate that the EPS from *C. closterium* possesses significant antioxidant and especially antiproliferative activity, supporting its potential as a natural bioactive agent.

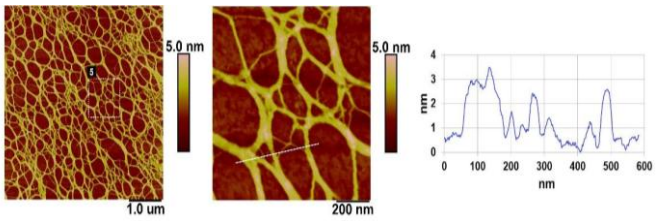

Fig. 1. Atomic force microscopy (AFM) height images of *C. closterium* EPS (100 µg ml^{-1}) acquired using tapping mode in air: (a) scan size 5 µm x 5 µm, vertical range 5 nm, (b) scan size 1 µm x 1 µm, vertical range 5 nm with vertical profile along the indicated line showing the fibril heights [1].

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PP 32 EXPLORING THE POTENTIAL OF MICROALGAE FOR INDUSTRIALLY RELEVANT ENZYMES

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Microalgae have emerged worldwide as a versatile renewable resource with extensive applications in multiple industries. Unlike other biomass sources, microalgae can rapidly grow in non-arable environments using wastewater or saline water, avoiding competition with food crops[1]. These aquatic microorganisms can efficiently convert carbon dioxide into valuable biomass and produce a variety of high-value bioactive compounds, including carbohydrates, proteins, lipids, pigments, essential fatty acids, vitamins, and antioxidants[2]. These compounds have significant commercial applications, including bioenergy, biomedicine, nutraceuticals, cosmetics, environmental management, and other industrial production processes. The ability to adapt to adverse environmental conditions and their low resource requirements make them vital players in advancing a sustainable and circular bioeconomy.

This study investigated microalgae as a source of industrially relevant enzymes. We have explored the enzymatic potential of three microalgae: *Dunaliella* spp., *Tetradesmus* sp., and *Phormidium* sp. Among the most relevant characteristics of these algae, *Dunaliella* spp. lacks a rigid cell wall and can survive in extremely hypersaline environments[3]. *Tetradesmus sp.* can rapidly achieve high biomass, rich in proteins, unsaturated fatty acids, and bioactive compounds. *Phormidium* sp. grows by forming unique filamentous mats and biofilms that allow it to thrive in hypersaline and alkaline environments. Enzymatic activities such as lipase, protease, carbonic anhydrase, lipoxygenase, and esterase were assessed in extracts of the three algae described above. Additionally, the antioxidant activity of algal extracts was also evaluated. More details of the results will be presented during the poster session.

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PP 33 MARINE-DERIVED COLLAGEN AS A KEY COMPONENT IN BONE BIOMATERIAL DEVELOPMENT

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Introduction: Collagen is a fundamental component of the organic phase of bone, providing the structural framework necessary for mineral deposition and cell-matrix interactions. It plays a key role in bone regeneration by supporting osteoblast attachment, proliferation, and extracellular matrix remodeling[1]. It makes up 89% of the organic matrix and 32% of the volume composition of bones[2]. While collagen can be derived from various sources, marine organisms have gained attention as sustainable and low-immunogenic alternatives. Jellyfish-derived collagen, in particular, is considered a promising biomaterial due to its high biocompatibility and bioactivity[3]. In addition, collagen can be easily integrated with other bioactive materials, improving the mechanical stability and biological activity of composite scaffolds[4].

Methods: In this study, composite scaffolds were developed using a combination of an inorganic phase and a marine-derived collagen-based organic phase, mimicking human bone composition (30% organic, 70% inorganic). These scaffolds were evaluated for their potential to be modified with blood-derived bioactive components to further enhance their regenerative capabilities. Scaffold preparation conditions and material ratios were optimized based on degradation and mechanical properties, aiming to develop a bone-like composite for regenerative applications.

Results: Scaffolds containing collagen demonstrated enhanced mechanical performance compared to those without collagen. Specifically, the addition of collagen improved elasticity and structural integrity, resulting in up to a 40% increase in compressive strength. These improvements align with the mechanical properties required for cancellous bone, which typically exhibits compressive strength in the range of 2–12 MPa and an elastic modulus of 0.1–2 GPa. In addition, the overall mechanical evaluation aimed to approach the bending strength (100–150 MPa) and elastic modulus (7–25 GPa) characteristic of human cortical bone.

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PP 33 FROM MARINE-BASED BIOPOLYMER COATINGS TO INJECTABLE HYDROGELS: A VERSATILE PLATFORM FOR SUSTAINED DELIVERY OF THERAPEUTICS

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Marine-derived biopolymers such as fucoidan, alginate, and chitosan offer a highly adaptable platform for the development of advanced drug and bioactive substance delivery systems. These polysaccharides exhibit inherent bioactivity, biocompatibility, and tunable physicochemical properties, enabling their use in both surface coatings for scaffolds and injectable hydrogel formulations. This work presents an integrated strategy for engineering multifunctional regenerative materials by leveraging the versatility of marine biopolymers across different delivery modalities.

In this study, we demonstrate how material formulation directly influences release behavior. When applied as coatings on calcium phosphate-based scaffolds, marine biopolymers act as diffusion barriers, modifying the drug release rate depending on polymer type and structure. For example, chitosan-coated scaffolds exhibited rapid initial lidocaine release (up to 70% within the first hour), while alginate coatings significantly delayed release, sustaining it for up to 60 hours. Drug release kinetics were strongly dependent on polymer-drug interactions and coating sequence, as confirmed by HPLC and SEM analysis of lidocaine crystal morphology[1].

In contrast, when marine biopolymers were formulated as self-assembled hydrogels, particularly fucoidan-chitosan systems, they enabled incorporation of bioactive agents such as platelet-rich fibrin (PRF). These hydrogels achieved sustained 7-day release of key growth factors (VEGF, EGF, IL-8, PDGF-BB, TGF-β1), as confirmed by ELISA and histological analysis, offering a promising route for localized regenerative therapy[2].

To further enhance injectability and structural stability, chitosan was combined with bacterial cellulose and pectin, forming interpenetrating networks with rapid gelation, desirable swelling behavior, and excellent syringeability. These injectable systems exhibited good antibacterial properties and high biocompatibility, maintaining >80% cell viability with primary cells, making them attractive for minimally invasive delivery in soft tissue regeneration[3].

These findings highlight the versatility of marine-based materials in forming bioactive, sustainable, and tunable delivery systems. The approach integrates green chemistry, functional biomaterial design, and advanced drug delivery principles, offering a strong foundation for future applications in orthopedic, dental, and soft tissue therapies.

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PP 34 SEAWEED-DERIVED COMPOUNDS INHIBIT KEY SKIN AGING ENZYMES AND PROMOTE PHOTOPROTECTION

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The marine environment is a prolific source of structurally diverse and biologically active natural products with promising biomedical applications[1]. In the field of skin health, inhibiting of extracellular matrix-degrading enzymes and mitigating ultraviolet (UV)-induced oxidative stress are considered key strategies for developing novel anti-aging and photoprotective agents[2]. This study aimed to evaluate the enzymatic inhibitory activity of eight seaweed-derived compounds and their synthetic analogues against hyaluronidase, elastase, collagenase, and tyrosinase enzymes and their photoprotective capacity in HaCaT human keratinocytes exposed to UV radiation. The cytotoxicity was evaluated in HaCaT cells (1 - 100 µM; 24h) to determine non-toxic concentrations. The photoprotective activity was assessed in HaCaT cells exposed to UVA/B-stimulated radiation (7.9 mW/cm^2; 15 min) in the presence or absence of compounds (1 hour), at non-toxic concentrations, through the quantification of reactive oxygen species (ROS) levels. Bromosphaerol (48.77 ± 8.84 %) and eleganolone (13.48 ± 2.22 %) compounds exhibited significant inhibition of hyaluronidase and tyrosinase enzymes activities. On the other hand, 12*R*-hydroxy-bromosphaerol and SPA5 compounds were able to inhibited the elastase enzyme activity by 21.00 ± 5.18 % and 18.00 ± 5.95 %, respectively. Regarding photoprotective activity, eleganolone demonstrated protection against UVA/UVB radiation in HaCaT cells by decreasing ROS in a concentration-dependent manner, with a 52.26 ± 7.37% reduction observed at the highest non-toxic concentration tested (100 µM). SPA5 analogue also decrease the production of ROS by 25.45 ± 7.21 %. Overall, our results highlight the potential of seaweed marine natural products and their analogues as promising candidates to incorporate in the development of novel dermocosmetic formulations aiming to prevent skin aging.

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5. Chemical ecology and ecosystems functioning linked to biotechnology

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OC 22 CHEMICAL ECOLOGY OF PARASITE (*PARVILUCIFERA* SP.) INDUCED METABOLIC ADAPTATIONS IN THE TOXIC DINOFLAGELLATE *Alexandrium minumtum*

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Dinoflagellates are pivotal primary producers in aquatic ecosystems, yet the proliferation of toxic species such as *Alexandrium* can trigger harmful algal blooms (HABs) that disrupt coastal environments[1]. These blooms are further modulated by intricate interactions with various microorganisms, including alveolate parasites of the genus *Parvilucifera*, which infect and lyse dinoflagellate cells, thereby naturally curbing bloom intensity[2]. This infection process is crucial, as it impacts biogeochemical cycles by shaping plankton community structure. Our research on metabolites involved in these interactions contributes to understanding chemical processes that influence ocean ecosystem functioning and has implications for sustainable marine management practices.

In this study, we combine comparative untargeted endometabolomics, with microalgal culturing and infection experiments, to investigate metabolic changes that occur during the infection of *Alexandrium minutum* by two *Parvilucifera* species (*P. infectans* and *P. rostrata*). Utilizing ZIC-HILIC chromatography coupled with high-resolution electrospray ionization mass spectrometry, we monitored zwitterions and polar metabolites throughout the infection process. Our results reaffirm the involvement of metabolites such as dimethylsulfoniopropionate (DMSP) and guanine in parasite reproduction and algal cell death, substantiating their roles in mediating host-pathogen dynamics[3,4]. Additionally, we also identify metabolites such as trigonelline, gonyol, betaine, and 2-homoectoine in parasite treated algal cultures, suggesting novel biochemical pathways involved in parasite-host interactions.

These findings provide new insights into the chemical dialogue between parasite and host. The identified metabolites could play key roles in parasite mediated regulation of HABs and could be useful in engineering novel predictive tools to manage and sustain marine ecosystem health.

