

Advances in Biome Research of Ulva



SeaWheat
COST Action CA20106

SeaWheat COST Action Workshop

March 18-19, 2025

**Auditorium 1.4, Edf 9 – complex Pedagógico
Universidade do Algarve, Campus da Penha,
Faro, Portugal**

Venue

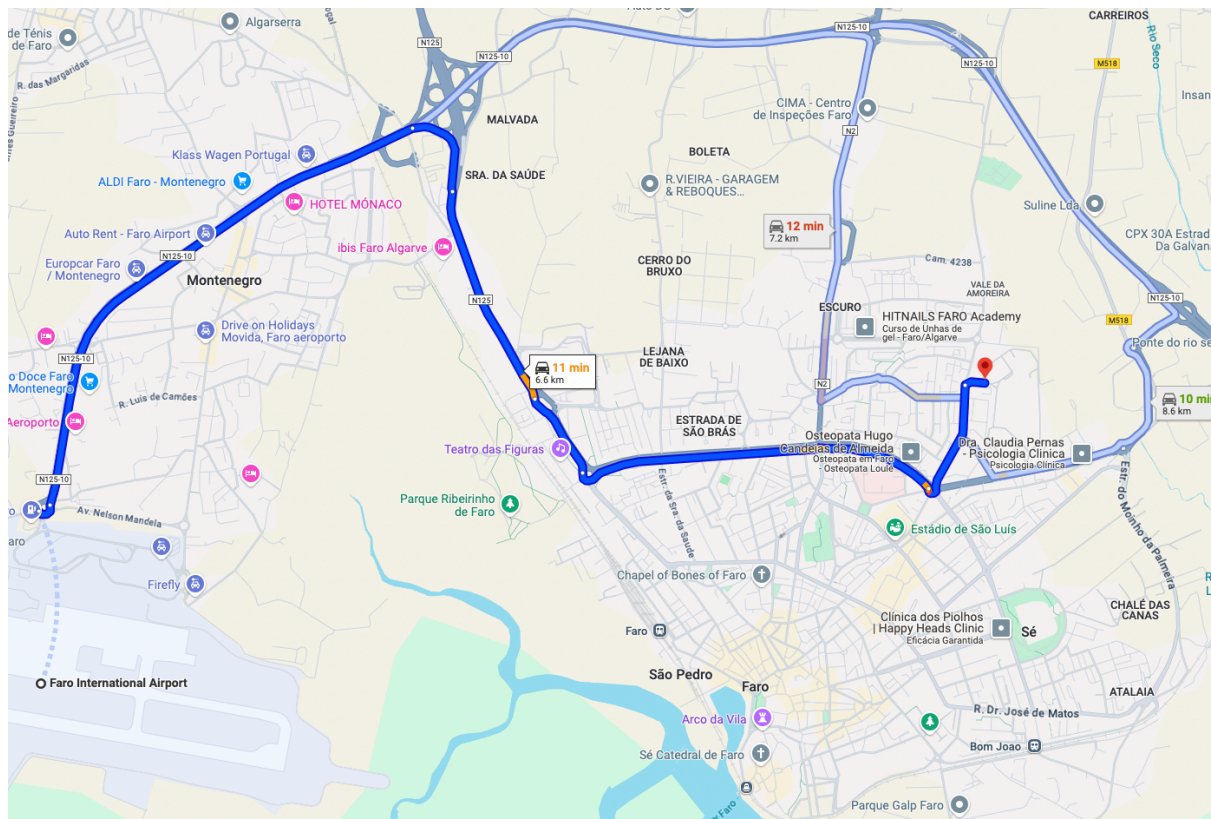
Contact Aschwin Engelen: 00351 934977238

How to get to the meeting venue

The meeting venue is situated in the Penha campus of the Universidade do Algarve, Auditorium 1.4 in building 9: Edf 9 – complex Pedagógico, 8005-139 Faro.



Map of the Campus da Penha with the venue as number 9 on the map and the campus entrance indicated as 1.



Program

March 17		
17:00-19:00	ICEBREAKER	Bar/Pub/Restaurant O Castelo, Rua do Castelo 11, 8000-243 Faro
Workshop programme		Advances in Biome Research of Ulva
March 18		
	Topic	Speaker
9:00-9:15	Welcome	Aschwin Engelen + SeaWheat representative
9:15-10:00	RIDING THE MICROBIAL TIDE: PAST, PRESENT AND FUTURE DIRECTIONS IN MARINE HOST-MICROBE INTERACTIONS	Gerard Muyzer (UvA, The Netherlands)
10:00-10:15	COFFEE BREAK	
Session 1	The Biome of Ulva - an introduction (e.g., bacteria, epiphytes, virus, fungi)	
10:15-11:00	STRUCTURE, DIVERSITY, AND FUNCTION OF THE CORAL MICROBIOME	Christian Voolstra
11:00-11:25	THE ULVA MICROBIOME: BEYOND BACTERIA	Luna van der Loos
11:25-11:50	AN EXPERIMENTAL TEST OF THE INFLUENCE OF MICROBIAL MANIPULATION ON SUGAR KELP (<i>SACCHARINA LATISSIMA</i>) SUPPORTS THE CORE INFLUENCES HOST FUNCTION HYPOTHESIS	Laura Wegener Parfrey
11:50-12:15	<i>Ulva</i> associated fungi and oomycetes from <i>Ulva</i> production industry	Cristiana Maia
12:15-13:30	LUNCH BREAK	
Session 2	Ecophysiological function and testing of e.g. microbial traits	
13:30-14:15	DECODING THE HIDDEN SECRETS OF PLANT MICROBIOMES	Adam Ossowicki
14:15-14:40	Unlocking the Secrets of Ulva: How Microbes Shape the Growth, Morphogenesis, and Survival of Sea Lettuce	Thomas Wichard

14:40-15:05	EVOLUTION OF METABOLIC COMPLEMENTARITY IN ALGAL-BACTERIAL SYMBIOSES	Simon Dittami
15:05-15:30	Light-regulated interactions between <i>Phaeobacter</i> sp. and <i>Ulva ohnoi</i> (Chlorophyta): Effects on microbiome dynamics, metabolome composition, and tropodithietic acid production.	Zujaila QuiMinet
15:30-16:00	TEA BREAK	
16:00-16:25	THE CHEMICAL 'LANGUAGE' OF THE ALGAL HOLOBIONT	Mahasweta Saha
16:25-17:00	Day Discussion	Thomas Wichard
19:30	DINNER	Tertúlia Algarvia - Praça D. Afonso III, 13-15, 8000-167 Faro, Portugal
Session 3	Microbiome analysis & microbiome dynamics	
March 19		
9:00-9:45	DIVERSITY, DISTRIBUTION AND ROLE OF CORAL PROTIST SYMBIONTS	Javier del Campo
9:45-10:10	DIVERSITY AND STRUCTURE OF THE ULVA MICROBIOME IN INDUSTRIAL PRODUCTION	Aschwin Engelen
10:10-10:35	HOW MANY CORE MICROBIOMES EXIST IN A SEAWEED HOLOBIONT?	Florian Weinberger
10:35-10:50	COFFEE BREAK	
10:50-11:15	Micropollutants challenge the core microbiome of <i>Ulva compressa</i> .	Justus Hardegen
11:15-11:40	TEMPORAL DYNAMICS IN THE MICROBIAL COMMUNITY ASSOCIATED WITH <i>ULVA FASCIATA</i> IN AN INTEGRATED MULTI-TROPHIC AQUACULTURE SYSTEM	Lior Guttman
Flash talks		
11:40-11:50	The cultivable bacteria of <i>Ulva</i> and <i>Codium</i> from wild and production	Myrsini Lymperaki
11:50-12:00	Seagrass microbiome engineering to improve seed germination for restoration	Julia van Duijnhoven

12:00-12:10	Microbiome of early life stages of temperate gorgonians	Rita Camacho
12:10-12:20	Frontiers special issue announcement	Erik-jan Malta
12:20-12:30	EUlva update	Luna vd Loos & Aschwin Engelen
12:30-13:30	LUNCH BREAK	
Session 4	Microbiome/Biome engineering/Stress	
13:30-14:15	HUMAN GUT MICROBIOME ENGINEERING: UNLOCKING THE GENETIC VAULT	James Marsh (gut, MPI Tübingen)
14:15-14:40	VISUALIZING MICROBIAL INTERACTIONS IN ULVA MUTABILIS WITH FLUORESCENTLY LABELLED BACTERIA	Sebastian Jeß
14:40-15:05	BIOREMEDIATION OF OZONE-PRODUCED OXIDANTS IN MARINE RAS USING ULVA: BENEFITS AND IMPACTS ON SEAWEED PHYSIOLOGY AND ASSOCIATED MICROBIOMES	Sabine Weidlich
Session 5	Commercial applications of <i>Ulva</i> microbiomes	
15:05-15:30	THE PLANT MICROBIOME: ECOLOGY, FUNCTIONS AND BENEFITS FOR SUSTAINABLE CROP PRODUCTION	Stéphane Compant
15:30-15:45	TEA BREAK	
15:45-16:10	CAN ULVA IN IMTA-RAS WITH FISH MODIFY THE GLOBAL MICROBIOME OF THE SYSTEM?	José Pintado
16:10-16:35	COMMERCIAL POTENTIAL OF ULVA MICROBIOMES IN AQUACULTURE APPLICATIONS	Erik-Jan Malta
16:35-17:00	MICROBIAL COMMUNITY DYNAMICS AND ENVIRONMENTAL INFLUENCES IN ULVA OHNOI LAND-BASED AQUACULTURE: IMPLICATIONS FOR DISEASE CONTROL	Ricardo Cruz-Lopez
17:00-17:25	BACTERIOME-MEDIATED IMPROVEMENT OF INDUSTRIALLY PRODUCED CHLORELLA VULGARIS	João Varela
17:25-18:00	Workshop discussion	



18:00	Closure	

Abstracts

RIDING THE MICROBIAL TIDE: PAST, PRESENT AND FUTURE DIRECTIONS IN MARINE HOST-MICROBE INTERACTIONS

MUYZER G.

