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ABSTRACTS

Keynote Speaker Abstracts

Keynote Lecture 1

Significance and challenges of microbial resource centers in a changing world

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Some estimates of the global prokaryotic diversity exceed 1 billion species whereas the number of bacterial species that are validly described to date amounts to only 21,400. Clearly, novel biology, novel biogeochemical transformations and new sources of biochemical innovation await their discovery. While the composition and expression patterns of unknown microorganisms can be analyzed by high throughput genomics, transcriptomics and proteomics, a major fraction of the genes identified in a genome may have unknown functions. Improved data science analyses of heterogenous and highly distributed data for not-yet-cultivated types of microorganisms can guide the development of novel cultivation approaches that better mimic their natural niche and hence underpin cultivation and phenotypic characterization of novel target microorganisms. A combination with high throughput, automated methods that allow multifactorial testing of different cultivation conditions (“culturomics”) is particularly promising and has begun to return novel types of bacteria. Through these approaches, however, microbial resources attain a substantial monetary value (~10,000 Euro) which microbial culture collections preserve in a highly cost-effective manner. Still, the diversity, accessibility and quality of the information on microbial resources needs to be improved, and the offer of different types of microbial resources be expanded, to meet novel demands of bioeconomy and pandemic preparedness. In particular, the more recent focus on microbiome analysis and the development of synthetic microbial communities opens up new gateways to bioeconomy and public health. Still, a better understanding of the links between the composition and activity of microbial communities, and of keystone species and their interactions, is needed for future climate change mitigation, One Health, and the improvement of agricultural practice, among others. This also involves establishing advanced methods for ecosystem monitoring that integrate data from microbial communities in a more consistent way and yield novel, valuable indicators for ecosystem functioning. Finally, the research, provision and application potential of microbial resources continues to have a direct societal impact. Thus, the knowledge on the biodiversity, biogeography, and genomic variability of microorganisms has significantly contributed towards establishing future-proof solutions for benefit sharing and promises novel opportunities for the collaboration between the Global North and South.

Keynote Lecture 2

Isolating, culturing and dissecting the arbuscular mycorrhizal fungal cell

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Arbuscular mycorrhizal (AM) fungi are ancient plant symbionts that play a central role in nutrient exchange, plant growth, ecosystem diversity, and global carbon cycling. They form extensive multinucleate mycelial networks, where nutrients and organelles move bidirectionally through a continuous cytoplasm. Despite their ecological importance, most AM fungi are notoriously difficult to isolate and culture, limiting progress in understanding their cellular biology. Recent advances in semi-sterile and in-vitro culture systems now open the way for detailed investigation of AM fungal development and organization across taxa. These systems reveal unique cellular features, including dynamic cytoplasmic flow and intriguing nuclear and lipid behavior. In parallel, emerging tools such as advanced microscopy, robotic imaging, and high-throughput image analysis are beginning to expose processes that were previously inaccessible, opening new avenues for better understanding the cellular basis of AM fungal ecological function.

Keynote Lecture 3

Fungal species concepts in the genomic era: lessons from genera of common fungi

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Fungal species delimitation has moved from morphology and the biological species concept to Genealogical Concordance Phylogenetic Species Recognition (GCPSR, Taylor et al. 2000), which in the past twenty-five years has revealed extensive cryptic diversity and provided a practical DNA-based standard. With the advent of genome sequencing, it was expected that whole-genome data would resolve borderline cases. Instead, genomes frequently reveal gene-tree incongruence, lateral gene transfers, introgression, and reticulate evolutionary histories that complicate GCPSR-based delimitation (Cai and Druzhinina 2021).

I will use *Trichoderma* (*Hypocreales*) together with comparisons to other common fungi to illustrate these issues. In *Trichoderma*, taxogenomic analyses of 66 strains resolved major clades but also revealed widespread discordance, signatures of ancient gene flow, and hybridization events (e.g. within *Longibrachiatum*), including ghost-lineage introgression. Despite the availability of genomic data, infrageneric “taxonomic clouds” or putative metaspecies—comprising overlapping biological species, agamospecies, and relict lineages (e.g. *T. harzianum* s.l.)—remain unresolved due to the lack of genealogical concordance and suitable species concepts.

Genomes are most informative when coupled with ecologically relevant traits. In *Trichoderma*, a genus-wide AI-supported analysis of genotype–phenotype linkages demonstrated that up to ~10% of the core genome encodes fitness-related “phenogenes”, which correspond to striking phenotypic differences when fitness traits are considered (Steindorff et al. 2025, unpublished). Moreover, subtle variation in key proteins such as hydrophobins can drive speciation by altering spore dispersal, stress tolerance, and reproduction, producing pronounced ecological divergence between species previously regarded as cryptic (Cai et al. 2020).

In the genomic era, tree-topological criteria alone are insufficient. A pragmatic species concept that ensures taxonomy remains useful—by explaining biology and predicting properties—requires integration of phylogenomics with ecological and multiparametric phenotypic evidence. Such a framework should accommodate metaspecies and reticulate evolution while safeguarding the taxonomic stability essential for science, policy, and application.

