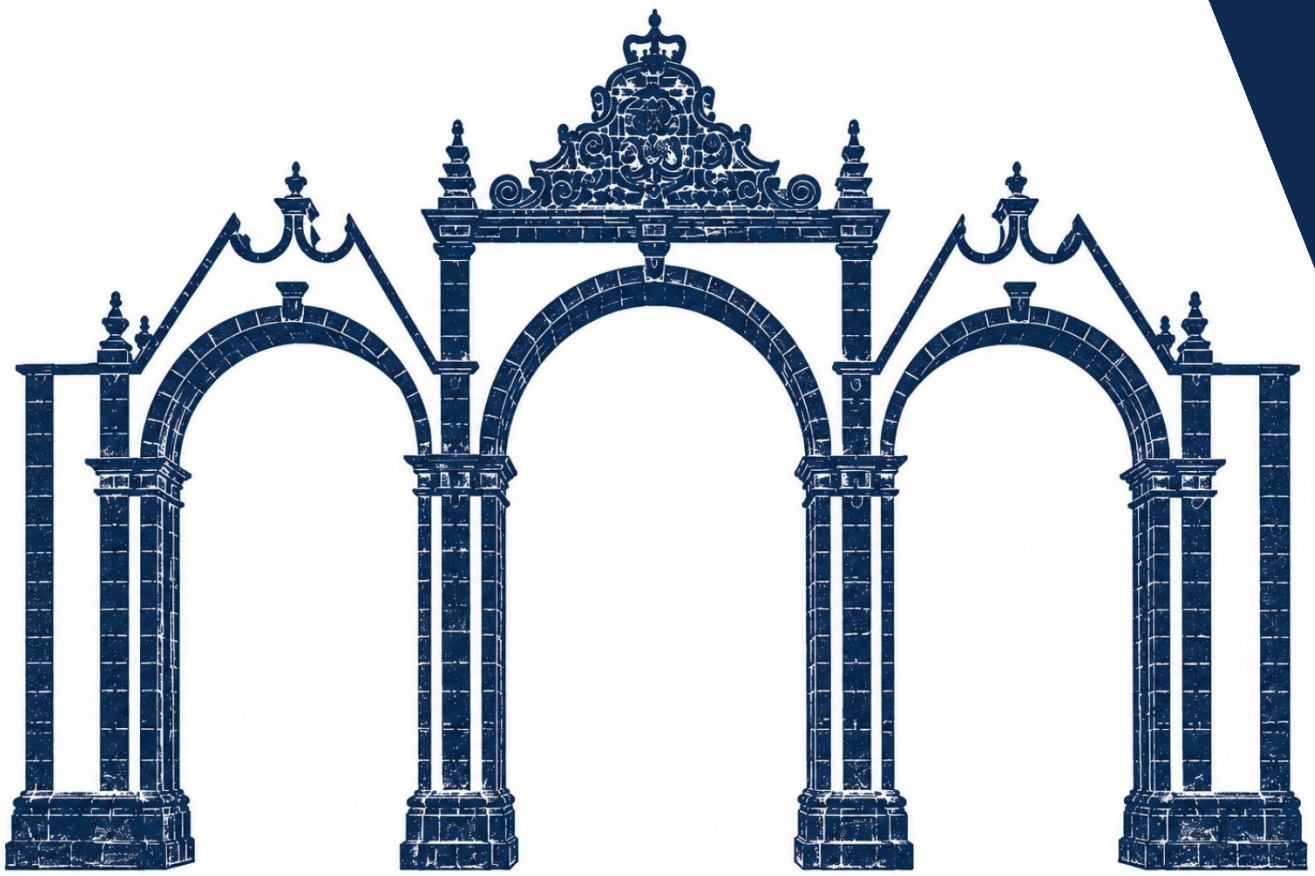
ECC | XLIV

14-16 SEPTEMBER 2026

The 44th Annual Meeting of the European Culture Collection's Organization

Integrative OMICs for a changing planet:

New frontiers in Taxonomy, Ecology and Biotechnology



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BACA Bank of Algae and Cyanobacteria of the Azores

ECCO European Culture Collections' Organisation

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Welcome Message

The European Culture Collections' Organization (ECCO) brings together culture collections and professionals dedicated to the preservation, characterization, management, and sustainable use of microbial and other biological resources. Through cooperation, exchange of expertise, and the promotion of high-quality standards, ECCO has played an important role in strengthening the culture collection community across Europe and beyond.

The annual ECCO Meeting is a central moment for this community, providing a forum to share scientific advances, technical developments, best practices, and new perspectives on the management and use of biological resources. It also offers an important opportunity to discuss emerging challenges, forge new collaborations, and strengthen links among culture collections, researchers, infrastructures, and other stakeholders.

The XLIV ECCO Meeting is hosted by the BACA collection (CIBIO-A, University of the Azores), in Ponta Delgada, Azores, a remote North Atlantic archipelago renowned for its distinctive biogeography, rich biodiversity, and strong links between terrestrial and marine ecosystems. Hosting the meeting in the Azores offers an appropriate setting to reflect on the importance of biological collections for documenting biodiversity, preserving genetic resources, supporting research, and fostering innovation to address present and future societal challenges.

Over the course of the meeting, more than 120 participants from 25 countries will have the opportunity to engage in scientific sessions, workshops, poster presentations, and discussions covering a broad range of topics related to culture collections and microbial resources.

On behalf of the Organizing Committee, we are delighted to welcome all participants to Ponta Delgada and the University of the Azores. We hope the XLIV ECCO Meeting will provide a stimulating environment for discussion and the development of new collaborations, while also offering the opportunity to explore the natural, cultural, and scientific richness of the Azores.

We wish you an inspiring and enjoyable meeting.

The Organizing Committee

XLIV ECCO Meeting 2026

Organizing Committee

- **Vítor Gonçalves** — BACA Director, CIBIO, University of Azores, Portugal
- **Rúben Luz** — BACA Curator, CIBIO, University of Azores, Portugal
- **Rita Cordeiro** — Researcher, CIBIO, University of Azores, Portugal
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- **Marizeth Groenewald** — Yeast Curator, CBS Collection, WI-KNAW, the Netherlands
- **Meriem Paris** — Head of CIP, France
- **Nelson Lima** — Head of MUM, Portugal
- **Olga Matantseva** — Curator of CCAC, Germany
- **Raquel Hurtado-Ortiz** — Head of CNCM, Institut Pasteur, France; Collection Officer, ECCO Board
- **Rosa Aznar** — Head of CECT, Spain
- **Rúben Luz** — Curator of BACA, CIBIO-Açores, Portugal
- **Vítor Gonçalves** — Head of BACA, CIBIO-Açores / University of the Azores, Portugal
- **Vítor Vasconcelos** — Head of LEGE-CC, Portugal
- **Wieland Meyer** — Director of WI-KNAW, the Netherlands
- **Wouter De Schamphelaire** — Curator of Confidential Collections and Service Manager, BCCM/Genecorner, Belgium; Secretary, ECCO Board

ECCO XLIV Scientific Program

Monday, 14th September

12:00-14:00	**Registration and poster mounting**
14:00-14:30	**Opening Ceremony** **Francisco Martins,** Vice-Rector for Administration, Planning, and Infrastructures of the University of the Azores **Rute Gregório**, Regional Director for Science, Innovation and Development, Regional Government of the Azores **Ana Costa**, Director of the Research Centre in Biodiversity and Genetic Resources - Açores **Gerard Verkley**, President of the European Culture Collection Organization **Vítor Gonçalves**, Director of the Bank of Algae and Cyanobacteria of the Azores
14:30-15:15	**Keynote Lecture 1 - Chris Bowler** (CNRS, France): *Exploring the Tara Oceans multiverse*
15:15-16:30	**Session 1 - Biodiversity, Systematics & Phylogenomics in the OMICs era & Session 2 - New approaches in Genomics and Genome-Scale Insights** *Chairs: Gerard Verkleij & Nelson Lima*
15:15-15:30	**O1. Aniket Saraf** (Institut Pasteur, France): *Hidden diversity of microcystin-producing cyanobacteria*
15:30-15:45	**O2. Marino Santos** (University of Porto, Portugal): *Phenotypic differentiation of Portuguese Erwinia amylovora collection strains using Fourier-transform infrared spectroscopy (FT-IR)*
15:45-16:00	**O3. Neža Čadež** (University of Ljubljana, Slovenia): *Origin of thermotolerant Hanseniaspora yeast populations and their adaptation to European vineyards*
16:00-16:15	**O4. Charles Bachy** (RCC, University of Sorbonne, France): *Culture collections as genomic infrastructures: supporting the large-scale sequencing of marine microbial eukaryotes within ATLASEA*
16:15-16:30	**O5. Michael Ross** (CCAP, SAMS, UK): *Metabolomics at the Culture Collection of Algae and Protozoa (CCAP)*
16:30-17:00	**Posters Session & Coffee Break**

17:00-18:45	**Session 3 - Microbiomes: Maintenance, Function, and Applications & Session 4 - Valorization of culture collections and strains: Biotechnology, Pharmaceutical and Ecological applications** *Chairs: David Novotný & Marizeth Groenewald*
17:00-17:15	**O6. Perrine Portier** (INRAE, France): *From single strains to complex microbiota: how can biological resource centres tackle this challenge and adapt?*
17:15-17:30	**O7. Luigi Chessa** (Agris Sardegna, Italy): *Microbial Biodiversity as a Living Resource for the Conservation of Typicity and the Valorisation of Traditional Food Systems*
17:30-17:45	**O8. Lars Möller** (DSMZ, Germany): *Long-term preservation of complex soil microbial communities and their functions*
17:45-18:00	**O9. Giancarlo Perrone** (ISPA, CNR, Italy): *The challenge of microbiome preservation from fermented food: the successful story of preserving the microbial consortia associated with Italian table olives*
18:00-18:15	**O10. Nelson Simões** (CBA, UAc, Portugal): *The repository of entomopathogens of Centre of Biotechnology of the Azores: cultures and libraries*
18:15-18:30	**O11. Duarte Toubarro** (CBA, UAc, Portugal): *Valorization of the Azorean Microbial Culture Collection through Biorefinery and Bioactive Molecule Discovery*
18:30-18:45	**O12. Eyal Kurzbaum** (SRI, University of Haifa, Israel): *Strain diversity and biotechnological characterization of Psilocybe cubensis cultures*
19:00-21:30	**Welcome Cocktail**

Tuesday, 15th September

09:00-09:45	**Keynote Lecture 2 - Pedro Leão** (CIIMAR, Portugal): *Discovery of unique chemistry and enzymology from the LEGE-CC cyanobacteria*
09:45-11:00	**Session 4 - Valorization of culture collections and strains: Biotechnology, Pharmaceutical and Ecological applications & Session 5 - Ethical and legal challenges of collection management** *Chairs: Wieland Meyer & Raquel Hurtado-Ortiz*
09:45-10:00	**O13. João Manoel** (BACA, CIBIO, Uac, Portugal): *Unlocking the potential of the Bank of Algae and Cyanobacteria of the Azores : From Native Diversity into Applied Biotechnology*
10:00-10:15	**O14. Federica Spina** (University of Torino, Italy): *The Fungal Kingdom Against Micropollutants: Unveiling Its Potential for the Bioremediation of Contaminants of Emerging Concern*
10:15-10:30	**O15. António Machado** (CIBIO, UAc, USFQ, Portugal): *Antibiofilm activity of Lactobacillus -derived cell-free supernatants against mono-, dual-, and tri-species interkingdom biofilms*
10:30-10:45	**O16. Amber H. Scholz** (DSMZ, Germany): *More ABS?? What do culture collections need to know about the new High Seas Treaty and the WHO Pathogen ABS systems?*
10:45-11:00	**O17. Adil Ennaji** (BCCM, Belgium): *From Isolation to Valorisation: A Focus on the International Depositary Authority under the Budapest Treaty. A brief introduction to the international patent system for inventions making use of microorganisms, and a discussion of a topical issue*
11:00-11:30	**Posters Session & Coffee Break**
11:30-13:00	ECCO XLIV Annual General Meeting (Members only)
13:00-14:30	**Lunch**
14:30-19:00	**Social Event**
20:00-23:00	**Dinner**

Wednesday, 16th September

09:00-09:45	**Keynote Lecture 3 - Tanja Kostic** (AIT, Austria): *Microbiome Biobanking: Navigating Complexity – Insights from the MICROBE Journey*
09:45-11:00	**Session 6 - Culture collection management and maintenance & Session 7 - Projects, Networks and databases** *Chairs: Cristina Varese & Wouter De Schamphelaire*
09:45-10:00	**O18. Elias El Zouki** (BACA, CIBIO, Portugal): *Evaluation of Cyanobacterial and Dinoflagellate Extracts for Alzheimer's Disease-Relevant Effects Using Zebrafish Larvae (Danio rerio)*
10:00-10:15	**O19. Matteo Florio Furno** (University of Turin, Italy): *Insights from the Cladosporium cladosporioides Species Complex: MALDI-TOF MS identification in fungal culture collections*
10:15-10:30	**O20. Belén Baena** (BEA, ULPGC, Spain): *From culture collection to genomic resource: unlocking cyanobacterial biodiversity and biotechnological potential in the Spanish Bank of Algae (BEA)*
10:30-10:45	**O21. Marco Anteghini** (LifeGlimmer, Germany): *Metis: a Biosecurity-Aware Decision Support System for Microbial Strain Discovery in Biotechnology*
10:45-11:00	**O22. Felix Mikus** (University of Geneva, Switzerland): *ExÂME - An Expansion Microscopy atlas of microbial eukaryotes*
11:00-11:30	**Posters Session & Coffee Break**
11:30-13:00	**Session 7 - Projects, Networks and databases & Session 8 - Open Science, Data Sharing & Science Communication** *Chairs: Vítor Gonçalves & Rosa Aznar*
11:30-12:00	**O23. Ana Portugal** (MIRRI-PT, Portugal): MIRRI-ERIC's Roadmap for FAIR Microbial Resources
12:00-12:15	**O24. Lorenz Reimer** (DSMZ, Germany): From BacDive to MicrobeDive: Moving towards a multi-domain strain knowledge base
12:15-12:30	**O25. Gabriel Bombo** (GreenCoLab, Portugal): *Industrial Biotechnology Algal Bank (IBAB): Supporting Research, Innovation, and Scalability in Blue Biotechnology*

12:30-12:45	**O26. Edward Moore** (CCUG, SU, UGOT, Sweden): *The International Code of Nomenclature of Prokaryotes and the International Committee on Systematics of Prokaryotes and Relevance for Bacterial Culture Collections and Microbiology*
12:45-13:00	**O27. Rita Patarra** (Expolab, Portugal): *Science Communication for Diverse Audiences: The Role of Science Centres in Promoting Scientific Literacy*
13:00-13:15	Closing Ceremony
13:15-14:30	Lunch
14:30-18:00	**Workshops**
14:30-16:00	Davide Faggionato & Amber Scholz (DSMZ), Tanja Kostic (AIT): *Beyond Traditional Collections: Enabling Sustainable Microbiome Biobanking Services*
16:00-16:30	Coffee Break
16:30-18:00	Marco Anteghini (LifeGlimmer) & Lornz Reimer (DSMZ): *From natural-language questions to strain shortlists: co-designing Metis with the culture-collection community*

Workshops

Beyond Traditional Collections: Enabling Sustainable Microbiome Biobanking Services

16th September 2026 | 14:30–16:00

Davide Faggionato (DSMZ), Amber Scholz (DSMZ) & Tanja Kostic (AIT)
with support from MICROBE consortium members

Abstract

Microbiome biobanking represents a new opportunity for research collections to extend their role and enable access to complex microbial resources. However, established business models developed around axenic cultures and traditional biological resource collections do not directly translate to the specific requirements, workflows, and value propositions of microbiome resources. Within the MICROBE project, new scenarios have been developed to explore how existing collections and research infrastructures could evolve to offer sustainable microbiome biobanking services, with a particular focus on defined microbial communities (DMCs). These emerging resources require new considerations around preservation, quality management, characterisation, regulatory frameworks, access models, data integration, user communities, and long-term sustainability. This workshop will present the scenarios developed within the MICROBE project and focus on three key aspects: practical considerations for implementing microbiome biobanking services, prioritisation of new sample types and resources to be integrated into collections, and questions related to liability and responsibilities associated with these emerging resources. The workshop will adopt a train-the-trainer approach, to strengthen knowledge exchange and empower participants to act as multipliers within their own institutions and networks. Through exchanges among collections, research infrastructures, scientists, and other stakeholders, the workshop aims to critically discuss challenges, identify barriers and opportunities, build capacity, and refine potential approaches for sustainable microbiome biobanking.

From natural-language questions to strain shortlists: Co-designing Metis with the culture-collection community

16th September 2026 | 16:30–18:00

Marco Anteghini (LifeGlimmer) & Lorenz Reimer (DSMZ)
On behalf of the BIOINDUSTRY 4.0 consortium

Abstract

Selecting a suitable microbial strain is often the slowest step in Design-Build-Test-Learn and biotechnology workflows: strain-level information is fragmented across culture collections, sequence archives, and literature, each with its own identifiers, schemas, and access interfaces. Metis is an open decision-support prototype that translates natural-language strain-discovery questions into structured, auditable queries over resources such as BacDive, MIRRI, UniProt, and NCBI, ranks candidate strains, and returns provenance-linked answers together with a built-in responsible-access (biosecurity) module. Unlike a plain large-language-model assistant, Metis grounds every recommendation in explicit database evidence and audit logs. In this hands-on workshop, participants will (i) see Metis running live on real strain-discovery tasks, (ii) work in small groups on their own queries and compare Metis with conventional database search and with a plain-LLM baseline, and (iii) contribute structured feedback and feature priorities that will directly feed the next iteration of the tool. The session is designed as a co-design activity with the culture-collection community, whose expertise is central to shaping how such a decision-support layer should serve mBRCs and their users.

Keynotes

K1: Exploring the Tara Oceans multiverse

Chris Bowler[1]*, FRS

[1]Ecology and Evolutionary Biology Section, Institut de Biologie de l'Ecole normale supérieure (IBENS), Paris, FRANCE
***Corresponding author:** cbowler@biologie.ens.fr

Abstract

The ocean is the largest ecosystem on Earth and yet we know very little about it. This is particularly true for the plankton that drift within, even though they form the base of marine food webs and are key players in Earth's biogeochemical cycles. Ocean plankton are at least as important for the Earth system as the forests on land, but most of them are invisible to the naked eye and thus are largely uncharacterized. To increase our understanding of this underexplored world, a multidisciplinary consortium, Tara Oceans, was formed around the 36m research schooner Tara, which sampled plankton at more than 210 sites and multiple depth layers in all the major oceanic regions during expeditions from 2009-2013. This talk will summarize the foundational resources from the project, which collectively represent the largest DNA sequencing effort for the oceans, and analyses that illustrate several aspects of the Tara Oceans' eco-systems biology approach to address microbial contributions to ecological and evolutionary processes. The project provides unique resources for several scientific disciplines that are foundational for mapping ocean biodiversity of a wide range of organisms that are rarely studied together, exploring their interactions, and integrating biology into our physico-chemical understanding of the ocean, as well as for identifying new organisms and genes of biotechnological interest. These resources, and the scientific innovations emerging to understand them, are furthermore critical towards developing baseline ecological context and predictive power needed to track the impact of climate change on the ocean.

Acknowledgements: Research in Bowler's lab is funded by Horizon 2020 projects AtlantECO (Grant Agreement no. 862923), BlueRemediomics (Grant Agreement no. 101082304), and Marco-Bolo (Grant Agreement No. 101082021), the BNP Paribas Foundation, and an ERC Advanced Grant (Diatomic; Grant Agreement no. 835067).

K2: Discovery of unique chemistry and enzymology from the LEGE-CC cyanobacteria

Pedro Leão[1]*

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Abstract

The LEGE-CC harbours a large diversity of Cyanobacteria strains. Over the years, we have been intrigued by the secondary metabolism of these organisms, which is linked to the specific ecological niches they occupy. Not only do cyanobacteria compounds exhibit unique structural features, these are introduced by biosynthetic machinery that performs unusual biochemical tricks. Here, I will show how the continuous exploration of a key biological resource center has allowed for the discovery of several families of new compounds and how this has, in turn, gradually led into the discovery of exciting new enzymes.

K3: Microbiome Biobanking: Navigating Complexity – Insights from the MICROBE Journey

Tanja Kostic[1,2]*

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[2] MICROBE consortium
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Abstract

Microbiome biobanking is emerging as a critical foundation for preserving microbial diversity and enabling its long-term access, characterisation and reuse. Yet, the complexity, heterogeneity and dynamic nature of microbiomes present challenges that extend far beyond preservation of axenic samples. Building effective and sustainable biobanking systems requires the integration of harmonised workflows, analytical technologies, data infrastructures and governance frameworks across the entire resource lifecycle. The EU-funded MICROBE project has explored these challenges from a systems perspective, examining how existing technologies, infrastructures, expertise and resources can be better connected and leveraged to strengthen microbiome biobanking across diverse biological contexts. Rather than creating a new standalone infrastructure, MICROBE has focused on identifying bottlenecks, addressing interoperability gaps and supporting the uptake and further development of existing solutions. A key insight from the MICROBE project is the importance of standardisation—from pre-analytical procedures and sample processing to microbiome characterisation and quality assessment. Equally important is the ability to connect biological resources with rich contextual, taxonomic and functional data, enabling their discovery, comparison and reuse. These technical dimensions are closely intertwined with ethical, regulatory and governance considerations that influence how microbiome resources can be accessed, shared and translated into research and innovation.

This presentation will reflect on the MICROBE journey and the lessons learned in navigating the complexity of microbiome biobanking.

Oral Presentations

Session 1 - Biodiversity, Systematics & Phylogenomics in the OMICs era

O1: Hidden diversity of microcystin-producing cyanobacteria

Aniket Saraf[1]*, Boris Aleksovski[2], Eddy Blondet[1], Alexis Criscuolo[3], Muriel Gugger[1]

[1] Collection of Cyanobacteria, Institut Pasteur, Paris, France
[2] Faculty of Natural Sciences, Institute of Biology, Ss. Cyril and Methodius University in Skopje, North Macedonia
[3] GIPhy - Genome Informatics and Phylogenetics, Biological Resource Center of Institut Pasteur, Institut Pasteur, Paris, France
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Abstract

Cyanobacteria are ecologically important microorganisms that produce various natural products, including cyanotoxins such as microcystins (MCs). MCs are potent hepatotoxins and pose a significant risk to humans and animals. They are cyclic heptapeptides synthesized nonribosomally via an integrated polyketide synthase (PKS)/nonribosomal peptide synthetase (NRPS) system. Sporadically distributed within the cyanobacterial phylum, MC producers are currently reported from the orders Chroococcales, Oscillatoriales and Nostocales. However, the full diversity of microcystin-producing cyanobacteria remains unexplored. In this study, we conducted in-depth taxonomic characterization of three microcystin-producing strains using a polyphasic approach, leading to the identification of a novel genus and species, expanding the known diversity of microcystin-producing cyanobacteria. One of the strains (PCC 9237), isolated in 1986 from a Finnish lake, was the first report of microcystin production in *Nostoc*. However, our multilocus and 16S rRNA gene phylogenies confirmed that PCC 9237 does not belong to *Nostoc* or other *Nostoc*-like genera, instead represents a novel nostocalean genus for which the name *Kaarinaea lacus* gen. nov., sp. nov. was proposed [1]. The remaining two strains (NMCCC 011 and NMCCC 012) were isolated from the wetland in North Macedonia, and microcystin production was confirmed by sequencing of the *mcy*B gene and ELISA. These strains exhibited *Pseudanabaena*-like morphology, and the polyphasic characterization confirmed NMCCC 011 was a novel species, whereas NMCCC 012 represents a novel variety, for which the names *Pseudanabaena vesniana* sp. nov. and *Pseudanabaena suomiensis* var. *macedonica* were proposed [2]. This study reports the presence of *mcy*B gene in the order Pseudanabaenales for the first time and supports the hypothesis of an ancient origin of microcystin production in cyanobacteria.