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Abstract

In this presentation, I will provide a historical overview, examine current challenges, and propose future research directions to advance our understanding of host–microbe interactions in marine organisms. As a case study, I will focus on *Caulerpa*, a genus of green algae found in tropical and subtropical coastal waters¹. Certain *Caulerpa* species are invasive and toxic, while others are opportunistic and threaten marine flora and fauna. For instance, *C. cylindracea* disrupts seagrass meadows in the Adriatic Sea², *C. prolifera* reduces faunal diversity in southern Portugal³, and *C. filiformis* has sublethal effects on a key herbivore in Australia⁴. With global warming driving the tropicalisation of temperate ecosystems, it is likely only a matter of time before *Caulerpa* species expand into higher latitudes.

Despite its plant-like appearance, *Caulerpa* is a single giant cell containing multiple nuclei, chloroplasts, mitochondria, and symbiotic bacteria—collectively forming a “holobiont”^{5,6}. Although little is known about the roles of these bacterial symbionts, they may influence the host’s growth and development, facilitate adaptation to environmental stress⁷, and contribute to the ecological success of these so-called “killer” algae.

To investigate interactions between *Caulerpa* and its symbionts, we employed a systems biology approach that integrates manipulative experiments, “culturomics,” multi-omics, and metabolic modeling⁸. While such a holistic strategy is rarely applied in marine sciences, it is essential to test hypotheses, predict holobiont responses to climate change⁹, and evaluate the risk of further invasions. As part of this effort, we sequenced the hologenomes of three *Caulerpa* species (*C. prolifera*, *C. lentillifera*, and *C. racemosa*), analysed the impact of sulfide on both algae and their symbionts using metatranscriptomics, and developed a preliminary genome-scale metabolic model.

References

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Acknowledgments

I gratefully acknowledge the valuable contributions of Anastasiia Barilo, Evelien Jongepier, Aschwin Engelen, Verna Cola and Douwe Molenaar, whose expertise was instrumental to the research on *Caulerpa*. This work was supported by the University of Amsterdam’s Research Priority Area “Systems Biology.”

Short biography

Gerard Muijzer is a Professor of Microbial Systems Ecology at the University of Amsterdam, where his research explores the structure, function, and dynamics of microbial communities, emphasising their

roles in biogeochemical cycles and biotechnological applications. He employs a systems biology approach to integrate experimental methods with advanced omics techniques and metabolic modelling. His primary focus is on the microbial sulfur cycle, particularly sulfur bacteria in natural environments (e.g., soda lakes and stratified lakes) and engineered ecosystems, such as full-scale bioreactors designed to remove toxic sulfur compounds from wastewater. Since 2012, he has expanded his investigations to include host-microbe interactions in sponges, seagrasses, and marine algae, particularly the green macroalga *Caulerpa*. For further information, please visit his ORCID profile: <https://orcid.org/0000-0002-2422-0732>.

STRUCTURE, DIVERSITY, AND FUNCTION OF THE CORAL MICROBIOME

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Abstract

Coral reefs are important marine ecosystems, supporting immense biodiversity and providing significant ecological and economic benefits. Corals and the reefs they build face unprecedented decline from local and global anthropogenic pressure. Central to the health and resilience of coral reefs is the microbiome, a complex community of microorganisms that inhabit coral tissues, mucus, and the surrounding environment. Microbial communities play a critical role in maintaining coral health, mediating nutrient cycling, and enhancing stress tolerance. Given the importance of the microbiome to host physiology and resilience, current research aims to manipulate the microbiome to provide an alternative path to organismal environmental adaptation. Although the premise of microbiome stewardship and microbiome rescue are demonstrated in principle, the underlying mechanisms or the ability of microbes to form stable novel associations is unknown. The presentation will summarize the current state of knowledge regarding the structure, function, and specificity of the coral microbiome, our efforts regarding functional screening for microbes that ameliorate stress, and elucidation of the underlying mechanisms. Discovery of microbes and microbial mechanisms mediating stress tolerance and our ability to harness them may inform active interventions to protect natural populations and conserve organismal and ecosystem biodiversity.

References

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Short Biography of the speaker

Dr. Voolstra studies coral reefs combining ecological, environmental, microbial, and molecular approaches. His most recent research particularly advanced knowledge of how the microbiome contributes to coral acclimation/adaptation and the delineation of standardized analytical methods (SymPortal, CBASS short-term acute thermal assays, Coracle, etc.) to fasten the development of approaches to mitigate climate change. He is an advocate of open science, open access, and free data sharing. Dr. Voolstra has published over 300 peer-reviewed research papers, various book chapters, and holds patents related to bioactive lead structures from marine organisms. Dr. Voolstra is the current president of the International Coral Reef Society (ICRS), stressing the urgency of developing and applying science-based solutions to coral reef restoration following a rigorous, evidence-based decision framework. Dr. Voolstra received his PhD at the Institute for Genetics in Cologne, Germany, was a Postdoctoral scholar at the University of California, Merced, before joining KAUST's Red Sea Research Center in Saudi Arabia as faculty, where he served as the Associate Director from 2016 to 2019. In 2019, Dr. Voolstra moved to the University of Konstanz, Germany where he is Professor (Chair) of Genetics of Adaptation in Aquatic Systems.

THE *ULVA* MICROBIOME: BEYOND BACTERIA

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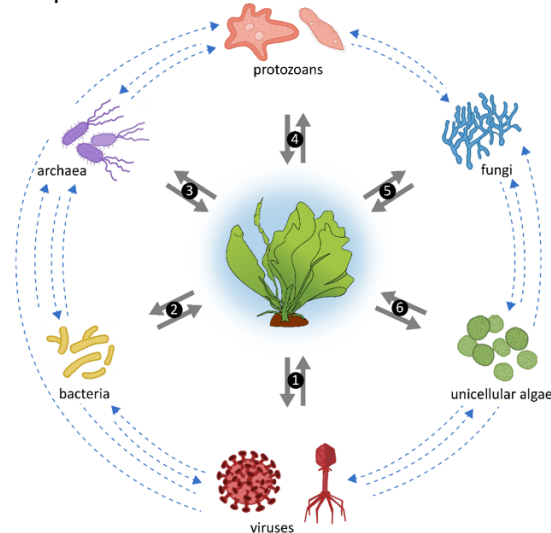
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Abstract

Seaweeds live together in symbiosis with numerous microorganisms, including bacteria, fungi, and viruses. These microorganisms are essential to the life and functioning of seaweeds. The green seaweed *Ulva* in particular is a model system to study seaweed-bacteria interactions, as they depend on their bacterial symbionts for normal morphological development and growth. Surprisingly little, however, is known about the other symbionts of the *Ulva* microbiome. Using metagenomic sequencing, we characterized viral communities associated with healthy and bleached specimens of *Ulva* for the first time. We identified 20 putative novel and divergent viruses, the majority of which belonged to undescribed viral families. Bleached *Ulva* samples contained particularly high viral read numbers. While reads matching assembled CRESS DNA viruses and picorna-like viruses were nearly absent from the healthy *Ulva* samples (confirmed by qPCR), they were very abundant in the bleached specimens. In addition, we assembled 37 near-complete (>90%) bacteriophage genomes associated with the *Ulva* biofilm, adding another layer of complexity to *Ulva*-bacterial interactions. Phage species often infect a small range of bacterial strains and the identified bacteriophages in our dataset included multiple phages specifically infecting, amongst others, *Alteromonas*, *Loktanella*, *Nonlabens*, *Roseovarius*, and *Sulfitobacter*. The bacteria that are infected by these phages are well-known symbiotic partners of the *Ulva* biofilm and some play a pivotal role in *Ulva* growth and morphogenesis. It is clear that a wealth of seaweed-associated microorganisms and symbiotic relationships remain to be discovered, if we look beyond bacteria.

Graphical abstract:



Short Biography of the speaker

Luna van der Loos conducted her PhD at Ghent University focusing on the *Ulva* microbiome. After her PhD, Luna continued exploring *Ulva* biodiversity within the European *Ulva* Taxonomy Initiative and worked on *Ulva* genomics. She recently started her tenure track at the Naturalis Biodiversity Center in the Netherlands.

AN EXPERIMENTAL TEST OF THE INFLUENCE OF MICROBIAL MANIPULATION ON SUGAR KELP (*SACCHARINA LATISSIMA*) SUPPORTS THE CORE INFLUENCES HOST FUNCTION HYPOTHESIS

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Abstract

Microbial symbionts influence many aspects of the biology of kelp and other macroalgae. Manipulating the microbiome through addition of probiotics may be a sustainable way to improve macroalgal productivity, health, and resilience for aquaculture and conservation. The core microbiome hypothesis suggests that the bacteria that are consistently found on a host (the core microbes) are likely to have a disproportionate impact on host biology, making them an attractive target for microbiome manipulation. In this study, we surveyed wild *Saccharina latissima* and their surrounding environment to assess bacterial distributions and identify core bacteria on sugar kelp and experimentally tested how cultured bacterial isolates affect kelp development. We found a significant positive relationship between ecological distribution and impact on gametophyte settlement and sporophyte development in kelp co-culture experiments. These findings are consistent with predictions from the core microbiome influences host function hypothesis and suggest that incorporating knowledge of ecological distribution when designing microbiome manipulation trials will increase success rates.

Short Biography of the speaker

Laura Wegener Parfrey is a biologist studying microbial ecology and evolution. Her lab at the University of British Columbia works to understand how symbiosis with kelp and other macroalgae shape the ecology and evolution of microbes, how these relationships change in changing environmental conditions, aims to use this knowledge to develop microbiome-based strategies to enhance the productivity and sustainability of macroalgal aquaculture. She holds a Ph.D. in organismal and evolutionary biology from the University of Massachusetts and BS in Biology from SUNY at Albany.