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Session Speaker Abstracts

Theme: Research and Development

Session 1: Advances and challenges in preservation of axenic cultures and microbiomes (synthetic and natural communities)

Preserving microbial diversity: from pure cultures to complex communities

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Microbial culture collections generally apply cryopreservation and freeze drying (lyophilisation) as methods of choice when preserving fungi and bacteria (Ryan *et al.* 2000). The methods utilised were developed in the 1960's, with collections in Europe leading the way in 'preservation technology'. Over the intervening years the basic principles of both cryopreservation and lyophilisation have remained unchanged, the aim of which is to optimally store samples without change to their viability, genomic and physiological integrity. Notwithstanding, that all collections use these methods, few have active programmes to develop and improve methodology, albeit there are reports in the literature of protocol development of fastidious/recalcitrant microbes. The rapid development and interest of microbiome research and 'biobanking' has necessitated culture collections to broaden their approach, from pure (axenic) single cultures of microbes to more complex microbial communities including synthetic microbial communities and 'microbiomes' (Ryan *et al.* 2021). One example is the UK Crop Microbiome Cryobank (Ryan *et al.* 2023), which has developed a resource of 40,000 cultures and soil samples, representing 3 soil types and 6 crop varieties. The starting point for preservation has been to develop and optimise the methods used for axenic microbes. However, there are additional challenges of preserving complex communities including the need to retain functional potential. The EU MICROBE project has been conducting experiments to develop, test and apply cryopreservation to a range of use cases including soil, seed and marine systems and then assess the effectiveness of preservation regimes using metagenomic and functional bioassays. As part of this, a large experiment on preservation of soil microbiomes has been undertaken across three European institutions. The results of this experiment, the rationale for the preservation approaches and challenges for the future will be discussed.

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Preserving bioremediation consortia: an evaluation of cryopreservation and lyophilization methods

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Background and aim. The present study set out to investigate the effects of different preservation methods on viability, composition and functionality of three bioremediation microbiomes. The present study set out to investigate the effects of different preservation methods on viability, composition and functionality of three bioremediation microbiomes.

Methods. Cells of diesel (PHC), cyanide (CYA) or lindane (HCH)-degrading microbiomes were resuspended in 14, 14, or 8 preservation media, respectively. A total of 630, 350 and 127 aliquots were prepared and stored, respectively. For the PHC-degrading consortium, preservation has now been monitored for 2 years, with 5 fixed time-points (TP) for measuring outcome parameters. For the others, preservation was initiated and will be monitored for 1 year, with 2 fixed evaluation TPs. Per TP and preservation method, 5 aliquots were/will be analyzed through flow cytometry to conduct a total and viability count. To date, data has been collected up to 2 years (PHC) and for <1 week (CYA, HCH) post-preservation.

Results. After two years of preservation, the cell viability decreased from 86.7% before preservation to 60-80% (cryopreservation) and 45-60% (lyophilization) after preservation. Pairwise comparisons of all 14 methods confirmed that overall, cryopreservation resulted in significantly higher average bacterial survival than lyophilization. When comparing cryopreservation methods, a greater survival was obtained after preservation in liquid nitrogen rather than at -80°C. When comparing lyophilization methods, a greater survival was obtained after preservation using 10% (w/v) skim milk rather than horse serum. A reduction in bacterial survival was observed at the first post-preservation TP (3 months) for all 14 conditions. Subsequent TPs yielded few statistically different survival rates. A significant reduction in average cell survival was observed between cell numbers before and after less than one week of preservation, for all conditions used for the CYA-degrading and HCH-degrading consortia.

Conclusions. Cryopreservation methods generally resulted in higher cell survival than lyophilization methods. The average viability of cells was significantly better when lyophilization methods involved the use of 10% (w/v) skim milk compared to horse serum. For all 14 preservation methods used for the diesel-degrading consortium, viability was significantly reduced after 3 months of preservation. However, for none of these 14 methods significant differences were observed between post-preservation measurements, suggesting that the initial preservation step, rather than preservation time, determines cell viability, which was confirmed by data obtained from the cyanide- and lindane-degrading consortia.

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How to preserve viable Microbiota?

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Culture collections, such as CIRM-CFBP, the French Collection for Plant-associated Bacteria (<https://cirm-cfbp.fr/>) have stored and distributed single strains for decades, bringing a much-appreciated service to scientists, permitting them access to reliable resources.

Microbiology is nowadays shifting its focus more and more to whole communities. The closer study of these microbiota is impaired by technicalities and often limited to descriptive approaches. One way to overcome some of these hurdles would be to preserve these communities as viable entities. However, this is easier said than done, as microbiota are complex and heterogeneous communities comprising a significant fraction of non-cultivable organisms. Hence, the preservation of microbial community will have a heterogeneous effect on the members of the community, leading to heterogeneous survival, which may in turn affect the metabolic capacities of the whole community.

The MICROBE project (<https://www.microbeproject.eu/>) aims at paving the way for microbiome biobanking. Within the framework of this project, we focused on seed microbiota extracted from beans. Three partners of the MICROBE project, INRAE, CABI and AIT, teamed up to conduct parallel experiments to determine which preservation condition is least disruptive to the taxonomic composition and functional diversity of the preserved communities. For each tested condition, the taxonomic diversity, assessed by metabarcoding (16S rRNA, ITS, *gyrB*), and the functional diversity, assessed with Biolog EcoPlates, were measured before preservation and after 1 week, 3 months and 12 months of preservation. The initial results indicate that some preservation conditions are more effective in preserving the functional diversity of the communities. The next steps are to compare the results from the functional assessment to metabarcoding data.

Session 2: Microbial reference materials for new diagnostic tools for plant, animal and human pathogens

Insights from a collection of historical *Trichosporon* strains from clinical, environmental, and food sources

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Background:

Trichosporon yeasts are opportunistic pathogens that may cause severe invasive infections in immunocompromised patients. Their taxonomy has been repeatedly revised, leading to the creation of new genera such as *Apiotrichum* and *Cutaneotrichosporon* (Guého *et al.* 1992; Liu *et al.*, 2015). Accurate identification is crucial for surveillance and treatment, as these species display intrinsic resistance to echinocandins and variable azole susceptibility.