References

[1] Saraf, A., Blondet, E., Boullié, A., Criscuolo, A., Gugger, M. (2025). Insight on the heterocyte patterning and proheterocyte division in the toxic cyanobacterium *Kaarinaea lacus* gen. nov., sp. nov., and its genomic potential for natural products. *Harmful Algae*, *142*, 102792.
[2] Aleksovski, B., Saraf, A., Stefanoska, E., Kiprijanovska, S., Vuchurević, A., Pakovski, K., Dimovski, A., Gugger, M., Krstić, S. (2025). Molecular and cytomorphological characterization of *Pseudanabaena vesniana* sp. nov. and *Pseudanabaena suomiensis var. macedonica var. nov.* (Pseudanabaenales, Cyanobacteriota) with evidence of microcystin-producing Pseudanabaena taxa. *Journal of Phycology*, *61*, 1057-1082.

O2: Phenotypic differentiation of Portuguese *Erwinia amylovora* collection strains using Fourier-transform infrared spectroscopy (FT-IR)

Marino Costa-Santos[1,2,*], Laura Regalado[1,2], Paulo R. Oliveira-Pinto[1,2], Nuno MarizPonte[1,2]

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Abstract

Erwinia amylovora, the causal agent of fire blight, is generally regarded as a genetically homogeneous species. Nevertheless, previous phenotypic characterization of portuguese isolates revealed variability in traits such as carbon source utilization and chemical susceptibility profiles [1]. In this study, we evaluated the ability of Fouriertransform infrared spectroscopy (FT-IR) [2] to discriminate among strains from a Portuguese *E. amylovora* collection. An *E. amylovora* collection isolated from Portugal in different years (2010-2024) and counties (117 strains), previously characterized through phenotypic assays and Genome-Wide Association Studies (GWAS), together with the reference strain LMG 2024 and type strain CFBP 1430, was analysed in this study using the IR Biotyper® system. All bacterial isolates were cultured under standardized conditions in Nutrient Agar plates (1.5% agar) and incubated at 28°C for 24 h. Following incubation, bacterial cells were processed using the IR Biotyper® Kit (Bruker, Germany). Infrared spectral data were acquired and analysed using the IR Biotyper® software, with clustering performed following the manufacturer's recommended workflow. To ensure reproducibility, three independent biological replicates were analysed per strain, each comprising four technical replicate measurements. FT-IR clustering analysis revealed the presence of distinct phenotypic profiles among the isolates. Notably, for some isolates, the clustering pattern and the dissimilarity matrix showed similar grouping patterns previously obtained through metabolic and chemical susceptibility characterization (e.g. Ea230 and Ea490), suggesting that FT-IR captures biologically relevant phenotypic variation within the collection. These findings demonstrate the potential of FT-IR spectroscopy as a rapid and cost-effective approach for the characterization and management of bacterial collections. Furthermore, the observed FT-IR-based clustering highlights its value as a fast and complementary tool for exploring intraspecific diversity in *E. amylovora*.

References

[1] Mendes, R. J., Amaro, C., Luz, J. P., Tavares, F., & Santos, C. (2022). Variability within a clonal population of *Erwinia amylovora* disclosed by phenotypic analysis. *PeerJ*, *10*, e13695.
[2] Martak, D., Valot, B., Sauget, M., Cholley, P., Thouverez, M., Bertrand, X., & Hocquet, D. (2019). Fourier-transform infrared spectroscopy can quickly type gramnegative bacilli responsible for hospital outbreaks. *Frontiers in microbiology*, *10*, 1440.

O3: Origin of thermotolerant *Hanseniaspora* yeast populations and their adaptation to European vineyards

Neža Čadež[1]*, Katja Doberšek[1]

[1] University of Ljubljana, Biotechnical faculty, Ljubljana, Slovenia
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Abstract

Hanseniaspora yeasts are characterised by accelerated evolution, reduced genomes with low GC content, and extensive gene loss compared to other Saccharomycotina yeasts. Their genomes are highly dynamic, displaying strong variation in heterozygosity, structure, and ploidy both between species and among isolates, representing a rare example of long-term hypermutator lineages in fungi. In this study, we investigated two closely related species with different ecological histories: *H. uvarum*, long associated with wine environments in Europe, and *H. opuntiae*, originally isolated from cacti in Hawaii but now increasingly found in European vineyards. Many of the European *H. opuntiae* isolates show hybrid ancestry with *H. pseudoguilliermondii*, suggesting hybridization facilitated their spread into wine-associated habitats. To explore the genomic basis of adaptation to vineyard environments, we generated haplotype-resolved genome assemblies for representative *Hanseniaspora* isolates and sequenced and phenotyped a collection of 200 isolates comprising *H. uvarum*, *H. opuntiae*, and putative hybrids originating from diverse environments. Population structure analyses revealed distinct lineages within each species that largely correlate with geographic origin, indicating ongoing local adaptation and region-specific evolutionary histories. Phenotypic assays uncovered predominantly species-specific profiles, while hybrid isolates consistently outperformed both parental species under vineyard related stress conditions. Ploidy estimation revealed that most hybrids are triploid, supporting a 2:1 genomic contribution from *H. opuntiae* and *H. pseudoguilliermondii*. Overall, our results indicate that hybridization and changes in genomic architecture are likely important contributors to fitness variation and adaptation in *Hanseniaspora*.

Session 2 - New approaches in Genomics and Genome-Scale Insights

O4: Culture collections as genomic infrastructures: supporting the large-scale sequencing of marine microbial eukaryotes within ATLASEA

Charles Bachy[1], Katell Hervéou[1], Michele Grego[1], ATLASEA consortium, Priscillia Gourvil[1], Ian Probert[1]*

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Abstract

Large-scale genome sequencing projects like ATLASEA, which aims at producing 4,500 high-quality marine eukaryotic reference genomes, depend not only on technological advances but also on having access to authenticated, viable, and well-characterized biological material. The Roscoff Culture Collection (RCC), a key partner in this initiative, plays a central role in providing such resources. The RCC maintains a diverse collection of marine microbial eukaryotes and applies standardised procedures for strain authentication, voucherisation, cultivation, biomass production, cryopreservation, and metadata management. Selected strains are processed using a BGA-compliant strategy that combines long- and short-read sequencing, Hi-C scaffolding, and transcriptome sequencing to generate high-quality reference genomes. Since October 2024, the RCC has provided 180 strains spanning seven major eukaryotic phyla to the ATLASEA consortium. To date, 25 genomes have been sequenced and submitted, and another 50 are currently in assembly and quality assessment. The project goal is to contribute ~900 genomes from RCC strains, representing nearly 20% of ATLASEA total target. This effort demonstrates that culture collections are not merely passive repositories but essential genomic infrastructures, providing the cultivation expertise, quality control, and taxonomic knowledge needed to transform living strains into high-quality genomic resources. Many of the targeted taxa currently lack such resources, underscoring the central role of the RCC and other culture collections in expanding genomic coverage for microbial eukaryotes.

O5: Metabolomics at the Culture Collection of Algae and Protozoa (CCAP)

Michael Ross[1,2]*, Rachel Allen[1,2], Matthew Davey[2], Frederik De Boever[2], Joanne Field[1,2], Alice Flint[2], David Green[2], Rachel Saxon[1,2], Naomi Thomas[1,2], Evie Whyte[1,2], Cecilia Rad-Menéndez[1,2]

[1] Culture Collection of Algae and Protozoa (CCAP), Scottish Association for Marine Science (SAMS), Oban, UK
[2] Scottish Association for Marine Science (SAMS), Oban, UK
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Abstract

The Culture Collection of Algae and Protozoa (CCAP) is one of the world's oldest, largest, and most biodiverse biological resource centers for living algae and protozoa. CCAP maintains over 3,200 strains of microalgae, macroalgae, cyanobacteria, and protozoa. At recent ECCO meetings, CCAP has presented our curatorial progress and innovative updates regarding bioinformatics, digital platforms and data accessibility, and genomic research. In this presentation, we shall present a corresponding overview of our research into the phenotypic and metabolomic characterization of our collection. This presentation will begin with a brief overview of CCAP and of our algal scale-up and -omics facility (CCAP-ARIES). This will include a brief case study coupling together cultivation scale-up and time-resolved changes in biochemical composition of the microalga *Chromochloris zofingiensis* (SAG 211-14), supporting production of high-value compounds in algal biotechnology. The primary focus of this presentation, however, will be on the Natural Product BioHUB (NP BioHUB) project. The NP BioHUB is one of five UKRI Green Economy Centres and is led by Swansea University, in partnership with SAMS, CCAP, and CABI. By exploring the biological and chemical diversity of algae, protozoa, and fungi, the NP BioHUB aims to develop and promote the use of primary and secondary metabolites in biotechnology, with an emphasis on agritech. To achieve this and supporting discovery science, CCAP and SAMS have been systematically screening the CCAP collection to obtain metabolomic profiles using FT-IR, HPLC, and GC-MS. We will present the progress made and novel results from this endeavor. Finally, I will look towards the future in integrating these -omic datasets, future challenges and opportunities, and what is on the horizon for culture collections and the advancement of biotechnology.

Session 3 - Microbiomes: Maintenance, Function, and Applications

O6: From single strains to complex microbiota: how can biological resource centres tackle this challenge and adapt?

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Abstract

The French Collection for Plant-associated Bacteria (CIRM-CFBP, https://cirm-cfbp.fr/) was created in 1973. Since then, it expanded and now holds more than 7000 strains representative of the known diversity of the diversity of plantpathogenic bacteria. Lately more and more resources isolated from the microbiome of healthy plants are included in the collection, making the CFBP strains strategic resources for plant health. The resources from CIRM-CFBP are used widely by researchers, plant breeders, and national plant protection organisations, for basic research, design of diagnostic tools, epidemiology, etc. CIRM-CFBP is also part of infrastructures such as MIRRI-ERIC (https://www.mirri-eric.eu/). The scientific community exploring the interactions between plants and bacteria has shifted to models taking the whole microbiome into account, integrating the complexity into their researches. The collections are now facing an upscale in their activities. Beside single strains, some questions arise toward the preservation of a high number of samples or complex samples such as Defined Complex Communities or even native living microbiota. The preservation of microbiomes is not trivial. Applying the usual techniques for isolated strains will not be as effective as not all microbiomes' members are cultivable. Thus, preservation will alter the taxonomic composition and in turn will alter the functional diversity of these communities. Within the framework of the MICROBE project (https://www.microbeproject.eu/), we are now exploring new ways to preserve seedassociated microbiota. Microbiota were extracted from bean seed lots and preserved following nine different preservation modalities. The experiments were conducted jointly among three partners of the project (INRAE / AIT / CABI). The taxonomic composition had been assessed by metabarcoding (ITS/*gyrB*/16S rRNA markers) and the functional diversity by Biolog Ecoplates. The first results show that, even if there is a high variability between the replicates, the preservation of at least a part of the complexity of the sample is possible. This project and these findings will enable the collection to better preserve whole communities and pave the way to a new era for biological resources centres.

O7: Microbial Biodiversity as a Living Resource for the Conservation of Typicity and the Valorisation of Traditional Food Systems

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Abstract

Microbial Natural *scotta-innesto* consortia historically used in Pecorino Romano PDO embody a unique microbial heritage. Their progressive replacement by defined commercial starters threatens strain-level diversity and weakens the link between product, territory, and tradition. Culture collections play a pivotal role in converting static preservation into a dynamic conservation strategy that delivers characterised, safe, and reusable microbial resources. Historically preserved consortia (*scotta-innesto)* from the Agris Sardegna BNSS Microbial Collection were characterised at species and strain level (whole-genome sequencing, phenotypic profiling), screened for safety determinants (antibiotic resistance, virulence genes, biogenic amine production), and benchmarked against a commercial starter in pilot-scale cheesemaking trials. Metabolomic (GC-MS/LC-MS) and sensory analyses tracked ripening dynamics over 120 days. The natural consortia were taxonomically diverse, genomically distinct from the commercial culture, and devoid of safety concerns. They displayed technological robustness (acidification kinetics, proteolysis) comparable to the commercial starter while driving divergent metabolic trajectories, characterised by richer volatile profiles, distinctive peptide signatures, and yielding cheeses with stronger sensory identity and territorial recognisability. Whole-genome data confirmed strain-level heterogeneity that underpins functional resilience. **Conclusions**: This case study demonstrates a dynamic conservation pipeline: ex situ preservation > deep characterisation > quality-controlled reintroduction as functional starter/adjunct. The collection operates not as a static repository but as a FAIR-compliant resource enabling innovation without homogenisation. Embedding such consortia in PDO specifications safeguards microbial diversity, product typicity, and future biotechnological options for both artisanal and industrial production.

References

[1] Chessa, L. et al. (2021). Autochthonous natural starter cultures: a chance to preserve biodiversity and quality of Pecorino Romano PDO cheese. Sustainability, 13(15), 8214. https://doi.org/https://doi:10.3390/su13158214

[2] Chessa, L., Paba, A., Daga, E., Dupré, I., & Comunian, R. (2021). Biodiversity and safety assessment of half-century preserved natural starter cultures for Pecorino Romano PDO cheese. Microorganisms, 9(7), 1363. https://doi.org/https://doi.org/10.3390/microorganisms9071363

O8: Long-term preservation of complex soil microbial communities and their functions

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Abstract

In the last decades microbiology research has undergone a paradigm shift, from a traditional focus on individual strains to complex communities, their composition and functionality. However, while technologies and methods for microbiome analysis have rapidly advanced, standardized methods and infrastructure for preserving complex environmental microbial communities have not yet found their way into biobanks. This is largely due to the fact that, while methods for the preservation of axenic strains are highly refined and the infrastructure for their storage is well developed, many techniques cannot be directly transferred to microbiomes, and studies on the long-term preservation of microbiomes remain scarce. The MICROBE project (https://www.microbeproject.eu/) addresses these key aspects and aims to close this fundamental gap in microbiome research. In two long-term experiments, complex soil communities originating from two distinct soil types from the Biodiversity Exploratories (www.biodiversity-exploratories.de) were preserved for up to one year. Different storage temperatures were combined with various cryoprotectants to identify optimal conditions for long-term preservation of microbial communities and their functionality. While the first experiment evaluated preservation success, the latter built on these findings and emphasized standardization of promising methods among three participating institutes. Efforts ensured reproducibility and comparability of results. Preservation quality was evaluated by DNA and RNA amplicon sequencing of the 16S rRNA gene (bacteria and archaea) and ITS region (fungi), cultivation experiments, and functionality assessments.The analysis revealed, depending on the methods applied, varying levels of preservation success in terms of maintaining functionality, active community members, and reculturability. Based on these insights, harmonized protocols were established among project partners using accessible methods to maintain complex microbial communities and their functions. This represents a first step toward understanding the requirements for long-term microbiome preservation and the development of supporting infrastructure, including standardized biobanking protocols for environmental microbiome samples.

O9: The challenge of microbiome preservation from fermented food: the successful story of preserving the microbial consortia associated with Italian table olives

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Abstract

Microbial biodiversity in fermented foods is a valuable source of functional traits with important applications for human health. However, its exploitation is strictly linked to preservation methods that need to maintain the viability, structure, and metabolic activity of complex microbial communities over time. While single-strain preservation is well established, maintaining the viability, structure, metabolic activity, and functionality of entire microbiomes remains a significant challenge for Culture Collections. This gap has been addressed by focusing on the microbiomes associated with table olives, a globally significant fermented plant-based food that is central to the Mediterranean diet (Gialluisi et al., 2026). Naturally fermented olives microbiomes from two typical Italian region cultivars, *Leccino* and *Bella di Cerignola*, were conserved for long-term by cryopreservation and freeze-drying, respectively. To ensure a comprehensive assessment of preservation success, the microbial community was characterized before and during storage using culture-dependent methods, metabarcoding, and metabolic profiling. The results showed that, after long-term storage using both cryopreservation and freeze-drying approaches, there was a high retention of microbial viability regardless of the cryoprotectant used. Metabarcoding analysis confirmed the stability of relative abundances across preservation methods. Furthermore, no significant alterations were detected in the metabolic profiles, indicating that the functional potential of the consortia was fully maintained during storage. Overall, our findings demonstrate the effectiveness of both cryopreservation and the newly developed freeze-drying protocol as robust tools for the long-term conservation of olive-associated microbiomes. The viability, structure, and functionality of olive-associated microbial consortia provide valuable tools for their long-term conservation, scientific valorisation and future biotechnological exploitation.

Acknowledgements: We acknowledge the contribution and support from the Italian national Node (MIRRI-IT) of the European Research Infrastructure MIRRI-ERIC.

References

[1] Gialluisi *et al.* 2026. Food Research International, 228:118430, doi:10.1016/j.foodres.2026.118430.

Session 4 - Valorization of culture collections and strains: Biotechnology, Pharmaceutical and Ecological applications

O10: The repository of entomopathogens of Centre of Biotechnology of the Azores: cultures and libraries

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Abstract

The Azorean archipelago represents a unique natural laboratory where geographic isolation has promoted the diversification of microbial and nematode communities with considerable biotechnological potential. The CBA owners a repository of entomopathogens. Entomopathogens are important both from fundamental perspective, because they are important models in the study of host-pathogens interactions, and also under a perspective of plant protection, because they can control populations of important pests. The collection preserves more than 250 bacterial isolates of *Bacillus thuringiensis* collected on the nine islands of the Azores, exhibiting a great morphological, molecular and genetic diversity. We have strains with 5 different crystal forms, from bipyramidal to amorphous, belonging to several serovars and with 12 distinct genotypes of cry genes. The virulence and specificity of these microorganisms have been shown to be high with strains active against Lepidoptera, Coleoptera and a few actives against Diptera, including vectors of human diseases. The collection of entomopathogenic nematodes is small but representative of the diversity observed in the Azores. These biological resources are complemented by genomic and transcriptomic datasets generated from both laboratory and natural conditions, providing a comprehensive platform for studying host-pathogen interactions. Integration of omics approaches with functional bioassays has enabled the discovery of novel bioactive molecules affecting insect physiology while also revealing compounds with promising pharmaceutical potential in mammalian cell models and experimental organisms. These collections demonstrate how biodiversity repositories can simultaneously support sustainable crop protection, fundamental research and bioactive molecule discovery. Moreover, some of identified molecules have also shown promising activities in mammalian cells and model organisms, highlighting their potential for pharmaceutical applications.

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O11: Valorization of the Azorean Microbial Culture Collection through Biorefinery and Bioactive Molecule Discovery

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Abstract

Island microbial diversity represents an underexplored source of biotechnological innovation shaped by geographic isolation and distinct environmental conditions. The Azorean Microbial Culture Collection (AzMCC) preserves environmental bacterial isolates from marine, terrestrial and volcanic ecosystems, constituting a valuable resource for biotechnology and the sustainable exploitation of regional biodiversity. Here, we present an integrated valorisation pipeline illustrating how microbial culture collections can support both marine biorefineries and the discovery of high-value bioactive molecules. Bacterial strains from the AzMCC were functionally screened for biomass deconstruction and the production of extracellular bioactive compounds. Selected isolates were applied to biomass valorisation within the Shrimp4NanoCosmetics and Vertical Algae projects, focusing on the conversion of shrimp by-products and algal biomass into high-value ingredients. In parallel, bioactive metabolites were characterised using activity-guided purification, chromatography, mass spectrometry and genome mining to identify novel molecules with biotechnological applications. The collection yielded bacterial strains exhibiting complementary biotechnological potential. Several isolates efficiently degraded complex marine biomass, supporting sustainable biorefinery approaches for the recovery of cosmetic and nutraceutical ingredients. Simultaneously, different isolates produced extracellular compounds with promising pharmaceutical and cosmetic applications. Low-molecular-weight antimicrobial peptides exhibiting activity against clinically relevant pathogenic bacteria, including *Staphylococcus aureus*, *Streptococcus pneumoniae*, *Staphylococcus epidermidis* and *Cutibacterium acnes*, were isolated. Additional strains produced extracellular enzymes with promising thrombolytic activity, further demonstrating the pharmaceutical potential of the collection. The Azorean Microbial Culture Collection demonstrates how biodiversity repositories can constitute innovation platforms supporting the circular blue bioeconomy. By integrating biodiversity conservation, functional screening, genome mining and application-driven research, the collection enables the discovery of industrial enzymes and novel bioactive molecules with pharmaceutical, cosmetic and ecological applications. This integrated framework highlights the strategic role of microbial culture collections in accelerating biotechnology and sustainable resource valorisation.

Acknowledgements: This work was supported by the Recovery and Resilience Plan (PRR, Portugal) through the *Vertical Algae* project, by COMPETE 2030 through the *Shrimp4NanoCosmetics* project, and by the *PT-OPENSCREEN – Azores Node* project (ACORES2030-2025-10), co-funded by the Azores 2030 Programme, the European Union (ERDF), and the Regional Government of the Azores.

O12: Strain Diversity and Biotechnological Characterization of *Psilocybe cubensis* Cultures

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Abstract

Psilocybin producing mushrooms have a long history of traditional use and are now receiving renewed scientific attention because psilocybin and related tryptamines are being investigated in mental health research. At our institute, a new fungal culture collection has been established to support fungal biodiversity, strain characterization, and applied biotechnology. Within this framework, we examined strain level variability in *Psilocybe cubensis* to assess biochemical diversity in bioactive compounds within a single species. Multiple distinct *P. cubensis* strains maintained in the collection were cultivated under standardized laboratory conditions. Fruiting bodies were dried, extracted, and analyzed for psilocybin, psilocin, baeocystin, norbaeocystin, aeruginascin, and norpsilocin. In parallel, selected Psilocybe strains were evaluated in submerged fermentation systems to assess the effects of strain identity and cultivation parameters, including medium composition, pH, agitation, aeration, and mycelial disruption, on biomass production and metabolite accumulation. Despite standardized cultivation and analytical procedures, substantial differences in tryptamine profiles were observed among *P. cubensis* strains, with psilocybin consistently identified as the dominant compound. Analysis of individual fruiting bodies further revealed considerable within-strain variability, demonstrating that both strain identity and biological heterogeneity affect metabolite composition. Submerged cultivation experiments showed that biomass production and bioactive compound accumulation were also strongly influenced by strain selection and process conditions. These findings emphasize the importance of culture collections not only as repositories of fungal diversity but also as platforms for systematic phenotypic, biochemical, and biotechnological characterization. This study highlights the value of fungal culture collections for documenting strain diversity, selecting biotechnologically relevant isolates, and supporting reproducible production of bioactive fungal biomass. Because the concentration of psychoactive compounds affects standardization, dosing precision, safety, and the interpretation of therapeutic research, rigorous strain characterization and chemical profiling are essential for future pharmaceutical and biotechnology applications.

O13: Unlocking the potential of the Bank of Algae and Cyanobacteria of the Azores: From Native Diversity into Applied Biotechnology

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Abstract

The Bank of Algae and Cyanobacteria of the Azores (BACA) hosts a unique collection of microalgal and cyanobacterial diversity, autochthonous to the Azores Islands, with strong potential for applied biotechnology. Within the framework of the Interreg-MAC CALYPSO and ACORES2030 AlgaeFusion projects, 13 strains were pre-selected for targeted biochemical characterization. Growth performance was established for six strains, enabling a preliminary assessment of their suitability for biomass-based applications. Ongoing analyses include polysaccharide profiling for EPS-rich cyanobacteria (CALYPSO) and pigment and metabolite quantification relevant for microalgal feed supplementation in poultry production (AlgaeFusion). Early results highlight substantial inter-strain variability in growth kinetics and biochemical composition, with strains *Dictyosphaerium* sp. BACA0425 and Chlorophyceae BACA0801 reaching biomass concentrations of 1.65 (±0.17) and 2.69 (±0.15) g L^{-1}, and Lutein concentrations of 2.69 (±0.28) and 1.86 (±0.57) µg mg^{-1}, respectively. Additionally, strains *Nodosilinea* sp. BACA0422, *Monoraphidium* cf. *griffithii* BACA0234 and *Scenedesmus* cf. *obliquus* BACA0397 exhibit distinctive polysaccharide profiles, adding to the functional diversity identified within the collection, reinforcing the value of native Azorean biodiversity as a reservoir of functional traits. These findings demonstrate BACA's strategic role in translating the Azorean biodiversity into industrial biotechnology, supporting the development of sustainable bioproducts derived from autochthonous microalgae and cyanobacteria.