ULVA ASSOCIATED FUNGI AND OOMYCETES FROM THE ALGAE PRODUCTION INDUSTRY

MAIA, C.¹, LYMPERAKI, M. M.¹, AIRES, T.¹, MARTINS, M.², MENDES, C. M.^{2,3,4},
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Abstract

The genus *Ulva*, a green macroalgae commonly known as sea lettuce, has attracted significant attention in the macroalgal production industry due to its ecological and commercial potential. With its rapid growth rates and beneficial nutrient profile, *Ulva* is an ideal candidate for use in various sectors such as food, pharmaceuticals, nutraceuticals, and biofuels. Given its commercial importance, it is crucial to identify potential pathogens that could negatively affect *Ulva* production and result in financial losses. To investigate the fungal and oomycete microbiome associated with *Ulva* species and assess their pathogenic potential, seasonal isolations were carried out in 2024 and January 2025 on biomass provided by the seaweed producer ALGAplus and indirectly by deploying baiting rafts in *Ulva* production tanks and a sedimentation earthen pond. This approach led to the direct isolation of 16 fungal isolates and the indirect isolation of 43 fungal isolates. Sequencing of the ITS region identified several fungal genera, including *Cladosporium*, *Diaporthe*, and *Penicillium*, among others. As for oomycetes, no isolations were obtained from the *Ulva* biomass or production tanks; however, they were isolated from a sedimentation earthen pond where *Ulva* was growing. Infection trials with oomycetes on *Ulva* are currently underway.

Acknowledgments

The authors would like to acknowledge “Pacto da Bioeconomia azul” (Project No. C644915664-00000026) within the WP5 Algae Vertical, funded by Next Generation EU European Fund and the Portuguese Recovery and Resilience Plan (PRR).

Short Biography of the speaker

Cristiana Maia is a Microbiologist with an interest in oomycetes and fungi associated with seagrasses and seaweeds. She earned her BSc in Microbiology from Escola Superior de Biotecnologia, Universidade Católica Portuguesa and her MSc in Molecular and Microbial Biology from Universidade do Algarve. In the last years she worked with the marine oomycete *Halophytophthora* and more recently started working with fungi associated with algae. Currently she is a PhD student at CCMAR working with oomycetes and identifying their ecological roles and potential biotechnological activities and also analysing the fungal and oomycete microbiome from algal species from the algae production industry.

DECODING THE HIDDEN SECRETS OF PLANT MICROBIOMES

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Abstract

Plant roots harbor an extraordinary diversity of microorganisms, with cell densities often surpassing those of the plant itself. Studies have shown that the plant microbiome plays a key role in enhancing plant tolerance to both abiotic (e.g., drought) and biotic stresses (e.g., disease), while also contributing to nutrition, growth, and development [1]. However, the functions and mechanisms of most plant-associated microorganisms remain poorly understood. Recent advances in 'omics technologies have expanded our knowledge of microbiome diversity and function, shedding light on the complex interactions within plant-associated microbial communities.

This presentation will provide new findings on the role of rhizosphere and endosphere bacteria in protecting plants from biotic and abiotic stresses. Additionally, we introduce bacLIFE [2], a novel bioinformatics tool designed for genome annotation, large-scale comparative genomics, and the prediction of lifestyle-associated genes (LAGs) in bacteria. Using bacLIFE, we analyzed 16,846 genomes from the *Burkholderia/Paraburkholderia* and *Pseudomonas* genera, identifying hundreds of genes potentially linked to plant pathogenic lifestyles. Site-directed mutagenesis and plant bioassays confirmed that six predicted LAGs are indeed involved in the phytopathogenic lifestyle, including genes encoding a glycosyltransferase, extracellular binding proteins, and homoserine dehydrogenases. An overview will be given on the wealth of genes and functions of the plant microbiome.

References

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UNLOCKING THE SECRETS OF *ULVA*: HOW MICROBES SHAPE THE GROWTH, MORPHOGENESIS, AND SURVIVAL OF SEA LETTUCE

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Abstract

Microbial communities play a crucial role in the ecophysiology of *Ulva* (Chlorophyta), influencing its growth, development, stress tolerance, and ecological interactions, including biofilm formation and the settlement of epibionts. While monitoring microbial dynamics provides valuable insights, one of the most challenging research areas remains the functional examination of microbial traits and their impact on *Ulva*.

Ecophysiological Functions of Microbial Traits in Ulva: A key function of surface-associated microbes is their role in *Ulva*'s morphogenesis and growth regulation. The presence of bacteria from the Roseobacteraceae and the genus *Maribacter* is essential for suitable morphological development, as axenic (bacteria-free) cultures develop into a callus. Specific bacteria release algal growth and morphogenesis-promoting factors, such as thallusin, which induce cell differentiation and cell wall formation and organize thallus development. Without these bacterial signals, *Ulva* remains in an undifferentiated or irregular growth state [1]. Beyond morphogenesis, microbial communities are also crucial for nutrient uptake and metabolism. *Ulva* relies on associated bacteria to enhance nitrogen, carbon cycling, or metal homeostasis. Additionally, microbial partners contribute to stress tolerance, enabling *Ulva* to withstand fluctuating environmental conditions, including variations in salinity, temperature, light, and pH [2, 3]. For example, under temperature changes, specifically stress-adapted bacteria must provide "core functions" such as thallusin production, which is necessary for *Ulva*'s growth under Antarctic conditions at 2°C [3].

Testing of Microbial Traits in Ulva: Notably, a changing microbiome can exhibit consistent traits and maintain functional stability in a dynamic environment. In contrast, a stable microbiome may also exhibit functional shifts in response to biotic or abiotic factors [4]. Therefore, experimental testing of microbial features is required to separate the two situations or complement bacterial activity. Testing microbial traits in *Ulva* involves axenic vs. non-axenic cultures, microbiome sequencing, and stable isotope tracing to analyze microbial influences on nutrient cycling, growth, and stress responses. Additional methods, such as physiological measurements, metabolomics, and bacterial/algal co-cultivation, identify functional interactions and their impact on *Ulva*'s ecophysiology.

This presentation highlights the importance of integrating functional examinations with microbiome analysis to identify trait variations in the (core) microbiome, even when microbiome composition remains unchanged.

References

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Acknowledgments

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Short Biography of the speaker

Thomas Wichard is a research group leader and lecturer in Analytical Chemistry at the Institute for Inorganic and Analytical Chemistry of the Friedrich Schiller University Jena (Germany). After being awarded a PhD in Biochemistry (Max Planck Institute for Chemical Ecology), he investigated the metal recruitment of nitrogen fixers at the Princeton Environmental Institute (USA). His team applies various analytical chemistry, chemical ecology, and molecular biology methodologies to understand the basis of eco-physiological processes in bacteria-macroalgae interactions (cross-kingdom interactions).

EVOLUTION OF METABOLIC COMPLEMENTARITY IN ALGAL-BACTERIAL SYMBIOSES

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Abstract

Metabolic complementarity is hypothesized to underpin beneficial interactions between symbiotic organisms, allowing the partners to potentially expand their combined metabolic capabilities by offsetting metabolic deficiencies. While genome-based metabolic models offer a promising avenue to predict such complementarity *in silico*, empirical evidence validating these predictions remains scarce. Here we analyzed 1300 algal-associated bacterial and 40 algal host genomes to investigate the specificity and evolution of metabolic complementarity. We addressed two key questions: 1) Does metabolic complementarity preferentially occur between algae and their direct bacterial associates compared to free-living relatives? and 2) To what extent is complementarity specific to host-bacterial pairs?

The comparative analysis of algal-associated and free-living bacteria did not consistently demonstrate enhanced metabolic complementarity in host-associated strains. However, we identified 38 bacterial taxa exhibiting significantly higher complementarity with their host or closely related algae than with phylogenetically more distant relatives. Metabolic complementarity varied significantly across bacterial classes, with e.g. Bacteroidia displaying high levels of complementarity but low host specificity, while e.g. Gammaproteobacteria demonstrated greater host specificity. The precise metabolic exchanges underpinning these patterns are currently being explored. Our findings provide novel evidence supporting the co-evolution of metabolic complementarity between algal hosts and specific members of their microbiome.

Short Biography of the speaker

I am a permanent CNRS researcher working on the interactions between brown algae and their associated microbiome. My research subjects include metabolic cooperation between the microbiome and the host, but also role of the adaption of brown algae to environmental stress, or the transmission of the microbiome. To address these questions, I integrate genomic data, (meta-) transcriptomics, metabolite profiling, and genome-based metabolic networks to predict possible beneficial metabolite exchanges between partners. In parallel, I work on the isolation of bacterial partners and establishing co-culture experiments to be able to test any hypotheses generated *in vitro*. Most of my work is carried out on the species *Ectocarpus subulatus*, *Saccharina latissima*, and *Ascophyllum nodosum*.

LIGHT-REGULATED INTERACTIONS BETWEEN *PHAEOBACTER* SP. AND *ULVA OHNOI*(CHLOROPHYTA): EFFECTS ON MICROBIOME DYNAMICS, METABOLOME COMPOSITION, AND TROPODITHIETIC ACID PRODUCTION.