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OC 23 DO SEAWEEDS FROM HIGH UV-EXPOSURE AREAS OFFER NATURAL UV PROTECTION? INSIGHT INTO BIOACTIVE PROPERTIES OF MYCOSPORINE LIKE AMINO ACIDS (MAAs) AND ISOLATION OF NOVEL MAAs FROM *CHONDRIA CORNUTA*

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The intertidal macroalgae are exposed to high solar UV radiation and have evolved biochemical defenses against such damage by natural UV-absorbing sunscreens, such as mycosporine-like amino acids (MAAs). This study investigated the antioxidant, skin rejuvenating, and UV-protective properties of MAAs isolated from 19 species of seaweeds along the Kuwait coast of the Arabian Gulf, where conditions of high UV index (8-10), salinity (40-45 ppt), and water temperature (13-35°C) prevail. MAAs from *Sargassum oligocystum*, *Sargassum aquifolium, Padina gymnospora*, and *Chondria cornuta* showed high antioxidant activity in different assays, anti-wrinkle properties, and were able to protect *E. coli* and HEK293 mammalian cells from UV radiations. MAAs from *Sargassum oligocystum*, as well as *Sargassum aquifolium*, showed high skin-whitening properties. The MAAs from *Chondria cornuta*, with a high content of MAAs, were subjected to individual MAA isolation. The NMR and LCMS analysis revealed the presence of four known MAAs (palythene, usjerine, palythine, and asterina 330), seven novel MAAs, and several unknown MAAs. The seven novel MAAs identified in this study includes the following: (1) mycosporine-ornithine derivative (MW: 348.4, λmax: 356 nm), (2) 7-O-(α-arabinopyranosyl)-porphyra 334 (MW: 474.4, λmax: 356 nm), (3) a porphyra 334 derivative (MW: 284.4 nm, λmax: 356 nm), (4) a porphyra 334 derivative (MW: 302.3, λmax: 330 nm), (5) a shinorine and cis-3,4-dehydrolysine derivative (MW: 302.3, λmax: 330 nm), (6) a mycosporine glycine-alanine derivative (MW: 245.3, λmax: 330 nm), and (7) an Asterina 330 derivative (MW: 288.3, λmax: 330 nm). This information could be useful in developing natural and sustainable UV protection agents for various applications, including cosmetics. The exciting results will be presented at the conference.

OC 24 EXOMETABOLOMICS TO ILLUMINATE THE WATERBORNE PATHOGEN SUPPRESSION EFFECT OF SEAGRASSES IN WATER COLUMN

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Seagrasses provide numerous ecosystem services in coastal environments, such as supporting marine biodiversity, protecting coastal regions and sequestering CO2. Seagrass habitats have been recently shown to reduce the abundance of various waterborne pathogens affecting human, fish and invertebrates in their vicinity[1]. However, chemical, spatiotemporal and geochemical aspects of this sanitation effect have remained unstudied. We hypothesized that seagrasses release key defensive secondary metabolites in the surrounding water column and the abundance of these allelochemicals would be indicative of pathogenic (and other environmental) pressures. We aimed to identify these metabolites dissolved in seawater and explore their potential involvement in waterborne pathogen regulation under varying environmental conditions.

We collected seawater (SW) samples sourced from eelgrass (*Zostera marina*)-vegetated (V) and non-vegetated (NV) areas in multiple sites and multiple months in the German Baltic Sea in order to assesss spatiotemporal variations in i) environmental parameters (e.g., nutrient, chlorophyll a, salinity, SW temperature, eutrofication, anthropogenic effects), ii) the abundance of three common pathogenic taxa commonly found in SW (enterococci, *Vibrio* spp., *Escherichia coli* and other coliforms), and iii) the exometabolome profile of all SW-V and SW-NV samples (with each other and against the eelgrass leaf metabolome) by untargeted metabolomics tools such as Feature-Based Molecular Networking and SIRIUS, statistical analyses and machine learning approaches. This study unveiled the correlation of pathogen biomass and pathogen suppression effect of eelgrass meadows with physical factors, e.g., increasing SW temperature, eutrophication and anthropogenic influences. A qPCR analysis showed a significant reduction of overall bacterial load in highly contaminated meadows. A pairwise comparison of the SW metabolomes against the eelgrass leaf metabolome indicated that i) the latter comprised a major portion of overall seawater dissolved organic matter (DOM) composition, and ii) SW-V samples contained a significant fraction of metabolic features distinct to eelgrass (exo)metabolome. Most strikingly, we identified four flavone molecules as key features distinguishing the SW-V and SW-NV samples. Their abundance was dramatically elevated as a response to pathogen (and other) pressures in eelgrass beds where we observed the highest pathogen removal. These combined microbiological and analytical approaches show that flavones in eelgrass exudates are key allelochemicals that structure seawater microbiome in eelgrass beds and contribute to their sanitary effect. This the first report of a seagrass exometabolome, which is highly relevant to public and coastal ecosystem health.

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OC 25 METABOLOMIC CHANGES IN ANTARCTIC MARINE INVERTEBRATES IN A WARMING OCEAN

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The Western Antarctic Peninsula is undergoing rapid warming due to global change, posing a threat to the rich communities of benthic marine invertebrates inhabiting there[1,2]. Here, we examined the chemical responses of two Antarctic species, the sponge *Dendrilla antarctica* and the colonial tunicate *Synoicum adareanum*, to gradual seawater temperature increases in controlled aquarium experiments, simulating global change scenarios. From *D. antarctica* specimens collected at Deception Island (Jan 2023), we isolated a novel β-lactone diterpene, dendrillolactone, along with seven previously described compounds: deceptionin, a gracilane norditerpene, cadlinolide C, a glaciolane norditerpene, membranolide, aplysulphurin, and tetrahydroaplysulphurin-1[3]. Some of these natural products are known to act as chemical defences against predators[4]. Upon moderate temperature increase, compounds such as deceptionin, cadlinolide C, membranolide, and tetrahydroaplysulphurin-1 showed higher concentrations, suggesting an upregulated chemical response. However, temperatures above 4°C disrupted sponge metabolism and led to premature mortality. Similarly, *S. adareanum* collected at Livingston Island (Jan 2022) exhibited significant changes in secondary metabolism. This species has been previously described as possessing several bioactive compounds[5,6]. UPLC-HRESI-MS analysis revealed increased production of some of its compounds with ecological and pharmacological significance. At 4–5°C, tunic necrosis was observed, indicating thermal limitation. This is the first comparative study addressing the effect of ocean warming on the secondary metabolism of Antarctic benthic invertebrates. Our results highlight that although natural product biosynthesis may respond to temperature stress, both species exhibit physiological thresholds that constrain resilience. These insights are key to understanding the vulnerability of polar organisms to climate change.

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OC 26 CHEMODIVERSITY OF MARINE INVERTEBRATES IN HIGHLY ANTHROPIZED ENVIRONMENTS

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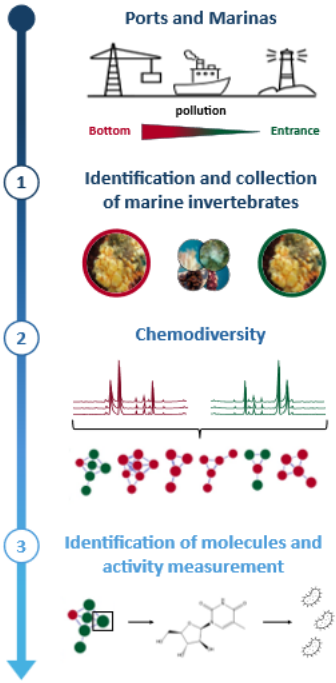
Ports and marinas are highly anthropized marine environments where pollution shapes biodiversity and the production of secondary metabolites[1]. Unlike natural habitats, these ecosystems remain largely unexplored, despite being primarily colonized by ascidians and bryozoans, well-known producers of bioactive metabolites[2]. These organisms may adapt their metabolism in response to environmental conditions, producing metabolites involved in detoxification with potential antimicrobial properties[3]. The herein presented study aims to characterize the metabolic diversity of a total of 10 well-identified and abundant sessile invertebrates dwelling in marinas, and to assess the influence of pollution gradients on the production of their bioactive metabolites.



Samples were collected in different marinas around Brest (Atlantic coast) and Marseille (Mediterranean sea), France. Standardized extraction protocols were implemented in biological replicates. MS-based metabolomics combined with chemometric analyses were performed to reveal metabolic shifts in line with pollution gradients. Antibiotic assays were performed to asses the bioactivities of all extracts and enriched fractions on mutlidrug-resistant bacteria of the ESKAPE group. The presented results will focus on a few species of interest including *Clavelina lepadiformis* (Tunicate) and *Schizoporella errata* (Bryozoan). These findings highlight the potential of port-associated marine invertebrates in the fight against antibiotic resistance[4] while also emphasizing the influence of environmental conditions on the production of bioactive metabolites. Studying these polluted environments not only helps to uncover new antimicrobial resources but also provides insights into the impact of pollution on chemical biodiversity

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OC 27 CHEMO-TAXONOMICAL MARKERS OF PHYLLIDIIDAE SPECIES (HETEROBRANCHIA) FROM KOH TAO ISLAND (THAILAND)

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Marine Heterobranchia, particularly recognized for their evolutionary innovations, represent a paradigmatic group due to their secondary loss of the shell and the development of alternative defence mechanisms. These adaptations include a range of strategies, such as the bioaccumulation or de novo biosynthesis of specialized secondary metabolites, and have led to the discovery of a high number of previously unrecognized cryptic species[1,2].

Among these, the family Phyllidiidae is one of the most widespread and extensively studied taxa of marine sea slugs inhabiting Indo-Pacific coral reefs. Significant efforts have been made to elucidate their phylogenetic relationships through molecular analyses[3]. From a chemical ecology perspective, Phyllidiidae are known for producing a wide array of sesquiterpene and diterpene secondary metabolites, many of which feature isocyanate and isothiocyanate functional groups[4]. However, due to the prevalence of cryptic speciation, taxonomic identification within this group remains challenging, and their overall phylogenetic framework is still unresolved[5].

This study investigates the potential of chemo-taxonomic approaches to improve species identification within Phyllidiidae, based on specimens collected from various dive sites around Koh Tao Island. By integrating molecular data with chemical profiling and advanced bioinformatic analyses, we identified key metabolites that serve as reliable chemo-taxonomic markers and uncovered minor and potentially novel isocyanate derivatives. These findings underscore the importance of multidisciplinary methodologies in resolving complex taxonomic and evolutionary questions in marine gastropods.

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OC 28 NEW TETRAHYDROFURAN CONTAINING LIPID AS FIRST CHEMICAL EVIDENCE OF THE KLEPTOPREDATION IN *Cratena peregrina* (AEOLIDIOIDEA: FACELINIDAE) NUDIBRANCH

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Specialized molecules play a pivotal role in chemical ecology by elucidating predator-prey interactions and exhibiting remarkable chemical and biological properties. Among marine invertebrates, heterobranchs, soft-bodied gastropods, stand out as a particularly promising group due to their remarkable chemical diversity. These organisms are capable of biosynthesizing or sequestering and storing secondary metabolites for a range of eco-physiological functions, including defense, communication, reproduction, development, and growth[1].