O14: The Fungal Kingdom Against Micropollutants: Unveiling Its Potential for the Bioremediation of Contaminants of Emerging Concern

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Abstract

Freshwater resources are increasingly threatened by the continuous release of contaminants of emerging concern (CECs), including pharmaceuticals and personal care products, which are only partially removed by conventional WWTPs. Sewage sludge represents a hotspot for the accumulation of these micropollutants, exerting selective pressure on resident microbial communities. Within the SusWater project, this study investigated the fungal biodiversity of contaminated sludge and evaluated its potential as a source of biocatalysts for the biodegradation of CECs. Fungi were isolated from contaminated WWTP sludge using liquid enrichment cultures supplemented with selected CECs commonly detected in wastewater. The isolates were taxonomically characterized and screened for their ability to degrade representative contaminants. Removal efficiencies were quantified using an HPLC-UV analytical method, and the most promising strains were selected for further investigation in more complex experimental systems. A total of 104 fungal isolates were isolated, predominantly belonging to the Ascomycota, while Basidiomycota (9%) and Mucoromycota (7%) were less represented. The isolates displayed diverse degradation capabilities, highlighting the remarkable metabolic versatility of fungi adapted to contaminated environments. Estriol and diclofenac were readily transformed, whereas carbamazepine proved considerably more recalcitrant. Overall, approximately 30% of the isolates reduced the concentration of at least one CEC by more than 50%, and several strains achieved removal efficiencies exceeding 70%. The degradation products were also monitored confirming that an active degradation process was occurring. Once the most performing strain was selected, process scale-up was set in bench reactor where it was possible to follow CECs transformation as well as the toxicity decrease. Indigenous fungi from contaminated wastewater sludge constitute promising candidates for the sustainable removal of CECs from wastewater. Ongoing research is exploring their immobilization in innovative hydrogel-based systems.

O15: Antibiofilm activity of *Lactobacillus*-derived cell-free supernatants against mono-, dual-, and tri-species interkingdom biofilms

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Abstract

Polymicrobial and interkingdom biofilms are highly tolerant microbial communities in which bacterial–fungal interactions can modify biofilm architecture and reduce treatment efficacy. This study evaluated the antibiofilm potential of *Lactobacillus*-derived cell-free supernatants (CFS) against clinically relevant mono-, dual-, and tri-species biofilms formed by *Pseudomonas aeruginosa* P28, Methicillin-resistant *Staphylococcus aureus* (MRSA) 333, and *Candida albicans* ATCC 10231. Four CFS obtained from *Lactobacillus reuteri* NCFB 2656T, *Lactobacillus acidophilus* IM-USFQ, *Lactobacillus jensenii* IM-USFQ, and *Lactobacillus gasseri* V193B were tested at 0.5× to 4× minimum inhibitory concentration (MIC). Biofilm inhibition and eradication assays were performed in 96-well plates. Antibiofilm activity was assessed by biomass quantification, viable cell counting expressed as log colony-forming units (CFU)/mL, and LIVE/DEAD fluorescence microscopy. CFS showed concentration-, species-, and biofilm complexity-dependent antibiofilm activity. *L. acidophilus* IM-USFQ displayed the most consistent performance, achieving 96.39–100% inhibition of mono-species biofilm biomass at 4× MIC, with viable-count reductions of 2.98–6.48 log CFU/mL. In tri-species biofilms, *L. reuteri* NCFB 2656T, *L. acidophilus* IM-USFQ, and *L. gasseri* V193B achieved more than 95% biomass inhibition at 4× MIC. However, biomass reduction did not always correspond to equivalent reductions in each microbial population, particularly in complex interkingdom biofilms. Eradication of mature biofilms was less effective than inhibition, indicating that CFS act preferentially during early biofilm establishment. Fluorescence microscopy confirmed that *L. acidophilus* IM-USFQ CFS reduced attached cell load and disrupted biofilm organization, although residual viability

depended on biofilm composition. *Lactobacillus*-derived CFS represent promising preventive or complementary antibiofilm candidates, particularly for limiting early biofilm formation in complex bacterial–fungal communities.

References

[1] Van Dyck, K., Pinto, R. M., Pully, D., & Van Dijck, P. (2021). Microbial interkingdom biofilms and the quest for novel therapeutic strategies. *Microorganisms, 9*(2), 412.
[2] Nithyanand, P., Boya, B. R., Lee, J., & Lee, J. (2025). Polymicrobial biofilms: Interkingdom interactions, resistance and therapeutic strategies. *Microbial Biotechnology, 18*(8), e70218.

Session 5 - Ethical and legal challenges of collection management

O16: More ABS?? What do culture collections need to know about the High Seas Treaty and the WHO Pathogen ABS systems?

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Abstract

Culture collections must operate within the national and international policy frameworks that govern the use of microbial resources. While still challenging, most ECCO collections have, over time, learned to manage the requirements around access and benefit-sharing (ABS) under the Convention on Biological Diversity and the Nagoya Protocol. However, two new legally-binding benefit-sharing frameworks are emerging that will likely pose new administrative issues for culture collection community. The new High Seas Treaty on Biodiversity Beyond National Jurisdiction (BBNJ) entered into force in January 2026 and many EU Member States have ratified. Soon new reporting requirements and the use of so-called BBNJ Batch Identifiers will be required. Secondly, the World Health Organization is finalizing the Pathogen Access and Benefit-Sharing Annex to the Pandemic Agreement and significant new responsibilities for collections are also envisioned in the current text. An overview of these two new agreements and the opportunities for ECCO members to collaborate and work collectively will be presented.

O17: From Isolation to Valorisation: A Focus on the International Depositary Authority under the Budapest Treaty

A brief introduction to the international patent system for inventions making use of microorganisms, and a discussion on a topical challenge

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Abstract

The presentation will cover a specific function that can be fulfilled by a culture collection: acting as an International Depositary Authority (hereinafter "IDA") under the Budapest Treaty system for the deposit of microorganisms in patent procedures. As a substantial proportion of ECCO members already hold this status, whereas others do not, the presentation will address both basic elements of intellectual property rights and their interaction with the Budapest Treaty system, as well as an overview of a current issue within the system to be addressed by culture collections. After a brief introduction to intellectual property rights, with a particular focus on patents and their role in the biotechnology innovation pipeline, the presentation will move on to the Budapest Treaty system, which provides for the deposit of microorganisms to satisfy the sufficiency of disclosure requirement for inventions. This part will also highlight the advantages of obtaining this status under international law. The key topic will be a current issue faced by the IDAs: the so-called "end-of-storage deposits". The Budapest Treaty requires IDAs to conserve deposited microorganisms for at least five years after the most recent request for a sample, and in any case for at least 30 years after deposit. However, it is silent on the fate of biological material after this mandatory storage period. This is not only theoretical but a pressing practical issue for IDAs. The presentation will draw on a synthesis of IDAs' practices recently shared by WIPO, in order to open a broader discussion[1] with the audience on best practices, thereby highlighting the role that an organisation such as ECCO can play in harmonising standards between culture collections in the absence of further guidance from legal institutions.

References

[1] World Intellectual Property Organization (1977). Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure.
[2] World Intellectual Property Organization. (1977). Regulations under the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure.
[3] World Intellectual Property Organization. (n.d.). *Handling of deposited microorganisms after the prescribed storage period*. https://www.wipo.int/en/web/budapest-system/handling-of-deposited-microorganisms-after-the-prescribed-storage-period

Session 6 - Culture collection managements and maintenance

O18: Evaluation of Cyanobacterial and Dinoflagellate Extracts for Alzheimer's Disease-Relevant Effects Using Zebrafish Larvae (*Danio rerio*)

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Abstract

Alzheimer's disease (AD) is a multifactorial neurodegenerative disease and the most common cause of dementia worldwide, primarily characterised by memory impairment and cognitive and behavioural changes. Cholinergic dysfunction, related to reduced acetylcholine levels, and oxidative stress are among the underlying mechanisms of the disease and form the basis of current therapeutic targets. Cyanobacteria and microalgae represent promising sources of secondary metabolites with reported neuroactive and antioxidant effects. This study screened crude methanolic extracts from eight cyanobacterial strains and one dinoflagellate from the Bank of Algae and Cyanobacteria of the Azores (BACA) for AD-relevant bioactivities in zebrafish larvae (*Danio rerio*). Toxicity assays established sublethal test concentrations for downstream evaluation of extracts, including acetylcholinesterase (AChE) inhibition using a modified Ellman assay, spontaneous locomotor and sensorimotor effects using a custom-trained SLEAP model and Megabouts analysis, and attenuation of D-galactose-induced oxidative stress using DCFH-DA fluorescence imaging. *Microcystis aeruginosa* BACA0148, *Kamptonema* sp. BACA0007, and *Symphyonema* sp. BACA0090 significantly inhibited AChE by approximately 40%, 34%, and 31%, respectively. BACA0148 produced the broadest locomotor and sensorimotor profile, while BACA0007 also increased several monitored parameters. BACA0090 showed little behavioural modulation despite significant AChE inhibition, while no extract altered bout displacement or thigmotaxis. As for the antioxidant, *Aliinostoc* sp. BACA0355 and *Aphanizomenon gracile* BACA0809 significantly reduced ROS-associated fluorescence by approximately 25% relative to the D-galactose-only control, without significant AChE inhibition. Bioactivity-guided fractionation, chemical characterisation, concentration-response analysis, and validation in an established AD-like model are required before therapeutic relevance can be determined. Nevertheless, the distinct cholinergic, neurobehavioural, and antioxidant activity profiles identified across the tested extracts highlight their promise as sources of bioactive compounds with potential relevance to neurodegenerative disorders.

O19: Insights from the *Cladosporium cladosporioides* Species Complex: MALDI-TOF MS identification in fungal culture collections

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Abstract

Microbial culture collections preserve authenticated biological material, but ongoing taxonomic revisions and the description of new species require periodic strain reauthentication of taxa that occurred many years ago. Within the European MALDIBANK project, this study evaluated MALDI-TOF MS as a tool for fungal strain authentication and quality control. In this study, a total of 172 strains belonging to the *Cladosporium cladosporioides* species complex and preserved in the *Mycotheca Universitatis Taurinensis* (MUT) culture collection were re-evaluated using a polyphasic approach combining previous morphological and molecular data with multilocus phylogenetic analyses. MALDI-TOF MS performance was assessed using three reference databases: MBT HT database (Bruker), the online MSI-2 reference database (msi.happy-dev.fr) and a curated in-house library (TUCC_FF) developed from molecularly validated strains. Multilocus phylogeny showed that 53.5% of the analysed strains required taxonomic reassignment, and 16 lineages were identified as putative novel taxa. To support strain authentication, the TUCC_FF library comprising 77 Main Spectra Profiles (MSPs) from phylogenetically validated strains was established. Species-level performance strongly depended on database representativeness: the Bruker database, containing only 18 *Cladosporium* MSPs, achieved the lowest species-level identification rates (10%), whereas the curated TUCC_FF library and the MSI-2 database reached up to 48.6% and 57.1%, respectively. Correct or closely related phylogenetic identifications reached 70.7% (MSI-2) and 78.2% (TUCC_FF), whereas assignments to distant taxa remained rare (<4%). MALDI-TOF MS represents a rapid and cost-effective tool for strain authentication in microbial culture collections. Its performance is strongly influenced by database quality and taxonomic coverage, highlighting the importance of expanding curated spectral resources. Initiatives such as MALDIBANK will support standardisation and improve the adoption of MALDI-TOF MS for routine collection management.

O20: From culture collection to genomic resource: unlocking cyanobacterial biodiversity and biotechnological potential in the Spanish Bank of Algae (BEA)

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Abstract

The culture collections of algae and cyanobacteria of the Spanish Bank of Algae (BEA) preserve more than 700 cyanobacterial strains from different environments of the Canary Islands and Macaronesia, as well as additional bioprospected strains from other regions worldwide. These collections constitute an important resource for the preservation and study of cyanobacterial diversity. However, many strains remain insufficiently characterized from taxonomic, evolutionary and functional perspectives. This study applies a polyphasic approach integrating morphological, molecular and genomic data under current taxonomic frameworks to improve strain characterization and assess their biotechnological relevance. Twenty cyanobacterial strains from different islands and habitats of the Canary Islands were selected from the BEA collection. A polyphasic framework was applied, combining morphological observations, 16S rRNA gene phylogeny and draft genome analyses. Genomic data were obtained through DNA extraction, sequencing (Sanger/Illumina) and bioinformatic pipelines for genome assembly and functional annotation. Comparative genomic analyses and pangenome reconstruction were performed, including publicly available cyanobacterial genomes for broader context. Biosynthetic gene clusters (BGCs), metabolic pathways, and core, accessory and singleton genes were analysed to assess functional diversity and biosynthetic capacity. The integration of morphological, molecular and genomic data improved the taxonomic resolution of the studied strains and clarified their evolutionary relationships. Pangenome analyses revealed variation in gene content among lineages, while biosynthetic gene cluster analyses enabled the *in silico* classification of strains according to their secondary metabolite profiles. These results highlight the value of genomic approaches for refining strain characterization within culture collections and for revealing hidden functional diversity. The combination of polyphasic taxonomy with phylogenomics, pangenomics and biosynthetic analyses increases the scientific value of cyanobacterial culture collections by improving strain characterization and functional assessment. This framework supports biodiversity studies, taxonomic refinement and the prioritization of strains for future biotechnological capacities.

References

[1] Dvořák, P., Jahodářová, E., Stanojković, A., Skoupý, S., & Casamatta, D. A. (2023). Population genomics meets cyanobacterial taxonomy. Algal Research, 72, 103128.
[2] Zhang, X., Xiao, L., Liu, J., Tian, Q., & Xie, J. (2023). Genome dynamics and adaptive evolution in cyanobacteria. BMC Genomics, 24, 462.
[3] Zammit, G., Zammit, M. G., & Buttigieg, K. G. (2023). Emerging approaches for cyanobacterial diversity and metabolite discovery. Diversity, 15(11), 1142.

Session 7 - Projects, Networks and databases

O21: Metis: a Biosecurity-Aware Decision Support System for Microbial Strain Discovery in Biotechnology

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Abstract

Microbial strain selection is an essential element in biotechnology and Design-Build-Test-Learn workflows. Strain-related data are distributed across culture collections, databases such as BacDive, and scientific literature. Access to this information is hindered by multiple identifiers and metadata formats (Reimer et al., 2022). While large language models (LLMs) can facilitate access, their outputs may contain hallucinated, unverifiable, or unsafe information (Chelli et al., 2024). Furthermore, integrating biosafety and misuse prevention remains challenging, limiting democratized access to these resources. We developed Metis, an open-access, modular decision support system designed to translate scientific questions into structured database operations. In our system, an LLM generates schema-validated queries without direct access to the database, thereby preventing information leakage. These queries are executed against a knowledge base that integrates identifiers, phenotypes, growth conditions, genomes, provenance data, and literature. The safety system classifies queries as low, moderate, high, or disallowed risk using deterministic rules, semantic similarity to a risk-reference corpus, and session context. All operations are comprehensively logged. Metis implements the complete query-to-answer workflow. Metis was benchmarked against a general-purpose LLM baseline, with evaluation criteria including retrieval effectiveness, accession resolution, evidence grounding, recommendation quality, and safety mediation. By grounding outputs in curated records, Metis enhances traceability and reduces unsupported claims. Biosecurity is addressed as an operational requirement integrated into the workflow. Metis provides a reproducible, evidence-based, and biosecurity-aware decision layer for microbial biological resource centers and the biotechnology industry. Additionally, it operates as a reference architecture for safer AI-assisted access to biological data.

References

[1] Chelli, M., Descamps, J., Lavoué, V., Trojani, C., Azar, M., Deckert, M., Raynier, J. L., Clowez, G., Boileau, P., & Ruetsch-Chelli, C. (2024). Hallucination rates and reference accuracy of ChatGPT and Bard for systematic reviews: Comparative analysis. Journal of Medical Internet Research, *26*(1), 1-11.
[2] Nielsen, J., & Keasling, J. D. (2016). Engineering cellular metabolism. Cell, 165(6), 1185–1197.
Reimer, L. C., Sardà Carbasse, J., Koblitz, J., Ebeling, C., Podstawka, A., & Overmann, J. (2022). BacDive in 2022: The knowledge base for standardized bacterial and archaeal data. Nucleic Acids Research, 50(D1), D741–D746.

O22: ExÂME - An Expansion Microscopy atlas of microbial eukaryotes

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Abstract

Cell biology has long centred on a handful of model organisms, driving methods tailored to those few species. To extend immunofluorescence microscopy across the eukaryotic tree, we employ expansion microscopy, a technique that physically expands fixed cells within swellable hydrogels, increasing antigen accessibility and enabling imaging of non-model organisms often impermeable to commercial antibodies and dyes (Mikus et al.,2025). In close collaboration with culture collections and laboratories providing cultures and expertise, samples are staged, treated, and fixed during on-site visits; expansion and imaging are performed at our home laboratory. A standardised label panel targeting the cytoskeleton, bulk proteome, and DNA determines whether protocol optimisation is required before proceeding to antibody screening and high-throughput confocal microscopy. Over 180 distinct species have been fixed, spanning the eukaryotic tree. Beyond mapping morphology and cytoskeletal organisation, within the euglenozoa alone we have begun quantifying mitotic progression, protein localisation diversity, and endosymbiont co-division. Screening commercial antibodies raised against human epitopes identified reagents recognising conserved targets as well as those robustly labelling unintended structures, including volvocean eyespots, rootlet fibres in *Naegleria*, endosymbionts, and mitochondria across lineages. We are currently evaluating options for sharing imaging volumes and integrating these data with existing genome and transcriptome resources. This project aims to produce an atlas of ultrastructural microscopy spanning the eukaryotic tree of life, while identifying dyes and antibody panels compatible with non-model organisms and expanding the molecular toolbox available to the broader research community. The collections and their expertise are central to this effort, and we hope the resulting dataset will serve as a shared resource for all.

References

[1] Mikus, F., Rubio Ramos, A., Shah, H., Hellgoth, J., Olivetta, M., Borgers, S., Saint-Donat, C., Araújo, M., Bhickta, C., Cherek, P., Bilbao, J., Txurruka, E., Eglit, Y., Leisch, N., Schwab, Y., Husnik, F., Seoane, S., Probert, I., Guichard, P., … Dudin, O. (2025). Charting the landscape of cytoskeletal diversity in microbial eukaryotes. *Cell*, *188*(26), 7610–7628.e13.

O23: MIRRI-ERIC's Roadmap for FAIR Microbial Resources

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Abstract

Microbial Biological Resource Centres (mBRCs) are the trusted custodians of microbial diversity, yet their collective value has long been constrained by fragmentation — inconsistent quality standards, uneven metadata, and disconnected digital services. As an ESFRI Landmark and a European Research Infrastructure Consortium (ERIC), MIRRI holds a distinctive mandate and legal standing to close these gaps, transforming a distributed network of European culture collections into a coordinated, service-oriented research infrastructure, and to act as a bridge connecting culture collections to other research infrastructures, and vice versa, expanding the reach and relevance of microbial resources across disciplines. This mandate is put into practice through a portfolio of projects funded by the EU Horizon Europe programme coordinated by MIRRI and implemented in collaboration with other Research Infrastructures. MIRRI-FIRM harmonises quality management and sustainability practices across mBRCs, strengthening traceability and long-term service reliability. MICROBES4CLIMATE provides transnational access to specialised technologies, resources, and expertise for climate change-related microbial research. MALDIBANK extends FAIR data principles into a domain that has so far lacked a shared reference resource: mass spectrometry-based microbial identification. It is building a global, cloud-based, open MALDI spectra archive and analytical platform supporting rapid identification, epidemiological surveillance, antimicrobial resistance monitoring, and environmental applications, with the ambition of becoming for spectral data what genomic repositories became for sequence data. Notably, MALDIBANK is co-developed with an industry consortium spanning a major diagnostics company (bioMérieux), an SME, and a startup, illustrating how MIRRI-ERIC brokers collaboration across the full innovation chain, from public research infrastructure to industrial partners. Together, these initiatives show how MIRRI-ERIC's institutional status translates into concrete services — harmonised quality, open data, coordinated access, and public-private co-development — for the European mBRC community and its industrial and academic users. Beyond service provision, MIRRI-ERIC is increasingly positioned as a strategic asset for Europe, providing the evidence base, technical standards, and biological resources needed to support emerging EU policy priorities for biotechnology and the bioeconomy. Realising this role fully will depend on continued collaboration across the European microbial resource community, including networks such as ECCO, to ensure that policy ambitions are matched by the infrastructure and expertise needed to deliver them.

O24: From BacDive to MicrobeDive: Moving towards a multi-domain strain knowledge base

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Abstract

Since its initial release more than a decade ago, the bacterial diversity database Bac*Dive* (https://bacdive.dsmz.de) has grown tremendously in terms of content and functionality. Today, Bac*Dive* is a comprehensive resource covering the phenotypic diversity of prokaryotes with data on taxonomy, morphology, physiology, cultivation, and more. As the leading database for strain-level information on bacteria and archaea, it has been designated as an *ELIXIR Core Data Resource* and a *Global Core Biodata Resource*. Here we present our plans to expand the Bac*Dive* concept and create a new overarching infrastructure for microbial strain-level information covering all domains of life. In recent years two Bac*Dive* offshoots for viral data were released: Phage*Dive* (https://phagedive.dsmz.de) for data on bacteriophages and PV*Dive* (https://pvdive.dsmz.de) for plant virus information. Further extensions for fungal and algal strain data are planned. Together with the StrainInfo database (https://straininfo.dsmz.de) serving as a metadatabase for resolution of microbial strain identities, these databases will provide the basis for Microbe*Dive*, a new infrastructure covering multi-domain strain data. Microbe*Dive* will manage data specific to certain organism groups, retaining the strengths of each established database, and catering to differing needs of users from different research communities. At the same time, a common ontology and data standard will enable their integration into a shared infrastructure and allow users to explore a comprehensive strain knowledge base beyond the barriers of domains and data silos.

O25: Industrial Biotechnology Algal Bank (IBAB): Supporting Research, Innovation, and Scalability in Blue Biotechnology

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Abstract

The biotechnology sector demands robust, specialised biobanks to overcome bottlenecks in the rapid scale-up of algae GreenCoLab established the Industrial Biotechnology Algal Bank (IBAB) as a high-standard bioresource provider and a catalyst for intersectoral cooperation, offering production-ready strains alongside rigorous intellectual property protection. Integrated within the Portuguese Blue Biobank, IBAB implements a dual-layered safeguarding approach and a sequential coding system to ensure confidentiality. A curated selection of individually relevant strains is dynamically maintained across various physiological states, ranging from cryopreserved stock to active exponential-phase cultures in up to 100 L bioreactors. Furthermore, IBAB features dedicated cryobanks to preserve non-GMO mutant algae, eliminating the need for continuous subculturing. By maintaining this portfolio of production-ready strains, IBAB significantly reduces industrial scale-up downtime from months to days. The collection supports the development of non-GMO mutants with tailored traits and provides a secure depository for commercially valuable strains. Additionally, thorugh GreenCoLab's Chemistry and Molecular Platforms, a comprehensive portfolio of scientific and technical services is available, including bioprospection, taxonomic identification and classification, metabolic optimisation, analytical characterisation, and advanced training programmes for research, education, and capacity building. IBAB represents a different approach to algal biobanking. By merging rapid-response strain availability, stringent data management, and dedicated mutant repositories, IBAB provides a secure, traceable, and scalable biological foundation, solidifying its role as an innovator in global blue biotechnology.