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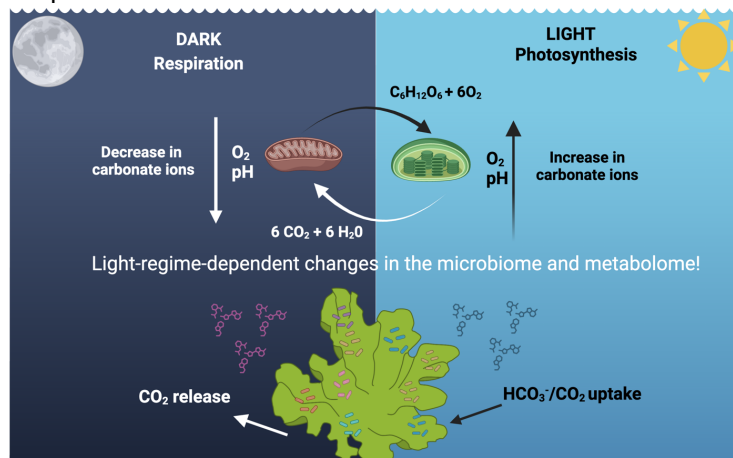
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Abstract

Ulva spp. are economically important macroalgae with various industrial applications, including as biofiltration agents for fish effluents in integrated multi-trophic aquaculture recirculating systems (IMTA-RAS) [1]. Recent works have proposed inoculating *U. ohnoi* with the probiotic bacterium *Phaeobacter* sp. strain 4UAC3 to tackle fish pathogens such as *Vibrio* spp. in IMTA-RAS [2]. However, the disappearance of *Phaeobacter* sp. 4UAC3 upon inoculation of *U. ohnoi* under a regular photoperiod presents significant challenges [3]. This study aimed to investigate how different light regimes impact the relationship between the *U. ohnoi* holobiont and *Phaeobacter* sp., focusing on how the colonization of *Phaeobacter* sp. strain 4UAC3 on *U. ohnoi* surfaces affects the alga's microbiome and metabolome dynamics. We also sought to validate the presence of tropodithietic acid (TDA), which can act as a probiotic. The study revealed the critical role of light in shaping microbial interactions between *Phaeobacter* sp. and *U. ohnoi*: The light regime significantly altered the microbial community structure, metabolite production, and physiological responses of both the bacterium and the alga. *Phaeobacter* sp. strain 4UAC3 thrived in darkness, modulating the microbiome and the *exo*- and *endo*-metabolomes of *U. ohnoi*. TDA was only identified under dark conditions and released into the algal chemosphere, while *Phaeobacter* antimicrobial properties were most pronounced in close association with the alga. These findings underline the importance of environmental factors, such as light regime, in driving microbial and molecular dynamics in marine holobionts. In addition, our results have direct implications for the application of *U. ohnoi* and *Phaeobacter* sp. in aquaculture, providing valuable insights for future research and practical applications in the field.

Graphical Abstract



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Acknowledgments

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Short Biography of the speaker

Zujaila N. Qui-Minet completed her PhD at the Station Biologique de Roscoff (Sorbonne University), where she investigated the physiology and ecology of coralline seaweed. She then worked in research and development in the private sector, focusing on plant and microalgae applications. In 2022, she began a postdoctoral position at IIM-CSIC (Spain) in collaboration with the University of Jena (Germany), studying seaweed-probiotic bacteria interactions for aquaculture applications. Since 2023, she has been working at LEMAR – IUEM – UBO (Brittany, France), examining how environmental factors shape the performance and senescence of proliferative seaweeds, and how these processes are associated with shifts in the microbiome and metabolome.

THE CHEMICAL 'LANGUAGE' OF THE ALGAL HOLOBIONT

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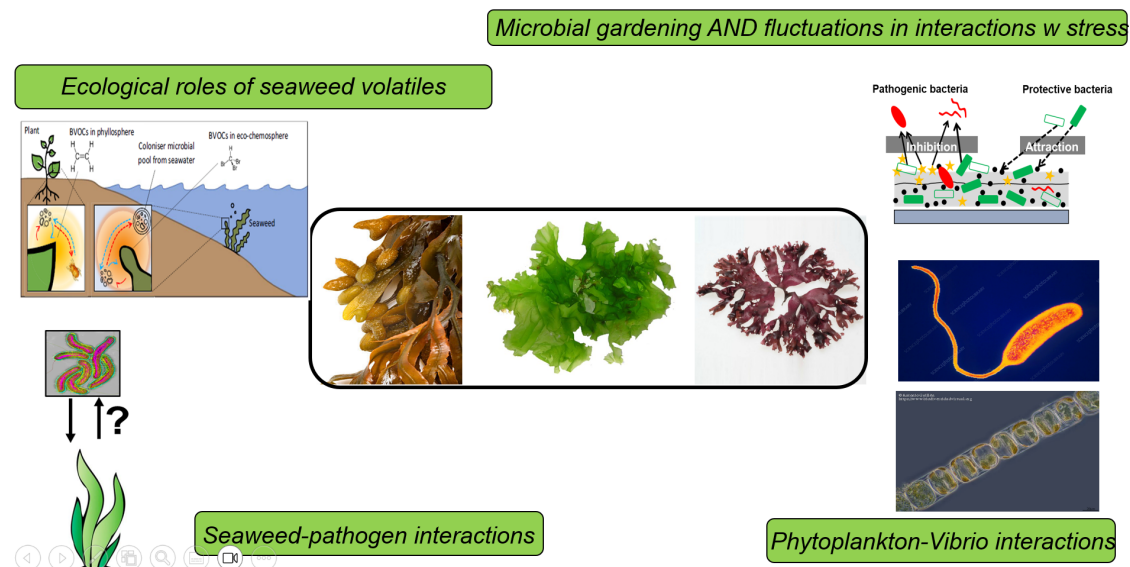
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Abstract

Marine algae form intimate relationships with microbes, collectively known as the 'algal holobiont'. These relationships often depend on chemical 'language', yet our understanding of them is limited compared to terrestrial environments. Climate-driven changes like rising temperatures, acidification, hypoxia, and desalination can significantly alter these interactions. My presentation will focus on how algae-bacteria interactions including interactions with pathogenic bacteria can fluctuate in response to stressors such as warmer oceans seaweeds and phytoplankton as model systems. I will also briefly touch upon the concept of microbial 'gardening' and how marine algal volatiles can influence interactions with microbes under temperature and light stress.



Short Biography of the speaker

Dr Saha currently leads the algal chemical ecology group at Plymouth Marine Lab. She has pioneered cross-cutting research on marine info-chemicals, holobionts, trace-gas info-chemistry, climate change and disease ecology and embraces an interdisciplinary approach. She completed her PhD in Algal Chemical Ecology at Helmholtz Centre of Ocean Research (GEOMAR), Germany with a German Academic Exchange fellowship. She sits on the editorial board of multiple international journals and has been awarded the Asian Women of Achievement award in Science category in 2021 and the Paul Somerfield mentorship award in 2024.

DIVERSITY, DISTRIBUTION AND ROLE OF CORAL PROTIST SYMBIONTS

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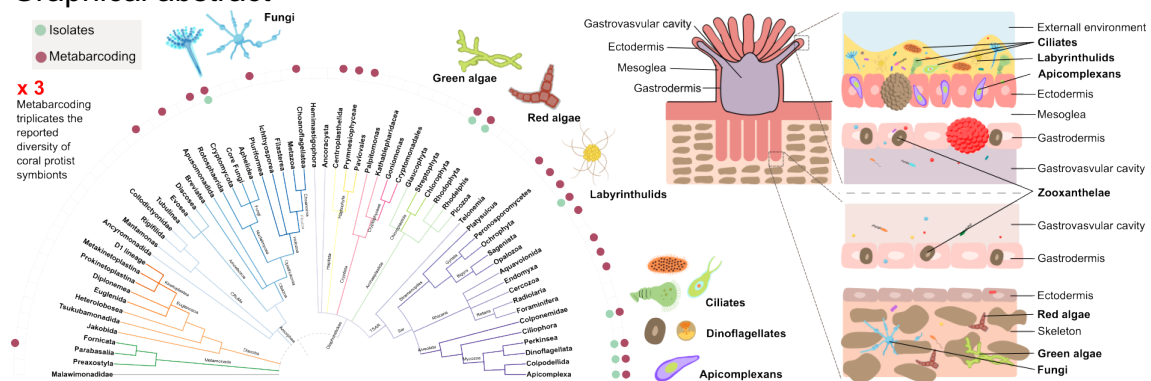
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Abstract

Corals are threatened by the current climate crisis in the form of ocean acidification and recurrent heat waves. Coral reefs and coralligenous habitats are biodiversity hotspots, provide many ecosystem services for the local communities and protect the shore from the effects of the rising seas. Losing the corals will dramatically impact the earth's biodiversity and the livelihood of coastal communities. The microbial members of the coral holobiont (the coral and its microbiome) strongly influence the host's evolution, physiology, and ecological functions. While some elements of the holobiont have been studied in detail and are well characterized, such as the zooxanthellae (Symbiodiniaceae), a unicellular eukaryotic alga that is essential for the survival of reef-forming corals or specific widespread bacterial symbionts such as *Endozoicomonas*, the study of other unicellular eukaryotes (protists) forming the holobiont has been neglected. Protists represent one of the primary sources of hidden genomic diversity (genomic dark matter) in most of the microbial habitats, including the coral holobiont. Not knowing this genomic diversity will not allow us to access the potential functions that these protists are playing in corals and how they might impact the resilience of corals to the effects of the climate crisis. Being ignorant of one of the components of the holobiont limits our capacity to fully understand coral biology and subsequently the coral reef and coralligenous ecosystems. My research group has already shown a sneak peek at the protist diversity hidden within the coral holobiont. Our preliminary data shows that we can describe 3 times more diversity of coral protist symbionts using metabarcoding than previously reported. Not only that, our preliminary data suggest that for at least one coral, the Mediterranean red gorgonian *Paramuricea clavata*, the composition of the protist symbionts community can predict how the coral will respond to heat stress. One question arises after these discoveries: could protists be key to understanding coral's resiliency to climate change?

Graphical abstract



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losses of chlorophyll biosynthesis in apicomplexan parasites. *Current Biology*, 2025.

Short Biography of the speaker

Dr. Javier del Campo is a microbial ecologist, Group Leader at the Institute of Evolutionary Biology (CSIC-UPF) in Barcelona, and an Adjunct Professor at the Rosenstiel School of Marine, Atmospheric, and Earth Science at the University of Miami. Dr. del Campo's research focuses on microbial symbionts and the effects of global warming on the microbiota of benthic and planktonic marine animals. While climate change significantly impacts free-living marine microbial communities, its effects on symbiotic microbes remain poorly understood. Microbial symbionts, both prokaryotic and eukaryotic, are essential to their host evolution, physiology, and ecological function. His work examines how global warming-driven environmental changes alter the composition and function of symbiotic microbial communities in key marine organisms—including corals, mollusks, and teleost fish—and how these shifts affect host health.