Cratena peregrina (Aeolidioidea: Facelinidae) is notable for its striking aposematic coloration. Field observations and ecological assays indicate that, like many aeolid nudibranchs[2], it employs nematocysts derived from its hydrozoan prey as a means of defense[3]. Recent findings suggest an additional trophic relationship involving the feeding of *C. peregrina* on hydrozoans that have recently ingested phytoplankton, indicating a form of indirect planktivory behavior and subsidized predation named kleptopredation[3].

Cratena peregrina has been deeply examined for the use of chemical defence in addition to nematocysts[4]. However, previous chemical studies are limited to the reports of prenylchromanols and steroids[5]. Recently, during a new investigation of this opisthobranch and its prey, the hydrozoan *Eudendrium racemosum*, we have isolated a novel secondary metabolite that can be biogenetically linked to plankton metabolism. The compound features a previously undescribed tetrahydrofuran-containing lipid structure, which was fully elucidated using spectroscopic and spectrometric methods. Biogenetic analysis suggests that the metabolite originates from the transformation of docosahexaenoic acid (DHA), providing the first chemical evidence supporting kleptopredation in this species. Here, I discuss these results of our study, including the determination of the absolute configuration of the new compound by a combination of instrumental techniques and chemical conversion.

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OC 29 CROSSING ECOSYSTEMS: HOW *OCEAN4BIOTECH* BRIDGED MICROBIAL RESEARCH IN EXTREME HABITATS

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Participation in the COST Action Ocean4Biotech (CA18238) marked a transformative step in expanding collaborative frameworks for research on microbial communities in subterranean habitats. Although the primary aim of Ocean4Biotech was to advance marine bioprospecting by fostering a European transdisciplinary platform for the sustainable use of marine biodiversity, this initiative also welcomed complementary perspectives from other extreme environments. In this context, research focused on microbial diversity and biotechnological potential in karst aquifers and caves of the Dinaric region was introduced into the network, enabling the establishment of meaningful collaborations with scientists investigating the deep-sea and other marine extreme habitats, including marine caves.

Despite their distinct physical settings, subterranean and submarine extreme habitats share key ecological features: isolation, persistent stress conditions, and the presence of specialized microbial life with unique biosynthetic capabilities. These ecosystems host a remarkable range of microniches and highly specialized microorganisms, shaped by intense environmental pressures and complex intra- and interspecies interactions among all three domains of life. Such shared features created fertile ground for interdisciplinary knowledge exchange and methodology alignment, particularly in the context of bioprospecting for novel bioactive compounds in karst caves.

The Ocean4Biotech platform not only facilitated scientific dialogue across ecological boundaries, but also strengthened capacity building, innovation potential, and integrative approaches to studying life in extreme environments. This experience underscores the critical role of structured networking initiatives in fostering cross-ecosystem collaboration and accelerating biotechnological discovery.

POSTER SESSION 2

PP 35 ALIEN CHEMICAL DEFENSE IN PHLEGREAN WATERS

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The introduction of alien species poses a significant threat to coastal ecosystems, particularly in the Mediterranean Sea, where newcomers often engage in chemical warfare with native fauna. Here, we report a novel polypropionate metabolite produced by the non-native cephalaspidean *Haloa japonica* (Pilsbry, 1895) (= *Haminoea japonica*, *Haminoea callidegenita*) in the Phlegraean lagoons, along the central Tyrrhenian coast. The compound, isolated from the mucus secreted upon disturbance, elicited a dose-dependent feeding deterrence in the native generalist shrimp *Palaemon elegans*, indicating its role as a defensive allomone. These results add new insight to the previous studies that reported the presence of alkylphenols acting as alarm pheromones in the external tissue of *H. japonica*, while the presence of polypropionates was only hypothesized based on TLC comparisons with related species[1-4]. Echoing hypotheses proposed for another alien cephalaspidean[5], we suggest that this unpalatable allomone protects *H. japonica* from predation, thus giving a selective advantage during its initial Mediterranean colonisation. This may also have facilitated the establishment of thriving populations and the subsequent spread throughout the Mediterranean coastline. Preliminary bioassays revealed no cytotoxicity, but rather induced a pro-inflammatory response, opening potential avenues for the pharmacological exploration of this metabolite.

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PP 36 CONTRIBUTION OF EELGRASS (*Zostera marina*) MICROBIOME IN PATHOGEN REDUCTION IN WATER COLUMN

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Seagrasses are a distinct group of submarine plants that form extensive underwater meadows in coastal regions. These foundational species are ecosystem engineers and provide a variety of ecosystem services that directly benefit human. A recently discovered ecological function of seagrass meadows is the suppression of pathogenic bacteria in the water column[1,2]. Several mechanisms underlying this complex effect have been suggested, but the potential involvement of the seagrass microbiome has not been investigated. Seagrasses harbor complex assemblies of microorganisms on their surfaces and inner tissues, and live intimately with both beneficial and harmful microbes in seawater. We hypothesized that the microbiome of the Baltic eelgrass *Zostera marina*, especially the leaf epiphytes that are at direct interface between the seagrass host and surrounding water, inhibit waterborne pathogens thereby contributing to their removal. Using a culture-dependent approach, we isolated approx. 90 bacteria and fungi associated with the surfaces and inner tissues of the eelgrass leaves (healthy and decaying) and the roots. We assessed the antibiotic activity of each microbial extract against a large panel of almost 30 common aquatic, human (fecal) and plant pathogens, and mined the metabolome of the most active extracts. The healthy leaf epibiotic bacteria, particularly *Streptomyces* sp. strain 131, displayed broad-spectrum antibiotic activity superior to some control antibiotics. Gram-negative bacteria abundant on healthy leaf surfaces, and few endosphere-associated bacteria and fungi also displayed remarkable activities. UPLC-MS/MS-based untargeted metabolomics analyses showed rich specialized metabolite repertoires with low annotation rates, indicating the presence of many undescribed antimicrobials in the extracts. This study contributes to our understanding on microbial and chemical ecology of seagrasses, implying potential involvement of the seagrass microbiome in suppression of pathogens in seawater. Such effect is beneficial for the health of ocean and human, especially in the context of climate change that is expected to exacerbate all infectious diseases. It may also assist future seagrass conservation and management strategies.

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PP 37 MS-BASED METABOLOMICS OF ATLANTO-MEDITTERRANEAN *APLYSINA* SPECIES: A KEY STEP FOR THE IDENTIFICATION OF THEIR SPECIALIZED EXOMETABOLITES

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Aplysina aerophoba (Nardo, 1833) and *Aplysina cavernicola* (Vacelet, 1959) are well known sponge species of Atlanto-Mediterranean ecosystems. While *A. cavernicola* is rather sciaphilic and found on overhanging cliffs or at the entrance of underwater seacaves, *A. aeroboba* can grow in shallower habitats and is often found on well-lit seabed. Both species produce specialized metabolites known as bromotyrosine spiroisoxazoline alkaloids **(Figure 1)**, such as aerophobin 2 and purealidin L. However, they differ in their production of certain compounds, with aerothionin being specific to *A. cavernicola* and isofistularin-3 to *A. aerophoba*[1,2]. We previously demonstrated that *A. cavernicola* releases part of its alkaloids (i.e exometabolites: EMs) into its surroundings, both *in aquaria* and *in situ* using (as observed with I-SMEL: In Situ Marine moleculE Logger)[3,4]. These EMs, may serve as distant chemical cues, possibly contributing to the sponge defensive or communication toolbox[5,6].

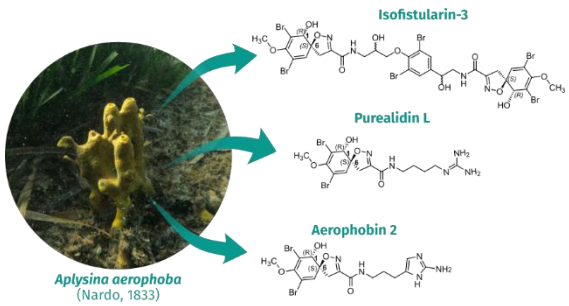

Figure 1. *Bromotyrosine alkaloids produced by* A. aerophoba.

As opposed to *A. cavernicola*, little is known about the exometabolome of *A. aerophoba*. In that context, the present study aims at **(I)** comparing the chemical diversity of both *Aplysina* species in order to **(II)** better determine the EM composition of *A. aerophoba* and identify unique, species-specific bromotyrosine alkaloids among them. To achieve this, comparative MS-based metabolomic analyses were performed on different samples collected in the Mediterranean Sea. Chemical discrimination of each *Aplysina* species, with the selection of differential markers, was conducted through chemometrics. Next, captures of *A. aerophoba* EMs were performed in shallow waters using I-SMEL. Building on the acquired knowledge, spectral analyses deriving from MS-based metabolomics led us to identify a series of brominated EMs, whose production is currently being monitored through time. These analyses will help to identify environmental factors influencing the production and release of such specialized metabolites.

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6. Synthesis of MNP and medicinal chemistry

XIV ECMNP
EUROPEAN CONFERENCE ON
MARINE NATURAL PRODUCTS

ORAL COMMUNICATIONS

OC 30 A SAR STUDY OF TETRAHYDRO-β-CARBOLINE AND β-CARBOLINE CONTAINING NATURAL PRODUCTS

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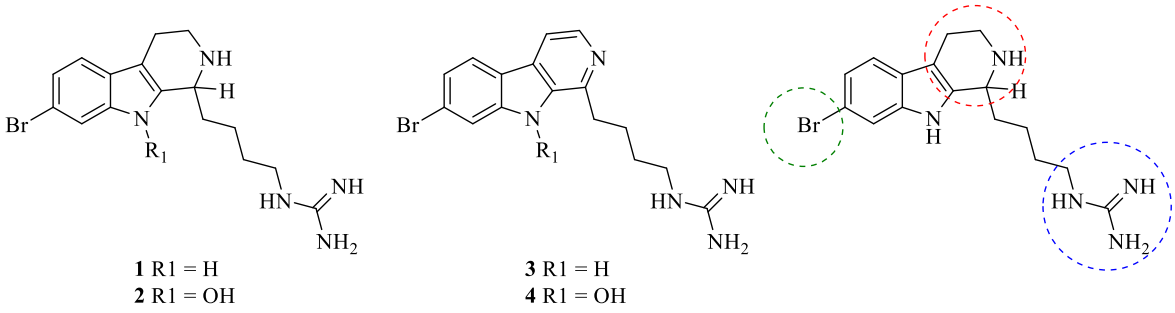
The alkyl-guanidine containing β-carboline natural products, opacalines A-C and their tetrahydro- variants (-)-7-bromohomotrypargine (**1**) and 7-bromo-*N*-hydroxyhomotrypargine (**2**), isolated from the New Zealand ascidian *Psuedodistoma opacum* have been shown to exhibit antibiotic potentiating properties against Gram-negative strains of bacteria. Of the isolated compounds, the tetrahydro-β-carboline **2** and β-carboline **3** both exhibited potentiating activity with doxycycline against *Pseudomonas aeruginosa* at 50 μM and 12.5 μM, respectively.