Session 8 - Open Science, Data Sharing & Science Communication

O26: The International Code of Nomenclature of Prokaryotes and the International Committee on Systematics of Prokaryotes: Relevance for Bacterial Culture Collections and Microbiology

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Abstract

A code of nomenclature for prokaryotes has been developing since before 1930, when R.E. Buchanan and colleagues proposed a separate code for Microbiology, splitting away from the Botanical Code. From the beginning, emphasis was placed on cultural characteristics and type cultures. The International Code of Nomenclature of Prokaryotes (ICNP or 'The Code') has undergone several revisions, most recently in 2025, following Principles that established the foundation of The Code, Rules, designed to effect the Principles, and Recommendations, intended as guidelines. Furthermore, The Code resolves that names should be: i) stable; ii) unambiguous; and iii) necessary, and is entrenched in the understanding that it serves for all prokaryotes. The International Committee on Systematics of Prokaryotes (ICSP) oversees emendations of The Code through an Editorial Board and an Editor-in-Chief. A Judicial Commission issues opinions and makes recommendations on matters of interpreting The Code. Subcommittees on Taxonomy support research and provide recommendations regarding classification and identification. The names of prokaryotic taxa should conform to the The Code for valid publication in the International Journal of Systematic and Evolutionary Microbiology (IJSEM); valid publication is necessary for names to acquire standing in prokaryotic taxonomy. Descriptions of novel taxa include deposition of designated type strains in public culture collections and evidence must be presented that cultures of the strains are present and available. The Code is evolving and has been modified with changing demands. Most recently, The Code was emended to establish regulations for bacteria that are evidenced only through digital sequence information (DSI). And, a List of Recommended Names (LoRN) for bacteria of medical importance has been published, providing guidance for microbiologists and addressing the impacts of name changes in prokaryotic taxonomy. The mandate of the ICSP and an overview of recent activities, particularly in context of culture collections, will be presented.

O27: Science Communication for Diverse Audiences: The Role of Science Centres in Promoting Scientific Literacy

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Abstract

ExpoLab – Centro Ciência Viva (Expolab-CCV), located in the Azores, Portugal, has promoted scientific literacy, public engagement with science and active citizenship since 2009. As part of the national Ciência Viva network and the regional network of science centres, Expolab-CCV acts as an interface between scientific institutions and society, translating research and complex scientific topics into accessible and participatory learning experiences. Its programmes address diverse audiences, including children from pre-school to secondary education, students with special educational needs, teachers, families, adults, senior citizens and the wider public. This diversity requires science communication strategies that adapt language, content, formats and levels of interaction to participants' ages, backgrounds, interests and previous engagement with science. The Centre combines interactive exhibitions, laboratory experiments, maker and technology activities, workshops, field trips, storytelling, environmental cinema, training, science festivals and outreach initiatives in schools and community settings. Its main thematic areas include biodiversity, climate, digital skills, oceans, and environmental sustainability, complemented by activities promoting critical thinking, scientific culture and active citizenship.These approaches are strengthened through collaboration with universities, research centres, schools, public authorities and civil society organisations, and through participation in European, national and regional funding programmes, including Horizon Europe, Horizon 2020, Erasmus+, the Portuguese Blue Fund and Azores 2020. Such projects provide opportunities to test new educational methodologies, connect locally relevant challenges with international research, and bring researchers and citizens into closer dialogue. Expolab-CCV's experience demonstrates how science centres can support the communication of research, while adapting scientific knowledge to different publics. It also highlights a continuing challenge for non-formal science education, moving beyond already science-engaged audiences and creating inclusive opportunities for meaningful participation by communities that remain less represented in science-related spaces. This contribution reflects on strategies and lessons learned through sustained science communication practice.

Posters

Session 1 - Biodiversity, Systematics & Phylogenomics in the OMICs era

P01: CCVIEO microalgae culture collection

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Abstract

The Oceanographic Centre of Vigo (IEO-CSIC) harbours a culture collection of marine microalgae (CCVIEO), with a particular focus on harmful and toxic dinoflagellate species. The collection comprises around 250 strains, characterised by morphological and molecular means by the "Harmful microalgae and plankton ecology (VGOHAB)" group, obtained from sampling work and collaborations with other national and international research groups. The CCVIEO collection is included in the CSIC's catalogue of services for the sale of cultures, growth media, and reference kits for taxonomic purposes. Collection management involves preparing culture media, periodical seeding of microalgae and microscopical examination, isolation of new strains mostly from NW Iberian Peninsula, accompanied by their morphological and molecular identification. Last but not least, management of the website, online database and handling of service requests. The strains are maintained in various sterile culture media according to the nutritional requirements of these. Seeding is carried out approximately every 2-3 weeks. The strains are distributed in three culture chambers at different temperatures (15, 19 and 25 °C), depending on their origin, under controlled irradiance and photoperiod conditions. The CCVIEO collection is placed in Galicia, the main shellfish producer in the country, periodically affected by harmful algae proliferations which cause harvesting closures in the region. Therefore, it is worth noting the importance of establishing cultures of the dinoflagellates responsible for toxic episodes by e.g. lipophilic (genus Dinophysis) and paralytic toxins (*Alexandrium minutum* and *Gimnodinium catenatum*). Laboratory strains facilitate the elaboration of studies to understand the effects of abiotic and biotic factors on their seasonal development, as well as other research including taxonomy, genetics, toxins (e.g. MARINNONET project), pigments, satellite, training host-parasite range experiments and functionally relevant ecological characteristics. Information about the culture collection and supply service for microalgae and related products are available on the CCVIEO website.

References

[1] CIFGA. Final MiTOXin (MARINNONET project: EAPA_0017/2022, Interreg Atlantic Area) report. pp.84 (2026).
[2] CCVIEO website: microalgaeccvieo.csic.es
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P02: Integrated Analysis of the Microbiota, Fatty Acid Composition, and Antioxidant Activity of Donkey Milk from Greece

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Abstract

Donkey milk has attracted considerable attention due to its unique nutritional composition, potential therapeutic properties, and favorable sensory characteristics. Donkey milk resembles human milk, and, due to its low casein content and bioactive properties, is suitable for individuals with cow milk protein allergy, supports cholesterol management, and benefits elderly nutrition. Despite extensive information on the physicochemical and nutritional properties of donkey milk, knowledge of its authochonous microbiota, including both bacteriota and mycobiota, remains limited. Recent metataxonomic studies have begun to shed light on the microbial ecology of raw donkey milk. The aim of the present study was to investigate the microbial diversity of donkey milk produced in all seven currently operating donkey farms in Greece. Towards this, both classical microbiological and metataxonomic analyses were employed. Complementary, classical chemical analyses were performed alongside the profiling of milk fatty acid composition and antioxidant activity of donkey milk. Finally, correlations between bacterial and fungal taxa and the chemical composition of milk were investigated. Milk composition analyses showed no significant differences with published values, with variation observed only in fat content. The fatty acid profile was also in agreement with published data, being characterized by relatively low levels of short chain fatty acids (SFAs) and a predominance of unsaturated fatty acids (UNFAs). Metataxonomic analysis identified *Acinetobacter, Enterococcus, Pseudomonas* and *Staphylococcus* among the most abundant bacterial genera, while *Alternaria*, *Debaryomyces* and *Udeniomyces* were the predominant fungal genera. Both classical microbiological and metataxonomic analysis confirmed the presence of lactic acid bacteria species. Several bacterial and fungal taxa correlated positively with donkey milk fatty acid content, whereas others were negatively associated with milk total antioxidant capacity, thus affecting its composition and antioxidant potential. Overall, this study provides valuable insights into the unique nutritional properties and the microbiome of raw donkey milk produced in Greece, further supporting its potential as a valuable alternative dairy source.

P03: Integrative taxogenomics redefines species and subspecies boundaries within the genus *Enterobacter*

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Abstract

The taxonomy of the genus *Enterobacter* remains controversial, limiting accurate identification despite its clinical and epidemiological significance. We re-assessed the taxonomic structure of the genus using an integrative taxogenomic approach. We analyzed 170 genomes from type and non-type strains, representing validly published species. An integrative framework combining core-genome phylogeny, multilocus sequence analysis (*gyrB*, *rpoB*, *atpD*, *infB*), comparative analysis of *hsp60* sequence fragments, and genome relatedness metrics [i.e., Average nucleotide identity (ANI) and digital DNA–DNA hybridization (dDDH)] were performed. Core-genome phylogeny identified 30 well-supported clusters and revealed several taxonomic inconsistencies. Genome relatedness values, interpreted together with monophyletic separation and type-strain placement in the core-genome phylogeny, supported the recognition of several former subspecies as distinct species-level lineages. Specifically, *E. hormaechei* subsp. *hoffmannii* and *E. hormaechei* subsp. *hormaechei*, as well as *E. cloacae* subsp. *cloacae* and *E. cloacae* subsp. *dissolvens* exhibited ANI values <95.5% and dDDH <63%, supporting their recognition at species rank. Conversely, *E. hormaechei* subsp. *oharae* and *E. hormaechei* subsp. *steigerwaltii* clustered within *E. xiangfangensis* lineage (ANI ≥96.8%; dDDH ≥75.2%), supporting their reassignment as subspecies of *E. xiangfangensis*. Additionally, a 968 bp *hsp60* fragment correctly delineated most species and provided substantially improved resolution compared with the classical 341 bp fragment. This study provides an integrative genome-based framework that resolves longstanding ambiguities in *Enterobacter* taxonomy and supports key nomenclatural revisions. The proposed framework improves the reliability of species identification and has direct implications for diagnostics, surveillance, comparative genomics, and evolutionary studies of this clinically relevant genus.

P04: Polyphasic characterization supports *Gardnerella minuta* sp. nov. as a novel species from the female urinary microbiome

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Abstract

The genus *Gardnerella* has undergone major taxonomic revision, yet its species level diversity remains incompletely resolved, particularly in the female urinary tract. During culture-based investigation of the urinary microbiome of an asymptomatic postmenopausal woman, strain CCPDSM^T was recovered and evaluated as a putative novel *Gardnerella* species. Strain CCPDSM^T was characterized using a polyphasic taxonomic approach combining culture conditions, morphology, physiological and biochemical profiling, wholegenome sequencing, 16S rRNA and *cpn60* phylogenies, phylogenomic reconstruction, and genome-based relatedness indices, including ANIb, ANIm, TETRA and dDDH. Functional genome annotation was also used to infer metabolic potential. The 16S rRNA gene sequence confirmed that strain CCPDSM^T belings to the genus *Gardnerella*, with *Gardnerella* genomic species 10 as its closest relative, showing 99.9% sequence identity. In contrast, phylogentic analysis based on *cpn60* and phylogenomic reconstruction demonstrated that strain CCPDSM^T did not cluster with any currently validly *Gardnerella* species or previously defined genomic species. Genome relatedness values were clearly below accepted species thresholds when compared with all *Gardnerella* type strains (ANIb ≤86.7%, ANIm ≤89.4%, TETRA <0.986 and dDDH ≤32.2%), and *G. greenwoodii* represented the closest relative according to genome-based indices. Phenotypically, CCPDSM^T is a Gram-staining-positive, non-motile, non-spore-forming coccobacillus with fastidious growth under anaerobic and microaerophilic conditions. Genome-based functional prediction indicated a compact, fermentative metabolic repertoire with expanded transport capacity, consistent with adaptation to a host-associated niche. Combined phylogenetic, genomic and phenotypic evidence supports strain CCPDSM^T (=CECT 31324^T=CCP 588^T) as representing *Gardnerella minuta* sp. nov. This study expands *Gardnerella* taxonomy and reinforces the female urinary tract as a reservoir of previously unrecognized bacterial diversity.

P05: *Sivoneniella epilithica* gen. et sp. nov.: A new phycoerythrin-rich, non-toxic, cryptic cyanobacterial genus from Suomenlinna Fortress (UNESCO WorId Heritage Site), Finland

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Abstract

Cyanobacteria are an ancient and diverse group of oxyphototrophic bacteria found across a wide range of environments. *Leptolyngbya* is genus of thin filamentous cyanobacteria characterized by simple morphology and lack of distinctive morphological features. Members of this genus inhabit a variety of environments in both terrestrial and aquatic systems. The polyphyletic nature of *Leptolyngbya* has been demonstrated in several studies, leading to the establishment of several new cryptic genera. Nevertheless, many strains assigned to *Leptolyngbya*, continue to fall outside the *Leptolyngbya sensu stricto* clade, highlighting the need for further taxonomic revision within the genus. This contribution focuses on the polyphasic characterization of two *Leptolyngbya*-like strains from previously unstudied epilithic habitats on the Suomenlinna Fortress. The 16S rRNA analyses revealed that the two strains form a distinct and well-supported clade within the family Leptolyngbyaceae and supported the establishment of a new monospecific genus, *Sivoneniella*, following the International Code of Nomenclature for Algae, Fungi, and Plants. Secondary structures of conserved 16S–23S ITS regions, ITS per cent dissimilarity, multi-locus phylogenies, and genome-based phylogenomic analyses further corroborate the recognition of this novel cryptic genus. Genome mining and LC-MS analyses revealed the absence of known cyanotoxins and other bioactive compounds in both UHCC 1019^T (=ULC 791) and UHCC 1020 (=ULC 808). These findings advance our understanding of cyanobacterial diversity in terrestrial ecosystems, highlight the importance of polyphasic approach workflows in cyanobacteria taxonomy and pave the way for further exploration of the biotechnological, antioxidant and nutraceutical potential of *S. epilithica*. Both strains have been deposited in the HAMBI/UHCC (University of Helsinki) and BCCM/ULC (University of Liege) culture collections and are available for further studies. This underlines the important role of culture collections in providing access to microbial biodiversity while minimizing the environmental impact associated with repeated field expeditions as well as in promoting research.

References

[1] Christodoulou *et al.* (2026) *Eur. J. Phycol* 61(1), 79–98

P06: Diversity and membrane fatty acid adaptation strategies of oligotrophic bacteria from Antarctic freshwater lakes

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Abstract

Antarctic freshwater lakes harbour a wide spectrum of bacteria that have evolved diverse mechanisms to cope with cold and extreme environmental conditions, including adaptations in membrane fatty acid composition. In this study, we investigated the diversity and fatty acid profiles of 205 oligotrophic bacterial strains isolated from freshwater lakes and ponds on James Ross Island, Antarctica. A polyphasic approach combining fatty acid methyl ester (FAME) profiling, MALDI-TOF MS protein profiling and 16S rRNA gene analysis was used to compare phenotypic characteristics with phylogenetic affiliation. The predominant taxa identified by 16S rRNA belonged to the families *Flavobacteriaceae* and *Pseudomonadaceae*, followed by *Oxalobacteraceae* and *Sphingomonadaceae.* Gram-positive bacteria were less abundant and mainly affiliated with *Micrococcaceae* and *Microbacteriaceae.* Clustering based on MALDI-TOF MS and FAME profiles revealed multiple distinct clusters that generally corresponded to phylogenetic clades. However, the class *Gammaproteobacteria* exhibited higher fatty acid variability and was distributed across several clusters. To assess adaptive responses, selected strains were cultivated at different temperatures. Lower temperatures were associated with increased proportions of monounsaturated fatty acids, reflecting adjustments in membrane fluidity. However, higher cultivation temperatures in temperature-tolerant strains increased the proportions of hydroxylated fatty acids, suggesting a role in membrane stabilisation under thermal stress. Our results show that fatty acid variability in cold-adapted Antarctic isolates does not always correspond to their phylogenetic relationships. Together with the observed temperature-related changes among genera, these findings provide valuable insights into the diversification and adaptive strategies of Antarctic freshwater bacteria. Future work will involve whole-genome sequencing of selected isolates to provide insight into the genetic basis of fatty acid variability of cold-adapted strains. This work was supported by the GAMU CAREER RESTART project (Muni/R/1443/2024) and the Czech Antarctic Research Programme.

P07: The phytopathogenic fungus *Roesleria subterranea* – its occurrence in *Vitis vinifera* roots in the Czech Republic and its sensitivity to fungicides and essential oils

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Abstract

The fungus *Roesleria subterranea* (Ascomycota) is an economically important pathogen of *Vitis vinifera* that causes root rot in Europe, including the Czech Republic. During 2021–2023, the mycobiota of grapevine (*Vitis vinifera*) roots was investigated in 27 vineyards in the Czech Republic. Roots were taken from 343 plants that were very old (plants uprooted as part of the vineyard restoration) or dead or showed esca symptoms, for a total of 1,029 roots. The roots were surface-sterilised, cut into small pieces and the pieces were incubated on 2% malt extract agar in Petri dishes. The isolated strains were identified to species level by using DNA sequencing. The inhibitory effect of 17 chemicals fungicides and six essential oils on the growth *R. subterranea* in *in vitro* condition (on agar medium in Petri dishes) was evaluated. *R. subterranea* was found in 16.33% of the roots examined, in 32.36% of the grapevines studied, and in 81.48% of the vineyards investigated. There were recorded differences in the frequency of occurrence between individual vineyards. The fungicides Bellis, Signum and Tessior with the active ingredients boscalid and pyraclostrobin showed 90-100% inhibition rate of all five evaluated strains of *R. subterranea* in *in-vitro* tests. Of the evaluated essential oils, origanum oil showed the highest inhibition rate 65,8 – 100%, comparable to the best tested chemical preparations.

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P08: Cultivating to Preserve: Microbiological Strategies for the Conservation of Prokaryotic Diversity

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Abstract

Microbial Culture Collections play a fundamental role in preserving microbial biodiversity by ensuring the long-term viability, purity, authenticity, and genetic stability of microbial resources. Achieving these objectives depends not only on preservation methods but also on the physiological state of cultures prior to conservation. Therefore, optimizing cultivation conditions is a critical step in the preservation workflow. The extraordinary metabolic diversity of prokaryotes is reflected in their ability to utilize a wide range of organic and inorganic compounds. As a result, culture collections require a large diversity of media to obtain sufficient biomass for preservation. At the Spanish Type Culture Collection (CECT), more than 6,800 prokaryotic strains are maintained, requiring approximately 400 different culture media. Over the last two decades, experience at CECT has shown that the culture medium recommended by depositors is not always the most suitable for preservation purposes. In many cases, successful cultivation and conservation require modifications to the proposed conditions. This challenge is particularly evident for fastidious microorganisms such as strict anaerobes, halophilic archaea, and members of the phylum Planctomycetota. As an example, CECT currently preserves around 100 strains representing 35 species of Planctomycetota. Their cultivation requires 13 specialized media, some prepared with ultrapure water and, in certain cases, alternative gelling agents instead of agar. More than half of these strains have been preserved using culture media different from those originally recommended by depositors. In addition, the optimal medium for liquid cultivation is not always the most suitable for growth on solid media. This contribution will present representative examples illustrating how cultivation conditions directly influence preservation success, highlighting the importance of culture optimization as an essential component of microbial biodiversity conservation.

P09: Characterization of *Actimicrobium* strains isolated from Antarctic cryoconites within a study of microbial biodiversity

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Abstract

From a microbiological perspective, Antarctica remains a largely unexplored region offering a wide diversity of unique sample types. Among these are cryoconites - aggregates of dust particles on glacier surfaces that, through the absorption of solar radiation, promote the formation of cryoconite holes. Between 2016 and 2021, more than 40 cryoconite holes were sampled on James Ross Island in Antarctica. These samples were subjected to basic bacteriological examination, followed by analysis of 16S rRNA gene sequences obtained from the isolated bacterial strains. Among the taxonomically diverse Gram-negative bacteria identified, a group of 15 strains isolated from 11 different cryoconite holes exhibited the highest sequence similarity to *Actimicrobium antarcticum*, with similarity values ranging from 97.5% to 100%. The strains were further characterized by repetitive sequence-based PCR (rep-PCR) fingerprinting with $(GTG)_5$, REP, and BOX primers to assess potential clonality among the isolates. While the rep-$(GTG)_5$ and BOX profiles showed very high similarity across strains, PCR with REP primers (REP-PCR) yielded more heterogeneous fingerprint patterns, enabling finer strain-level discrimination. Nevertheless, all approaches consistently distinguished a cluster comprising strains with high 16S rRNA gene sequence similarity to *A. antarcticum*. Additionally, REP-PCR analysis revealed two further well-separated clusters comprising isolates that all shared 100% 16S rRNA gene sequence similarity.These results indicate that five strains can be assigned to *A. antarcticum*, whereas the remaining isolates represent two different strains belonging to a novel *Actimicrobium* species. This novel species will be further defined through ongoing whole-genome sequencing and comprehensive polyphasic characterization.

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P10: Morpho-molecular and phylogeographic analysis of *Rosellinia necatrix* from western Portuguese orchards

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Abstract

The Western region of Portugal relies heavily on fruit production, yet its orchards are increasingly threatened by persistent soilborne pathogens. Among them, *Rosellinia necatrix* (RN) stands out as a highly destructive and polyphagous fungus that causes root rot, often leading to tree decline and death before above-ground symptoms become evident. This study aimed to improve the understanding of its occurrence in the region through morpho-molecular analysis, supporting future and sustainable integrated management strategies. Culture-based isolation and molecular identification were combined to characterize the autochthonous fungal diversity. Samples were processed through multiple isolation approaches to improve recovery of RN, while also enabling the recovery of cooccurring fungi. RN isolates were examined morphologically, using proteomic profiling and molecular barcoding. The obtained RN molecular data was then evaluated with phylogenetic and phylogeographic analyses. Phylogenetic and phylogeographic reconstruction confirmed the presence of RN in the area and placed the Portuguese strain within an Iberian lineage, suggesting introduction from Spain rather than local emergence. The phylogeographic analysis suggests a globally dispersed pathogen with distinct lineages, and a pattern consistent with human-mediated movement, highlighting that the pathogen's presence in Portugal is part of a wider epidemiological and evolutionary process. This work confirms the presence of the pathogen and reveals that its distribution reflects historical dispersal associated with plant movement and trade. These findings provide a basis for future integrated management strategies, underscoring the value of traceability and preventive orchard management in limiting the spread and impact of the pathogen.

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P11: From the DSMZ Cyanobacteria & Protist Collection: Metagenomic Profiling of Non-Axenic Cyanobacterial Cultures – Exemplified by *Coleofasciculus* Strains

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Abstract

The cyanobacteria and protists collection at the Leibniz Institute DSMZ comprises approximately 1,100 cyanobacterial strains across 150 genera, including organisms from extreme or symbiotic habitats. Crucially, 98% of these cultures are currently maintained as non-axenic mixtures. To overcome traditional characterization challenges, we utilize modern metagenomic workflows to systematically resolve their complex taxonomy and uncover hidden heterotrophic biodiversity. This comprehensive approach is demonstrated here using the globally distributed, filamentous cyanobacterial genus *Coleofasciculus*, which acts as a major primary producer in intertidal microbial mats. The microbiomes of 32 non-axenic *Coleofasciculus* strains sourced directly from the DSMZ repository were analyzed using a dual-layered high-throughput sequencing approach. High-resolution PacBio full-length amplicon sequencing of the complete 16S rRNA gene and the adjacent internally transcribed spacer region (16S-ITS) provided detailed taxonomic profiling. Concurrently, a representative subset of 14 strains underwent deep metagenomic sequencing using the Illumina NovaSeq 6000 platform followed by genomic binning to fully capture the associated heterotrophic community. High-resolution 16S-ITS sequencing of the 32 cultures provided exceptional taxonomic profiling down to the strain level and successfully identified distinct intragenomic ribosomal operon variants (Marter et al., 2025). Parallel deep metagenomics of the 14 selected cultures yielded 320 high-quality metagenome-assembled genomes (MAGs), uncovering massive taxonomic novelty dominated by *Pseudomonadota*, *Bacteroidota*, and *Planctomycetota*. Functional profiling revealed widespread phototrophic potential, including 32 MAGs with rhodopsin operons and the landmark discovery of *Candidatus* Photomyxococcus marinus—a novel, facultatively phototrophic myxobacterium possessing a complete photosynthesis gene cluster (Marter et al. 2026). Regarding methodology, long-read 16S-ITS amplicon sequencing provides superior taxonomic resolution down to the strain level, proving to be the ideal tool for rapid profiling and quality control of non-axenic culture collections. In terms of biology, the cyanosphere of mat-forming cyanobacteria represents a significant ecological hotspot for taxonomic novelty, functional versatility, and previously unknown phototrophic lineages.