Methods:

Thirty lyophilized *Trichosporon* strains, isolated between 1941 and 1994 and preserved in the CFIP, were revived and assessed for purity via macroscopic and microscopic examination. Identification was performed using MALDI-TOF mass spectrometry (Bruker MBT Compass Library) and confirmed by sequencing of ITS, IGS1, and 26S rDNA regions. Sequences were compared with public databases and used to build phylogenetic trees. Minimum inhibitory concentrations (MICs) for amphotericin B, azoles, and echinocandins were determined according to EUCAST guidelines.

Results:

MALDI-TOF identified 28/30 strains at species level, with sequencing confirming and refining identifications. Taxonomic updates included reclassification of *T. cutaneum* as *T. asahii*. Phylogenetic analysis showed >97% similarity with type strains. MICs confirmed intrinsic echinocandin resistance and moderate azole susceptibility, with no major differences between historical and contemporary isolates.

Conclusion:

A combined phenotypic–molecular approach enables robust reclassification of historical fungal collections. Updated taxonomy and susceptibility data enhance the research and clinical relevance of CFIP *Trichosporon* strains.

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Microbial collections and their role to provide reference materials and databases as basis for the diagnosis of mycoses

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With the ever-increasing number of fungal infections, due to the raise of immunocompromised patients the need for fast and accurate diagnostic methods is paramount. Invasive fungal infections (IFIs) alone cause world-wide ~1.6 million deaths annually and account for 10% of all nosocomial infections. IFIs are suspected as major cause of the 15-25% of pneumonia, 40-60% of meningitis/encephalitis and 20% of fever/sepsis cases which are currently undiagnosed, resulting in a death rate of about 50%, even though antifungal drugs are available. This is largely due to the fact that fungal infections are under-recognized and conventional techniques used for diagnosis take days to weeks for results to become available, and lack specificity and sensitivity. Microbial culture collections play an increasing critical role in providing quality-controlled reference strains for the development of rapid and accurate clinical microbiology diagnostics methods and for antifungal resistance testing (MIC). Advances in proteomics (MALDI-TOF) and molecular biology, especially the development of next generation long-read sequencing and metagenomics, enable fast generation of diagnostically valuable data. However, correct identification of the causative agents is currently hampered by the lack of comprehensive reference databases. Here again microbial collections play a second fundamental role in provide accurately identified reference strains as basis for the establishment of those urgently needed quality controlled reference databases, including: 1) reference fungal DNA barcode databases (e.g. the (ISHAM)-ITS database for human/animal pathogenic fungi, <http://its.mycologylab.org>, which contains ITS1/2 and TFl1alpha reference sequences for metabarcoding based ID; 2) reference whole genome sequence databases (e.g. MycoCosm, <https://mycocosm.jgi.doe.gov/mycocosm/home>) for metagenomics based ID, and 3) reference protein spectra database (e.g. MSI-2 database, <https://msi.happy-dev.fr>) for MALDI-TOF based ID. However, there are still major gaps in reference data sets for fungal species. Currently, ITS barcode data are available for most of the human pathogenic fungi but for only half of them TFl1alpha DNA barcodes are available. Only 1/3 of the human pathogenic fungi have a genome with a similar ration having validated MALDI-TOF reference spectra. The final and third major role of microbial collections is to provide an accurate taxonomy and maintaining nomenclature stability in view of clinical relevance. As such, microbial collections have a basic role in interlinking environment, agriculture, and human health (One Health Concept).

100 Years of collecting biological materials: The diversity of the ATCC® collection and its use as biological standards

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For more than 100 years, ATCC® has been supplying the global scientific community with authenticated, high-quality biological resources and standards that support research with the power to transform lives. At its inception in the 1920s, ATCC® was regarded as simply a microbial culture collection—a repository of microorganisms that scientists could draw from to conduct their research to make new discoveries. Today, ATCC® provides the world's leading scientists with one of the largest and most diverse collection of biological materials, including microbes, cell lines, molecular genomics tools, and nucleic acids. ATCC® also serves as both a type strain and patent depository. Our vast collection boasts more than 70,000 microbes and 4,000 eukaryotic cell lines used in various industrial applications, and we are continuing to expand. In this poster, I will highlight the diversity and importance of the collection built over the last 100 years. I will describe the whole cell and molecular standards developed from our collection that support drug discovery, food, clinical and diagnostic labs. The collection and derived products can be used as a valuable resource for the present and future generations of scientists.

Session 3: Microbes for food safety & security and to promote human health (see excel)

Innovation at a cost: comparing single-cell dispensing and conventional spiral plating for cultivating kombucha microbiota

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Background and Aims: Recent advances in single-cell dispensing (SCD) technology offer a novel approach for isolating microbial taxa. The present study aimed to assess the effect of different plate types and dispensing parameters of a single cell dispenser (B. sightTM, Cytena) on the growth output and/or dispensing time of kombucha-derived axenic cultures of bacteria and yeasts. Subsequently, the optimized dispensing parameters were used to compare the effectiveness of conventional spiral plating and single-cell dispensing in recovering microbial diversity from kombucha samples.