A structure-activity relationship study was conducted on the β-carbolines by altering various components of the structure (**Figure 1**), such as the presence or absence of bromine substituent, guanidine group and the aromaticity of the rings, to identify the minimum requirements for activity. A total of four target β-carboline containing compounds were synthesized with two compounds identified as the first known total syntheses of the natural products' opacaline A (**3**) and 7-bromohomotrypargine (**1**). The results of this SAR study and their ability to enhance antibiotic activity against resistant bacteria will be presented.



1 R1 = H
2 R1 = OH

3 R1 = H
4 R1 = OH

OC 31 SYNTHESIS AND ANTIMICROBIAL ACTIVITIES OF ACARNIDINE C12:0 AND ANALOGUES

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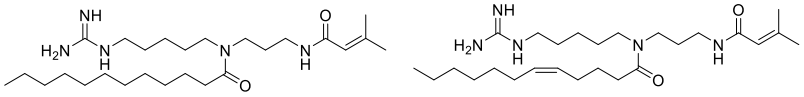
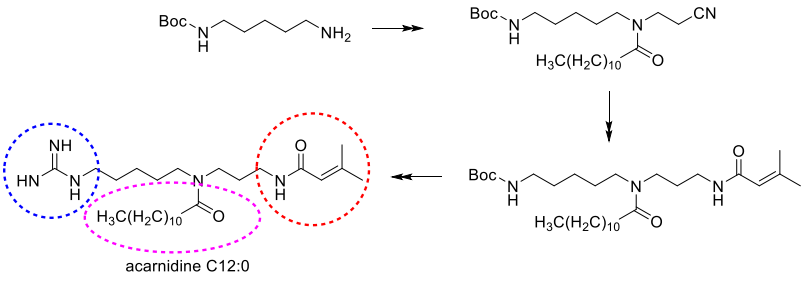
Acarnidines C12:0 and C12:1 are acylpolyamines isolated as antimicrobials from the sponge *Acarnus erithacus*[1].



While the synthesis of acarnidine C12:0 has been disclosed[2,3] no studies have been published on the structure-activity relationship of these compounds. In our search for new classes of antimicrobial agents and antibiotic enhancing compounds, we now report on our studies of the acarnidines.

Our synthetic route to acarnidine C12:0 started from mono Boc protected cadaverine by first introducing a nitrile group, functionalised by a C_{12} fatty acid chain, followed by reduction and addition of the isobutene moiety and finally Boc deprotection to allow installation of the guanidine group (Scheme 1). A second route has also been developed to allow the introduction of unsaturated fatty acids to the alkyl amine core which will enable our exploration of the structure-activity relationship of the acarnidines for the first time. This poster will present the synthesis of acarnidine C12:0 and analogues with the related biological activities as antimicrobials and antibiotic enhancers.



Scheme 1. Synthetic route of acarnidine C12:0.

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POSTER SESSION 2

PP 38 BIOINSPIRED SYNTHESIS OF SHERMILAMINE B AND KUANONIAMINE D

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Shermilamine B and kuanoniamine D (**Figure 1**) are biologically active sulfur-containing pyridoacridine alkaloids that were isolated from several marine organisms. The shermilamine family of alkaloids have a thiazinone subunit, whereas the kuanoniamine family of alkaloids have a thiazole subunit.[1]

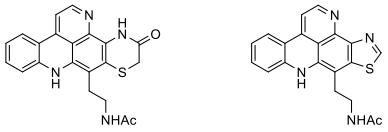
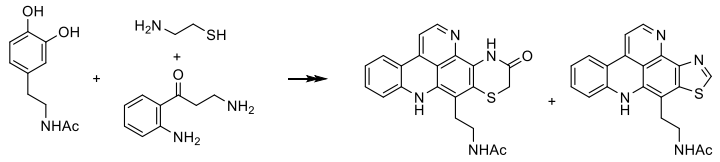


Figure 1 Structures of shermilamine B and kuanoniamine D.

Shermilamine B was found to have moderate antimicrobial activities towards *Escherichia coli* and *Micrococcus luteus*. Kuanoniamine D exhibits insecticidal activity toward neonate larvae of the polyphagous pest insect *Spodoptera littoralis* and toxicity in the brine shrimp lethality test.[1]

To be able to achieve further biological investigation and determination of structure-activity relationships, resupply of these marine alkaloids is a significant issue. Total synthesis of these two alkaloids were reported in early 1990s, but the synthetic route involved multiple steps, low yields and the use of hazardous reagents.[2]

We have now developed a novel bioinspired synthesis of both shermilamine B and kuanoniamine D. This process utilizes biogenic-related starting materials (cysteamine, *N*-acetyldopamine and kynuramine), combined with a mild oxidant to form the pentacyclic scaffolds (**Scheme 1**).



Scheme 1 Bioinspired synthesis of shermilamine B and kuanoniamine D.

The synthesis and biological activities of these two compounds will be presented in the poster.

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PP 39 LAUREQUINONE-BASED SYNTHETIC QUINONES AS AGENTS AGAINST *Leishmania amazonensis*

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Leishmaniasis affect millions of people worldwide and current treatment options against these protozoa parasite are limited and induce multiple undesired effects. To develop alternative treatments against *Leishmania amazonensis*, this work explores new synthetic compounds based on the marine natural sesquiterpene laurequinone[1].

Using a molecular simplification strategy focused on the elimination of stereogenic centers, the fragment 2-(1*S*,2*R*,5*R*)-1,2-dimethylbicyclo [3.1.0]hexan-2-yl in laurequinone was modified to a cyclopentyl moiety in 2 position to afford an active lead compound prototype. Optimization by homologation of the cyclopentyl ring to a cyclohexyl leads to the most active compound of the series, 2-cyclohexyl-5-methylcyclohexa-2,5-diene-1,4-dione, with an IC_{50} of 0.29 ± 0.05 μM and a selectivity index of 43.0 against promastigotes of *L. amazonensis*[2]. The compound, which pharmacophore moiety resembles that of ubiquinone, causes a decrease in the mitochondrial membrane potential and a reduction in ATP production levels, leading to an excess of ROS. These effects in the parasite mitochondrion could be rationalized by a blockage in the electron transport chain, where ubiquinone intervenes.

Acknowledgements

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7. Natural products isolation and downstream processing

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OC 32 BIOASSAYS FOR NATURAL RESOURCES: USE WITH CAUTION

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Bioassays play a central role in revealing the bioactivity of natural resources and are the cornerstone of effective bioprospecting. Their careful selection and high quality are crucial to ensure meaningful and reproducible results. Bioassays are indispensable in the early stages of research, where they guide the isolation, purification and identification of bioactive compounds by detecting the most promising candidates. In addition, bioassays are equally valuable in the later stages of research and development when it comes to rigorously evaluating the safety and efficacy of identified compounds to ensure they meet the required standards for further development in pharmaceutical or other industrial applications. By bridging the gap between exploration and validation, bioassays provide a structured and reliable framework for transforming natural resources into functional and impactful discoveries. The role of bioassays in bioprospecting is fundamental and irreplaceable. However, numerous practical considerations should be taken into account in both the selection and implementation of bioassays to obtain reliable bioassay results, as these serve as a starting point for application-based development and further testing, as well as for consideration by regulatory authorities. An overview of frequently used bioassays in marine biodiversity research is given in order to highlight current research trends in marine natural products research[1].

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OC 33 UNVEILING THE METABOLIC POTENTIAL OF THE DEEP-SEA-DERIVED *Streptomyces profundus* THROUGH THE OSMAC APPROACH

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Deep-sea environments represent one of the last frontiers in NP exploration[1]. The extreme conditions of these habitats drive deep-sea microorganisms to evolve unique biochemical, metabolic, and physiological adaptations, often resulting in the production of new metabolites[2]. Deep-sea Actinomycetota remain underexplored, yet studies suggest these environments harbor unique strains that are potential sources of new molecules[3, 4]. Actinomycetota are known to harbor multiple biosynthetic gene clusters (BGCs) within their genomes, enabling a single strain to produce various NPs. However, many of these BGCs are not expressed under conventional laboratory conditions. In recent years, the OSMAC (One Strain - Many Compounds) approach has proven highly effective in activating the expression of dormant BGCs through modifications in culture conditions[5]. As a result, its application has led to the discovery of novel bioactive compounds[6, 7].

In this study, we present the findings from applying a specific growth condition - cultivation in GYM medium - as part of an OSMAC approach applied to a strain of *Streptomyces profundus*[8] isolated from a deep-sea sample collected in the Madeira archipelago, in order to find novel bioactive compounds with pharmaceutical relevance. This condition was found to significantly stimulate anticancer activity of *S. profundus*. Following a bioactivity-guided pipeline, a compound was isolated that initially showed features consistent with a novel structure, but was subsequently identified as a known molecule. Additional bioactivity assays will be carried out with this molecule, along with the determination of its IC_{50} value.

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OC 34 FROM ALGAL CELLS TO SELF-ASSEMBLED VESICLES: UNLOCKING DRUG DELIVERY POTENTIAL

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Marine microalgae are a diverse group of photosynthetic organisms that fulfill an important ecological function and have considerable biotechnological potential. Recently, the use of microalgae as drug delivery systems has attracted considerable interest. There are various approaches based on intact algal cells, cellular fragments and extracellular vesicles. However, there are still obstacles such as low vesicle yield, instability, complicated isolation processes and lack of standardization. To overcome these problems, we have developed an innovative approach for vesicle preparation in which osmotic stress of cells leads to self-assembly of membrane segments[1,2]. The resulting vesicles have complicated, puzzle-like structures. Understanding their structure and function as alternative drug delivery systems requires a combination of top-down and bottom-up biophysical approaches. The morphology, composition, overall properties, biocompatibility and transportability of the vesicles will be presented. This study could help in the development of algae-based delivery systems that improve drug delivery while being biocompatible, environmentally friendly and sustainable.

Acknowledgments

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OC 35 CHLOROPHYLL DERIVATIVES FROM *Arthrospira platensis* FOR NOVEL NUTRACEUTICAL APPLICATIONS

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Metabolic syndrome increases risk of developing life-threatening diseases such as diabetes and obesity. Cyanobacterium *Arthrospira platensis* consumption has shown beneficial effects on metabolic syndrome conditions proving its potential to produce bioactive molecules for these conditions and diseases. Through a natural product bioassay-guided approach, two isomers - 13^2-*S*-hydroxypheophytin a (*S*-hpa) and 13^2-*R*-hydroxypheophytin a (*R*-hpa) - were isolated and characterized.

A DCM:MeOH (2:1) extract was sequentially fractioned through chromatography using Hex:EtOAc gradients. Each fractionation set was assessed on zebrafish larvae lipid metabolism assays, ultimately leading to the isolation of the bioactive isomers. Structure elucidation was performed by 1D and 2D (COSY, HSQC, HMBC) NMR and mass spectrometry. The stereochemical differences were inferred based on proton chemical shifts at the diagnostic positions (C-13^2, C-13^4, C-17) ROESY correlations, and comparison with literature data.