DIVERSITY AND STRUCTURE OF THE *ULVA* MICROBIOME IN INDUSTRIAL PRODUCTION

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Abstract

The *Ulva* microbiome plays a critical role in the industrial production of *Ulva* species in aquaculture, as it significantly influences the growth, health, and biochemical composition of the algae. Beneficial bacteria within the microbiome contribute to morphogenesis, nutrient cycling, enhance nutrient availability, and produce growth-promoting compounds, thereby improving biomass yield and quality. Additionally, the microbiome provides defense against pathogens through competitive exclusion and the production of antimicrobial substances, reducing the need for chemical treatments. A well-balanced microbiome also aids in maintaining the structural integrity of *Ulva* and enhances its nutritional value, making it more suitable for applications in animal feed, bioplastics, and pharmaceuticals. Understanding and managing the *Ulva* microbiome is thus essential for optimizing large-scale cultivation and ensuring sustainable production in aquaculture industries. Our seaweed microbiome knowledge regarding differences among *Ulva* species/strains and different cultivation systems across the year are still very rudimentary. Here we present the current state of a 16S rRNA metagenomic *Ulva* microbiome monitoring effort across 'strains' and within different cultivation facilities of a seaweed production company across different times of the year.

Acknowledgments

This work was financially supported by "Pacto da Bioeconomia azul" (Project No. C644915664-00000026) within the WP5 Algae Vertical, funded by Next Generation EU European Fund and the Portuguese Recovery and Resilience Plan (PRR), under the scope of the incentive line "Agendas for Business Innovation" through the funding scheme C5 - Capitalization and Business Innovation.

Short Biography of the speaker

Dr. Aschwin Engelen leads the Marine Microbial Ecology and Biotechnology group that studies microbiomes of mainly marine foundation species like seagrass, corals, and seaweeds. He did his Masters degree in Marine Biology and PhD at the University of Groningen, The Netherlands. Since 2002 he has been working on marine ecology at CCMAR in Faro, Portugal.

HOW MANY CORE MICROBIOMES EXIST IN A SEAWEED HOLOBIONT?

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Abstract

Microbial taxa that are consistently associated with a seaweed host may represent important core symbionts (beneficial or harmful) [1]. However, such microbiota may be negatively affected by certain environmental conditions tolerated by their host. This raises the question of whether functionally similar taxa could replace each other in different environments. On the other hand, microbial symbionts have occasionally been shown to increase the resilience of algal hosts under suboptimal conditions, suggesting that specific core functions may be required in some environments [2]. To gain insight into such relationships, we studied the microbiome of *Gracilaria vermiculophylla* - a species with a very broad ecological amplitude - across its Northern hemisphere range [3] and at two selected sites over three years [4], based on 16S rDNA amplicon analysis and subsequent prediction of microbial genome functions. We identified a permanent taxonomic core that was present throughout all populations, regardless of season. However, most epibiota were taxonomically distinct between and even within populations, while functionally more similar. Furthermore, our results reveal pronounced seasonal shifts, both taxonomically and functionally, oscillating between late winter and early summer in consecutive years. Apparently, seasonal variability is a driver of functional changes, whereas spatial variability is functionally more redundant. As some microbiota are predictably associated with the host at certain seasons, they could be considered as members of seasonal core microbiomes.

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Short Biography of the speaker

Dr. Florian Weinberger is a scientist at the GEOMAR Helmholtz Centre for Ocean Research at Kiel, Germany. As a trained botanist and microbiologist, he has been involved in various projects on physiological, biochemical and molecular biological aspects of the ecology, aquaculture and utilization of algae and aquatic plants since 1990. His research focuses on seaweed management ecology in natural habitats and aquaculture and covers seaweed biodiversity, the ecological interactions of seaweeds with symbionts, epibionts, consumers and competitors, the ecology of nuisance algae and the eco-evolutionary implications of algal invasions.

MICROPOLLUTANTS CHALLENGE THE CORE MICROBIOME OF *ULVA COMPRESSA*.

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Abstract

The exceptional growth rate, robustness, and adaptability of the green macroalga *Ulva*, combined with its high potential for nitrogen and phosphorus removal, have made it a promising candidate for wastewater treatment and bioremediation. However, micropollutants in wastewater pose a potential threat to the holobiont. We explored the effect of emerging contaminants commonly found in ground- and wastewater on the microbiome of *Ulva compressa* (cultivar *U. mutabilis*). We challenged the core microbiome of *U. mutabilis*, which has been under cultivation for more than 70 years, with four antibiotics (chloramphenicol, erythromycin, oxytetracycline, and sulfamethoxazole), two herbicides (atrazine and glyphosate), and three endocrine disruptors (bisphenol A, estradiol, and ethinylestradiol). By comparing the microbiome of long-term cultivation to the native microbiome of *U. compressa*, we aim to understand the significant impact of emerging contaminants and long-term laboratory cultivation on the microbiome of *Ulva* and its potential implications for wastewater treatment and bioremediation. The long-term cultivation of *Ulva* resulted in the homogenisation and reduction of microbiome diversity; however, the key functional taxa persisted. The impact of micropollutants was found to be distinct, with antibiotics exhibiting a more profound effect than herbicides and endocrine disruptors. These findings highlight the sensitivity of *Ulva* microbiomes to environmental changes, which has implications for algal aquaculture and ecosystem management.

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Short Biography of the speaker

Justus Hardegen is a Ph.D. candidate under the supervision of Dr. Thomas Wichard at the Friedrich Schiller University Jena (Germany) and is currently in the final stages of completing his dissertation. His research, supported by the State Graduate Scholarship of Thuringia (Germany), explores the interactions between *Ulva compressa* and its associated microbiome stressed with selected model micropollutants. Ultimately, his work aims to assess the potential of *Ulva* for wastewater treatment and the bioremediation of micropollutants.

TEMPORAL DYNAMICS IN THE MICROBIAL COMMUNITY ASSOCIATED WITH *ULVA FASCIATA* IN AN INTEGRATED MULTI-TROPHIC AQUACULTURE SYSTEM

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Abstract

The inseparable relationship between *Ulva spp.* and their associated microbiome has been studied extensively, given its significance in shaping the well-being and functioning of the macroalgae. Previous studies showed that cultivation settings, such as integrated multi-trophic aquaculture (IMTA) systems, could impact the *Ulva* bacterial community significantly¹. Though temporal dynamics is also among the driving forces contributing to community assembly², how microbial communities assemble within and between seasons is still unclear. In the current study, we characterized the microbiota associated with *Ulva fasciata* grown as a biofilter in an IMTA system in the Gulf of Aqaba (Eilat, Israel) over a developmental period of 5 weeks across two seasons of spring and winter. The *Ulva*-associated microbial community was identified using the 16S rRNA gene amplicon sequencing, and ecological indices were further analyzed. Composition-wise, the *Ulva* microbiome was dominated by three phyla: Proteobacteria, Bacteroidetes, and Planctomycetes. A significant difference in alpha and beta diversity was observed between and within communities across different time scales, where different taxonomic groups characterized each season. Distinction in functionality was also found across different seasons along the weeks. Most nitrogen metabolism genes are found in *Ulva*'s microbes, and the microbial community benefits the alga by converting nitrate to ammonia through the DNRA metabolism. Characterizing bacterial communities associated with *Ulva fasciata* from an IMTA system along different seasons enriched our knowledge about macroalgal micro-inhabitants and provided a deeper understanding of their functions and dynamics, thus revealing this macroalgae's adaptation to such a habitat.

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Short Biography of the speaker

Lior Guttman is an associate professor at the Department of Blue Technologies and Sustainable Mariculture, at The University of Haifa. His expertise is set in microbial ecology in marine ecosystems and mariculture systems, where microbes present various services that are crucial to the system and cultured organisms in terms of performance, resilience, and health. A primary goal of the studies in Guttman's lab is to characterize the forces that govern the dynamics in microbial communities and their effects on the host organism and the environment. Understanding these forces enables us to predict and modulate the microbiome's composition, interactions, and metabolisms toward optimized eco-services. The research combines state-of-the-art omics, molecular biology, bioinformatics, classic microbiology, and chemistry.

UNRAVELING THE CULTIVABLE MICROBIOME OF *ULVA* AND *CODIUM*: SEASONAL INSIGHTS FROM INTEGRATED MULTI-TROPHIC AQUACULTURE SYSTEMS AND NATURAL HABITATS

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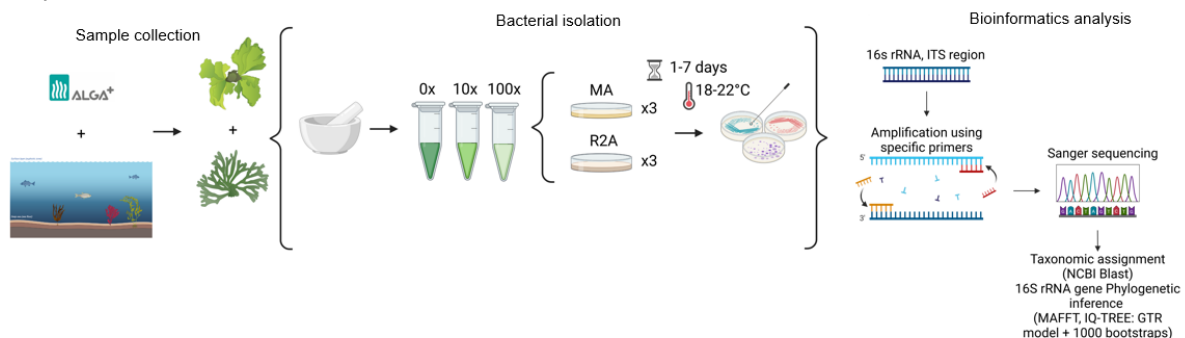
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Abstract

Seaweed-associated microbial communities play an important role in host growth, development, and health [1]. These symbiotic interactions are primarily shaped by host species and geography, while environmental factors such as seasonality and the life cycle of the host organism can further influence the composition of the associated bacterial communities [2,3]. To fully harness the potential of these microbes, their function and capacity need to be identified. Moreover, in order to experimentally test their relationship with the seaweed host and to industrially apply them, we need to be able to cultivate them first. The present study aims to isolate and characterize the cultivable microbiome of the industry highly important green macroalgal genera *Ulva* and *Codium*, in Portugal. We assessed the diversity and composition dynamics of their cultivable associated microbial communities from natural habitats and Integrated Multi-Trophic Aquaculture (IMTA) systems across different seasons. To achieve this, microbes associated with wild and cultivated seaweeds from the IMTA systems at the seaweed producer ALGAplus were seasonally isolated using different culture media. Environmental reference control samples were collected from natural and tank seawater, inlet water, and sediment, while physical parameters were measured in situ. Subsequently, the culturable microbial strains were identified to the lowest taxonomic level through full 16S rRNA gene amplicon Sanger sequencing, and the total community was analysed through Illumina MiSeq technology. Through this process, a cutting-edge biobank of more than 500 isolated bacteria from both macroalgal genera was created. The collection includes various strains with potential growth-promoting capacity and high-value metabolites. Our findings indicate a diverse range of bacterial communities associated with seaweed across cultivated and wild habitats, as well as in distinct culture media. Beneficial microbes such as *Cobetia*, *Pseudoalteromonas*, *Pseudomonas*, *Sulfitobacter*, *Ruegeria*, and *Roseovarius* were identified among others. High throughput sequencing will elucidate the non-culturable part of the microbiome and unveil the biotechnological potential of the whole community. The outcomes of this study are promising for advancing seaweed research and further biotechnological applications of seaweeds in various fields.