P12: Unraveling the Complexity of Environmental *Bacillus* spp. Using Fourier-Transform Infrared Spectroscopy (FT-IR)

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Abstract

The genus *Bacillus* comprises a highly diverse group of species characterized by substantial genetic heterogeneity and high intra-species diversity, posing significant challenges for accurate identification and typing. Conventional typing approaches often lack sufficient discriminatory power to reliably differentiate closely related *Bacillus* species and strains [1]. In contrast, Fourier-transform infrared spectroscopy (FT-IR) through the Bruker IR Biotyper (IRBT), has recently emerged as a rapid and accurate tool for bacterial strain typing [2]. Therefore, this study aimed to characterize and type a collection of environmental *Bacillus* species using IRBT. Environmental isolates of *Bacillus cereus*, *B. pumilus*, and *B. nitratireducens*, isolated in Portugal, were previously identified by genome sequencing. Strains were cultured on Nutrient Agar (1.5% agar) and incubated at 28°C for 24 h. Bacterial cells were processed according to the IR Biotyper® Kit protocol (Bruker Daltonics, Germany). Fourier-transform infrared (FT-IR) spectra were acquired using the Bruker IR Biotyper (IRBT) system and subsequently analyzed for strain typing and characterization. Hierarchical clustering based on Euclidean distance/UPGMA algorithm clearly discriminated the isolates, accurately separating the three *Bacillus* species included in this study. This classification was supported by 2-D Principal Component Analysis (PCA), in which the first two principal components explained 98.6% of the total variance. Significant differences among species were observed ($p < 0.05$). *B. pumilus* strains clustered in the lower-left quadrant of the PCA plot, whereas *B. cereus* and *B. nitratireducens* were predominantly distributed in the lower-right and upper-right quadrants, respectively. This study highlights the potential of the IRBT as a rapid, accurate, and high-throughput approach for *Bacillus* species identification. Ongoing work aims to validate its application across a wider diversity of *Bacillus* species and to evaluate its discriminatory power for strain-level typing based on environmental origin and phenotypic traits. Overall, IRBT represents a promising tool for the characterization and management of *Bacillus* culture collections.
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References

[1] Xu, X., & Kovács, Á. T. (2024). How to identify and quantify the members of the *Bacillus* genus?. Environmental Microbiology, 26(2), e16593.
[2] Al-Fraihat, E., Barker, K. R., & Tadros, M. (2025). The IR Biotyper as a tool for typing organisms of significance for hospital epidemiology-A subject review. Diagnostic Microbiology and Infectious Disease, 111(3), 116676.

P13: The first two protocols for characterization of *Trichoderma* strains using IR-Biotyper

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Abstract

Fourier-transform infrared spectroscopy (FTIR) is a high-throughput approach for microbial typing. The IR Biotyper (IRBT) has been extensively used as an FTIR-based platform for bacterial typing. However, its application to environmental microorganisms, namely filamentous fungi, remains unexplored. This work aimed to develop and evaluate two protocols for typing *Trichoderma* strains using IRBT. Two protocols were developed using *Trichoderma* strains, based on [1]. Conidia were harvested from 12-day-old cultures grown on potato dextrose agar (PDA) at 25 °C using 10 mM $MgSO_4$. The suspension was filtered through a cotton column to remove hyphae. Subsequently, 15 µL of a suspension (5.0×10^9 conidia/mL) was deposited onto a 96-spot silicon microtiter plate and analysed using the IRBT. In the second protocol, *Trichoderma* strains were cultured in PDB (24 h, 25 °C). Cultures were filtered through a 70 µm cell strainer to retain hyphae and eliminate conidia. Hyphae were washed with 10 mM $MgSO_4$ and homogenised using a bead mill (three cycles of 1.5 m/s for 20 s). Subsequently, 60 µL of the hyphal suspension was mixed with 50 µL of 70% (v/v) ethanol and vortexed for 1 min at 3,500 rpm. Finally, 15 µL of the suspension was deposited onto a 96-spot silicon microtiter plate and analysed using IRBT. Both protocols generated reproducible FTIR spectra and enabled discrimination among *Trichoderma* strains. Each strain formed a unique cluster, while strains of the same species exhibited greater similarity than strains from different species. These findings demonstrate that both conidial and hyphal preparations can be used for FTIR-based typing of *Trichoderma* collections. This work presents two protocols for FTIR-based typing of *Trichoderma* strains using IRBT. The methodologies provide a basis for applying this technology to fungal collections and support the fast/low-cost method for FTIR-based typing in other filamentous fungi.

References

[1] Kirtil, H. E., Cebi, N., Yildirim, R. M., Metin, B., & Arici, M. (2024). A rapid spectroscopic method for the identification of the filamentous fungi isolated from Turkish traditional moldripened cheeses. *Journal of Microbiological Methods*, *217*, 106884.

P14: CBMAR: A curated bacterial biobank from temperate mesophotic sediments of the North Atlantic coast of Portugal

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Abstract

Temperate mesophotic ecosystems, found at intermediate depths (30–150 m) represent unique transitional zones between shallow and deep waters supporting critical ecological processes. Yet, these ecosystems remain among the most uncharacterized marine habitats globally, particularly in what concerns the microbial component. Within the ATLANTIDA II North Atlantic coastal observatory (NORTE2030-FEDER-01799200), which establishes marine biobanks as conservation instruments, we are building the first curated bacterial collection from the Portuguese mesophotic zone, the CBMAR biobank, capturing microbial diversity from these understudied sediments. Bacteria were isolated from sediments at depth ranging 30-70 m across 25 stations on the NW Portuguese mid-shelf off Viana do Castelo over three campaigns (2023-2025) and Sanger-sequenced (16S rRNA). A reproducible pipeline built consensus sequences and assigned taxonomy through a quality- and length-weighted consensus of BLAST, SINTAX and lowest-common-ancestor calls. QC-failing isolates were flagged provisional. Records were curated and deposited into a web-application with Nagoya ABS tracking and Arctos/EMBRC export. To date, from 436 high-confidence identifications (≥1200 bp; median 1405 bp), CBMAR spans 111 species across 46 genera. The collection is Gram-positive-dominated (310; 71%; *Bacillota* 301, *Actinomycetota* 9), led by *Bacillus*, *Paenibacillus* and *Priestia*, with a Gram-negative fraction (126; *Pseudomonadota*) led by *Pseudomonas* and *Enterobacteriaceae*. Most isolates matched a described species (≥98.7%), but 7 distinct lineages fell below 98.7% and could not be assigned at species level, including *Pseudomonas*, *Pseudoalteromonas, Peribacillus* genus representatives, and a mesophotic *Psychrobacter* resembling the deep Southern-Ocean *P. nivimaris*. A literature assessment further indicated that the collection is rich in taxa with documented biotechnological potential (biosurfactants, cold-active enzymes, bioplastics, ectoine, bioremediation). Of these, the *Psychrobacter* and *Pseudoalteromonas* lineages will be prioritized for detailed molecular and functional characterization. CBMAR delivers a queryable, network-integrated mesophotic bacterial collection that advances ATLANTIDA II and provides a curated, FAIR-compliant resource for marine conservation and bioprospecting.

P15: Cyanobionts in embryophytes: studies on the symbiotic competence of cyanobacteria

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Abstract

It was a cyanobacterial symbiont that was eventually turned into the chloroplasts for carbon fixation. Yet, there is another prominent type of cyanobacteria in symbiosis: the cyanobionts. While cyanobacteria provide fixed nitrogen to their hosts, the hosts provide sugars for the cyanobacteria. Best described in several embryophytes (e.g. *Gunnera, Azolla* and *Anthoceros*), these cyanobionts are tightly integrated into the host body but have not (yet) been domesticated into an organelle. The manifold occurrence of symbiotic cyanobacteria warrants the question of what manifests the symbiotic competence of these cyanobacterial lineages (de Vries & de Vries 2022). Yet, in current genomic comparisons, the 'symbiotic toolkit' appears to grow smaller when datasets are expanded. To understand the cyanobacterial competence, we address this in three aspects: (i) We combine comparative genomics and genome-wide association studies to pinpoint genetic factors that are common to all cyanobacteria that are clearly capable of symbiosis: We are leveraging the SAG algal culture collection and sequencing cyanobacterial strains isolated from symbiotic and non-symbiotic conditions. Experimentally, we use the *Anthoceros* lab system (Chatterjee *et al.* 2022) to phenotype the cyanobacterial strains sequenced for symbiotic competency and efficiency in the Anthoceros–cyanobacteria symbiosis after cyanobacterial reconstitution, (ii) study motility in cyanobacterial symbioses, and (iii) investigate cyanobacterial-symbiotic performance under stress conditions. Here we present the first results of determining factors linked to the symbiotic capabilities of the cyanobacteria.

References

[1] Chatterjee, P., Schafran, P., Li, F. W., & Meeks, J. C. (2022). *Nostoc* Talks Back: Temporal Patterns of Differential Gene Expression During Establishment of *Anthoceros-Nostoc* Symbiosis. *Molecular plant-microbe interactions : MPMI*, *35*(10), 917–932. https://doi.org/10.1094/MPMI-05-22-0101-R
[2] de Vries, S., & de Vries, J. (2022). Evolutionary genomic insights into cyanobacterial symbioses in plants. *Quantitative Plant Biology*, 3:e16. https://doi.org/10.1017/qpb.2022.3

P16: The diversity of yeasts in fruit kefir reveals the different contributions of each species and the occurrence of multiple interspecific hybridisation events

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Abstract

Fruit kefir has become a very popular probiotic beverage. This drink is typically produced by fermenting a mixture of water 40-60 g/L of sugar with a dry fig, and a slice of lemon using a microbial community containing yeast and bacteria that produces translucent grains. In this project, we explored the diversity of the five main yeast species encountered, using the genomic data of 53 strains isolated from kefir and data from shotgun metagenomics. *Saccharomyces cerevisiae* was always present in the different fruit kefirs and originated mainly from one group associated with the "M1 mosaic" origin as described in the recent overview of *S. cerevisiae* diversity (1) with some originating from the Brazil-bioethanol cluster and some from the mosaic beer cluster. Similarly, *Zygotorulaspora florentina* strains, which were present at lower frequencies, appeared as closely related. In contrast, *Pichia fermentans* and *Pichia membranifaciens* isolates showed wide diversity and did not originate from a single source. Finally, strains characterised as *Hanseniaspora valbyensis* revealed a complex origin, with the presence of several interspecific hybrids echoing the hybrids encountered in *Saccharomyces* or *Pichia species*. This fermented beverage represents an interesting system to study the domestication of a microbial community.

References

[1] Loegler, V., Friederich, A., Schacherer, J., 2024. Overview of the Saccharomyces cerevisiae population structure through the lens of 3,034 genomes. G3 14, kae245.

Session 2 - New approaches in Genomics and Genome-Scale Insights

P17: Scaling genome assembly and annotation across bacterial and viral culture collections: lessons from long- and short-read sequencing of NCTC and NCPV strains

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Abstract

Genomic characterisation of microbial culture collections is essential to maximise their long-term scientific value, enabling improved annotation, data reuse, and integration into modern bioinformatics workflows. This study presents complementary approaches to genome assembly and annotation across bacterial and viral datasets from the UK's National Collection of Type Cultures (NCTC[1]) and National Collection of Pathogenic Viruses (NCPV[2]), highlighting practical challenges and solutions in working with taxonomically diverse collections. Oxford Nanopore Technologies (ONT) sequencing data generated during a pilot project on 27 NCTC strains were analysed using Autocycler[3] to produce high-quality, complete genome assemblies. In parallel, short-read Illumina sequencing data for 176 NCPV strains were assembled using IVA[4] and SPAdes[5], followed by annotation with VIGOR4[6]. To ensure consistent and meaningful annotation across diverse viral taxa, bespoke viral family-specific reference databases were developed. Long-read assemblies enabled the generation of complete bacterial genomes and demonstrated scalability, contributing to the development of a larger sequencing initiative. Short-read approaches proved effective for many viral genomes; however, limitations were identified for larger and more complex viruses. The development of family-specific reference databases enabled consistent and accurate annotation across diverse viral taxa and will be made available as a community resource to support standardisation and broader data reuse. This work demonstrates practical approaches to scaling genome assembly and annotation across diverse culture collections. Combining tailored bioinformatics workflows with fit-for-purpose reference resources supports improved data quality, standardisation, and interoperability. Building on these findings, further work is planned to explore the application of ONT sequencing to address challenges associated with complex viral genomes.

References

[1] NCTC (https://www.culturecollections.org.uk/about-us/nctc/)
[2] NCPV (https://www.culturecollections.org.uk/about-us/ncpv/)
[3] Wick RR *et al*. Bioinformatics. 2025;41(9):btaf474.
[4] Hunt *et al*. Bioinformatics. 2015;31(14):2374-2376.
[5] Bankevich *et al*. Journal of Computational Biology, 2012;19(5): 455-477
[6] Wang *et al*. BMC Bioinformatics, 2010;11, 451.

Session 3 - Microbiomes: Maintenance, Function, and Applications

P18: Whole-community cryopreservation reaches the phylogenetic blind spots of culture collections: an RNA-based cross-validation of soil microbiome biobanking

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Abstract

Whole-community cryopreservation offers biological resource centres an opportunity to extend their reach beyond taxa currently tractable by isolation-based methods. Cross-referencing the Global Catalogue of Microorganisms (GCM; ~600,000 strains, 162 Collections) against sequence databases reveals bacterial representation at ~76% of soil taxa at class level, but fungal coverage drops to ~50% and protist coverage to ~33%. Taxa well-described in sequence databases, including obligate biotrophs and arbuscular mycorrhizal fungi, remain absent from collections, forming a phylogenetic "red zone" of low GCM availability. Within the MICROBE project (https://www.microbeproject.eu/), we tested whether preserving whole communities could capture and revive these red-zone taxa where isolation-based approaches cannot. Two distinct soils (Histosol; Cambisol) from the DSMZ Biodiversity Exploratories sampling campaign were preserved using four cryopreservation protocols (glycerol, trehalose, no cryoprotectant, encapsulation). After one year, post-thaw viability was assessed by RNA extraction following 24-hour resuscitation, a conservative proxy for metabolic activity. Amplicon sequencing (ITS and 16S) of rRNA fractions was cross-referenced against GCM availability scores to identify red-zone taxa showing post-cryopreservation activity. For bacteria, 82 of 85 red-zone classes (97%) showed RNA activity in at least one cryopreservation treatment. Among fungi, 32 of 52 red-zone classes (62%) were RNA-active. Canonical arbuscular mycorrhizal genera (*Glomus, Rhizophagus, Funneliformis)* were absent from post-cryopreservation RNA, representing a defined failure class. Conversely, corticioid basidiomycetes (*Sertulicium*) showed consistent enrichment across protocols. These results illustrate the reach and limits of community-level cryopreservation as a biobanking tool. Whole-community cryopreservation is not a substitute for isolated-strain biobanking but a complementary approach that can preserve a taxonomically broader snapshot of soil biodiversity. We propose whole-community archiving as a conservation strategy for biological resource centres. Ongoing work within MICROBE is exploring methods to propagate preserved whole microbiomes and develop defined microbial communities, with the longer-term aim of making these uncultured taxa accessible.

P19: Towards a curated culture collection of bacteria from the female urogenital microbiome

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Abstract

Culture collections are essential for preserving microbial diversity and transforming microbiome research into experimentally accessible biological resources. The female urogenital microbiome (FUM) remains poorly represented by cultivated and taxonomically curated strains, limiting species-level studies, functional validation and future microbiome-based applications. The Culture Collection of Porto is establishing a curated culture collection of bacteria from the FUM, based on isolates recovered from culturedependent studies of asymptomatic women[1,2]. Urine and vaginal samples were processed using extended culturomics. Strains were initially by MALDI-TOF MS/gene marker sequencing, and selected representatives of different species/genera are being subjected to WGS. Strains are being preserved and curated with associated metadata. In recent years, particular attention has been given to taxonomically complex and underexplored urogenital taxa (e.g. *Corynebacterium*, *Gardnerella* and *Lactobacillaceae*). The collection under development includes isolates representing 131 bacterial species and 54 genera from the FUM. Polyphasic characterization of selected lineages has already supported the description of novel species, including *Lactobacillus mulieris*, *Limosilactobacillus urinaemulieris*, *Limosilactobacillus portuensis*, *Gardnerella pickettii*, *Gardnerella greenwoodii*, and eight novel *Corynebacterium* species. These findings highlight the value of culture-based strategies for revealing, preserving and characterizing previously unrecognized bacterial diversity from the female urinary tract. This initiative will establish a curated FUM culture collection as a foundation for taxonomy, strain preservation, comparative genomics and future functional studies. By linking viable isolates with genomic, phenotypic and contextual metadata, the collection will support species discovery and promote the longterm valorization of urogenital microbial diversity.

References

[1] Ugarcina Perovic S, Ksiezarek M, Rocha J, et al. Urinary Microbiome of Reproductive-Age Asymptomatic European Women. *Microbiol Spectr*. 2022;10(6):e0130822. doi:10.1128/spectrum.01308-22.
[2] Ksiezarek M, Ugarcina-Perovic S, Rocha J, Grosso F, Peixe L. Long-term stability of the urogenital microbiota of asymptomatic European women. *BMC Microbiol*. 2021;21(1):64. Published 2021 Feb 25. doi:10.1186/s12866-021-02123-3

P20: Multi-omic approach for assessing microbial viability, taxonomic composition, and metabolic activity after freeze-drying of fermented olives microbiomes

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Abstract

The development of food microbiome biobanks within research infrastructures aims to preserve viable, well-characterized microbial consortia for both scientific and industrial applications. Preservation strategies support positioning culture collections as key infrastructure for enabling safe, resilient, and sustainable fermentations. In this study, we evaluated an integrated workflow that combines culture-dependent and culture-independent approaches to assess the microbial viability, taxonomic composition, and metabolic activity of the microbiome in fermented table olive *cv. Bella di Cerignola* during freeze-drying. An integrated multi-omic workflow combining viability assays, MALDI-TOF-MS identification, metabarcoding analysis, and phenomic profiling was applied before and after the freeze-drying procedure. Microbial viability was assessed by plate counting on selective culture media. The taxonomic profile was evaluated by a metabarcoding approach, and representative colonies were randomly selected for identification based on MALDI-TOF-MS analyses. Functional diversity and metabolic potential were assessed using the Omnilog EcoPlate™ system. Culturomics enabled quantification of viable populations after freeze-drying and reliable taxonomic identification. Culture-dependent results were consistent with metabarcoding data and MALDI-TOF-MS identification, confirming workflow robustness. Functional profiling indicated that the microbial consortium retained substantial metabolic versatility after freeze-drying, supporting preservation of community functionality. The integrated multi-omic workflow provides a high-resolution framework for assessing microbiome preservation. These findings also support the development of standardized freeze-drying protocols for preserving microbial consortia, alongside cryopreservation methods.

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P21: Isolation and characterization of strict anaerobic strains in a microbial biobank

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Abstract

As part of cross-biobank initiatives involving human microbiota and derivative microbial strains at the CRBIP, a study was conducted to isolate strict anaerobic bacterial strains from human faecal samples collected from a cohort of healthy donors. The aim was threefold: to establish expertise on strictly anaerobic bacteria within the CIP, to enrich the CIP biobank with fully characterized strains, and to examine the valorization potential of strains of interest. Samples from 11 stools from human healthy donors were processed by fast and targeted culturomics using four culture media in strict anaerobic conditions (1). A total of 385 isolated colonies were obtained and identified using full 16S rRNA gene sequencing and MALDI-TOF mass spectrometry. In addition, new bacterial species candidates were evaluated by whole genome sequencing. Those were further biochemically characterized including short fatty acids (SCFAs) production and Oxford Technologies sequencing was also performed. The 16S rRNA gene sequencing analysis of isolates revealed a broad range of bacterial genera belonging to the phylum Bacillota (Firmicutes), such as *Dialister*, *Mediterraneibacter*, *Collinsella*, *Ligaoa*, *Faecalibacterium*, *Ruminococcus*. At species-level, 38 different bacterial species were distinguished. Among them, 4 were ambiguously defined, those belonging to *Dysosmobacter sp*, *Neglecta sp*., *Verrocomicrobia sp., Barnesiella sp.* A special effort is being for the phenotypic characterization of a *Faecalicatena contorta* strain, focusing on metabolic pathways of SCFA synthesis (2). Based on the blast analysis of gene markers, predicted SCFA metabolic capabilities are being tested by measuring SCFA concentrations by gas chromatography in the culture supernatant. This work forms part of an initiative to further characterise the human gut microbiota of healthy donors. The culturomics approach has enabled the isolation and characterisation of strict anaerobic bacteria, which remain largely under-represented in microbial biobanks. The genomic analysis, supplemented by SCFA phenotypic analysis, is of taxonomic importance and supports potential valorisation of these strictly anaerobic strains.

References

[1] Bellais S, Nehlich M, Ania M, Duquenoy A, Mazier W, van den Engh G, Baijer J, Treichel NS, Clavel T, Belotserkovsky I, Thomas V. (2022). Species-targeted sorting and cultivation of commensal bacteria from the gut microbiome using flow cytometry under anaerobic conditions. *Microbiome*, Feb 3;10(1):24. https://doi/10.1186/s40168-021-01206-7

[2] Sakamoto M, Iino T, Ohkuma M. (2017). *Faecalimonas umbilicata* gen. nov., sp. nov., isolated from human faeces, and reclassification of *Eubacterium contortum*, *Eubacterium fissicatena* and *Clostridium oroticum* as *Faecalicatena contorta* gen. nov., comb. nov., *Faecalicatena fissicatena* comb. nov. and *Faecalicatena orotica* comb. nov. *Int J Syst Evol Microbiol.* May;67(5):1219-1227. https://doi//10.1099/ijsem.0.001790.

P22: First eukaryotic metagenome-assembled genomes from stone monument biofilms reveal potential for biogeochemical cycling

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Abstract

Stone monuments subaerial biofilms (SABs) are key drivers of cultural heritage biodeterioration and have been increasingly investigated through metagenomics methods. However, genome-resolved studies have almost exclusively focused on prokaryotes, leaving the genomic architecture and ecological functions of eukaryotic biodeteriogens largely unexplored. This study aimed to recover and characterize eukaryotic metagenome-assembled genomes (MAGs) from stone monuments SABs and evaluate their potential roles in biogeochemical cycling. An Oxford Nanopore® metagenomic dataset obtained from SABs colonizing UNESCO World Heritage stone monuments in Coimbra (Portugal) was revisited using a co-assembly genome-resolved metagenomic approach. Eukaryotic contigs were identified, binned and evaluated using a tailored bioinformatics approach. Taxonomic and functional genomic annotation was conducted to understand MAGs general and biodeteriorative metabolic pathways. Two eukaryotic MAGs were recovered. MAG SM8 was assigned to *Trebouxiophyceae* (*Chlorophyta*) and comprised 56 scaffolds with a N50 of 1.16 Mb, a genome size of 35.3 Mb and 82.2% BUSCO completeness. MAG CM95 was assigned to *Cyanidiaceae* (*Rhodophyta*), comprising 73 scaffolds, with an N50 of 264 kb, a genome size of 12 Mb and 69.0% BUSCO completeness. Molecular analyses indicated that both MAGs putatively represent previously undescribed lineages. Functional reconstruction revealed that the *Chlorophyta* MAG encoded a complete assimilatory nitrate reduction and assimilatory sulphate reduction pathways, while the *Rhodophyta* MAG encoded a complete assimilatory sulphate reduction pathway and partial nitrate assimilation (reduction) capacities. Both genomes also contained metabolic pathways and gene contents associated with stress resilience, photosynthesis and photoprotective pigment biosynthesis. This work reports the first recovery and characterization of eukaryotic MAGs from cultural heritage biofilms, suggesting that stone associated microalgae have the potential to contribute to nitrogen and sulphur cycling, known biogeochemical biodeteriorative processes that have previously been mainly attributed to prokaryotic members of SAB communities.