Methods: Eight bacterial and four yeast isolates were used to evaluate the effect of dispensing parameters (detection threshold, velocity of droplet formation and cell roundness) and plate type on the number of dispensed cells leading to growth (the ‘growth output’). Live/dead and total counts for each cell suspension were measured using flow cytometry. Single cells were dispensed using a bright-field SCD (i) into wells of 96-well plates containing broth media, (ii) onto agar plugs in wells of 96-well plates, and (iii) onto a one-well rectangular agar plate. Each plate type was inoculated using three dispensing velocities (55, 65, and 75 $\mu\text{m}/\text{ms}$) and three detection threshold levels (1, 3, and 5). The first 8 wells of each plate were used as positive and negative controls. Forty-four wells per plate were inoculated with cells with low roundness (0–0.5), the remaining 44 wells with cells with high roundness (0.5–1.0). Based on this first experiment, optimized dispensing parameters were identified. These parameters were then applied in a pilot experiment comparing SCD with conventional spiral plating for isolating microbial diversity from kombucha. Both direct plating and plating after pre-enrichment were performed on five selective agar media targeting acetic acid bacteria, lactic acid bacteria, and yeasts. A total of about 800 isolates was picked for identification.

Results and Conclusion: The viability of the initial cell suspension influenced the growth output. Dispensing parameters, i.e. especially the velocity of droplet formation, and plate type only affected the growth output of bacterial isolates with a generally low growth output. For bacteria, dispensing time decreased as the detection threshold increased when selecting cells with low roundness. For yeasts, an overall increase in dispensing time was observed when selecting cells with high roundness. These findings suggested that in microbial communities containing both bacteria and yeasts, specific detection threshold and roundness parameters could selectively exclude certain cell types, impacting overall isolation success. Spiral plating and SCD allowed to recover largely the same species diversity. However, SCD was about ten times more expensive. The present study concluded that SCD may only be practical for routine use after further optimisation and cost reduction.

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**Cryopreservation of fermented olives microbiomes:
Viability, functional and taxonomic stability after long-term storage**

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Microbial communities are essential to the functioning of ecosystems, playing a central role in biological processes across the planet. In food ecosystems, the microbiomes of fermented products not only enhance food safety and shelf life but also contribute to human health and well-being. Within this framework, Microbial Culture Collections serve as vital infrastructures also for ensuring food safety and quality, as well as fostering the development of bio-based innovations. As the demand for sustainable food systems grows, both industry and researchers are increasingly focused on harnessing the potential of complex microbial consortia in fermentation and developing nature-inspired solutions. However, a significant challenge remains: the absence of standardised, effective methods for the long-term preservation of these microbiomes, along with reliable assessments of their post-preservation viability and functionality. Recent investigations conducted under the EU-funded SUS-MIRRI.IT project (N° IR0000005) have advanced our understanding of microbiome preservation, particularly in fermented food systems. This study presents novel findings on the cryopreservation of microbiomes derived from table olives and their brine. The protocols tested involved storage at ultra-low temperatures using a -150°C freezer, combined with the use of glycerol and dimethyl sulfoxide (DMSO) as cryoprotective agents. The microbial consortia were analysed before and after a one-year storage period by using culture-based techniques and RNA-based metabarcoding, as well as metabolic profiling by Biolog Ecoplate assays. Moreover, the oleuropein degradation ability was evaluated in microbiome samples recovered and propagated after 1 year of cryopreservation. Results indicated a slight reduction in microbial viability after one year, independent of the cryoprotectant used. Metabolic activity and functional performance, specifically the ability to degrade oleuropein, remained stable. Furthermore, metabarcoding analysis revealed no significant alterations in the composition of the microbial community. This integrated methodological approach offers a valuable model for preserving microbiomes from other fermented foods, reinforcing the crucial role of culture collections in maintaining viable and functionally robust microbial resources for future applications.

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A taxonomic revision of the *Fusarium sambucinum* species complex

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Devastating plant pathogens, endophytes, rare human opportunistic pathogens and saprotrophs, are some known lifestyles of the *Fusarium sambucinum* species complex (FSAMSC). The FSAMSC represents a clade of morphologically diverse, globally distributed, mycotoxigenic fungi. It is of central relevance for *Fusarium* taxonomy as it includes the conserved generic type of *Fusarium* (*F. sambucinum*), and that of the sexually typified *Gibberella* (*G. pulicaris*). We tested recent phylogenetic circumscriptions in FSAMSC using multigene phylogenetics, traditional cultural and morphological analyses, and coalescent-based species tree estimations methods using a large set of strains from four culture collections (*i.e.*, BBA, CBS, IMI and NRRL) plus recent isolations from diverse substrates. Seventy-five species are resolved in FSAMSC making it one of the most speciose groups in *Fusarium*. However, only 40 phylospecies are currently linked to types and Latin binomials. Thirty-four novel species are described, and illustrations are provided for all the species studied. Differences between coalescent-based methods and genealogical concordance results challenge the current species delimitations within *F. graminearum sensu lato* (*F. graminearum* species complex, a species aggregate within FSAMSC), and lesser-studied species like *F. armeniacum*, *F. longipes*, *F. sibiricum*, and *F. sporotrichioides*. In line with these results, narrower species circumscriptions are proposed, which correlate with distinctive morphological features. Fresh material of *F. sambucinum* was collected from its original substrate and location (*Sambucus nigra*, Germany), and its identity confirmed by morphological and mating experiments. An epitype is designated, thus finally stabilising the taxonomy of this important taxon, now circumscribed within a genetically and morphologically well-characterised phylogenetic clade.