Both compounds were tested for appetite modulation, β-cell regeneration and glucose uptake in zebrafish larvae, and steatosis in HepG2 cells. *S*-hpa reduced the liposomes uptake (IC50 = 22.50 µM), whereas both isomers reduced the *Paramecia* uptake with similar IC50 values in zebrafish larvae, suggesting distinct hormonal and neuronal interactions. Both isomers decreased neutral lipids accumulation, with *R*-hpa exhibiting a stronger effect than *S*-hpa, displaying an 8-fold lower IC50 value (1.18 µM) in zebrafish larvae and 2-fold lower IC50 value (4.8 µM) in HepG2 cells.

To support future applications, extraction procedures were optimized using industrially relevant GRAS solvents. An EtOH:Acetone (1:4) extraction resulted in 4-fold enrichment of *S*-hpa and 8-fold increase in *R*-hpa, showcasing scalable potential for enriched extraction and nutraceutical development.

This research uncovered varying degrees of bioactivity between hpa isomers, highlighting the significance of configurational changes in their action mechanisms. This discovery holds promise for the development of future health-related applications in the nutraceutical or even medicinal fields.

Acknowledgements

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OC 36 VALORIZATION OF THE BLUE CRAB (*Callinectes sapidus*) SHELL WASTES

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The blue crab (*Callinectes sapidus*), an invasive alien species in the Mediterranean, poses significant economic and environmental challenges[1]. In Rimini, Italy, the startup Mariscadoras has developed a supply chain for its meat, mitigating the impact of the invasion while generating economic benefits[2]. This study explores the valorization of the exoskeleton, a by-product of this process, for the production of high-value materials. Particular attention is given to chitin, a biopolymer with applications in biomedical, bioplastic, and cosmetic fields[3] and astaxanthin, a carotenoid with strong antioxidant activity[4].

Conventional chitin extraction relies on harsh acids and bases, raising safety and environmental concerns[5]. Looking for alternatives, we investigated Deep Eutectic Solvents (DES), testing Choline Chloride:Lactic acid (ChCl:LA) and Choline Chloride:Formic acid (ChCl:FA) at different concentrations of crab shell (3-5-10%). Through Fourier transform infrared spectroscopy (FTIR), X-Ray Diffraction (XRD), Scanning Electron Microscopy (SEM), and gravimetric analysis, the optimal extraction protocol for the highest yield was identified. In addition, astaxanthin was extracted using ultrasound-assisted extraction with ethanol and acetone as solvents. The antioxidant activity of the extract, pure astaxanthin and DES-extracted chitin was evaluated.

The ultimate goal of the work is to develop antioxidant chitosan films by combining chitosan (a water-soluble derivative of chitin) and astaxanthin, thus exploiting their bioactivity for improved packaging and cosmetic applications. These results contribute to the sustainable valorisation of marine wastes, supporting the principles of the Blue Economy while reducing the environmental impact of invasive species, as well as contrasting the use of non-biodegradable materials.

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OC 37 IN- VITRO WOUND HEALING ACTIVITIES OF CHITOSAN BASED FILMS CONTAINING ASTAXANTHIN EXTRACT (*Aristeaomorpha foliacea* and *Aristeus antennatus*)

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Wound healing using chitosan (CS) films has become the focus of interest for many researchers today. In this context, our research is to evaluate the wound healing efficacy of chitosan (CS)- sodium tripolyphosphate (TPP) films containing astaxanthin extract obtained from shrimp (*Aristaeomorpha foliacea* and *Aristeus antennatus*) shells at four different concentrations. For this purpose, astaxanthin extracts at varying concentrations (0,1-5%) were added to the chitosan – sodium tripolyphosphate solution. The resulting films were characterized using FTIR, UV-Vis, TGA, SEM, tensile strenght and elongation at break, and antioxidant activity (DPPH) analyses. Wound closure and cell migration were monitored over 72 hours, with significant observations recorded at 24, 48, and 72- hour time points. It was confirmed that increasing concentrations of astaxanthin extracts showed statistically positive correlation with wound healing properties ($p<0,05$). These findings suggest that the incorporation of astaxanthin extract into chitosan- sodium tripolyphosphate films presents a promising bio- material for wound healing applications by combining its benefical properties with the biocompatibility and biodegradability of chitosan.

POSTER SESSION 2

PP 40 A NEW CLASS OF CYTOTOXIC OXAZOLE DERIVATIVES FROM THE SPONGE *Rhabdastrella rowi*

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Sponges from the genus *Rhabdastella* are known to be a prolific source of terpene derivatives such as the cytotoxic globostelletins[1] and stelliferins[2].

We describe herein the first isolation and the structural elucidation of two unusual complex oxazole derivatives PM100618 and PM110049, isolated from the sponge *Rhabdastrella rowi* collected in Papua New Guinea.

These compounds were obtained by bioassay-guided fractionation of an organic extract of the organism, using VLC RP-18 chromatography and reverse phase semi-preparative HPLC. Structure elucidation of these new metabolites was carried out by spectroscopic methods including MS, ^{1}H, ^{13}C and 2D-NMR. The stereochemistry was deduced by NOEs correlations and Mosher and Marfey´s methods. Furthermore, the structure of PM100618 was confirmed by total synthesis (this will also be presented in this symposium) which allowed us to further investigate its mechanism of action and to initiate advanced *in vivo* evaluation for cancer treatment.

These compounds exhibit *in vitro* cytotoxicity activities at nanomolar concentrations against several different human tumor cell lines, including lung (A-549), colon (HT-29), breast (MDA-MB-231) and pancreas (PSN1).

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PP 41 BIOACTIVE METABOLITES FROM DESERT FUNGI: A NATURAL APPROACH TO COMBAT MARINE FISH PATHOGENS

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Hyper-arid ecosystems, such as deserts, presents underexplored sources of unique microbial biodiversity with potential for novel bioactive metabolite production[1]. This study focuses on the isolation and characterization of secondary metabolites from desert-derived fungi and their antimicrobial activity against key marine pathogens affecting aquaculture species. Fungal strains were isolated from desert soil samples and cultured under varied conditions to induce secondary metabolite production. Bioactivity-guided fractionation was employed, followed by compound purification using LC-MS, and structural elucidation was achieved through 1D and 2D NMR spectroscopy.

Several compounds displayed potent antimicrobial activity against marine bacterial pathogens, including *Tenacibaculum maritimum*, *Yersinia ruckeri*, *Vibrio crassostreae*, and others, which are known to cause significant mortality in farmed fish.

The application of these bioactive metabolites in aquaculture could reduce reliance on synthetic antibiotics, offering a sustainable approach to prevent pathogen colonization and chronic infections. By incorporating desert-derived antimicrobials, fish health and productivity may be enhanced, leading to more sustainable solutions in marine industries by incorporating natural, bioactive substances that are both effective and environmentally friendly.

This research highlights the promise of extreme-environment fungi as reservoirs of novel compounds with broad-spectrum bioactivity, paving the way for innovative biocontrol agents in aquaculture.

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PP 42 BIOPROSPECTING OF BACTERIAL SYMBIONTS OF THE MARINE HYDROID *Hydractinia*

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Symbiotic bacteria play critical roles in animal evolution, development and metabolism[1]. The molecular and cellular mechanisms underlying these fundamental interactions, however, are largely unknown. To fill this major knowledge gap, we have recently established the bacteria-*Hydractinia* symbiosis as a new marine model system to characterize key cross-kingdom signalling molecules and to explore the encoded biosynthetic wealth of its symbiotic bacteria[2,3].

Amongst others, the genus *Pseudoalteromonas*, has attracted much attention in the recent years due to its ecological[4], antibacterial[5], antibiofilm and antifouling capabilities[6,7,8] ,but still remains mostly unexplored for its natural product repertoire. Rapid technological developments in the field of genomics have enabled a renaissance of microbial natural product research[9], and thus we decided to study species of this peculiar genus more in depth. For this, *Hydractinia*-associated bacteria were isolated on different cultivation media and monocultures used for whole genome sequencing. Subsequently, we utilize state-of-the-art computational tools to predict and analyze the carbohydrate-active enzymes as well as the secondary metabolite biosynthesis potential of the isolated strains. From the predictions, we further select for biomolecules of putative bioactivity for inspection of their potential applications. Moreover, we specifically inspect bacterial isolates of the genus *Pseudoalteromonas* to uncover their undisclosed biosynthetic potential and their potential ecological significance for *Hydractinia*.

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PP 43 BIOPROSPECTING OF PIGMENT-PRODUCING HALOPHILIC MICROORGANISMS FROM THE SEČOVLJE SALT PANS

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Salt pans are extreme environments characterized by high salinity, harboring a unique and largely untapped microbial biodiversity. The microorganisms inhabiting these niches have evolved specific adaptation mechanisms, enabling survival under fluctuating and often harsh conditions. These adaptations can result in the production of bioactive compounds with significant biotechnological potential, including antioxidant, UV-protective, and antibacterial activities. However, replicating such extreme environments in laboratory conditions remains a challenge, and establishing pure microbial cultures is a time-consuming process.

This study focuses on the isolation and bioprospecting of microalgae from the Sečovlje Salt Pans (Slovenia). Petola samples were collected across different seasons, allowing for the assessment of seasonal shifts in microbial communities through metagenomic analysis. Clear differences in community composition were observed between high- and low-salinity periods. In parallel, a cultivation-based approach was employed to isolate and purify microalgal strains with potential biotechnological applications.

The obtained isolates were subjected to preliminary bioactivity screening, including determination of total phenolic content and antioxidant capacity. Additionally, their pigment profiles were extracted using environmentally friendly deep eutectic solvents (DES), which serve as a sustainable alternative to conventional organic solvents.

Our results demonstrate that despite the complexity of isolation and cultivation processes, salt pan-derived microorganisms—particularly microalgae—represent a promising reservoir of novel bioactive compounds for use in cosmetics, pharmaceuticals, and related industries.

PP 44 CHEMICAL AND BIOLOGICAL STUDIES ON THE CAPTIVE CORAL REEF SPONGE *Lendenfeldia chondrodes*

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Lendenfeldia Bergquist, 1980 is a marine sponge genus commonly found in flat reefs across the Indo-Pacific region. Despite their natural habitat, these sponges, known as the "Blue Photo Sponges", are also encountered in aquarium reef tanks and aquaculture facilities posing challenges as pests [1]. Previous chemical investigations into *Lendenfeldia* sponges, which are well known for their complex associated microbiome [2,3], have revealed a variety of bioactive secondary metabolites mainly belonging to the group of scalarane-type sesterterpenoids [4–7]. This communication deals with the isolation and structural characterization of new bis-homoscalaranes from a sample of *Lendenfeldia chondrodes* grown in aquarium. The results of both chemoecological studies and an anti-inflammatory activity screening will be presented, shedding light on the defensive roles and potential pharmacological properties of these new metabolites.