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Session 4 - Valorization of culture collections and strains: Biotechnology, Pharmaceutical and Ecological applications

P23: Recovering native microbial diversity from Fiore Sardo PDO: integrating on-farm monitoring and culture collection-based preservation

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Abstract

Raw-milk cheeses rely on complex native microbial consortia that shape product identity, technological performance, and sensory characteristics, representing an underexploited reservoir of dairy microbial resources. This aspect is particularly relevant in small-scale dairy systems, where cheesemaking still relies on spontaneous fermentation rather than commercial starter cultures, allowing indigenous microbial communities to drive product differentiation. Within this framework, the 4Fiori project was established to improve the overall quality of Fiore Sardo PDO, a traditional Sardinian raw ewe's milk cheese, through a multidisciplinary approach integrating technological, microbiological, chemical-nutritional, and sensory analyses, while preserving its authenticity and distinctive traits. A central objective of the project is to recover, characterise, and valorise the indigenous microbial resources associated with farms that have maintained traditional practices without routine use of starter cultures. During the first cheesemaking season, artisanal Fiore Sardo PDO productions without the addition of starter cultures were monitored under field conditions. Cheeses were characterised at 105 days of ripening through a multidisciplinary approach, providing a baseline for comparison with the subsequent cheesemaking campaign, in which a biodiverse starter culture composed of 13 strains from the Agris-BNSS microbial collection will be applied. In parallel, approximately 1500 microbial isolates were obtained from cheeses produced during the first season and are currently preserved in the Agris-BNSS collection. A selection of these isolates will be identified at species level, and target groups will undergo strain-level characterisation, thereby supporting the structured exploitation of the microbial diversity associated with Fiore Sardo PDO. Concurrently, the 13 strains composing the starter culture were subjected to whole-genome sequencing and annotation, combined with phenotypic characterization to assess acidification activity, growth kinetics, and volatile aroma production. The comparison between cheeses produced without starter cultures and those obtained using the selected multi-strain culture will allow the assessment of its impact on the main pro-technological and anti-technological microbial groups, as well as on product quality traits. Overall, this study provides a collection-oriented contribution to the understanding, preservation, and valorisation of native microbial diversity associated with Fiore Sardo PDO, while supporting its integration into national and European microbial resource infrastructures.

P24: Beyond genome mining: discordant bacteriocin repertoires and antimicrobial phenotypes in urogenital *Lactobacillaceae*

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Abstract

Members of the *Lactobacillaceae* contribute to female urogenital microbiome (FUM) stability and pathogen exclusion, yet the relationship between bacteriocin genomic potential and antimicrobial activity remains poorly resolved. This study characterized bacteriocin diversity and explored genotype-phenotype relationships in urogenital lactobacilli. Ninety-one isolates, representing 15 species recovered from urine/vaginal samples of 24 women, were analyzed. WGS was used for species assignment and identification of bacteriocin biosynthetic gene clusters (BGCs) using BAGEL4 and antiSMASH. Antimicrobial activity was assessed by overlay assay against 52 strains: 18 *Streptococcus agalactiae*, 15 *Escherichia coli*, 10 *Klebsiella pneumoniae*, 3 *Staphylococcus aureus*, 2 *Enterococcus faecalis*/*Enterococcus faecium*, 1 *Enterococcus lactis*/*Proteus mirabilis*. Genome mining identified 54 BGC types across 68 isolates (75%), including 45 putative novel clusters (<80% aminoacid identity with known bacteriocins). Genomes encoded 1-8 BGCs, with some cluster types associated with specific species and substantial strain-level variability within species. Class III bacteriocins predominated. Urinary isolates showed higher BGC richness than vaginal isolates, while carriage was similar (~74%). Antimicrobial activity was detected in 45% (n=41/91) of isolates, spanning diverse indicator taxa. Isolates displayed heterogeneous inhibitory profiles, ranging from full (n=9 strains) to narrow spectrum (n=17 strains). Isolates with similar BGC repertoires frequently exhibited divergent activity profiles, and no clear relationship emerged between BGC number and antimicrobial breadth. Bacteriocin genomic potential showed limited concordance with antimicrobial activity, under the conditions tested. Inhibitory effects may reflect additional mechanisms (e.g. regulation/expression/non-bacteriocin metabolites). These findings highlight substantial strainlevel functional variability and support integrated genomic and phenotypic approaches when identifying candidate strains for microbiome-based applications.

P25: Antimicrobial Resistance Profiles of Gram-Negative Bacterial Isolates Preserved in the HUMB Microbial Collection

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Abstract

Gram-negative (G-) bacterial pathogens are major causes of infections, with antimicrobial resistance (AMR) increasingly limiting treatment options. HUMB collection provides a valuable resource for monitoring resistance trends. We aimed to record the resistance profiles of a subset of G- isolates collected 2012-2014. 188 G- isolates collected from clinical specimens in frame of the project "Transfer Routes of Antibiotic Resistance" were included in the analysis. Isolates originated from 4 Estonian hospitals. Antimicrobial susceptibility was determined by E-test and interpreted according to EUCAST criteria. *Pseudomonas aeruginosa* isolates (n=109) originated from respiratory tract (46.8%), wound specimens (30.3%), urine (12.8%), and other clinical materials (10.1%). Testing revealed high resistance rates to imipenem (66.1%), meropenem (52.3%), piperacillin/tazobactam (52.3%), and ciprofloxacin (51.4%), indicating a high prevalence of carbapenem-resistant and multidrug-resistant *P. aeruginosa* strains. *Escherichia coli* isolates (n=79) were recovered from urine (53.2%), wound specimens (21.5%), blood (6.3%), and other clinical materials (19.0%). All 79 *E. coli* isolates were ESBL producers. High resistance rates to ciprofloxacin and trimethoprim/sulfamethoxazole were observed across isolates from all specimen types. Wound isolates exhibited the highest resistance to ciprofloxacin (88.2%) and amikacin (47.1%). In contrast, resistance to meropenem and colistin remained uncommon regardless of the source of isolation, indicating that these agents retain high activity against ESBL-producing *E. coli*. Clinical G- clinical isolates from period 2012-2014 demonstrate high levels of antimicrobial resistance, including multidrug resistance. These findings underscore the need for ongoing AMR surveillance and targeted antimicrobial stewardship measures.

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P26: Evaluation of *Trichoderma* spp. as biological control agents against fruit-associated fungal pathogens

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Abstract

Fruit quality and availability are strongly affected by fungal pathogens that cause disease and spoilage at different stages of the supply chain. Since the use of chemical treatments is increasingly limited by environmental concerns, biological control agents have emerged as promising alternatives. Therefore, this study evaluated the effectiveness of *Trichoderma* spp. as potential biological control agents against fruit-associated fungal pathogens. Eight fungal strains were selected as target pathogens. Isolates associated with 'Rocha' pear brown spot disease (*Alternaria arborescens* and *Stemphylium vesicarium*) and heat-resistant spoilage fungi from processed fruit products (*Talaromyces trachyspermus* and *Paecilomyces variotii*). Ten *Trichoderma* spp. strains from MUM culture collection were evaluated for their biocontrol potential. Dual culture assays were used for antagonistic activity, after which culture filtrates from selected isolates were used for the evaluation of antifungal metabolite activity. *T. atroviride*, *T. longibrachiatum*, *T. koningii*, *T. harzianum*, and *T. viride* dual culture assays inhibited pathogen growth, highlighting their potential as biological control agents. For culture filtrate assays, *T. longibrachiatum* showed the highest inhibition, indicating stronger antifungal metabolite activity. The results identify *T. longibrachiatum* as a promising biocontrol agent for fruit-associated fungal pathogens and support the use of *Trichoderma*-based strategies as sustainable alternatives.

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P27: Cyanobacterial Exopolysaccharides: Chemical Profiling and Effects on Development and Toxicity in Zebrafish

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Abstract

Cyanobacteria are photosynthetic microorganisms of high ecological and biotechnological relevance, notable for producing exopolysaccharides (EPS), extracellular compounds used in food, pharmaceutical, and biotechnological industries. This work aimed to identify cyanobacteria from the Bank of Algae and Cyanobacteria of the Azores (BACA) with potential for EPS production, characterize and quantify their main constituent monosaccharides, and evaluate their toxicity in *Danio rerio*. Genomic screening of 129 sequenced strains was performed using the epsSMASH tool, identifying biosynthetic gene clusters (BGCs) associated with EPS, of which 17 were selected for cultivation and exudate recovery. After lyophilization, exudates were tested for toxicity in *Danio rerio* embryos (2 hpf) and larvae (3 dpf). For chemical analysis, lyophilized exudates were hydrolyzed, derivatized, and analyzed by HPLC. Results revealed BGCs compatible with cellulose-like, curdlan-like, cyanocellulose, and PNAG/pga-like polymers, along with marked variability among strains in exudate and EPS production: *Maricoleus* sp. BACA0762 showed the highest exudate volume (2.9475 g/L), *Cryptocyanus* sp. BACA0588 the highest EPS amount (25.519 mg/L), and *Dulcicalothrix* sp. BACA0080 the highest EPS yield relative to exudate (4.50%). Glucose, mannose, and galactose were the predominant monosaccharides, with *Dulcicalothrix* sp. BACA0080, *Leptolyngbya* sp. BACA0262, and *Dulcicalothrix* sp. BACA0344 showing the most diversified profiles. In toxicity assays, embryos were more sensitive than larvae: exudates from *Leptolyngbya boryana* BACA0330 (75% mortality), *Leptolyngbya* sp. BACA0262, and *Wilmottia* sp. BACA0516 (both, 70% mortality) caused significant toxic effects compared to the negative control, while no exudate caused significant toxicity at the larval stage. These findings highlight the biosynthetic and structural diversity of EPS produced by Azorean cyanobacteria in the BACA collection, as well as their bioactive potential, reinforcing the need for further studies on the structural characterization of these polymers and on the mechanisms underlying the toxicity observed during early developmental stages of *D. rerio*.

P28: Assessment of Toxic and Behavioural Effects of Cyanobacterial Ethanol Extracts in Zebrafish (*Danio rerio*) Embryo and Larval models

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Abstract

Cyanobacteria are an important source of secondary metabolites with significant biotechnological and biomedical potential. However, many of these compounds remain poorly characterized, highlighting the need to evaluate their biological effects using appropriate experimental models. In this study, the bioactive potential of ethanolic extracts obtained from different cyanobacterial strains belonging to the Bank of Algae and Cyanobacteria of the Azores (BACA) was evaluated through genomic analyses, toxicity assays, and behavioural assessments using *Danio rerio*. The selected strains were analysed using antiSMASH and BiG-SCAPE to identify and compare biosynthetic gene clusters (BGCs) associated with secondary metabolite production. Toxicity assays were performed using *Danio rerio* embryos and larvae, evaluating lethality endpoints and teratogenicity, while behavioural analyses were conducted using SLEAP and Megabouts. The results revealed a high diversity of BGCs, including NRPS, PKS, RiPP, and terpene biosynthetic pathways, with many unidentified clusters. Toxicity assays showed marked differences among the extracts, with embryos being more sensitive than larvae. However, no relationship with the identified BGCs could be established, reinforcing the possibility of novel bioactive compounds. Overall, the results demonstrate that cyanobacteria from the BACA collection have the potential to produce biologically active compounds capable of inducing toxic and behavioural effects in *Danio rerio*. This study highlights the importance of integrating genomic and biological approaches to identify strains with potential for future biotechnological and pharmaceutical applications.

P29: Exploring Azorean Microalgae and Cyanobacteria for Nutraceutical Product Development: A Zebrafish-Based Safety Screening Approach

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Abstract

Microalgae and cyanobacteria are promising sources of bioactive compounds with potential nutraceutical applications due to their diverse metabolic profiles, including pigments, polyunsaturated fatty acids, vitamins, and other bioactive metabolites. Within the AlgaeFusion project, 20 autochthonous strains from the Bank of Algae and Cyanobacteria of the Azores (BACA) were selected for screening based on their biomass productivity and biotechnological potential. Biomass was harvested, freeze-dried, and extracted using environmentally sustainable solvents to obtain crude extracts for biological screening. A preliminary toxicity screening was conducted using zebrafish (*Danio rerio*) embryo and larval models. Embryos were exposed and monitored throughout embryogenesis according to the OECD Fish Embryo Toxicity (FET) guidelines[1]. Mortality, hatching success, developmental progression, and morphological abnormalities were recorded to assess teratogenicity. Complementary toxicity assays were subsequently performed in zebrafish larvae to evaluate post-embryonic tolerance under comparable exposure conditions. The results revealed marked differences among the tested strains, with several extracts inducing significant toxicity during embryonic development, whereas zebrafish larvae showed considerably lower toxicity at the same exposure concentration. These findings suggest that embryonic stages are more sensitive to metabolites present in the extracts and highlight the importance of evaluating developmental toxicity during the early stages of bioactive compound screening. The observed variability among strains reinforces the need for careful safety assessment before selecting candidates for nutraceutical applications. Based on these preliminary results, toxicologically safe extracts are being further investigated for their lipid-reducing potential using zebrafish larvae models. These findings contribute to the sustainable valorization of Azorean microalgae and cyanobacteria by establishing an integrated pipeline that combines safety evaluation with the screening of health-promoting bioactivities for future nutraceutical development.

References

[1] Organisation for Economic Co-operation and Development. (2013). *Test No. 236: Fish embryo acute toxicity (FET) test*.

P30: Bank of Algae and Cyanobacteria of the Azores – BACA culture collection

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Abstract

The Bank of Algae and Cyanobacteria of the Azores (BACA) was established in 2018 at the University of the Azores, Portugal, through the integration of existing microalgal and cyanobacterial culture collections into a centralized infrastructure. BACA currently maintains more than 800 strains of cyanobacteria and microalgae, predominantly isolated from diverse Azorean terrestrial, freshwater and marine habitats. Initially focused on biodiversity conservation and taxonomy, BACA has progressively developed into an integrated platform combining polyphasic taxonomy, genomics, metabolomics and biological screening. More than 130 cyanobacterial strains have been sequenced, substantially improving the phylogenomic representation of several poorly characterized cyanobacterial lineages. Analysis of 104 genomes representing more than 50 genera revealed 858 biosynthetic gene clusters (BGCs), grouped into 595 gene-cluster families, with a large proportion showing no close correspondence to characterized clusters in MIBiG, emphasizing the unexplored biosynthetic diversity retained within the collection. This genomic potential is increasingly being translated into bioactivity-guided natural-product discovery. Screening of BACA extracts using zebrafish larvae combines toxicity assessment, fluorescence-based phenotyping and behavioural analysis to identify biologically active strains while rapidly evaluating their in vivo safety. Recent screening has identified several promising, non-toxic cyanobacterial strains with lipid-reducing activity, including *Dulcicalothrix* sp. BACA0344, *Cyanobium* sp. BACA0019, *Pegethrix atlantica* BACA0077 and *Pseudocalidococcus azoricus* BACA0433. Other screening efforts have revealed strong biological activity in previously unexplored strains, including phenotypes associated with compounds for which no known cyanobacterial toxins have been detected, reinforcing the potential for discovering novel metabolites. This transition from biodiversity conservation towards biotechnology and biodiscovery has been progressively strengthened through successive research projects, including AlgaeFusion, CyanoFit, MARTAS, ALGA-X and CALYPSO. Together, these initiatives are consolidating BACA as a multidisciplinary platform connecting Azorean microbial biodiversity, genome mining, natural-product chemistry and zebrafish-based functional screening, transforming conserved microbial diversity into new knowledge and potentially valuable bioactive compounds.

P31: From Culture Collections to Environmental Metagenomics: Exploring Microbial Diversity in Azorean Aquatic Ecosystems

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Abstract

Culture collections provide essential biological resources for microbial research, preserving and making accessible microbial diversity for taxonomic, ecological and genomic studies. The Azores harbor diverse aquatic ecosystems, supporting microbial communities with important ecological roles. Part of this diversity is represented in the BACA culture collection, which preserves over 800 microalgal and cyanobacterial strains from nine islands. Environmental shotgun metagenomics offers a complementary perspective by enabling the characterization of microbial communities directly from their natural environments. Here, we present preliminary results from surface-water samples collected from eight freshwater lakes, four coastal sites and natural pools on São Miguel Island. Samples were filtered within 24 h of collection. Environmental DNA was extracted using a magnetic bead-based kit and sequenced by shotgun metagenomics (Illumina, 6 Gb per sample). Taxonomic classification was performed using Kraken2 and Bracken with standard reference databases. Following decontamination, downstream analyses were conducted in R using Phyloseq for community composition and Vegan for PERMANOVA and PCoA. Metagenomic profiles revealed clear separation between freshwater and marine communities. Freshwater systems showed higher diversity and were characterized by the presence of bloom-forming cyanobacteria, including *Dolichospermum* and *Microcystis aeruginosa*, together with *Polynucleobacter*. Marine samples displayed lower diversity and strong *Acinetobacter* dominance. These results highlight the ecological complexity of Azorean aquatic ecosystems and the potential of integrating environmental metagenomics with culture collection resources to improve the characterization of microbial diversity. Future work will explore the integration of BACA genomic data into these metagenomic analyses.

P32: Screening of cyanobacteria for antibacterial metabolites against clinically relevant pathogens

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Abstract

Clinically relevant pathogens pose a major threat to global public health, with the emergence of new pathogens and a surge in multidrug-resistant (MDR) ones. Cyanobacteria, characterized by their diverse metabolic pathways, represent a promising yet underutilized source of unique secondary metabolites. Genomically sequenced strains of the Bank of Algae and Cyanobacteria of the Azores (BACA) were genome-mined for the presence of biosynthetic gene clusters known to produce anti-microbial compounds (e.g. lanthipeptides), identifying 24 isolated strains. Biomass of those strains was produced in controlled conditions, harvested by centrifugation, and lyophilized. Intracellular metabolites were extracted via sonication-assisted extraction using methanol and methanol: water (1:3 v/v) in two extraction procedures. These extracts were tested against clinically relevant pathogens, such as *Staphylococcus aureus* ATCC 25923, *Bacillus cereus* ATCC 11778, *Escherichia coli* ATCC 25922, *Vibrio cholerae* 112, *Staphylococcus epidermidis* wildtype (WT) and *Candida albicans* ATCC 10231 in disc diffusion and spot-on-lawn assays. Early developmental and larvae toxicity assays of extracts were performed using the zebrafish (*Danio rerio*) model. The zebrafish toxicity assay reveals that methanolic extracts of *Neowestiellopsis persica* BACA0089 and Tolypothricaceae BACA0056 were toxic to larvae but not toxic to embryos, while the methanol:water extracts of both strains were non-toxic at the tested concentrations. The MIC test reveals that *N. persica* BACA0089 extracts methanol: water (1:3 v/v) exhibited (51.5 ± 2.0 %) and methanol (52.2 ± 7.6%) bacteria growth inhibition at 500 µg/mL against *Staphylococcus aureus* ATCC 25923. These findings reinforce the potential of cyanobacteria as a sustainable alternative bioresource for discovering next-generation antibiotics. Further analysis, bioassay-guided fractionation and LC-MS/MS based annotation of the bioactive compounds are recommended to characterize the specific therapeutic compounds.

P33: Use of Extracts from Amazonian Soils *Streptomyces* as Biological Control Agents Against *Fusarium oxysporum* and as Growth Promoters of *Coriandrum sativum* L.

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Abstract

Coriandrum sativum L. (coriander) is an economically important crop widely cultivated in tropical and subtropical regions, particularly in northern and northeastern Brazil. However, its productivity is often threatened by *Fusarium oxysporum*, the causal agent of *Fusarium* wilt, a soil-borne disease that leads to vascular wilt and significant yield losses. Conventional control relies heavily on chemical fungicides, which may promote pathogen resistance and generate environmental and health concerns. Biological control has emerged as a sustainable alternative, particularly through the use of microorganisms capable of suppressing pathogens and enhancing plant growth. Among them, *Streptomyces* species are known to produce a wide range of bioactive compounds, including antibiotics, hydrolytic enzymes, siderophores, and volatile organic compounds with antifungal activity. This study evaluated the biocontrol potential of *Streptomyces* isolates obtained from soils of the Brazilian Amazon. Thirty soil samples were collected from different depths, and two actinobacterial strains, designated ACT1 and ACT7, were selected. Morphological analysis identified both isolates as members of the genus *Streptomyces*. Organic extracts were produced using ethyl acetate and tested against *F. oxysporum* at concentrations of 2.5 and 5 mg/mL. Both extracts significantly reduced fungal mycelial growth compared with the control treatment. The ACT7 extract at 5 mg/mL showed the highest antifungal activity, achieving approximately 35.9% inhibition by the fifth day of evaluation. The results also demonstrated a dose-dependent response, with higher concentrations providing greater fungal suppression. The observed effects are likely associated with the production of secondary metabolites and extracellular enzymes capable of disrupting fungal development. Collectively, these results demonstrate the promise of Amazonian Streptomyces isolates as effective biological control agents and sustainable agricultural bioinputs, offering an environmentally friendly strategy to manage soil-borne pathogens, decrease reliance on chemical fungicides, and promote crop health and productivity.

P34: Fungi biodiversity to valorise Brewers' Spent Grain as innovative ingredient

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Abstract

Brewing industries generate millions of tons of brewers' spent grains (BSG) globally every year. Although nutrient-rich, high moisture content makes them perishable. This work aims to utilize wet BSG as a low-cost, nutrient-rich substrate for food-grade filamentous fungi, transforming a perishable agricultural by-product into a sustainable, high-protein, high-fiber food matrix (Cheriaparambil & Grossmann, 2025; Chin et al., 2022). *Fusarium venenatum* strains *Fv1* (type strain) and *Fv2* (MBDS-UNISSCC) converted BSG into alternative protein sources (Finnigan et al., 2019). Solid-state fermentation (SSF) on commercial BSG flour, using cellophane membrane as support, was optimized via a full factorial design assessing 15 nutritional combinations (Runs), with different concentrations of glucose (0%, 2.5%, 5%, 7.5%, 10%) and ammonium sulfate (0%, 1.25%, 2.5%) as supplementary carbon and nitrogen sources. Fungal growth was monitored for 10 days by biomass weight and diameter. Filter paper and cellophane were evaluated to isolate pure mycoproteins. Specific primers were designed to quantify fungal biomass in the matrix by qPCR (Sohlberg et al., 2022). The 15-run SSF optimization successfully identified the ideal nutrient combination for biomass maximization. For the *Fv1* strain, the optimal formulation (8.59% glucose, 1.76% ammonium sulfate) yielded 1.624 g of mycelium per 22.5 g of substrate. In comparison, the *Fv2* strain reached its maximum yield of 1.472 g of mycelium per 22.5 g of substrate using 7.47% glucose and 1.74% ammonium sulfate. The qPCR assay provided accurate monitoring of fungal kinetics, while cellophane membranes enabled effective isolation of pure mycoproteins from the commercial flour. This study establishes a scalable framework to upcycle BSG into premium mycoprotein via *Fusarium venenatum*. The optimized SSF process minimizes environmental waste while delivering an economically viable, high-protein alternative for the expanding sustainable food market.

References

[1] Finnigan, T. J., Wall, B. T., Wilde, P. J., Stephens, F. B., Taylor, S. L., & Freedman, M. R. (2019). Mycoprotein: the future of nutritious nonmeat protein, a symposium review. *Current developments in nutrition*, *3*(6), https://doi.org/10.1093/cdn/nzz021

[2] Cheriaparambil, R., & Grossmann, L. (2025). Properties and cultivation of Fusarium spp. to produce mycoprotein as an alternative protein source. *Sustainable Food Proteins*, *3*(1), https://doi.org/10.1002/sfp2.70002

[3] Chin, Y. L., Chai, K. F., & Chen, W. N. (2022). Upcycling of brewers' spent grains via solid-state fermentation for the production of protein hydrolysates with antioxidant and techno-functional properties. Food Chemistry: X, 13, 100184.