Session 4: Unlocking the treasure chest: Whole Genome Sequencing of collection holdings

Great diversity, great opportunities and great challenges: Insights into decoding genomes from the Central Collection of Algal Cultures

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The Central Collection of Algal Cultures (CCAC) of the University of Duisburg-Essen, Germany, hosts more than 7,000 algal strains, which represent a vast and largely untapped reservoir of biological diversity. This diversity holds enormous potential for basic and applied research, environmental management, biotechnology, and industrial applications. Realizing this potential requires access to high-quality genome sequences, which provide critical insights into algal biology and enable broad applications.

Recent advances in sequencing technologies now make large-scale comparative genomic exploration feasible, paving the way for international collaborations. One such initiative is GENIAL, a partnership between the University of Duisburg-Essen and the Joint Genome Institute (California). GENIAL aims at generating genome sequences for more than 120 representative algal strains from CCAC, along with their associated prokaryotes and viruses. In addition, the Advanced Light Source at Lawrence Berkeley National Laboratory also supports this endeavour, where the exact same strains are investigated via synchrotron radiation-based Fourier transform infrared spectromicroscopy to decipher the production of biomolecules.

The opportunities are immense: sequencing a diverse range of strains can substantially expand the genomic foundation needed to attract further large-scale initiatives, while also enhancing the use of culture collection resources. This, in turn, will open new avenues for both fundamental research and applied innovation. At the same time, the challenges are considerable. Cultivating sufficient biomass from such taxonomically diverse algae is demanding, as growth requirements and rates vary widely among species. Isolating large quantities of high-molecular-weight DNA adds further complexity, given the diversity of cell morphologies, cell wall structures, and metabolite compositions. Moreover, the genomic architecture of algae – often characterized by large sizes, abundant repeats, and structural complexity – creates serious obstacles for genome assembly.

By sharing CCAC's experiences and highlighting both the promises and challenges of algal genomics projects, this presentation underscores the importance of coordinated efforts to unlock the full potential of phototrophic biodiversity.

Analysis of virulence factors in whole genome sequences of zoonotic *Serratia marcescens* and *Serratia liquefaciens* strains, deposited in Polish Collection of Microorganisms

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Bacteria of the *Serratia* genus belong to the phylum *Enterobacterales* and the family *Yersiniaceae*. They are Gram-negative rods from the group of opportunistic human pathogens. Infections with *S. liquefaciens* and *S. marcescens* in humans can cause diseases such as endocarditis, arthritis, meningitis, urinary tract infections, and bacteremia, which may develop as a result of direct contact with animals.

The subjects of this study are isolates of two species *Serratia marcescens* and *Serratia liquefaciens*. Both strains were obtained from cattle examined in the Silesian Voivodeship in Poland and deposited in PCM, respectively, under accession numbers PCM 3246 and PCM 3254.

The aim of the study was to determine the virulence factors of *Serratia marcescens* and *Serratia liquefaciens* isolates obtained from cattle in Poland.

Obtained isolates were identified using MALDI Biotyper Sirius (Bruker). Subsequently, tests were performed on differential media (DNase agar, lipase agar, gelatinase agar, and Columbia agar) to assess the presence of extracellular enzymes such as deoxyribonuclease, lipase, and gelatinase, as well as to evaluate hemolytic activity. In the following steps, the length of the O-specific LPS chain was determined using SDS-PAGE electrophoresis, and serum resistance to a commercial human serum preparation (Sigma-Aldrich) was assessed using the spot assay method.

Whole-genome sequencing was conducted on Illumina MiSeq, raw paired-end reads were assessed with FastQC tool and then trimmed and assembled with Fastp and Spades tools. After such preparation, genomes were annotated with Prokka, in order to identify occurring genes. The final step was to use the Panaroo tool in order to create a summary of core genes and differentiate them from genes unique to each *Serratia* strain.

Results of conducted biochemical tests revealed that *S. marcescens* PCM 3254 and *S. liquefaciens* PCM 3246 produce enzymes deoxyribonuclease, lipase, and gelatinase, and also show hemolytic activity. Both isolates express LPS with a long O-specific chain and exhibit resistance to human serum.

Bioinformatic analysis discovered presence in *S. marcescens* PCM 3254 genes responsible for e.g. multidrug efflux MFS transporter Bcr/CflA, outer membrane porin OmpC/OmpF/PhoE, OprD, multidrug efflux RND transporter SdeA/SdeB, hemolysin, class A beta-lactamase and virulence factor SrfA, SrfB, SrfC related protein. In *S. liquefaciens* PCM 3246 genes responsible for e.g. macrolide transporter MacAB-TolC, multidrug resistance protein mexA, ABC-type multidrug transport system SmdA/SmdB, multidrug efflux RND transporter MdtC, MdtB/MuxB, MdtA/MuxA and hemolysin III family protein were identified.

Autocycler Express: rapid and interactive consensus assembly generation for bacterial genomes

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Long-read sequencing technologies enable the generation of near-complete bacterial genome assemblies. However, no *de novo* assembler is perfect – issues like duplicated or missing plasmids, spurious contigs, and failures to circularize sequences remain common problems. Achieving optimal results still requires manual consensus generation. While tools like *Trycycler* simplify this process, they are labor-intensive and require command-line expertise. Its successor, *Autocycler*, automates many steps, but manual, command-line-based supervision is still recommended. With the ability to sequence hundreds of datasets quickly and affordably, there is a growing need for more accessible solutions.

Here, we present *Autocycler Express*, a browser-based user interface designed to streamline the manual curation capabilities of the *Autocycler* pipeline. Key features include: (i) overview of all samples; (ii) visualization of *Autocycler* outputs at each stage, including on-demand dotplot generation and direct submission contig subsequences to NCBI's Blast servers for approximate taxonomic identification; (iii) support for iterative refinement including removal of assemblies or contigs, curation of clusters, graph cleaning); and (iv) postprocessing steps including contig reorientation and generation of FASTA files which are directly compatible with the NCBI annotation pipeline *PGAP*.