Graphical abstract



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Acknowledgments

This work was financially supported by “Pacto da Bioeconomia azul” (Project No. C644915664-00000026) within the WP5 Algae Vertical, funded by Next Generation EU European Fund and the Portuguese Recovery and Resilience Plan (PRR), under the scope of the incentive line “Agendas for Business Innovation” through the funding scheme C5 - Capitalization and Business Innovation.

Short Biography of the speaker

Myrsini is a Marine Biologist and Oceanographer with interests in molecular biology, seaweed cultivation, oceanography, and water quality. She holds a BSc in Oceanography and Marine Biosciences from the University of the Aegean, Greece, and an MSc in Freshwater and Marine Biology from the University of Amsterdam, Netherlands. Currently, she is pursuing a PhD at the University of Algarve, Portugal, in the Marine Microbial Ecology & Biotechnology group of CCMAR. Her research explores the microbiome of macroalgal species relevant to **the** seaweed industry, identifying bacterial communities that enhance growth and induce high-value metabolites to improve industrial macroalgal productivity and biomass quality.

UTILIZING PROBIOTICS TO ENHANCE SEAGRASS RESTORATION SUCCESS

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Abstract

Seagrass meadows are globally declining due to anthropogenic stressors. Therefore, urgent restoration efforts are required to recover and expand these crucial ecosystems (1). The role and importance of the seagrass microbiome has gained more attention in the last decades. As soil bacteria have been leveraged to enhance terrestrial crop productivity for many years, growth-promoting bacteria are now proposed as a tool to improve seagrass health and recovery (2;3).

This study investigates the microbiome's role in seagrass health, growth, and resilience. We identified and characterized novel and known bacteria isolated from different parts of Portuguese seagrass species, including *Zostera marina*, *Zostera noltii*, *Cymodocea nodosa*, and *Ruppia maritima*, to expand the list of putative beneficial microbes associated with seagrasses.

Bacterial isolates were identified using comparative analysis of 16S rRNA sequences. Subsequently, whole genome sequencing was performed on selected strains. We annotated the genes and identified potential growth-promoting properties within the genomes. In a laboratory experiment, five bacterial strains were tested for their impact on seagrass seed germination and early development, with *Bacillus* spp. significantly enhancing both.

These bacteria may serve as probiotics to facilitate seed viability, stimulate the health and growth of transplanted seagrass shoots, and thus promote the success of seagrass restoration initiatives.

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Acknowledgments

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Short Biography of the speaker

I am a PhD candidate at CCMAR since 2022, focusing on seagrass restoration and conservation using nature-based solutions. My research aims to deepen our understanding of healthy microbiome communities and involves the isolation and identification of growth-promoting bacteria. These beneficial microbes are applied as probiotics to support the restoration of seagrass seeds and shoots. My main study topics and interests are in Marine Biology, Ecology & Biodiversity Conservation, Microbiology, Evolution and Nature-based Solutions to mitigate Climate Change.

MICROBIOME DYNAMICS IN EARLY LIFE STAGES OF THE TEMPERATE GORGONIAN, *EUNICELLA VERRUCOSA*

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Abstract

Corals form ecosystems of high ecological importance such as coral reefs or coral gardens. These ecosystem builders depend on interactions with and assemblage of microorganisms including bacteria, dinoflagellates, viruses, and archaea, which together with the coral host form the coral holobiont. Despite the importance of these interactions, not much is known about how these microorganisms are acquired, such as bacteria. Bacteria can be transferred to early life stages in tropical scleractinian corals vertically (parental source), horizontally (environmental source) or both, independent of their sexual reproductive strategy (brooder or broadcast spawner). However, no information is available on temperate octocorals, such as gorgonians.

In this work we analysed the bacterial community in the early life stages of the temperate octocoral *Eunicella verrucosa*: how coral associated bacterial communities differ and develop among different early life stages and how those bacteria are transmitted.

To do this, samples of the broadcast spawner *Eunicella verrucosa*, were collected from colonies kept in aquaria. During the reproductive season early life stages were collected (eggs, embryos, larvae, juvenile polyps), as well as samples of potential sources (adult tissue, sclerites, seawater, sediments). Samples were sequenced using high throughput Illumina amplicon sequencing of the V5-V7 region of the bacterial 16S rRNA gene, followed by multivariate analysis to assess the change of bacterial communities over life stages, and possible sources.

The results showed differences in bacterial community composition among life stages of in *E. verrucosa*. Eggs, early polyp, and adult tissue bacterial communities were significantly different from the ones in Embryos, larvae, and skeleton. Considering the embryos, larvae, and skeletons, these bacterial communities differed from every life stage considered.

Both vertical and horizontal bacterial transmission occurred, which unveils parental and environmental influences on bacterial acquisition. We identified vertical transmission of *Cutibacterium*, *Straphylococcus* and *Salinisphaea*; and horizontal transmission of *Pseudoalteromonas*, which have been linked to cues on larval settlement [1] and *Winogradskella* linked to bleaching protection in tropical corals [2].

Ontogeny microbiome dynamics in gorgonians and other octocorals are poorly explored. This work presents to our knowledge the first study of bacterial assemblages in early life stages of temperate gorgonians, which makes this work useful insight for this knowledge gap for an ecologically important species.

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Acknowledgments

The Marine Microbial Ecology and Biotechnology was the group that allowed this work to be developed as my master thesis, under the supervision of Aschwin Engelen and Tânia Aires; and the Plant A Coral organization collaborated with the contribution of the coral samples collection and also with the insight on the biological information on the early life stages biological of the coral species here considered.

Short Biography of the speaker

Rita Camacho graduated last year from the IMBRSea master's programme, with the thesis «Microbiome Dynamics in Early Life Stages of Temperate Gorgonians», on which this presentation is partly based. After graduating she joined the Marine Microbial Ecology and Biotechnology group where she is currently investigating cryopreservation media for bacteria preservation from different seaweed commercial species.

HUMAN GUT MICROBIOME ENGINEERING: UNLOCKING THE GENETIC VAULT

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Abstract

The human gut microbiome—a complex ecosystem of microorganisms—fundamentally influences human health through its effects on metabolism, immunity, disease prevention, and neurological function. While traditional research has established correlations between microbial species abundance and various factors including diet, disease states, and therapeutic interventions, realizing the microbiome's therapeutic potential requires a deeper understanding of microbe-microbe and microbe-host interactions [1]. Recent advances in microbiome genetics and engineering offer promising methods to manipulate and precisely control gut microbial function for understanding the mechanistic basis for community dynamics. However, progress faces a significant challenge: the limited availability of genetic tools for most gut microbial species [2]. As a result, our current perspectives on gut microbial ecology are unrepresentative and vastly incomplete. To address this challenge, we have taken a systematic approach to identify and overcome the barriers to genetic tractability. By developing customized genetic tools for specific microbial targets, we have moved beyond relying on standardized techniques originally designed for non-gut model organisms. This tailored approach has significantly accelerated our ability to engineer and investigate previously inaccessible branches of the gut microbial tree.

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Acknowledgments

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Short Biography of the speaker

James Marsh is a microbiologist specializing in microbiome genetics and engineering. He earned his PhD from Queensland University of Technology in Brisbane, Australia, where he focused on infectious disease microbiology, followed by postdoctoral research at the University of Technology Sydney, studying host-pathogen genetics and transcriptomics. Marsh later joined Ruth Ley's department at the Max Planck Institute for Developmental Biology, where he shifted to host-commensal interactions, developing innovative genetic systems to study these relationships. Currently, he leads a research group at the Max Planck Institute for Biology in Tübingen, Germany. His group uses genetics to uncover fundamental principles of microbial ecology and explore applications in biotechnology, medicine, and ecosystem management.

VISUALIZING MICROBIAL INTERACTIONS IN *ULVA MUTABILIS* WITH FLUORESCENTLY LABELLED BACTERIA

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Abstract

Ulva mutabilis depends on specific bacterial species for its development. *Roseovarius sp.* releases algal growth- and morphogenesis-promoting factors which are essential for normal growth, while *Maribacter sp.* produces thalassin, a compound required for proper rhizoid formation [1]. The interaction between *U. mutabilis* and its associated bacteria is a well-regulated symbiosis, where the alga provides organic compounds like glycerol in exchange for bacterial signals that control its development [1]. When studying this system, *U. mutabilis* can be tracked and quantified via chlorophyll fluorescence, however differentiating and measuring the microbiome remains a challenge. Conventional microbiome analysis techniques, such as nucleic acid staining, do not allow for continuous observation of bacterial dynamics in live samples. Here we developed a reliable method to visualize heterotrophs in the microbiome by expressing different coloured fluorophores. First, we labelled *Roseovarius sp.* with mVenus and showed that growth measured with optical density at 600 nm correlated well with the growth measured by fluorescence, thus allowing us to track the bacterium with ease in a microplate format. We then investigated whether fluorescence microscopy with genetically labelled *Roseovarius sp.* is a suitable method for analysing its interaction with *U. mutabilis*. Fluorescently tagged *Roseovarius sp.* was introduced into axenic *U. mutabilis* cultures, and its localization was monitored over time. The bacterium remained detectable for several days, confirming the stability of the fluorescence protein. Live-cell imaging facilitated the observation of bacterial accumulation near rhizoids and gametangia formations, supporting the hypothesis of active chemotactic responses and metabolic exchange.