[4] Sohlberg, E., Virkajärvi, V., Parikka, P., Rämö, S., Laitila, A., & Sarlin, T. (2022). Taqman qPCR quantification and Fusarium community analysis to evaluate toxigenic fungi in cereals. Toxins, 14(1), 45. https://doi.org/10.3390/toxins14010045

P35: Exploring Microbial Diversity and Yeast Typing in Traditional Sourdoughs from Villaurbana (Sardinia, Italy)

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Abstract

Sourdoughs are complex microbial ecosystems central to traditional breadmaking and regional food heritage. Despite extensive research on Italian sourdoughs, Sardinian microbiota remain comparatively understudied. Within the TRIGU citizen science project, the MBDS-UNISSCC culture collection of the University of Sassari partnered with the Municipality of Villaurbana to co-design a participatory characterisation of local sourdough starters, aiming to assess bacterial and fungal diversity and identify candidate strains for a locally representative microbial consortium. Thirteen sourdoughs were characterised using an integrated approach combining NGS-based amplicon sequencing (16S rRNA and ITS regions) for community profiling, enzymatic quantification of organic acids and residual sugars, and culture-dependent isolation of 130 yeast isolates. Yeast identification was performed by D1/D2 ribosomal sequencing and MALDI-TOF mass spectrometry. Intraspecific typing of *Saccharomyces cerevisiae* and *Torulaspora delbrueckii* isolates was conducted by inter-delta fingerprinting and microsatellite analysis. Bacterial communities were strongly dominated by the genus *Fructilactobacillus* across all samples. Fungal communities were dominated by yeasts, with *S. cerevisiae* being the most abundant species (58.46%), followed by *T. delbrueckii* (15.38%), *Pichia fermentans* (9.23%), *Wickerhamomyces anomalus* (7.69%), *Maudiozyma humilis* (6.92%), and *Monosporozyma unispora* (2.31%). Microsatellite typing revealed high intraspecific diversity in *S. cerevisiae*, with isolates distributed across multiple distinct and well-differentiated genetic clusters. Notably, *T. delbrueckii* isolates from two different sourdoughs formed two clonal groups with no phylogenetic overlap with globally characterised reference strains, suggesting possible endemic Sardinian diversity. Despite originating from a single municipality, these sourdoughs harbour remarkable microbial and genetic diversity. Candidate *S. cerevisiae* strains isolated from samples SD107, SD105, SD42, and SD15, together with *T. delbrueckii* strains from SD97 and SD106, are proposed for the design of a locally anchored sourdough consortium, pending experimental validation of co-culture compatibility.

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References

[1] Coronas, R., Sanna, A. M. L., Cabizza, R., Reale, A., Bianco, A., Grondin, C., Legras, J. L., Zara, G., & Budroni, M. (2026). Exploring Microbial Diversity and Yeast Typing in Traditional Sourdoughs from Villaurbana (Sardinia, Italy) Using an Integrated Approach. *Foods*, *15*(13), 2307. https://doi.org/10.3390/foods15132307

P36: Culture-Dependent Exploration of Wheat-Associated Drought-Tolerant Microbiota Reveals Geographic Structuring and Plant Growth-Promoting Potential

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Abstract

Increasing drought frequency across global agroecosystems poses a major threat to wheat productivity and underscores the need for sustainable microbiome-based strategies to enhance crop resilience. Within the MICROBES-4-CLIMATE project, this study aimed to identify drought-adapted bacterial and fungal strains associated with wheat (*Triticum aestivum*) and establish a workflow for the development of synthetic microbial communities (SynComs) capable of improving plant performance under water-limited conditions. Wheat plants and associated bulk soil, rhizosphere, and root endosphere were sampled from five geographically distinct agricultural sites in Italy and Greece. Microbial communities were isolated using culture-dependent approaches. Fungi and bacteria were cultivated on rich medium and low water activity ones. In Italy, a total of 616 fungal and 379 bacterial isolates were isolated and identified. Plant growth-promoting traits, including phosphorus solubilization, indole-3-acetic acid production, siderophore production, and biofilm formation, are currently being evaluated. Fungal communities were dominated by Ascomycota (>90%) across all sampling sites and plant compartments, with *Aspergillus* representing the most abundant genus. Distinct enrichment of *Penicillium, Cladosporium,* and *Talaromyces* was observed depending on the site and compartment, suggesting geographical and ecological structuring of cultivable fungal diversity. Among bacteria, *Pseudomonas* predominated in bulk soils regardless of sampling location, whereas *Bacillus* and *Variovorax* were consistently recovered from the rhizosphere and root endosphere. These taxonomic patterns indicate that wheat-associated microbial communities harbour diverse drought-adapted microorganisms with potential plant-beneficial functions, representing a valuable resource for microbiome engineering. This study provides a comprehensive collection of cultivable drought-adapted bacterial and fungal isolates associated with wheat and establishes a robust pipeline for selecting microbial candidates for SynCom development. Ongoing functional characterization and compatibility screening will support the assembly of microbial consortia aimed at enhancing wheat drought tolerance and promoting more resilient and sustainable agricultural systems under future climate change scenarios.

P37: Antimicrobial resistance of selected strains deposited in Polish Collection of Microorganisms

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Abstract

Between 2016 and 2023 WHO recorded a continuous increase in reported cases of bacterial resistance in various regions of the world. Many factors contribute to bacterial resistance to antibiotics [1]. These include horizontal transfer of resistance genes, inhibition of cell wall synthesis, inhibition of metabolic pathways, depolarization of cell membranes, and inhibition of nucleic acid synthesis [2]. The aim of the study was to determine the potential antibiotic resistance profile of selected Gram – negative and Gram – positive bacteria deposited in Polish Collection of Microorganisms. The subject of the study were 60 strains selected from *Klebsiella pneumoniae* (15), *Enterococcus faecalis* (15), *Staphylococcus aureus* (15) and *Streptococcus pyogenes* (15) species. Antibiotic resistance in the tested strains was determined using VITEK 2 Compact system with applying designated cards. The analysis showed resistance of all tested *Enterococcus faecalis* to the antibiotics quinuptistin/dalfoprostin, 66% of resistant strains for streptomycin and 46% for gentamicin. Among *Staphylococcus aureus* 7% of strains were resistance for antibiotics like: cefoxitin, oxacillin, erythromycin and clindamycin and 20% of strains were resistance for tetracycline. All of tested *Staphylococcus aureus* were intermediate resistant for ciprofloxacin and levofloxacin. In *Klebsiella pneumoni*ae we observed resistance for piperacillin in all of tested strains and additionally 13% of strains were resistance for piperacillin/tazobactam. All of *Streptococcus pyogenes* strains were resistance for gentamicin and intermediate resistance for levofloxacin. We detected one strain resistant for rifampicin. Studies indicate that the tested strains of *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Enterococcus faecalis*, and *Streptococcus pyogenes* are sensitive to the most of tested antibiotics. It was also confirmed the occurrence of natural antibiotic resistance of *Enterococcus faecalis* to quinuptistin/dalfoprostin and *Staphylococcus pyogenes* to gentamicin.

References

[1] WHO (2023) *Antimicrobial resistance.* https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance
[2] Reygaert, W.C. (2018) An overview of the antimicrobial resistance mechanisms of bacteria. *AIMS Microbiol. 26;4(3):482-501*. doi: 10.3934/microbiol.2018.3.482.

P38: Screening and Selection of Chitinolytic Yeast Strains for Biotechnological Valorisation of Chitin

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Abstract

Chitin is the second most abundant polysaccharide in nature and a renewable resource with significant biotechnological potential, particularly for the production of chito-oligosaccharides and N-acetylglucosamine, with applications in the pharmaceutical, food, and cosmetic industries. Its valorisation depends on the availability of efficient chitinolytic enzymes, with yeasts representing a promising yet still underexplored source. This study aimed to optimise the conditions for assessing chitinolytic activity in yeasts using 96-well plates and to select yeast strains with high chitinolytic capacity. The screening assay was performed in minimal medium with colloidal chitin as the sole carbon source. Assay conditions were first optimised by comparing different medium volumes and evaluating the effect of pre-centrifuging the chitin, leading to the selection of total medium with 100 µL as the standard condition. Eighteen strains belonging to seven species of the genus *Candida* and to *Saccharomyces* were then screened, with growth monitored by spectrophotometry. To quantify specific enzymatic activity, a DNS assay was performed on extracts obtained by mechanical lysis. *S. cerevisiae* PYCC 4072, *C. auris* 17-270-10, and *C. albicans* SC5314 stood out as the strains with the highest chitinolytic potential. The DNS assay results revealed extremely low reducing sugar values across all samples, with the likely cause identified as the extraction protocol used, which predominantly recovered cytosolic proteins while discarding cell wall fragments, where chitinases are mostly retained. These findings highlight the need to adapt the extraction protocol to target cell wall-associated fractions in order to accurately quantify chitinolytic activity. The identified strains nonetheless represent promising candidates for further investigation as sources of chitinolytic enzymes for biotechnological applications.

P39: CIIMAR Microbial Culture Collection (CM2C): Preserving Microbial Diversity for Bioremediation Technologies

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Abstract

CIIMAR Microbial Culture Collection (CM2C) is a biobank of non-photosynthetic microorganisms that provides access to strains with diverse biotechnological applications. Within CM2C, bacterial strains, isolated from different aquatic environments, have been investigated for their ability to degrade major classes of contaminants, including hydrocarbons, pesticides, and pharmaceuticals. [1-3]. Most of these strains belong to the Pseudomonadota phylum, including the genera *Pseudomonas*, *Acinetobacter* and *Hydrogenophaga*, which have been associated with the biodegradation of hydrocarbons, pharmaceuticals or pesticides. Moreover, CM2C includes representative members of the phyla Bacteroidota and Actinomycetota, which have been reported to play important roles in contaminant transformation [1,3]. CM2C contributes to the long-term preservation, accessibility, and use of microbial resources through the maintenance of microbial strains and associated metadata. The organisation of strain-associated metadata and datasets in compliance with the FAIR (Findable, Accessible, Interoperable, and Reusable) principles further supports their traceability and scientific reuse. Samples and associated data are overseen in compliance with Access and Benefit Sharing (ABS) requirements and the Nagoya Protocol. CM2C further provides access to genomic resources for selected strains, enabling the identification of metabolic pathways, enzymes, and adaptive traits underlying pollutant degradation and stress tolerance. By providing curated strains and interoperable data, CM2C supports the development of microbial-assisted bioremediation solutions, contributing to the EU Zero Pollution ambition and the EU Mission "Restore our Ocean and Waters".

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References

[1] Perdigão et al, (2020) https://doi.org/10.3390/w13010066
[2] Alexandrino et al. (2020) https://doi.org/10.1016/j.jhazmat.2020.122545
[3] Fernandes et al. (2020) https://doi.org/10.1016/j.jece.2020.103881

P40: Functional and Genomic Characterization of Microbial Resources for Applications in Biotechnology, Food Industry and Sustainable Agriculture

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Abstract

Microbial culture collections represent valuable reservoirs of genetic and functional resources for developing sustainable biotechnological solutions. The Collection of Industrial Microorganisms (KKP) preserves approximately 3,000 bacterial, yeast, filamentous fungal and bacteriophage strains and supports their characterization for applications in biotechnology, food production and agriculture. This study focused on selected *Bacillus* strains preserved in KKP as candidates for microbial biopreparations and biocontrol agents. Selected *Bacillus* isolates were characterized using phenotypic, biochemical, genomic and microbiome-based approaches. The strains were evaluated for CotA-associated laccase activity, antagonistic activity against phytopathogenic fungi and application-related traits. Whole-genome sequencing was performed for selected isolates to confirm taxonomy and assess functional and safety-related characteristics. The impact of bacterial inoculation on soil microbial communities was analysed by 16S rRNA amplicon sequencing. Selected strains were also evaluated in postharvest plant protection models. The investigated strains displayed diverse functional traits relevant to sustainable agriculture and environmental biotechnology. Selected *B. pumilus* isolates exhibited strain-dependent CotA-associated laccase activity, with the highest ABTS oxidation observed for KKP 4078. Strong but pathogen-specific antagonistic activity was detected. *B. subtilis* KKP 3899 and *B. pumilus* KKP 3900 effectively inhibited *Botrytis cinerea* and *Alternaria alternata*, whereas activity against *Fusarium oxysporum* was limited. In postharvest assays, *B. subtilis* KKP 3897 and *B. pumilus* KKP 3902 reduced *A. alternata* symptoms on pepper fruits, demonstrating their practical biocontrol potential. Soil microbiome analyses revealed strain- and soil-dependent effects. Some strains, including *B. subtilis* KKP 3894 and KKP 3901, induced only moderate microbiome changes and remained similar to untreated controls, indicating favourable ecological compatibility. Comprehensive characterization of *Bacillus* strains preserved in KKP demonstrates the importance of culture collections as active research infrastructures supporting the discovery and validation of application-ready microorganisms. Integrating enzymatic, genomic, microbiome and biocontrol analyses enables effective valorization of microbial resources for sustainable agriculture, food biotechnology and environmental applications.

P41: Real-Time PCR as a Rapid Approach for the Detection of *Listeria monocytogenes* in Cured Azorean Cheeses

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Abstract

Listeria monocytogenes is a major foodborne pathogen, and the cause of listeriosis, a severe disease of considerable public health relevance. Its ability to survive stressful environmental conditions facilitates persistence in food-processing settings and contamination of different food matrices, particularly dairy products. Virulence determinants such as *hlyA*, *inlA*, *inlB* and *prfA* contribute to its pathogenicity, highlighting the importance of rapid and reliable detection methods for food safety monitoring. This study evaluated the occurrence of *L. monocytogenes* in Azorean cheeses and assessed a TaqMan real-time PCR (qPCR) assay targeting the virulence-associated *hlyA* gene alongside the Enzyme-Linked Fluorescent Assay (ELFA) used for routine screening. DNA from selected ELFA-positive and ELFA-negative samples was also subjected to Illumina sequencing, and subsequently analysed using a python-based bioinformatics pipeline. Among 262 cheese samples screened by ELFA, 24 (9.2%) yielded positive results, all of which originated from non-certified cheeses. The 11 ELFA-positive samples selected for qPCR were confirmed positive and 6 ELFA-negative samples were also confirmed positive by qPCR. Notably, the same molecular target was also detected in six samples previously classified as negative by ELFA. Genomic analysis of the 3 samples submitted for sequencing (54, 93 and 298) revealed the presence of genomes from several bacterial species, including *L. monocytogenes* and *Listeria innocua*. Furthermore, *hlyA*, *inlA*, *inlB* and *prfA* were identified in the draft genome of *L. monocytogenes*. Overall, qPCR showed a greater capacity to detect the molecular target within the analysed subset, supporting its potential as a complementary rapid method for *L. monocytogenes* detection and food safety monitoring in Azorean cheeses.

P42: Examining the chemotaxonomic potential of heterocyte glycolipids through expanded phylogenetic coverage of Azorean Nostocales strains

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Abstract

Heterocyte glycolipids (HGs) play a crucial role in regulating gas fluxes in diazotrophic cyanobacteria of the order Nostocales. Closely related species often yield similar HG distribution patterns, promising potential for chemotaxonomic profiling. Accordingly, HG data obtained from monospecific cultures can be integrated into polyphasic approaches to help elucidate taxonomic relationships between Nostocales species (Bauersachs et al., 2019). To extend the volume of available HG inventories, we analyzed the lipid extracts of 31 Nostocales strains isolated from the Azores, including 24 genera of which 18 have not been analyzed for their HG content so far. Eight of these genera were described in the past ten years. Their exact taxonomic placement is currently ongoing, making polyphasic approaches particularly valuable for robust classification. All Azorean strains were dominated by one or two alcoholic HGs that were accompanied by the corresponding keto-derivatives. Clustering of species, based on their HG inventories, allowed the comparison with current phylogenetic taxonomies. Twenty-three of the 31 strains expressed HG distribution patterns similar to those previously described in other members of the respective cyanobacterial families to which they were assigned. Interestingly, the other eight strains expressed very different HG inventories, pointing towards ambiguities in the current classification of these species. In addition, differences in the distribution of structural HG isomers revealed species-specific characteristics. Our data on Azorean Nostocales strains significantly extend the current coverage of HG inventories and will help refine the taxonomy of heterocytous cyanobacteria in polyphasic approaches.

References

[1] Bauersachs, T., Miller, S. R., Gugger, M., Mudimu, O., Friedl, T., & Schwark, L. (2019). Heterocyte glycolipids indicate polyphyly of stigonematalean cyanobacteria. *Phytochemistry, 166*, 112059.

Session 6 - Culture collection managements and maintenance

P43: Ukrainian Microalgal Culture Collections Under Wartime Conditions

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Abstract

Microalgal culture collections play an important role in biodiversity conservation and scientific research. The Algae Culture Collection of Kyiv University (ACKU, WDCM994) and the Microalgae Culture Collection of the M.G. Kholodny Institute of Botany (IBASU-A, WDCM1282) are the two leading microalgal culture collections in Ukraine and contain numerous original, authentic, and biotechnologically valuable strains. The collections include strains isolated from diverse terrestrial and aquatic habitats, including soils, freshwater ecosystems, hypersaline habitats, and Antarctic terrestrial biotopes. Many strains originate from regions affected by war or temporary occupation, including Crimea and eastern and southern parts of Ukraine. Both collections are actively used in research, education, and international collaboration. The large-scale russian invasion of Ukraine caused severe challenges for the preservation of living algal cultures. In 2022, buildings housing both collections were damaged during missile attacks. Continued attacks on the Ukrainian energy infrastructure later caused prolonged power outages, unstable temperature conditions, and interruptions in routine collection maintenance. As a result, some strains were lost, while others required purification and recovery. In 2024–2025, support from the EURIZON project (grant agreement No. 871072) allowed us to revise of the ACKU and IBASU-A collections and evaluate their current state. After the revision, the ACKU collection currently includes 235 algal strains representing 85 genera, while IBASU-A contains about 500 strains belonging to 186 species and 100 genera. Most ACKU strains were isolated from non-aquatic environments, particularly soil and aerophytic habitats, and the collection currently includes 31 authentic strains. The IBASU-A collection contains halophilic, freshwater, and terrestrial algae, including biotechnologically valuable and rare strains; 23 strains are authentic. Despite ongoing wartime conditions and infrastructure instability, both collections continue to function, preserve the Ukrainian microalgal biodiversity heritage, and remain open for international cooperation and future integration into the European research infrastructure.

P44: 30 Years of Micoteca da Universidade do Minho (MUM): Enhancing Knowledge In Mycology

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Abstract

In 2026, Micoteca da Universidade do Minho (MUM) celebrates 30 years of continuous service to science, innovation, and the preservation of fungal biodiversity. Founded in 1996 at the Centre of Biological Engineering of the University of Minho, MUM has since its foundation an active role in the international settings being nowadays recognized as a microbiological resource centre, supporting research, education, biotechnology, environmental sciences, and public health. Today, MUM preserves more than a thousand fungal strains and operates under internationally recognised quality standards, supported by an ISO 9001 based Quality Management System that serves researchers and industry worldwide. As a certified biological resource centre and an International Depositary Authority under the Budapest Treaty, the collection guarantees the long-term preservation, authentication, and accessibility of microbial resources. Over three decades, MUM has also contributed to capacity building through training courses and supported the organisation of scientific congresses and conferences. Over the past thirty years, MUM has played a crucial role in the discovery and dissemination of fungal biodiversity. To date, 59 strains preserved in the collection have been associated with the description of species new to science and has supported scientific publications, including 8 books carrying the MUM ISBN. These activities have been further strengthened through participation in at least 16 nationally and internationally funded research projects. One of the most exciting challenges for the coming years is MUM's contribution to MALDIBANK, the European initiative creating an open, cloud-based repository of MALDI-TOF mass spectrometry spectra for microbial identification. The inclusion of well-characterized reference strains from MUM, including type strains and newly described species, will significantly enrich the MALDIBANK database. By providing high-quality authenticated biological material and associated metadata, MUM helps improve the accuracy, reliability, and taxonomic coverage of MALDI-TOF identification systems, enabling faster and more precise identification of fungi and other microorganisms in clinical, environmental, food, and industrial settings. As it enters its fourth decade, Micoteca da Universidade do Minho continues to build bridges between biodiversity, technology, and scientific discovery, ensuring that fungal resources remain a powerful driver of innovation and knowledge for years to come.

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P45: Analyses, services and research activities of the public BCCM/ULC cyanobacteria collection

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Abstract

Cyanobacteria are a phylum of morphologically diverse photosynthetic bacteria. Their long and complex evolutionary history has contributed to the successful colonization of a wide range of habitats from polar to temperate, tropical and equatorial regions.
BCCM/ULC is a public collection funded by the Belgian Science Policy Office (BELSPO). It currently hosts more than 500 cyanobacterial strains, of which approximately 140 derive from Antarctic, Arctic and alpine environments followed by tropical, subtropical and mediterranean biotopes as well as strains of Belgian origin. Public deposition and distribution of strains are covered by an ISO 9001 certification, granted as part of a multi-site certification for the Belgian Coordinated Collections of Microorganisms (BCCM) consortium. All strains are studied by applying a polyphasic approach integrating morphological, molecular, and ecological data. The catalogue of all publicly available strains can be found on https://bccm.belspo.be/catalogues/catalogue-search?collection=ULC. Furthermore, the collection hosts more than 20 reference (or "type") strains for newly described taxa, including *Plectolyngbya*, *Shackletoniella*, *Timaviella, Parakomarekiella*, *Petrachloros, Leptochromothrix, Vermifilum*, *Tigrinifilum, Affixifilum, Sirenicapillaria, Ophiophycus*, *Floridanema, Dapis* and *Sivoneniella*. Lastly, our team of experts offers services in cyanobacterial strain isolation, maintenance, preservation, and characterization using light microscopy and standard genetic markers (e.g. 16S rRNA). Customized, on-demand training sessions are also available. Our analyses and services are available via https://bccm.belspo.be/services-ULC.

P46: Evaluation of RS and RSp Media for the Cultivation of Phylogenetically Diverse Marine Protists

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Abstract

A large fraction of abundant marine protists remains unavailable in culture despite their ecological importance in oceanic food webs and carbon cycling. Recently, the fully defined RS medium was developed to mimic oligotrophic open ocean conditions and support the cultivation of diverse protists. In this study, we evaluated the performance of RS and its version designed to support the growth of photosynthetic organisms (RSp) across a broad range of marine protists with different trophic modes and phylogenetic affiliations. Ten protist strains representing major eukaryotic supergroups were cultivated in RS/RSp media and compared with their standard maintenance media. The tested taxa included heterotrophic, osmotrophic, and photosynthetic species, including representatives of Apusomonadida, Euglenozoa, Haptophyta, Rhizaria, Stramenopiles, Rhodophyta, and Chloroplastida. Cell growth was monitored using flow cytometry or hemocytometer counts, microscopy, and PAM fluorometry. Most tested species successfully grew in RS/RSp media and showed growth dynamics comparable to those observed in standard media. PAM measurements showed that most photosynthetic species remained physiologically active in the RSp medium during the experiment. Microscopy observations also revealed some life-cycle related features not present when grown in standard media, such as auxospore formation in *Minidiscus variabilis* and the presence of non-calcified cells in *Emiliania huxleyi*. RS and RSp media can support the growth of phylogenetically diverse marine protists with different trophic modes. These fully defined media may be useful for future cultivation and experimental studies of marine protists.