Autocycler Express enables the semi-automatic processing of hundreds of genomes in just a few hours, significantly reducing manual effort while maintaining high assembly completeness and accuracy. Moreover, the browser-based UI enables biologists without programming skills but domain specific knowledge to perform or participate in the curation process. This can potentially lead to superior results.

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On overview of CCAP's molecular curation

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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 3,000 strains of microalgae, macroalgae, cyanobacteria, algal pathogens, and protozoa. These strain holdings have been isolated from across the globe, and through time. The biological and chemical diversity, as well as untapped datasets locked within our collection is truly staggering! CCAP has been involved with several innovations in the molecular sphere. For instance, we launched the Bioinformatics Gateway; a free and user-friendly access portal to all of our 18S DNA barcoding data from our collection. Through this Gateway, users are able to view and download sequence information pertaining to each of our strains. Furthermore, CCAP has taken a key role in a wide range of international genome sequencing projects to help answer fundamental questions in evolution, comparative genomics, ecosystem assembly, and global carbon cycles (i.e., the Chinese-led 10KP and the UK-USA 100 Diatom projects). More recently, CCAP's major genomic commitments have been to the Macroalgal Deep Genomics project (Nelson et al. 2024), which increased the number of available seaweed genomes from 14 to 124 at the time of publication, and to the protistan group of the Darwin Tree of Life initiative, the UK branch of the Earth Biogenome Project, which aims to sequence all eukaryotic life on earth (Darwin Tree of Life Consortium 2022). During this presentation, we will initially provide a brief overview of CCAP, our core functionality, and curatorial activities. Afterwards, we will present a brief history of time relating to our molecular biological progress; beginning with our background in taxonomy and DNA fingerprinting, digital sequence curation, our recent projects involving Whole Genome Sequencing, before rounding off with areas of future exploration and direction to harness the value from data generated.

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Theme: Collection management & legal and regulatory challenges

Session 5: Culture collections for sustainable development

Utilization of VTTCC resources in biotechnology

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VTT Culture Collection (VTTCC) was established in 1959. Since then, microorganisms, isolated from diverse industrial and environmental samples, were deposited in the VTTCC making it a valuable resource of microorganisms for various applications. Many of these organisms have been passively stored in the collection for many years. However, with developments of new high-throughput technologies for screening and modelling, our collection is evolving from passive repository to active collection for discovering microbial strains with interesting properties.

With increasing pressure on environmental resources, bioeconomy and particularly microbial bioeconomy became important for ensuring a sustainable and resilient future. VTT is actively working on innovative solutions for the sustainable food and feed ingredients traditionally derived from animal or plant sources, as well as bulk ingredients for industry, application of microorganisms for transforming various underutilized resources such as industrial and agricultural side-streams into valuable products, and the production of biomaterial.

Generally, microbial culture collections serve as important infrastructures for biotechnology, offering access to quality-assured microbial strains. VTTCC exemplifies this role by supporting VTT's research in diverse biotechnology fields. The presentation will give an overview of the VTTCC's role in biotechnology research and give some examples of biotechnological applications.

Decoding the plastic-degrading potential of marine yeasts: A multi-omics perspective on microplastic-associated fungi

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Microplastic (MP) contamination poses a growing threat to marine ecosystems, disrupting biodiversity and environmental stability. In this study, we investigated the genomic, metabolomic, and physiological characteristics of four marine basidiomycete yeasts isolated from MP-contaminated sediments in the Livorno coastal area (Italy).

The strains, *Cystobasidium slooffiae* MUT6565, *Sakaguchia dacryoidea* MUT6569 (Cystobasidiomycetes), *Vishniacozyma carnescens* MUT6591 (Tremellomycetes), and *Kondoa aerea* MUT6563 (Agaricostilbomycetes), resulted effective in the degradation of plastic polyurethanes with ether and ester bonds. In this study, we report for the first time the whole-genome sequencing of four marine basidiomycete yeasts. Their genomes exhibited enriched repertoires of genes coding for putative plastic-active enzymes (Pazy), including esterases, laccases, lipases and hydrophobins that may promote MP adhesion. Genomic analysis also revealed horizontally acquired genes, such as a bacterial-derived plastic depolymerase in *C. slooffiae* MUT6565, suggesting niche-specific adaptive evolution.

In parallel, we performed metabolic profiling through mass spectrometry, which revealed a broad array of secondary metabolites, including terpene-like compounds of potential biotechnological interest. Furthermore, phenotypic microarray analysis using Biolog FF MicroPlates™ was conducted under varying salinity conditions (0% and 3% w/v NaCl) to explore salt-dependent metabolic versatility. While *V. carnescens* MUT6591 showed no significant metabolic changes across salinities, the remaining strains exhibited differential metabolic responses. These variations may reflect osmotic stress-induced modulation or the activation of specific metabolic pathways, underscoring their adaptive capabilities in fluctuating marine environments and highlighting a strong prospect for industrial applications.

This integrative multi-omics approach highlights the potential of these marine yeasts as promising candidates for MP biodegradation and the development of sustainable biotechnological applications. By combining genomic, metabolomic, and phenotypic data, this strategy enables a comprehensive understanding of both the functional capabilities and adaptive responses of microorganisms in complex environments. This systems-level perspective is essential for selecting and optimizing microbial strains for targeted environmental interventions and bioprocess design and for the development of sustainable biotechnological applications.