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PP 45 CONVENTIONAL AND GREEN CHITIN EXTRACTION METHODS

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Seafood production is increasing worldwide and with it the amount of waste, which represents around 35 % of raw materials[1]. Most of it is landfilled, leading to environmental pollution and resources loss[2,3]. On the other hand, seafood waste is still rich in nutrients such as proteins, lipids, minerals, chitin and others, that can be recovered[4]. Chitin is second most abundant biopolymer on earth, with excellent biomedical and physicochemical properties (such as non-toxicity, biodegradability, and biocompatibility)[5], with high potential for utilization. It can be extracted from shellfish waste and used in numerous applications such as cosmetics, food packaging, textiles, biomedicine, environmental engineering and others[1,2,3]. The main challenge is to close the gap between laboratory-scale chitin extraction and sustainable, large-scale production. This requires the development of more environmentally friendly and efficient extraction methods without affecting the bioactivity and quality of the extracted chitin.

The aim of our research was to extract chitin from seafood waste (crustacean shells), which are the most frequently discarded sources of chitin in the northern Adriatic region. We tested and compared conventional (acid-base) and more environmentally friendly (deep eutectic solvent - DES) extraction methods. We characterised the chitin extracts with different analyses (FTIR, TGA, XRD, NMR, SEM, elemental analyses, measurement of protein, ash content and degree of acetylation). We also evaluated the extraction methods in terms of energy, chemicals, costs, time and water consumption.

The poster presentation will address the question of which tested (green) methods are superior for chitin extraction.

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PP 46 DISCOVERY AND CHARACTERIZATION OF NEW CYCLIC DEPSIPEPTIDES FROM A FILAMENTOUS CYANOBACTERIUM COLLECTED IN BOA VISTA, CAPE VERDE

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Marine microorganisms are a rich source of structurally diverse natural products with specialized ecological roles and potent bioactivities. In this study, we explored the chemodiversity of environmental cyanobacteria from underexplored insular and continental regions of northwest Africa, specifically Cape Verde and Morocco, to assess their pharmaceutical potential against infectious diseases. GNPS MS/MS molecular networking[1] was performed on crude extracts and primary fractions, followed by dereplication using the MarinLit database, as well as bioactivity screening against parasites and cytotoxicity assays on cancer cell lines. This strategy led to the isolation of promising novel natural products named here as boavistamides. Advanced NMR-based AI tools, such as SMART NMR 2.1[2] and DeepSAT 0.2[3], accelerated the structure elucidation of these cyclic depsipeptides. Their planar structures were determined using a combination of HRMS and 1D/2D NMR spectroscopy techniques. Chemical methods such as Marfey's analysis were used to establish their absolute configuration. Finally, boavistamide A, isolated from a fraction exhibiting strong antiparasitic activity, was tested against *Plasmodium falciparum* and *Trypanosoma brucei*, the causative agents of malaria and human African trypanosomiasis (HAT), respectively. Malaria remains a major global health concern with hundreds of thousands of deaths reported annually. HAT, is almost always lethal and classified as a neglected tropical disease (NTD) by the World Health Organization (WHO), highlighting the need for improved research and treatment options. Our findings underscore the therapeutic potential of marine cyanobacteria from remote and poorly studied regions as a promising source of new antiparasitic agents.

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PP 47 FROM SEA TO SOIL: ISOLATION AND BIOACTIVITY PROFILING OF MARINE-DERIVED ANTIFUNGAL COMPOUNDS AGAINST PLANT PATHOGENS USING OSMAC AND HTS APPROACHES

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Plant pathogenic microorganisms can cause severe annual crop losses with economically devastating consequences[1]. Plant safety is intrinsically linked to human and animal health, as plants constitute a significant portion of their diet[2].

In this study, a library of marine fungal extracts from 365 strains from Fundación MEDINA collection was generated using an OSMAC approach, in which each strain was cultured in five different media. Extracts were screened against plant pathogens via high-throughput screening (HTS) assays, and active extracts underwent LC-HRMS and LC-MS/MS analyses for dereplication.

Strains *Paraconiothyrium* sp. CF-301740 and *Pyrenochaetopsis indica* CF-301929, both cultivated in a rice-based solid-state medium (BRFT) and originating from the Coral Sea in Australia, were selected for large-scale cultivation. The organic extracts of both strains displayed activity against the fungal phytopathogens *Zymoseptoria tritici*, *Fusarium proliferatum*, and *Magnaporthe grisea*, while the extract of *Pyrenochaetopsis indica* showed additional activity against *Colletotrichum acutatum*.

Following large-scale cultivation, extraction, and bioassay-guided fractionation, ten compounds were isolated: five from *Paraconiothyrium* sp., belonging to the orcinol family, and five from *Pyrenochaetopsis indica*, classified as spirodioxynaphthalenes, three of which are new natural products. The structures of the compounds were elucidated using HRMS, UV spectroscopy, and both 1D and 2D NMR. Bioactivity profiling of the isolated compounds revealed potent antifungal activity in some of them.

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PP 48 MARINE BIOPOLYMER-BASED SCAFFOLDS FOR BONE TISSUE ENGINEERING

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Tissue engineering is an emerging field in regenerative medicine which provides alternative therapeutic methods to restore the function, and repair damaged tissues. Porous extracellular matrix-like scaffolds have been employed in tissue engineering for enhancing cell adhesion, cell growth, differentiation, and mineralization.

Marine biopolymers have been used for the development of such scaffolds, due to the wide spectrum of biological activities they exhibit, as well as their biocompatibility, biodegradability, chemical tuning ability, osteoinductivity and sustainability[1]. So far, various polysaccharides[2,3], as well as gelatin[4], have been employed for the preparation of porous scaffolds and studied as extracellular matrix-compatible materials. Moreover, hydroxyapatite, a highly biocompatible mineral, provides a favorable environment for osteoconduction, protein adhesion, and osteoblast proliferation, and has been, therefore, widely used in tissue engineering[5].

In the framework of our research activities, a series of novel porous structures based on chemically cross-linked biopolymers, including the marine sulfated polysaccharides, ulvan and ι-carrageenan, and marine-derived gelatin, as well as chondroitin sulfate with or without the addition of marine origin hydroxyapatite, were designed, prepared and characterized. The IR spectra confirmed the presence of the constituents, with the peak intensities being analogous to the ratio of the biopolymers used. The impact of the composition on the scaffold's morphology, porosity, *in vitro* degradation rate, as well as on their thermal and water uptake properties was determined, while their osteoinductive potential was investigated through the evaluation of cell adhesion, viability and osteogenic differentiation of MC3T3-E1 mouse pre-osteoblastic cells. The results verified the lack of toxicity of the scaffolds and their ability to potentiate cells' differentiation into mature osteoblasts, thus confirming their potential in the development of biomimetic scaffolds for bone tissue engineering applications.

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PP 49 MARINE EXPLORATION AROUND THE UNION OF THE COMOROS

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The marine biodiversity surrounding the Comoros Islands has hardly been explored, offering a promising area for natural product discovery. In this study, an extensive marine exploration campaign was conducted in 2023 to collect biological samples from various marine organisms inhabiting this region. Advanced analytical techniques, including high-performance liquid chromatography (HPLC), mass spectrometry (MS) and nuclear magnetic resonance (NMR) were used to identify and characterize the chemical diversity present in these samples.

As a result, more than 200 distinct chemical structures were identified, with approximately 20% of them being novel compounds. These findings highlight the richness of marine natural products in this underexplored region and underscore the potential of marine ecosystems in the Comoros for pharmaceutical and biotechnological applications. The rapid and significant results obtained within a relatively short period emphasize the efficiency of the exploration approach and suggest that further studies in this region could yield even more valuable discoveries. This work provides a strong foundation for future research on marine-derived compounds and their potential applications, reinforcing the importance of continued efforts in marine bioprospecting.

These findings contribute to the global understanding of marine natural product diversity and pave the way for the sustainable exploitation of marine resources in previously neglected regions.

PP 50 NEW ACICULITIN FROM MARINE SPONGE AS INMUNOMODULATING AGENT

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Aciculitins are unique structures with two cyclic peptides joined by a histidinone-tyrosine fragment, bearing a fatty acid chain and a D-lyxose. Until now, only three analogues, aciculitins A-C, together with two artifacts, aciculitamides A and B, have been reported from the sponge *Aciculites orientalis*[1], and aciculitin D from the sponge *Poecillastra* sp.[2].

Herein, as part of our efforts to discover new anticancer structures by bioassay-guided fractionation, we selected a sponge from the genus *Aciculites*, collected by rebreather diving in Kapoposang (Indonesia, Indo-Pacific Ocean) for further studies. From this specimen a new aciculitin analog, aciculitin E, was isolated along with two known congeners. The new active molecule was identified using NMR and MS techniques, showing the presence of two additional sugar moieties.

For these bicyclic peptides only antitumoral and antifungal activities have been reported to date[1,2,3]. Our findings indicate that these molecules also exhibit immunomodulatory properties, encouraging us to study of these molecules in greater depth.

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PP 51 NEW ANTIMICROBIAL ACYCLIC DEPSIPEPTIDES FROM A MARINE *Lyngbia majuscula*

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Cyanobacteria are an ancient and prolific group of organisms recognized for their exceptional capacity to produce structurally diverse and biologically active natural products. To date, more than 500 new compounds have been identified from Cyanobacteria, with peptides (dolastatins, gatorbulins, coibamides), polyketides (caldorazoles), and their hybrids (iezosides) being the most representative classes[1].

In this study, three new peptides were isolated from a cyanobacterial sample collected off the coast of Melekeok, Palaos. A bioassay-guided isolation of the organic extract of this organism led to the identification of antimicrobial components, resulting in the isolation of new tumonoic acid derivatives[2,3].

The structural elucidation of these new metabolites was carried out using spectroscopic techniques, including MS, ^{1}H, ^{13}C and 2D-NMR and the stereochemistry of the amino acids was determined and confirmed by Marfey´s method. The cytotoxic and antimicrobial activities of these compounds were also evaluated.

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PP 52 NEW STEROIDAL GLYCOSIDES FROM MARINE SPONGES COLLECTED IN THE UNION OF THE COMOROS

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Monanchora is a genus of Demospongiae within the Poecilosclerida order, found worldwide. Dozens of structures such as guanidine-derived alkaloids[1] and pyrroloquinoline[2] have been isolated from this genus, some with potential anticancer properties and other therapeutic areas. However, no compounds have been reported specifically from *Monanchora lipochela*, a common species in the Comoros Islands.

This study presents the isolation and characterization of ulososide A, a saponin previously identified in sponges of a different genus of Poecilosclerida (*Ulosa* sp.) and in *Ectyoplasia ferox* (order Axinellida), along with two novel saponin derivatives from *M. lipochela* specimens collected from different marine sites in the Comoros Islands. Structural identification was performed using NMR and MS techniques. The cytotoxic activity of these compounds were also evaluated against four human tumor cell lines.

These findings emphasize the remarkable chemical diversity of saponins across sponge species and their potential as lead compounds for anticancer drug development.