P47: Discriminatory Power of MALDI-TOF MS in Microbial Taxonomy: The Impact of Commercial Databases

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Abstract

MALDI-TOF mass spectrometry (MALDI-TOF MS) is widely used for microbial identification and offers a taxonomic resolution comparable to 16S rRNA gene analysis. Its main limitation, however, lies in its dependence on commercial databases, which are largely focused on clinically and industrially relevant microorganisms. In addition, factors such as sporulation and exopolysaccharide production may affect identification performance, although optimization of cultivation conditions can improve results. At the Spanish Type Culture Collection (CECT), MALDI-TOF MS is routinely employed for quality control of reference strains, including authentication of newly deposited strains and stock replenishment, as well as for the identification of microbial isolates submitted by external users. In this study, the performance of MALDI-TOF MS was evaluated through a retrospective analysis of 10,529 isolates processed by the CECT identification service and 4,533 reference strains analyzed between 2020 and 2025. Among isolates submitted for identification, 85% were successfully identified at the species level, 12% at the genus level, and only 3% remained unidentified. In contrast, among reference strains analyzed for authentication, 56% were identified at the species level, 14% at the genus level, and 30% could not be identified. The higher proportion of unidentified reference strains was associated with the limited taxonomic coverage of commercial databases. While isolates submitted to the identification service mainly belonged to taxonomic groups commonly represented in these databases, the reference strains encompassed a much broader microbial diversity, including numerous taxa absent from the available reference spectra. Further details on the taxonomic distribution of both datasets will be presented during the communication. These results demonstrate that current commercial databases are particularly limited when dealing with taxonomically diverse collections and novel taxa. In this context, CECT participates in the MALDIBANK project, funded by Horizon Europe, which aims to develop a robust and openly accessible MALDI-TOF MS database for the scientific community.

P48: Czech Collection of Microorganisms: present status and future prospects

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Abstract

The Czech Collection of Microorganisms (CCM) is a specialised research and service facility located at the Faculty of Science of Masaryk University in Brno, Czech Republic (ccm.sci.muni.cz). Over the past 60 years, the CCM has developed into an internationally recognised repository, delivering high-level expertise in microbial taxonomy, cultivation, and characterisation. The CCM continuously expands its high-value bioresources while actively safeguarding *ex situ* microbial gene pools and biodiversity. The core activities of the CCM cover the deposition, preservation and distribution of cultures of bacteria, archaea, filamentous fungi, yeasts and staphylococcal bacteriophages. The collection currently maintains over 5,300 strains, complemented by more than 12,000 diverse isolates from Antarctica. The long-term maintenance of viable cultures is ensured by state-of-the-art preservation techniques. The CCM offers a selected set of reference strains used as quality control standards in microbiological laboratories. Additional services include culture deposition, patent deposition, lyophilisation, identification, and customised long-term storage. Beyond its service role, the CCM conducts research on microbial taxonomy and contributes to the Czech Antarctic Research Programme. The microorganisms collected in Antarctica represent a valuable source of strains with multiple potential applications, and some of them are available for scientific research through the Czech Antarctic Microbial Biobank (camb.carp.sci.muni.cz). The CCM is a member of international organisations such as the World Federation for Culture Collections and the European Culture Collections' Organisation, and is involved in the National Programme on Genetic Resources. Through its services, the CCM supports basic and applied research, including industrial applications, biotechnology, and education. Future goals emphasise maintaining high-quality services, improving data management and enhancing research excellence. The CCM aims to actively participate in national and international research infrastructures by establishing the microbiological consortium MIRRI-CZ, joining the Roadmap of Large Research Infrastructures, and finally the pan-European MIRRI-ERIC Consortium.

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P49: Saccharomyces and non-Saccharomyces yeast's biodiversity from Samtskhe-Javakheti region of Georgia

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Abstract

Samtskhe-Javakheti is an important wine-growing region of Georgia, where winemaking has been practiced since ancient times. It is one of the highest viticultural regions not only in Georgia but also in the world, where vineyards grown up to 1,500 meters above sea level, so the region has a cool climate. Differences in vine varieties, climate, topography and plant–microbial relations condition in fruit quality stipulating regional differences of wine. (Bokulich, et al. 2016). Therefore, the aim of our study was to study the biodiversity of yeasts common for Samtskhe-Javakheti region and create their collection. 130 Samples were taken, including 70 grapes and 25 wines. Obtained 442 yeast isolates identified by MALDI-TOF MS analysis. They represent to the 33 different species of 24 genera; *Metschnikowia pulcherrima* (16.3%), *Hanseniaspora uvarum* (9.9%), and *Saccharomyces cerevisiae* (10.8%) were the dominant. Such high occurrence frequency of *S. cerevisiae*'s strains differ to the results obtained for Qartli region of Georgia (Andiashvili et al., 2025) must be conditioned by the diversity of approaches for their isolation: grape juice, enrichment culture obtained at 25 °C and 10 °C (by the addition of alcohol), crushed grape juice fermented at 20 °C, grape juice inoculated and fermented in synthetic medium containing 18% glucose, grape berries inoculated on a solid medium. The created collection of Saccharomyces and non-Saccharomyces yeasts reflecting their diversity make the possibility their usage to produce high-quality unique regional wines with new taste properties.

Acknowledgements: This work was supported by Shota Rustaveli National Science Foundation of Georgia (SRNSFG) [grant number FR-23-11803].

References

[1] Bokulich, *et al*. Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. mBio, 2016, 7, 3, 1-12
[2] Andiashvili G., et al. Biodiversity of yeasts isolated from vineyards of Qartli region of Georgia. ECCO XLIII. September 15-17, 2025 Utrecht, Netherlands

P50: Take or Toss?-Hidden treasures or trash

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Abstract

Biological resource centers play a crucial role in advancing science, public health, and the bioeconomy. Therefore, the high-quality, long-term preservation of valuable biological materials is of utmost importance. To mitigate the risks of material loss due to staff shortages, supply issues, or unforeseen disasters, spatially separated backup solutions are strongly recommended and often required for biobanks. In response, DSMZ offers a secure deposit service for biological materials, ensuring that materials not included in the DSMZ catalog are stored safely and are not shared with third parties without the depositor's written consent. Since 1974, the DSMZ has also functioned as a depository for microorganisms intended for patent purposes. Since 1981, the DSMZ has been recognized as an International Depositary Authority (IDA) under the Budapest Treaty. Following Rule 9.1 Budapest Treaty, the biological material is stored for at least 30 years. In total, the DSMZ holds more than 10,000 patent and safe deposits. However, many patent deposits never make it into a patent and/or the patent or safe deposited material does no longer fall within the scope of the depositor. We would like to discuss the possible next steps for handling the material when the protection status of these deposits has expired. There are essentially two options for these strains: First, the destruction of the material, or second, the transfer of the strains to a public collection, where they would be preserved and made available to the international scientific community. We would like to encourage depositors to transfer the strains to our public collection. Such a transfer would ensure the long-term preservation of the material and contribute to the conservation of global microbial biodiversity. Furthermore, making the strains available for research purposes can increase their scientific visibility and potential impact.

P51: Connecting Cultures and Data: The Digital Evolution of LEGE-CC

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Abstract

The Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC), hosted at CIIMAR (Portugal), is one of the oldest and most diverse collection of cyanobacteria and microalgae in Portugal, currently preserving over 2000 strains from freshwater, marine, brackish, and terrestrial environments. Over more than three decades, LEGE-CC has evolved into an internationally recognized biological resource center, supporting biodiversity research, biotechnology, ecotoxicology, and the discovery of novel microbial taxa. The collection has contributed to the description of several new cyanobacterial genera and species, highlighting the scientific value of long-term culture maintenance and curation. As culture collections face increasing demands for data accessibility, traceability, and operational efficiency, LEGE-CC is undergoing a significant digital transformation. A key step in this process is the integration of collection data into the Blue Biobanks Digital Research Platform, a national infrastructure that connects marine biobanks and provides centralized access to biological resources, biodiversity records, and associated metadata. This integration promotes interoperability, supports FAIR data principles, and enhances the visibility and accessibility of biological resources for both academic and industrial users. In parallel, a dedicated mobile and web-based application is being developed to support the daily management of culture collections. The platform will facilitate strain tracking, inventory management, culture maintenance scheduling, workflow monitoring, quality control procedures, and data recording. By reducing manual tasks and improving traceability, the application is expected to increase efficiency, standardization, and long-term sustainability of collection management activities. The continued development of LEGE-CC is further supported by ongoing investments in the CIIMAR Blue Biobank, including new facilities and specialized equipment dedicated to the preservation, characterization, and management of biological resources. Together, these initiatives demonstrate how the combination of digital tools, integrated databases, and modern research infrastructures can strengthen culture collection management while expanding access to valuable biological resources for the scientific community and the Blue Bioeconomy.

References

[1] de Oliveira, F. L., *et al.* (2024). *Exploring the cyanobacterial diversity in Portugal: Description of four new genera from LEGE-CC using the polyphasic approach*. J. Phycol. 60(5), 1285-1304.
[2] Morais, J., *et al.* (2025). *Description of Vacuolonema iberomarrocanum gen. et sp. nov. (Oculatellales, Cyanobacteria): A new marine cyanobacterial taxon from the Portuguese and Moroccan Atlantic coast*. Phytotaxa, 708(2), 182–196.
[3] Hentschke G.S, et al. (2022). *Zarconia navalis gen. nov., sp. nov., Romeriopsis navalis gen. nov., sp. nov. and Romeriopsis marina sp. nov., isolated from inter- and subtidal environments from northern Portugal*. Int. J. Syst. Evol. Microbiol*.,* 72.
[4] Brito, Â., *et al.* (2017). *Description of new genera and species of marine cyanobacteria from the Portuguese Atlantic coast*. Mol. Phylogenet. Evol., 111, 18–34.
[5] Ramos, V., *et al.* (2018). *Cyanobacterial diversity held in microbial biological resource centers as a biotechnological asset: The case study of the LEGE Culture Collection*. J. Appl. Phycol., 30, 1437–1451.
[6] Vasconcelos, V. M. (2022). *30 Years of a Collection of Cyanobacterial and Microalgae Cultures: LEGE-CC and Its Contributions to Cyanobacterial Ecotoxicology and Biotechnology*. Biol. Life Sci. Forum, 14(1), 45.

Session 7 - Projects, Networks and databases

P52: Azole resistance surveillance of *Aspergillus fumigatus* in wastewater in Belgium

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Abstract

Azole-resistant *Aspergillus fumigatus* (ARAf) is an emerging public health concern that threatens the efficacy of first-line antifungal therapies. While environmental resistance is commonly linked to agricultural azole use, wastewater treatment plants (WWTPs) may act as monitoring points for resistant strains linked to agricultural practices. This study investigated the occurrence and azole resistance profiles of *A. fumigatus* in Belgian municipal wastewater. Between February 2022 and March 2024, 237 influent wastewater samples were collected from 10 WWTPs serving approximately 2.5 million inhabitants (22% of the Belgian population). Samples were cultured on malt extract agar with chloramphenicol (MC) and on tebuconazole-supplemented medium (MC+T) to screen for azole-resistant isolates. Suspected resistant isolates were identified by MALDI-TOF MS. Antifungal susceptibility testing against itraconazole, voriconazole, posaconazole, and isavuconazole was performed according to EUCAST guidelines. Phenotypically resistant isolates underwent *cyp51A* gene sequencing to screen for known resistance mutations. *A. fumigatus* was detected in 87.3% and 81.4% of samples on MC and MC+T media, respectively. A total of 1,422 isolates were recovered on MC and 714 on MC+T. Seasonal variation was observed, with the highest fungal burden in winter and the lowest in summer. Thirty-eight azole-resistant isolates were identified, corresponding to an overall resistance rate of 5.3%, with the highest prevalence in autumn (n = ; 8.8%). Most resistant isolates exhibited multi-azole resistance, with 76.3% resistant to all four azoles tested. The environmentally associated TR34/L98H mutation of the *cyp51A* gene predominated (73.7%), followed by TR46/Y121F/T289A/G448S (5.3%) and TR46/Y121F/T289A (2.6%). Three resistant isolates lacked known *cyp51A* resistance mutations, suggesting alternative resistance mechanisms. The predominance of TR34/L98H closely mirrors resistance patterns observed in Belgian clinical isolates, supporting a link between environmental and clinical reservoirs. Belgian WWTPs frequently harbor *A. fumigatus*, including azole-resistant strains. Wastewater surveillance represents a promising complementary approach for monitoring environmental antifungal resistance within a One Health framework.

P53: Unlocking the Potential of the CCAP Collection Through Genomics and Metabolomics

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Abstract

The Culture Collection of Algae and Protozoa (CCAP) is a biological resource centre comprising a wide range of biodiversity, with strain holdings spanning Prokaryotic cyanobacteria to macroalgae and most microbial Eukaryotic lineages. The origins of our strains correspond to a broad temporal and spatial diversity of environments. The collection comprises over 3200 strains in the public domain of which 371 are Type strains. With the aim of aiding with the collection curation and providing more valuable information to the scientific community, CCAP collaborates with a broad range of algal research projects, spanning genomics, metabolomics and biotechnology projects.
This poster highlights several of these collaborative projects, including updates from the Darwin Tree of Life (DToL) project, which is sequencing more than 100 genomes from CCAP strains, and the Natural Product BioHUB, which investigates the biological and chemical diversity represented across much of the CCAP collection. The DToL has already published 6 genomes, with 25 in the pipeline nearing publication. The Natural Products BioHUB has completed 20% of the CCAP collection analysed by Fourier-transform infrared (FTIR) spectroscopy, with an aim for characterisation of the entire collection. FTIR is a technique that enables determination of the proportion of lipids, carbohydrates and protein in a sample. Initial results display clustering by algal class based on variation in the FTIR metabolic fingerprint. CCAP will continue to build upon its world-class research and service provision, with which to investigate the unique and underexplored diversity of protistan organisms for the understanding of the natural world and the development of new biotechnological applications.

P54: A contribution towards lipidomic-enhanced microbial identification using negative-ion MALDI-TOF MS

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Abstract

Lipids are key components of living organisms, and their diversity in microorganisms reflects environmental adaptations. Although MALDI-TOF MS is widely used for rapid protein analysis, its application in lipidomics is still limited. Nevertheless, lipidomic profiles can complement proteomic data, potentially improving the identification of difficult to discriminate microorganisms. Within the MALDIBANK project, which aims to establish an open-access MALDI spectral database for microbial identification, this study evaluates the added value of lipidomic spectra for the identification of filamentous fungi and cyanobacterial strains. Spectra were obtained from filamentous fungi strains belonging to Micoteca da Universidade do Minho (MUM) and cyanobacterial strains from Blue Biotechnology and Ecotoxicology (LEGE-CC) culture collections. Lipids were extracted using Bruker's MBT Lipid Xtract kit, and spectra were acquired in negative-ion mode using a MALDI Biotyper® Sirius instrument. Preliminary negative-ion lipid spectra were successfully obtained from both filamentous fungi and cyanobacterial strains. The spectra showed reproducible lipid profile patterns. For filamentous fungi, ongoing analyses are evaluating whether lipid signatures can improve strain identification and support the discrimination of mycotoxigenic strains. For cyanobacteria, analyses are being conducted to evaluate the potential of lipidomic profiles to differentiate toxin-producing strains. The spectra generated will significantly expand the MALDIBANK database. The integration of lipidomic and proteomic data is expected to improve the discrimination of closely related species and provide additional information on microbial toxicity.

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P55: CECT and its contribution to applied microbiology and biotechnological innovation

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Abstract

The Spanish Type Culture Collection of the University of Valencia (CECT-UV) is the only public microbial Biological Resource Centre (mBRC) in Spain acting as a depositary collection and provider of yeasts, filamentous fungi, bacteria, and archaea. It hosts the Spanish node of the "MIRRI-ERIC" Infrastructure (Microbial Resource Research Infrastructure - European Research Infrastructure Consortium), which facilitates access to a broad catalogue of microorganisms, specialised services, consultancy, and training related to the use and preservation of microbial resources. Participation in European projects derived from MIRRI-ERIC, such as BIOINDUSTRY 4.0, MALDIBANK, and MICROBES-4-CLIMATE, contributes to strengthening CECT's capacities and expanding the scope of its services. Within BIOINDUSTRY 4.0, CECT participates in the development of new digital tools to promote the industrial exploitation of microbial biodiversity, contributing new physiological data from CECT strains. Within MALDIBANK, CECT leads WP4 and contributes by generating new MALDI-TOF spectra to expand the database and improve identification, detection of phenotypic traits (e.g. antimicrobial resistance and toxin production), and strain-level discrimination. To this end, well-characterized microbial strains preserved in culture collections have been selected to support the development and validation of innovative tools focusing on specific demonstrators across health, food and environmental applications. Within MICROBES-4-CLIMATE, CECT leads WP1, increasing the scientific impact of its microbial resources and associated services through the implementation of a centralised service catalogue focused on the study of interactions between microorganisms, plants, and soils, as well as their role in climate change response, adaptation, and mitigation. Through the transnational access programme, international researchers can access specialised CECT services to address transdisciplinary research challenges. Looking ahead, in 2027 CECT will also provide services within RISE-UP BIO, working closely with other research infrastructures to support biomanufacturing.

P56: MICROBES-4-CLIMATE: Advancing climate change research using microbial resources

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Abstract

MICROBES-4-CLIMATE (M4C) is a Horizon Europe INFRASERV project. It aims to deepen the comprehension of the complex relationships among microorganisms, plants, and soil within the framework of climate change. By offering access to advanced Research Infrastructures, training, and assistance, the project seeks to encourage research tackling the multifaceted challenges presented by climate change to terrestrial biodiversity and ecosystems. By exploring these interactions, M4C strives to advance the understanding and facilitate applied research directed at enhancing the resilience of plants and crops to the effects of climate change, thereby fostering sustainable and resilient agricultural methods. M4C enables researchers from a wide range of countries to carry out research projects at cutting-edge facilities in the microbiological domain, with a focus on climate change questions. M4C offers transnational access (TNA) to four distinct Research Infrastructures and 144 services spanning 20 countries. The available services provide opportunities to support research addressing climate change-related challenges, with the upcoming TNA call offering researchers a new opportunity to access these capacities.

A57: MALDIBANK (Multi-domain Open MALDI Spectra Archive for Identification of Microorganisms) to facilitate the identification of microbiotes associated to fermented foods

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Abstract

Identifying microorganisms is vital across all fields of microbiology to tackle global challenges such as epidemics, food security, and environmental sustainability. In recent years, matrixassisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry has transformed microbial identification by providing a rapid, high-throughput technique based on species-specific proteomic or lipidomic fingerprints. The efficiency of this approach relies on comprehensive taxonomic databases and standardized analytical protocols. In this context, the MALDIBANK European project (2025–2029), involving 24 partners across 12 countries [1], seeks to advance the use of MALDI-TOF through the development of AI-driven tools, harmonized methods, and validated identification procedures. By creating an open, FAIRcompliant platform integrating 100,000 reference spectra from over 20,000 microbial strains (bacteria, yeasts, and filamentous fungi) MALDIBANK aims to become a reference resource in microbial identification, comparable to GenBank in genomics. This initiative will enable improved microbial phenotyping and epidemiological surveillance while fostering the principles of Open Science. In our case, we decided to focus on fermented foods as they provide an interesting case study. Indeed, a meta-analysis of the microbial diversity of 47 different Swedish fermented foods identified over 2,400 bacterial species [2]. Several hundred prokaryotic species are described each year; in 2024, for example, nearly 220 new bacterial species were described [3]. First, we worked with the MALDIBANK consortium to define accurate metadata for the analyzed samples and establish standard operating procedures (SOPs) for generating spectra. We conducted a gap analysis to identify food-related taxa not currently present in databases, as well as targeting taxa present in databases with low intraspecific diversity. Thus, from our collections [4], we selected 376 strains of bacteria, among them a large number of lactic acid bacteria, and 98 strains of yeast, corresponding to 151 and 62 species, respectively, for which the genomes are available. More strains will be added within the next year. We also intend to generate lipidomic spectra from selected bacterial species to build a comprehensive lipidomic database, which could provide new insights and tools for bacterial identification and characterization. In a second step, focusing on the cheese and milk kefir models, we will explore the relevance of the MALDI-TOF and associated SOPs, as well as the implemented MALDI-TOF database, in describing the diversity of associated microbiomes. If possible, we will also explore its ability to facilitate exploration at the inter-species level.

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References

[1] https://maldibank.eu/ ou https://cordis.europa.eu/project/id/101188201/fr

[2] Palmnäs-Bédard M, de Santa Izabel A, Dicksved J, Landberg R. Characterization of the Bacterial Composition of 47 Fermented Foods in Sweden. *Foods*. 2023; 12(20):3827. https://doi.org/10.3390/foods12203827
[3] https://lpsn.dsmz.de/
[4] https://reseau-cirm.hub.inrae.fr/crb-collections-et-catalogues ; https://umrf.clermont.hub.inrae.fr/

P58: PT-OPENSCREEN Azores Node: Integrating Biodiversity Collections, Multi-Omics and Artificial Intelligence for Bioactive Molecule Discovery

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Abstract

Biodiversity collections are increasingly evolving from repositories of biological material into innovation platforms supporting biotechnology and drug discovery. The recently established PTOPENSCREEN Azores Node aims to integrate the biodiversity of the Azorean archipelago using omics, computational biology and functional screening to accelerate the identification of highvalue bioactive molecules for pharmaceutical and industrial applications. The platform combines microbial, marine and terrestrial biodiversity collections with highthroughput genomic, transcriptomic and eDNA sequencing to explore the potential of geretical resources. Primary and secondary databases, genome mining and gene prediction are integrated with AI, molecular docking and structure-based screening to identify molecules targeting specific therapeutic pathways. Candidate compounds are subsequently validated through chemical and biochemical assays, followed by in vitro screening using immortalised human cell lines (HaCaT keratinocytes, THP-1 monocytes, KMST-6 fibroblasts and PC-12 neuronal), as well as primary cell cultures (lymphocytes and DRG neurons). Promising candidates are evaluated in *D. melanogaster* disease models before validation in rodent models. The PT-OPENSCREEN workflow enables the prioritisation of bioactive molecules from biodiversity collections through the integration of omics, artificial intelligence and experimental validation. Representative applications include the identification of peptides targeting Kv1.3 ion channels for immune-mediated diseases, antimicrobial peptides active against clinically relevant pathogens, and natural products with antioxidant and cosmetic potential. The combination of computational prediction with biological models substantially reduces discovery time and increase translational potential. The PT-OPENSCREEN Azores Node provides an integrated infrastructure connecting biodiversity collections, multi-omics, artificial intelligence and functional validation into a single drug discovery pipeline. By transforming biological collections into dynamic innovation resources, the platform strengthens the role of biodiversity repositories in biotechnology, pharmaceutical research and the sustainable blue bioeconomy while positioning the Azores as a strategic European hub for natural product discovery.

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Session 8 - Open Science, Data Sharing & Science Communication

P59: Circular Relationship between Climate Change, Healthy Ecosystems and Soil Microbial Diversity: Challenges to Teaching Sustainable Development in Portugal and Brazil

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Abstract

This study analysed how Education for Sustainable Development (ESD) is addressed in the primary education curricula and textbooks of Portugal and Brazil, focusing on the relationships between climate change, healthy ecosystems, soil, and microbial diversity. The analysis was supported by the KVP model (Knowledge–Values–Practices), which has been widely applied to the study of teachers and pupils' conceptions, curricula, and textbooks. In the KVP framework, Knowledge (K) refers to scientifically validated information, Values (V) to beliefs, ideologies, and cultural perspectives that influence educational choices, and Practices (P) to teaching approaches, textbook design, and the social practices promoted through education. This model provides a useful lens for understanding how scientific concepts are selected, represented, and taught in school. Using a qualitative comparative methodology, official curricula and teaching materials for children aged 6–10/11 years were examined. The results show that Brazil introduces biodiversity, ecosystems, and soil concepts more explicitly and at earlier stages than Portugal. Climate change is only indirectly addressed in both countries through foundational environmental knowledge. Microorganisms are largely associated with health and hygiene, while their ecological role and contribution to soil biodiversity receive limited attention. From the KVP perspective, these findings suggest that the balance between scientific knowledge, educational values, and teaching practices influences how sustainability-related topics are incorporated into the classroom. Overall, microbial diversity remains underrepresented, with the Brazilian curriculum in the early years of schooling offering a more explicit approach to environmental sustainability, soil management, and climate change than the Portuguese curriculum.

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