The Moroccan Coordinated Collections of Microorganisms (CCMM): Safeguarding and valorizing microbial genetic resources

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Established in 1998, the Moroccan Coordinated Collections of Microorganisms (CCMM) represent the first national infrastructure dedicated to the collection, preservation, and documentation of microbial resources in Morocco. Hosted by the National Center for Scientific and Technical Research (CNRST) in Rabat, the CCMM safeguards Morocco's microbial genetic heritage through the conservation, characterization, and valorization of microbial strains, thereby supporting research, innovation, and sustainable development.

As the only microbial culture collection in North Africa and the second on the African continent, the CCMM occupies a strategic position in the regional scientific landscape. Recognizing its technical expertise, the CCMM was designated in 2018 as an International Depository Authority (IDA) under the Budapest Treaty, allowing it to receive and preserve microorganisms for patent purposes (Smith & Ryan 2012).

In parallel, the CCMM contributes to the implementation of the Nagoya Protocol on Access and Benefit-Sharing (ABS) of the Convention on Biological Diversity (CBD) with respect to microbial genetic resources, thus supporting compliance with international frameworks while promoting fair and equitable benefit-sharing practices.

This presentation will outline the organizational structure, strategic objectives, and flagship initiatives of the CCMM. It will also highlight the scientific and technical services provided through CNRST platforms to researchers, academic institutions, and industry stakeholders in Morocco and abroad. Selected research projects and activities will be presented, illustrating the CCMM's contribution to advancing microbial biotechnology and biodiversity knowledge in the region.

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Exploration and valorization of the microbial diversity of Malvasia di Bosa DOC

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Studying and valorizing microbial biodiversity associated with a specific wine terroir is fundamental to enhancing wine identity and quality. Particularly, non-*Saccharomyces* species have been revalued for their positive contributions to wine aromatic complexity and typicity (Ciani et al., 2010). In valorizing biodiversity, specialized infrastructures like microbial culture collections (MCC) and biological resource centers (mBRC) play key roles by guaranteeing the quality of preserved microbial resources and their availability for stakeholders. In this context, the study of microbial biodiversity associated with Malvasia di Bosa has particular importance, given that this wine is among the most characteristic of Sardinia, strongly linked to its territory of origin. In this work, 140 yeast colonies were isolated from different vineyards within the Malvasia di Bosa DOC territory. Following phenotypic and molecular (Esteve-Zarzoso et al., 1999) identification, different yeast species were identified: *Aureobasidium pullulans*, *Cryptococcus* spp., *Rhodotorula glutinis*, *Vishniacozyma carnescens*, *Wickerhamomyces anomalus*, *Starmerella apicola*, *S. bacillaris*, *Metschnikowia pulcherrima*, *Hanseniaspora uvarum*, and *H. opuntiae*. Non-*Saccharomyces* species of oenological interest were further characterized for their technological properties by evaluating H₂S production, β -glucosidase activity, and fermentative properties through micro-vinification assays on Malvasia di Bosa must. Based on the oenological and metabolic characteristics, strains of *Starmerella bacillaris* and *Metschnikowia pulcherrima* were selected to be used as starters in mixed culture fermentations with a *S. cerevisiae* starter strain under cellar conditions. Results showed that locally selected yeast species may define a territorial "microbial fingerprint" contributing to wine specificity. The MBDS-UNISSCC collection played a fundamental role in this process through conservation, characterization, and management of Malvasia microbial biodiversity. Operating under the ISO 9001:2015 standard, the collection applies protocols that ensure cell viability and traceability during prolonged storage. Strain associated data are managed through the publicly accessible MBDS database (www.mbds.it), in accordance with FAIR principles, promoting scientific collaboration, technology transfer, and industrial application. The case of Malvasia di Bosa illustrates how tradition and innovation can be integrated to build a sustainable and competitive model of wine production, supported by the MBDS-UNISSCC infrastructure.

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Screening of the fungal biodiversity and targeted genome sequencing to guide innovation in the circular bioeconomy

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CIRM-CF is a Biological Resource Center (BRC) preserving and offering to the scientific community more than 3,000 fungal strains, mostly isolated from wood. The capacity of fungal wood decomposers to degrade polysaccharides (cellulose, hemicelluloses and pectins) and polyaromatic compounds (lignin) makes them a source of inspiration for the valorization of residues issued from the biorefineries, and for bioremediation. However, because these fungi are filamentous, the automation of cultures is arduous, and one challenge on the route toward innovation is the identification of the most relevant strains among thousands of them.

At CIRM-CF, we have combined large-scale functional phenotyping and targeted genome sequencing to guide the selection of performing strains and to identify the enzymatic mechanisms involved. We ran a large-scale phenotyping of more than 1,000 fungal strains and evaluated their growth and degradation potential towards two lignocellulose-derived compounds, two synthetic dyes, and a synthetic plastic polymer. We drew a functional map over the phylogenetic diversity of Basidiomycota and Ascomycota, aimed to guide the selection of fungal taxa best suited for dedicated biotechnological applications.

Fungal strains from the order Polyporales, Basidiomycota, performed particularly well for the degradation of three out of the five tested compounds. To identify the enzymatic systems involved, we analysed the genome sequence information from 50 Polyporales species, including 26 newly sequenced genomes. We captured expansions of genes involved in lignin degradation in several lineages, which explained the performance of the strains applied to saccharide recovery from lignocellulose. More recently, the functional map was used to guide the selection of fungal strains aimed at the bioremediation of polyaromatic hydrocarbons (PAHs) in creosote-treated wood.