The method proved useful for visualizing microbial interactions in real-time without disrupting cell viability. It provides a basis for further research on bacterial dynamics in the *Ulva* microbiome and could contribute to a better understanding of host-microbe interactions in marine environments.

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Short Biography of the speaker

Sebastian Jeß is a master student in Chemical Biology at the University of Jena, building on a Bachelor's degree in Biology with a focus on Microbiology. Their research is driven by a deep interest in microbiome evolution and microorganisms. Their academic journey has been characterized by a dedication to exploring the development and dynamics of microbial communities.

BIOREMEDIATION OF OZONE-PRODUCED OXIDANTS IN MARINE RAS USING *ULVA*: BENEFITS AND IMPACTS ON SEAWEED PHYSIOLOGY AND ASSOCIATED MICROBIOMES

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Abstract

The maintenance of good water quality is essential for the success of recirculating aquaculture systems (RAS). Among water treatment tools, ozone (O₃) has garnered increasing interest from aquafarmers worldwide due to its wide array of beneficial effects. Beyond its germicidal properties, ozone improves solid removal, oxidises toxic nitrogen compounds, and degrades a broad spectrum of biogenic and artificial molecules. While its application in freshwater systems is generally straightforward, the ozonation of seawater produces by-products known as 'ozone-produced oxidants' (OPO). These by-products can accumulate in recirculating systems and pose significant risks to animal health. In this experiment, we evaluated the bioremediation capacity of the seaweed *Ulva* for OPO removal in an outdoor Integrated Multi-Trophic Aquaculture (IMTA) RAS setup that cultivated gilthead seabream (*Sparus aurata*). Effluent water was ozonated and then passed through a cultivation unit containing *Ulva*. OPO concentrations in the water were measured both before and after the seaweed unit, and the reduction in OPO was compared to control systems without *Ulva*. Additionally, we assessed the effects of OPO on the growth, metabolic composition, and photosynthetic efficiency of *Ulva* by comparing seaweed exposed to ozonated water with controls grown without ozonation. The results showed that systems containing *Ulva* achieved an 11 % reduction in OPO levels. However, ozonation also reduced *Ulva* growth, altered its morphology, and increased its chlorophyll, phenolic compound, and soluble sugar contents. Furthermore, the amino acid composition of *Ulva* changed under ozonation, with 15 - 128 % increases in proline, glutamic acid, glutamine, leucine, serine, valine, and phenylalanine. The microbiome associated with *Ulva* shifted, with a marked reduction in complex carbohydrate-metabolising bacteria, likely due to the biofilm-degrading properties of OPO. This study demonstrates that *Ulva* can effectively reduce OPO concentrations in marine RAS. However, this bioremediation process alters the chemical composition, morphology, and microbiome of the seaweed, highlighting both the potential and risks of using ozone to manipulate seaweed biomass quality.

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Short Biography of the speaker

Sabine Weidlich studied Biology (BSc) at the University of Salzburg and Ecology & Ecosystems (MSc) at the University of Vienna (2014–2021). Her Master's thesis, conducted within the international GAME program at GEOMAR Kiel (Germany), investigated the role of floating marine debris as a dispersal vector for the Mytilid mussel *Brachidontes puniceus* in Cabo Verde. She explored aquaculture through the ACES+ Erasmus program, studying at SAMS (Scotland), the University of Crete (Greece), and CCMar (Portugal). Currently, as a PhD researcher at ZMT Bremen, she examines the effects of ozonation as a water treatment tool on cultivated marine plants, animals, and their microbiomes. Her research interests include seaweed cultivation, integrated farming systems, and microbiome dynamics in aquaculture.

BACTERIOME-MEDIATED IMPROVEMENT OF INDUSTRIALLY PRODUCED *CHLORELLA VULGARIS*

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Abstract

The rising market demand for microalgal biomass for diverse biotechnological applications, such as human and animal nutrition and nutraceuticals, has increased the industrial-scale production of microalgae. In recent years, there has been a growing academic and industrial interest in microalgae-associated bacteria, recognizing the significant impact of bacteria on the growth and biochemical composition of microalgal cultures. This study focuses on assessing the influence of a synthetically designed bacterial consortium on the growth and nutritional profile of industrially produced cultures of *Chlorella vulgaris*. The coexistence of microalgae with bacteria improved production traits aimed at large-scale autotrophic production of microalgae, including growth, biomass quality, and a more efficient harvesting process. The innovative approach, previously successful at a laboratory scale, aimed to validate its efficacy on pilot and industrial scales. Initial testing occurred at Necton microalgae production facilities in Olhão, Portugal, using 100L flat-panel photobioreactors (PBRs). The tailored bacterial consortium demonstrated significant improvements in *C. vulgaris* cellular concentration, pigments (neoxanthin, violaxanthin, zeaxanthin, and lutein), and vitamin B₁₂ concentrations compared to those of control cultures. Scale-up production occurred at Allmicroalgae facilities in Pataias, Portugal, with *C. vulgaris* cultivated heterotrophically in industrial (250 L) fermenters and the chosen bacterial strains in pilot fermenters (5 L). Subsequently, the tailor-made consortium was introduced to the microalga cultures in 2.5-m³ tubular PBRs over nine days for autotrophic growth. Microalgal performance, assessed by cell counts, revealed a 20% increase in microalga concentration in treatments exposed to the synthetic bacterial consortium, along with a 50% increase in vitamin B₁₂. The remaining parameters of the nutritional composition remained consistent across all treatments, showing no significant differences. The results suggest the feasibility of growing selected bacterial strains heterotrophically and employing designed bacterial consortiums on an industrial scale to enhance the growth performance of *C. vulgaris*.

Acknowledgments

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Short Biography of the speaker

João Varela is an Associate Professor with Aggregation at University of Algarve and he has worked on the biology and biotechnology of microalgae for 26 years, leading the MarBiotech research laboratory at the Centre for Marine Sciences (CCMAR). He also helped the founding of the collaborative laboratory GreenColab, an interface between the industry and academia. He has worked on the elucidation of the carotenoid biosynthetic pathway in *Dunaliella salina* and *Tetraselmis striata*, isolation of novel industrial strains using a pipeline combining random mutagenesis and selection via flow cytometry and the use

of metabolic inhibitors. More recently, he has been working on the microalgal microbiomes to improve growth and production of high value-added metabolites by holobionts comprising industrial microalgae and associated microbiota.

THE PLANT MICROBIOME: ECOLOGY, FUNCTIONS AND BENEFITS FOR SUSTAINABLE CROP PRODUCTION

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Abstract

Global research on the plant microbiome has enhanced our understanding of the complex interactions between plants and microorganisms. Considerable research has been done on the microbial structure and composition of the plant microbiome, and their functions, but also on sources and niches of colonization of specific microbial strains. For decades, harnessing the plant microbiome has led to the development of various microbial applications to improve crop productivity in the face of a range of challenges, for example, climate change, abiotic and biotic stresses, and declining soil properties. This has involved the application of single microbial strains, microbial consortia, the development of plant breeding with microorganisms, but also of the development of new technology tools enabling the modulation of the plant microbiome. Although there are still some gaps in research to leverage all microbiome functions for sustainable plant production, some microbial strains and new technologies derived from the plant microbiome research are already commercialized. Using different crop models and microorganisms, I will show how some successes were obtained after studying the ecology and functions of some plant microbiome components. This involves strains to increase crop growth, promote plant health, and technologies to incorporate microbial strains inside plants.

Short Biography of the speaker

Dr. Stéphane Compant is a Senior Scientist at the AIT Austrian Institute of Technology in Austria, specializing in plant-microbe interactions and microbial ecology. He obtained his PhD degree from the University of Reims Champagne-Ardenne and his habilitation from the University of Bordeaux in France. Previously, he served as an Associate Professor of Microbiology at the National Polytechnic Institute of Toulouse in France before working at AIT. Dr. Compant is recognized for his extensive research on the ecology and functions of plant-associated microorganisms, particularly endophytic bacteria and fungi. His work focuses on beneficial plant-microbe interactions, biocontrol of plant diseases, biostimulation, and the development of biopesticides to combat pests and diseases. SC has over 20 years of experience in molecular microbiology and plant pathology, has coordinated numerous national and international research projects, and has served on various scientific boards and committees.

CAN ULVA IN IMTA-RAS WITH FISH MODIFY THE GLOBAL MICROBIOME OF THE SYSTEM?