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PP 53 POLYOXYGENATED CEMBRANOIDS FROM OCTOCORALS OF THE GENUS *SARCOPHYTON*

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The marine environment is one of the richest sources of diverse natural products with a wide array of biological activities[1]. The Red Sea, lying between Africa and Asia, is the world's warmest and most saline marine habitats, with its seawater inlet at the Indian Ocean. The more than 2000 km-long stretch of coral reef system of the Red Sea, hosting a rich biodiversity with a high number of endemic species, is among the five most extended reefs in the world. Nonetheless, the biota of the Red Sea, in comparison to that of other tropical areas, has not been as extensively investigated as a source of bioactive marine natural products[2].

Over the last decades, soft corals have been proven a rich source of biologically active compounds, featuring a wide range of chemical structures. Among them, octocorals of the genus *Sarcophyton* (Sarcophytidae) have been proven a prolific source of bioactive natural products, having afforded more than 1,000 metabolites to date[1], mainly sesquiterpenes, diterpenes, steroids and ceramides, displaying a wide range of biological activities[3].

In the context of our continuous interest towards the isolation of bioactive metabolites from marine organisms, we recently had the opportunity to examine two populations of *Sarcophyton* collected from the coastline of Al Lith in the Red Sea (Saudi Arabia). Fresh tissues of the organisms were extracted with mixtures of CH_2Cl_2/MeOH, and the resulting organic residues were subjected to multiple steps of chromatographic separations that have so far led to the isolation of 38 secondary metabolites, mostly featuring the cembrane skeleton, among which 11 are new natural products. The structures of the isolated metabolites were established on the basis of extensive analysis of their 1D and 2D NMR and MS data. The evaluation of the biological activity of the isolated compounds is currently in progress.

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PP 54 RED ALGAE *Furcellaria lumbricalis* AS A SOURCE OF ANTIOXIDANTS AND NATURAL UV FILTERS

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Furcellaria lumbricalis is a red algae found in the Baltic Sea. The drifting forms are washed out in the bays in huge amounts (the total amounts reach up to average 35 kg/m^2 (dry weight, after sand removal)[1] and aesthetic issues from tourism view-point occur. On the other hand this biomass may be considered as a source for various valuable products. The main efforts up to date are turned to extraction of algal polysaccharides[2] and natural red colorant R-phycoerythrin[3]. Some studies have revealed the Baltic red algae as a potential source of antioxidants[4].

Herein, we are presenting our results towards elaboration antioxidant rich extracts from *Furcellaria lumbricalis*. In order to prepare antioxidant rich extracts solvents with different polarities and hydrogen bond forming properties were used. The extracts were prepared both from new biomass and via sequential extraction starting with less polar solvent and gradually moving to the more polar ones. All the extracts were analysed for their polyphenol content, as well as they were characterized with NMR techniques. The extracts were tested for their antiradical and UV-filter properties.

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PP 55 RETHINKING SEAFOOD WASTE: GREEN EXTRACTION PATHWAYS FOR HIGH-VALUE BIOPRODUCTS

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The European Green Deal has paved the way for a holistic and integrated approach to tackling the interlinked challenges of climate change, environmental degradation and sustainability. The idea of a circular bioeconomy, based on reducing waste and reusing and/or recycling products, has shaped recent policy efforts in response to environmental and economic challenges.

Of the seafood traded annually, crustaceans are of particular interest. Of these, only 40% are meat, resulting in a global production of 7-9.7 million tonnes of crab, shrimp and lobster shell waste per year. In non-developed countries, which are the main producers of crustaceans, shells are often landfilled or discarded in the sea, which poses a significant environmental problem, as the high content of nitrogenous compounds in the shells releases considerable amounts of greenhouse gases during decomposition. On the other hand, the disposal of shells in industrialised countries can be a costly process. An attractive solution to overcome this bottleneck and reduce our current dependence on petroleum-based value chains is to utilise this abundant and low-value waste as a feedstock to develop a shell biorefinery. Crustacean shells are composed of chitin, proteins, minerals and astaxanthin, which are of great value for various applications in numerous industries.

Today, only chitin is industrially isolated from crustacean shells, using strong alkaline and acid solutions that generate significant amounts of toxic wastewater that must be further processed. In this sense, the development of more environmentally friendly and sustainable downstream processes is of great importance. The aim of this work is therefore to develop a cascade process using more environmentally friendly solvents for the selective extraction of the different compounds present in the shells. Due to the labile character of astaxanthin, the first step in a shell biorefinery should start with its extraction. So far, more than 20 solvents have been used for the selective extraction of this pigment, with 6 solvents showing promising results. The next steps are aimed at isolating the other compounds present in this biomass. By implementing a sequential extraction strategy, this study aims to establish a comprehensive and sustainable shell biorefinery concept that maximises resource valorisation while minimising environmental impact.

PP 56 SCREENING FOR FATTY ACID AND MYCOSPORINE-LIKE AMINO ACIDS FROM MICROORGANISMS OF THE SEČOVLJE SALTWORKS

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Organisms inhabiting extreme marine environments, such as saltpans, produce unique bioactive compounds to withstand high solar radiation, extreme temperatures, and changes in salinity. These include lipids and mycosporine-like amino acids (MAAs), which have light-protective and antioxidant properties. The cosmetics industry is interested in unsaturated fatty acids, such as omega-3 α-linolenic (ALA), docosahexaenoic acid (DHA), and eicosapentaenoic acid (EPA); omega-6 linoleic acid (LA); and omega-9 oleic acid. These can be incorporated into various formulations thanks to their antioxidant and anti-inflammatory functions, among others[1].

In this study, we explored the fatty acid and MAA profiles of microorganisms thriving in hypersaline environments. During a 2023-2024 biodiversity study of the Sečovlje saltworks (Piran, Slovenia), we isolated three biotechnologically relevant organisms: *Dunaliella* spp., *Phormidium* spp. and *Tetradesmus* spp. Gas chromatography (GC-MS) and liquid chromatography (LC-MS) analyses revealed that *Dunaliella* spp. and *Tetradesmus* spp. were rich in ALA, LA, and oleic acid. *Phormidium* spp. contained high levels of palmitic acid and palmitoleic acid but no omega-3 fatty acids, as previously reported[2]. In addition, in methanol extracts from *Dunaliella* spp. we observed spectrographic peaks consistent with the presence of MAAs.

This study underscores the potential of saltpan microorganisms as sources of valuable bioactive compounds for biotechnological applications, particularly in the development of novel, natural sunscreen formulations. In addition to their practical applications, this investigation highlights a commercially relevant selling point: prospective formulations can take advantage of locally sourced organisms.

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PP 57 SEAWEED EXPLORATION AND ADVANCEMENT - UNLOCKING POTENTIAL

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The UN 2030 Agenda for Sustainable Development has defined several strategies towards environment sustainability, biodiversity restoration and preservation, where biodiversity loss, marine and land pollution, and circular economy are paramount issues[1]. SEA-UP – "Seaweed Exploration and Advancement – Unlocking Potential" - aligns with this vision by promoting sustainable use of underexplored seaweeds to respond to emerging environmental challenges, while boosting blue bioeconomy.

SEA-UP will valorize *Gelidium corneum*, currently used exclusively for agar extraction, and *Sargassum muticum*, an invasive yet underutilized brown seaweed rich in valuable bioactive compounds[2,3]. Managing the spread of invasive *S. muticum* will contribute to mitigate biodiversity loss while offering an abundant resource for industrial exploration.

SEA-UP will implement for the first time an eco-friendly biorefinery strategy to maximize these seaweeds value through a cascade extraction, delivering sustainable bioactive ingredients for cosmetics, such as pigments, antioxidant, antimicrobial, photoprotective and anti-ageing ingredients, as well as antifouling agents for the maritime industry[2,3]. For higher valorization of seaweeds, the waste biomass derived from extractions will be converted into biochars and nanoporous carbons, to adsorb pharmaceutical contaminants from water, such as diclofenac and ibuprofen, which are emerging pollutants in aquatic ecosystems[4]. SEA-UP ensures scalability using safe solvents and aligning with industrial needs. Its integrated biorefinery model offers a sustainable, circular approach to creating environmentally friendly products, strengthening blue economy sectors while helping mitigate the negative impacts of invasive species on marine ecosystems through their collection from impacted areas.

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PP 58 SECONDARY METABOLITES FROM *Laurencia natalensis* COLLECTED IN SOUTH AFRICA

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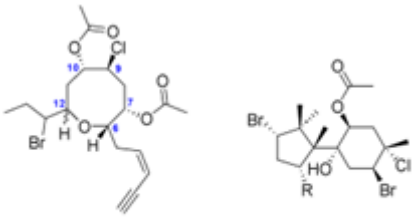
Marine red algae of the genus *Laurencia* are recognized as prolific producers of structurally diverse and biologically active secondary metabolites, such as halogenated terpenoids and C_{15}-acetogenins, many of which exhibit significant pharmacological properties[1,2]. Despite its wide distribution along the South African coastline, *Laurencia natalensis* remains largely unexplored from a chemical standpoint, and its secondary metabolite profile is poorly characterized[3].

In the present study, we report the isolation of four major secondary metabolites from *L. natalensis* collected from coastal waters of South Africa. The algal material was extracted and fractionated by high-performance liquid chromatography. This led to the identification of two known halogenated sesquiterpenes and two new C_{15}-acetogenins. The structural elucidation was accomplished through comprehensive spectroscopic analysis, including 1D and 2D NMR experiment, and the absolute configurations of the chiral centers were determined using a combination of experimental electronic circular dichroism (ECD) and time-dependent density functional theory (TD-DFT) calculations.



Biological evaluation of the isolated compounds is currently underway, with a focus on assessing antibacterial, antifungal, and cytotoxic activities. This work contributes to the chemical characterization of South African marine biodiversity and highlights the potential of *L. natalensis* as a source of novel bioactive natural products. Furthermore, this research is carried out within the framework of the European COMBO project, which promotes the exploration and sustainable utilization of marine biodiversity through collaborative, multidisciplinary approaches.

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PP 59 SECONDARY METABOLITES FROM MARINE SPONGES OF WALLIS AS ANTICANCER AGENTS AGAINST OSTEOSARCOMA

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MEREOS project is based on a multidisciplinary consortium of five research teams from the Great West of France involving chemists and biologists to target new metabolites from marine sponges as bioactive agents against osteosarcoma. Some cancers such as osteosarcoma, which is a pediatric cancer with a high metastatic risk, remain poor prognosis[1]. Thus, new molecules that can lead the development of anticancer agents are still one of the main priority for human health. Bioprospection from marine environment appears as one of the possible sources, exemplified by numerous secondary metabolites isolated from marine macroorganisms being the starting point of significant advances in some cancer treatments[2]. The objective of the project is the chemical study of marine sponges from Wallis Island[3] in Oceania to isolate and characterize active molecules on osteosarcoma cell lines, which can also modulate the activity of protein kinases[4] or ion channels, controlling calcium signalling[5], in specific signaling pathways involved in tumour development. In this context, 7 on 43 sampled marine sponge species have been selected based on the bioactivity of their extracts. Priority was initially given to 4 species (*Dendrilla* sp., *Fascaplysinopsis* sp., *Lissodendoryx* sp., and *Halichondria* sp.) to build bioactive-based molecular networks highlighting the potential metabolites responsible for the activity observed. Thus, a bioguided isolation approach led to the isolation and characterization of several natural products belonging to diverse chemical families such as bromotyrosines, sesquiterpene hydroquinones, pyrroloiminoquinones, or sulfated sterols. The potential of these natural compounds as anticancer agents against osteosarcoma is currently evaluated.