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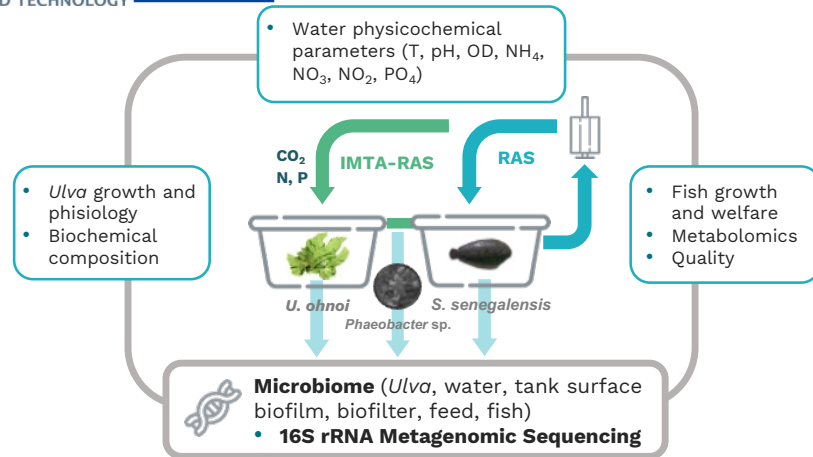
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Abstract

The green alga *Ulva ohnoi* has demonstrated to be an effective biofiltration agent of fish effluents in Integrated Multi-Trophic Aquaculture Recirculation Systems (IMTA-RAS), due to its high growth rate and high nutrient (N and P) removal. IMTA-RAS offers advantages over other *Ulva* cultivation systems, optimising algae biomass production and quality [1]. Moreover, *Ulva* spp. support microbial communities beneficial to fish health which are claimed to enhance resilience and disease prevention in RAS systems. Recent works have proposed inoculating *U. ohnoi* with the probiotic bacterium *Phaeobacter* sp. strain 4UAC3 to tackle fish pathogens such as *Vibrio* spp. in IMTA-RAS [2] and proposed a two-phase light intensity procedure [3] to optimise antagonistic activity [4]. However, studies to describe microbial communities and understand the impact of *U. ohnoi* introduction or its microbial manipulation in the overall microbiome of IMTA-RAS at an industrial-scale are lacking but urgently needed.

Different experiments were run in a pilot system with three replicate systems running one after another. Two control treatments: C1) *U. ohnoi* grown with inorganic nutrients in RAS and C2) *Solea senegalensis* in RAS, were compared with two IMTA-RAS treatments: E1) *S. senegalensis* and *U. ohnoi*; and E2) *S. senegalensis* and *U. ohnoi* inoculated with *Phaeobacter* sp. 4UAC3, a bacterium isolated from *Ulva* spp. known to antagonise fish pathogens. Samples were collected in at least triplicate for a metabarcoding study of bacteria by 16S rRNA gene sequencing from: algae (weekly), water (three times per experiment), and fish, tank surfaces, biofilter, and feed (at the beginning and end per experiment), making a total of 532 samples.

Samples were extracted with the Quick-DNA Miniprep kit and the 16S rRNA V5-V7 gene region, sequenced with Illumina NovoSeq PE250 technology. Those results, currently under analysis, will allow to: i) understand the impact of *Ulva* on the microbiome of the system (C2 vs E1), ii) understand the effect of fish effluents on *Ulva* microbiome (C1 vs E1), iii) evaluate the feasibility of microbial manipulation of *Ulva* at a pilot industrial scale (E1 vs E2). Moreover, the resulting microbial analysis is planned to be integrated with the other parameters analysed in *Ulva* (e.g., growth, physiology and biochemical composition), fish (e.g., growth, welfare) and water (e.g., pH, DO, NH₄, NO₃, NO₂, PO₄). This integrative analysis will potentially base the development of strategies for biofiltration and microbial management in IMTA-RAS transferable to industry, contributing to the sustainable growth of aquaculture.



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Acknowledgments

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Short Biography of the speaker

José Pintado is Researcher at IIM-CSIC in the Integrated Marine Ecology (InMare) group. After a PhD at the University of Santiago de Compostela, he was post-doctoral fellow at the *Institut de recherche pour le développement* (IRD) (1996-2000), Lecturer at the University of Montpellier (2002-2005) and visiting fellow at the University of New South Wales. His research is currently directed to the implementation of the ecosystem approach aquaculture, focusing on microbial ecology and interactions host-microbiota, applying the concept of holobiont to cultivated marine species. He has participated and coordinated projects related to integrated multi-trophic water recirculation systems (IMTA-RAS) with fish and macroalgae (*Ulva* spp.), focusing on host-specificity of bacterial communities in macroalgae and microbial management strategies. His research involves multi-disciplinary approach, from aquaria experiments to -omic techniques.

COMMERCIAL POTENTIAL OF *ULVA* MICROBIOMES IN AQUACULTURE APPLICATIONS

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Abstract

The microbiome associated with *Ulva* plays a pivotal role in its growth, health, and resilience, making it a subject of increasing research for its commercial potential in sustainable aquaculture systems. However, knowledge on the *Ulva* holobiont is still only in its infancy. In this talk, I will address potential commercial applications of the microbiome with particular focus on potential applications in aquaculture (both seaweed and animal) that are in my view promising and should be explored in detail in future research lines.

With respect to aquaculture applications, three main application lines can be distinguished. 1) Microbiome applications directly for seaweed aquaculture; 2) Applications for aquafeed production for other cultures; and 3) Using the microbiome as carrier for specific microorganisms with beneficial functional properties for aquaculture systems.

The microbiome can stimulate *Ulva* nutrient uptake capacity and thereby enhance its growth. However, cost-effectivity is doubtful for large scale cultivation, especially in open sea systems. A more promising line would be the application of microbiomes in hatchery phases of *Ulva* and other seaweeds. With respect to aquafeed production, microbiomes can be used to manipulate the biochemical composition of the *Ulva* biomass (for instance amino acid composition, vitamin content, etc.). Moreover, the microbiome is very important in post-harvest treatments as fermentation, which might greatly enhance protein digestibility of the seaweed biomass so that protein rich compounds, high in critical amino acids can be developed.

Finally, a potential application that evolved recently is the manipulation of the seaweed holobiont by including specific bacteria that will render specific functional properties to both the seaweed biomass as well as its surroundings. An example of this is the use of a manipulated holobiont as a component in a circulating fish aquaculture system, which has a potential of reducing fish diseases (Pintado et al. 2023 and related papers).

The development of cost-effective cultivation methods for *Ulva* and the scaling of microbiome-based solutions will be key to unlocking its full commercial potential. Overall, the integration of *Ulva* microbiomes into aquaculture systems presents a promising avenue for achieving more sustainable, efficient, and environmentally friendly aquaculture practices, with significant commercial opportunities across a range of industries.

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Acknowledgments

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Short Biography of the speaker

Erik-jan Malta PhD, is Chief Scientific Officer and researcher seaweed cultivation and sustainable aquaculture at the Aquaculture Technology Centre (CTAQUA), Spain. A biologist by training, Erik has more than 25 years of international research experience in marine ecosystem and seaweed ecology, seaweed cultivation and applications and sustainable aquaculture systems as Integrated Multitrophic Aquaculture (IMTA). He has been PI of several research projects in Spain and Portugal and is



coordinator of the Interreg Atlantic Area project AQUAFISH0.0 and collaborator and in various other past and present EU funded projects. He has published >25 papers in peer-reviewed journals (H-index = 19) as well as contributions to book chapters and various technical reports and is member of the editorial advisory board of the international journal Aquatic Botany and research topic co-editor of the journal *Frontiers in Marine Science*.

MICROBIAL COMMUNITY DYNAMICS AND ENVIRONMENTAL INFLUENCES IN ULVA OHNOI LAND-BASED AQUACULTURE: IMPLICATIONS FOR DISEASE CONTROL

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Abstract

The cultivation of *Ulva ohnoi* in land-based aquaculture systems offers a controlled environment to optimize seaweed productivity while shaping microbial community dynamics. This study explores the abundance, diversity, and taxonomic composition of epiphytic bacteria, under varying environmental conditions over a four-week cultivation cycle. Using epifluorescence microscopy and 16S rRNA gene sequencing, we identified three dominant bacterial morphotypes and a microbial community primarily composed of *Rhodobacterales*, *Gammaproteobacteria*, *Actinobacteria*, and *Bacteroidota*. Selective culturing on TCBS media, revealed a negative correlation between bacterial abundance and seawater pH, while *Vibrio* spp. concentrations were inversely related to temperature and irradiance. These findings suggest that physicochemical fluctuations influence microbial population shifts, potentially mediated by *Ulva*-associated metabolites such as dimethylsulfoniopropionate (DMSP) and sulfated polysaccharides. Additionally, preliminary results indicate the potential of *Ulva*-derived metabolites for disease control in aquaculture. This study underscores the intricate relationships between *Ulva*, its microbiome, and environmental variables, offering insights into microbiome-informed cultivation strategies for improved seaweed productivity and aquaculture biosecurity.

References

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Short Biography of the speaker

Bachelor in Biology from the Autonomous University of Baja California (UABC-México) working with fungal enzymes for insecticide bioremediation. Master in Science in Marine Biotechnology from the Center of Scientific Research and Higher Education from Ensenada (CICESE) working with microbial consortia for hydrocarbon bioremediation. Technician in the Department of Processes and Technology (Metropolitan Autonomous University – México) working on hydrocarbon bioremediation processes in water and soils. Doctor in Science in Marine Ecology from CICESE working with symbiotic processes between dinoflagellates and bacteria in the context of vitamins. Research associate at the Algal Biology Laboratory (CICESE) studying harmful algal blooms. Postdoctoral fellow at SDSU (USA) under the supervision of Prof. Carl Carrano, working with symbiosis processes in dinoflagellates and bacteria in the context of iron, as well as the molecular mechanisms involved in the formation of biofilms by marine bacteria. Repatriation program from overseas researchers (México) to CICESE (Dept. Biological Oceanography). Currently working at UABC-Institute of Oceanological Research (México). Also trained



in marine viruses in the laboratories of Curtis Suttle (UBC-Canada) and Forest Rohwer (SDSU-USA), and in in situ hybridization techniques (Max Planck Institute-Germany). Currently developing the line of “Microbial ecology associated with marine macrophytes under the holobiont perspective”.

Dinner

At



tertúlia algarvia

Praça D. Afonso III, 13-15, 8000-167 Faro, Portugal

Menu Buffet Tradition

Algarve at the table

only for groups of 20 or more adults

On the table

Bread,, Olives,
Tuna pâté with chives
Algarve style carrot salad,

Buffet Service

Starters

Gazpacho Andaluz
Selection of Algarve style 'Tibornas'

Main Courses

Xarém (maize porridge) with cockles and carob croutons
Duck rice with sausages from Monchique
Lettuce salad
Tomato salad

Dessert

Chococolate mousse with carob crumble
Seasonal fruits

Drinks

Still water
Lemonade, soft drinks and beer
Selection of wine (red, white and rosé)

Coffee or decaffeinated coffee

Price per pax

28,50€