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PP 60 SESQUITERPENES FROM A RED SEA ALCYONARIAN OF THE GENUS *LEMNALIA*

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Soft corals are recognized as a prolific source of structurally diverse bioactive metabolites. Alcyonarians of the genus *Lemnalia* (Neptheidae) are notably rich in sesquiterpenes and nor-sesquiterpenes featuring various carbocycles, including the nardosinane and neolemnane skeletons. Such sesquiterpenes have exhibited a wide range of biological activities, including cytotoxic, anti-inflammatory and antiviral[1].

In the framework of our ongoing research towards the isolation of new biologically active marine metabolites, we investigated the chemical profile of a population of *Lemnalia* sp. collected by SCUBA diving from the coral reefs of Shi'b Sulaym, located near Al Lith on the south-west coast of the Kingdom of Saudi Arabia. The animal tissues were exhaustively extracted with mixtures of CH_2Cl_2/MeOH and the resulting organic residue was subjected to a series of chromatographic separations, yielding 55 sesquiterpenes, 46 of which were previously reported and 9 are new natural products. The structures of the isolated compounds were determined on the basis of thorough analysis of 1D- and 2D-NMR and MS data.

The majority of the isolated metabolites featured the nardosinane and neolemnane carbon skeletons. Additionally, aristolane, aromadendrane and eremophilane type sesquiterpenes were isolated. In a previous study of our team on a different population of *Lemnalia* sp. collected from Al Jadir, another region of the south-west coast of the Kingdom of Saudi Arabia near Al Lith, a total of 31 sesquiterpenes were isolated[2]. Both alcyonarian populations were characterized by nardosinane and neolemnane type sesquiterpenes. However, the population from Shi'b Sulaym displayed a more complex chemical profile in terms of total number of isolated compounds, including also aromadendrane derivatives, a group of sesquiterpenes not previously isolated from the genus.

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PP 61 SPATANES AND SECO-SPATANES FROM THE INVASIVE BROWN ALGA *Rugulopteryx Okamurae*

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Brown algae of the family Dictyotaceae are primarily distributed in tropical and subtropical oceanic regions and are considered an abundant source of biologically active secondary metabolites. Among the structurally diverse compounds that characterize the secondary metabolome of these brown algae, terpenes represent the most characteristic group of metabolites[1]. Diterpenes isolated from various genera of this family have demonstrated a wide range of biological properties, including cytotoxic, antifungal, antiviral and anti-inflammatory. The species *Rugulopteryx okamurae*, although native to the northwestern Pacific Ocean, is rapidly expanding along the southwestern coasts of Europe and across the Mediterranean Sea as an invasive opportunistic species.

In the framework of our ongoing research towards the discovery of new bioactive compounds, we investigated the chemistry of two *R. okamurae* populations collected from deep and shallow waters along the Cadiz coastline. Specimens of both populations were exhaustively extracted with CH_2Cl_2/MeOH and the organic residues were subjected to multiple chromatographic separations leading to the isolation of 24 diterpenes featuring the spatane and seco-spatane skeletons. Specifically, 16 spatanes and 8 seco-spatanes were isolated and identified on the basis of extensive analyses of their NMR and MS spectroscopic data. Among them, 11 are new natural products. The evaluation of the bioactivity of the isolated compounds is currently ongoing.

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PP 62 STEREOCHEMICAL STUDY OF A PEROXIDE-DERIVED POLYKETIDE BY VIBRATIONAL CIRCULAR DICHROISM AND QUANTUM CHEMICAL CALCULATIONS

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Peroxide-derived polyketides isolated from marine sponges, resulting from peroxide rearrangement or reduction, are structurally diverse secondary metabolites with promising biological activities[1]. Since the stereochemistry of a given compound is often closely related to its biological activity, the determination of absolute configurations is an important step in the characterization of bioactive compounds[2]. The endoperoxide polyketide (**1**) (Figure 1), containing four stereogenic centers, was previously isolated from the Brazilian marine sponge *Plakortis angulospiculatus* and had its absolute configuration assigned based on the comparison of optical rotation data, biosynthetic considerations, and NMR calculations[3,4]. Herein, we describe the isolation of an structurally-related endoperoxide polyketide from the same species, collected at the Fernando de Noronha Archipelago. Detailed analyses of the ^{13}C and ^{1}H NMR data together with simulated NMR chemical shifts and DP4+ analysis suggest that the metabolite isolated in this work (**2**) is a diastereoisomer of **1**. Considering that the biological activity of these compounds can be affected by small structural changes[5], VCD associated with quantum chemical calculations was applied for the unequivocal assignment of the absolute configuration of **2**. Finally, this work highlights the advantages of using VCD for stereochemical analysis of natural product molecules and may contribute to chemotaxonomic studies on Brazilian marine sponges.

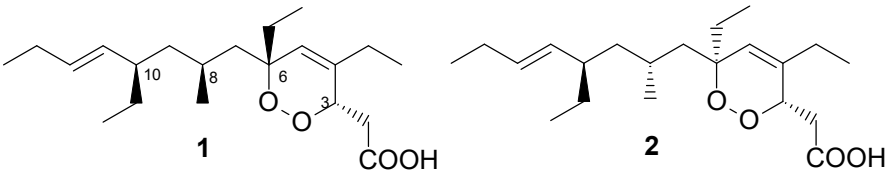

Figure 1. Structures of the endoperoxide polyketides **1** and **2**.

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PP 63 TERPENOIDS AND ACETOGENINS FROM *DICTYOTA* AND *LAURENCIA* SPECIES FROM THE GREEK SEAS

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The genus *Dictyota* (Dictyotaceae), comprising *c.* 40 species widely distributed in the tropical and subtropical regions of the Atlantic, Pacific and Indian Ocean, in the Sea of Japan, as well as in the Mediterranean Sea, is one of the most interesting genera of brown algae, with a rich chemical profile, characterized mainly by sesqui- and diterpenes[1].

Among red algae, the genus *Laurencia* (Rhodomelaceae), comprising approx. 140 accepted species distributed in tropical, subtropical and temperate coastal waters, is one of the richest sources of new secondary metabolites in the marine environment[1]. Up to now, almost 1,200 secondary metabolites, mostly halogenated C_{15} acetogenins and terpenes often displaying unprecedented carbon skeletons, have been reported from *Laurencia* sp. and mollusks of the genus *Aplysia* that feed on them.

Secondary metabolites isolated from *Dictyota* and *Laurencia* species exhibit a wide spectrum of biological activities, such as antibacterial, antifungal, antiviral and antifouling, as well as cytotoxic, anti-inflammatory, anti-platelet and anti-coagulant[1].

Over the last decades, we have collected from different localities in the Aegean and Ionian seas a high number of specimens belonging to the genera *Dictyota* and *Laurencia* species, which have been submitted to analysis of their chemical profiles either through metabolomic analyses or through phytochemical analysis, leading so far to the identification of several dozens of terpenoids and acetogenins, including a high number of new natural products.

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PP 64 UNLOCKING BLUE ECONOMY OPPORTUNITIES: A CRITICAL ANALYSIS OF SOUTH KOREA'S WEST SEA

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The West Sea of South Korea (Yellow Sea) supports a highly productive marine ecosystem, shaped by shallow depths, strong tidal forces, and nutrient-rich waters[1,2]. Extensive tidal mudflats, which rank among the most ecologically and economically valuable in the world, provide critical habitats for aquaculture and migratory species[3,4]. Despite this ecological richness, the full biotechnological and economic potential of the region's marine resources remain largely untapped. This analysis synthesizes available data on key biological groups—fish, seaweed, shellfish, halophytes, and microorganisms—and explores their emerging contributions to sustainable blue economy sectors[5]. Systematic literature searches and national reports identified high-value opportunities, including the extraction of bioactive compounds from endemic species and microalgae, functional polysaccharides and antioxidants from brown macroalgae, valorisation of macroalgal biomass waste for bioplastic and biosurfactant, and exploitation of marine invertebrates and microorganisms for novel antimicrobials. Integrated multi-trophic aquaculture (IMTA) systems and the upcycling of fisheries and seaweed residuals are also highlighted as critical pathways to enhance circular bioeconomy initiatives[6]. However, current valorisation efforts face challenges such as technological limitations and high processing costs. The review emphasizes the need for interdisciplinary innovation combining marine biotechnology, biology, and sustainability science. Advancing the valorisation of the West Sea's rich marine and mudflat resources offers a unique opportunity to drive blue economic growth, reduce marine waste, and contribute to Sustainable Development Goals (SDG 14: Life Below Water; SDG 12: Responsible Consumption and Production)[7].

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PP 65 GREEN EXTRACTION OF PIGMENTS FROM PREDATORY MACROALGAE IN THE GALICIAN SEA VIA SUPERCRITICAL FLUIDS

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Supercritical carbon dioxide ($scCO_2$) is a tunable, green solvent with exceptional transport properties, enabling efficient extraction of nonpolar and slightly polar compounds from biomass without generating solvent waste[1]. Its selectivity, inertness and scalability make it ideal for recovering high-value bioactive molecules, such as the pigment fucoxanthin, which exhibits antioxidant, anti-inflammatory, and potential anti-obesity properties[2]. The brown macroalga Wakame (Undaria pinnatifida), native to Asia, has become an invasive species in coastal ecosystems worldwide. In the Irish sea, its proliferation threatens native biodiversity by outcompeting local algae and disrupting marine habitats[3]. However, Wakame's high fucoxanthin content presents an opportunity for dual ecological and economic valorisation: removing this invasive species could restore coastal biodiversity while yielding commercially valuable extracts.

In this study, $scCO_2$ extraction was optimized for fucoxanthin recovery from European-harvested Wakame and compared to conventional solvent-based methods. $ScCO_2$ demonstrated superior selectivity and extract purity, minimizing co-extraction of polar impurities. A systematic optimization of different pressure and temperature profiles yielded a fucoxanthin extraction efficiency of 52.7 mg/g extract. This represents a 7-fold increase in purity compared to conventional extraction (7.5 mg/g extract).

By targeting invasive Wakame populations in coastal regions in Europe, this approach aligns with circular economy principles, transforming an ecological threat into a source of nutraceutical or cosmetic ingredients. Future work should explore the effects of increasing extraction pressure and yield optimization as well as possible encapsulation methods for the obtain fucoxanthin rich supercritical extracts. The use of green co-solvents may further improve extraction efficiency while preserving the environmental benefits of the process.

Acknowledgements

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