This work demonstrates that screening the natural biodiversity treasured in collections combined with targeted genome sequencing can help leverage technological bottlenecks for circular Bioeconomy.

Session 6: Ethical and legal challenges of collection management

**The changing landscape of access and benefit-sharing:
what ECCO members need to know**

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At the UN Biodiversity Conference (COP16) in Cali, Colombia in October 2024 new decisions were reached on how benefits can and should be shared from digital sequence information (DSI). This new benefit-sharing mechanism under the Convention on Biological Diversity (CBD) creates new financial obligations for commercial users of DSI but ensures that non-commercial users of DSI can continue to publish in and use genetic sequences in open access databases although DSI databases have new requirements imposed on them. In parallel, new benefit-sharing instruments under the World Health Organization and the High Seas Treaty will affect how collection managers handle pathogens and microbes from international waters. The talk will explain what these new international laws mean for ECCO members. The talk will also highlight recent efforts by DSMZ and other collections to streamline Nagoya Protocol compliance and “fast-track” agreements with partner countries including Costa Rica and Brazil. Taken together, new options for improving the sharing of benefits emerge but also caution, engagement and action from ECCO members continues to be needed.

Theme: Community, Networks & Databases

Session 7: Projects, networks and databases I

BIOINDUSTRY 4.0 – using AI to enhance biotechnology for smart biomanufacturing

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The rapid acceleration of developments in artificial intelligence (AI) has major implications for many socioeconomic activities. Among these, biotechnology stands out because so far, its development has occurred in parallel to that of AI, meaning that an exciting interplay between AI and biotechnology has been established.

My presentation will focus on the opportunities offered by the biotechnology-AI nexus. To illustrate these, speaking on behalf of my project colleagues, I will briefly describe the aims of the BIOINDUSTRY 4.0¹, an undertaking that involves 22 partners, including 6 major Research Infrastructures (RIs). Funded in the framework of Horizon Europe, the goal of this project is to build a series of AI-based tools that will be made available to the scientific community by RIs as cutting-edge research services.

For microbial collections, by enriching the available data, the aim is to develop a powerful search tool and decision support system. It is intended that these will accelerate the uptake of microbial biodiversity in industrial bioprocesses. For the bioprocesses themselves, BIOINDUSTRY 4.0 intends to lay the foundations of digital twins that will be used to monitor and control bioreactors. To enable the command-control loop, the project is also focusing on the development of advanced process analytical technology (PAT devices) that will provide access to hitherto inaccessible, or difficult to measure process parameters. Finally, I will conclude with brief insight about IBISBA², a RI that focuses its activity on biotechnology for biomanufacturing. Currently under development, this RI intends to spur European biotechnology and catalyze the structuring of R&D ecosystems across the Union.

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¹ <https://www.bioindustry4.eu/>

² <https://ibisba.eu/>

Microbes-4-Climate: Facilitating transnational access to advance research on climate change

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Microbes4Climate (M4C: <https://microbes4climate.eu/>) is a five-year project funded by Horizon Europe coordinated by MIRRI-ERIC, with a Consortium of thirty-one partners from all across Europe, involving five Research Infrastructures (RIs).

The main goal of this project is to deepen the comprehension of the complex relationships among microbes, plants, soil and atmosphere within a dynamic environment in times of climate change, by offering access to advanced services of RIs through an excellence-driven Transnational Access (TNA) programme. TNA is a vital resource for researchers, offering free access to tailored services (onsite and remote) of high-quality RIs across multiple countries.

We will present a catalogue of services from which users can select services and submit a simple application for access, which is assessed by independent evaluators. The catalogue offers includes 144 services covering areas such as biological resource supply and preservation, microbial isolation and characterization, access to microbial discovery and phenotyping facilities, soil and plant analysis techniques, big data and machine learning tools, as well as remote consultancy. It includes all the relevant “ingredients” for users to drive scientific innovation to adapt to climate change and related risks for terrestrial biodiversity and ecosystems, including agricultural and (agro)forestry ecosystems.

We will also present the results of the first TNA call for access and provide best examples of applications and recommendations for future calls.

This programme promotes global collaboration, helping researchers overcome geographical barriers and accelerating high-impact research. Therefore, M4C has the potential to be a game-changer in enabling curiosity-driven research and advancing frontier knowledge.

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The REBECA network: From biodiversity conservation to biomedical and feed applications

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The REBECA network (Blue Biotechnology Excellence Network) is a collaborative cluster of microalgae and cyanobacteria culture collections across Macaronesia, aiming to preserve regional biodiversity and foster an innovative bioeconomy. By linking conservation with applied biotechnology, REBECA serves as both a repository of unique strains and a catalyst for industrial development that contributes to economic growth and enhances quality of life in the region.

The network brings together five major collections: the Bank of Algae and Cyanobacteria of the Azores (BACA), the Spanish Algae Bank (BEA), the Madeira Algae Bank (MAB), the Cape Verde Algae Bank (BACV), and the Mauritania Algae Bank (BAM). As a founding member, BACA provides strains from the Azores and actively participates in research and innovation projects that translate biodiversity into societal value.

Currently, within the framework of the INTERREG-MAC 2021–2027 program, REBECA is developing the project CALYPSO – Contribution to the regeneration of industrial and agricultural waste through algae cultivation and the application of its polysaccharides in biomedical and environmental products that generate a positive impact on society. BACA's role focuses on providing novel biodiversity and evaluating the toxic, teratogenic, and anti-inflammatory properties of strains using zebrafish larvae as a biomedical model. In parallel, through the recently approved AlgaeFusion project (ACORES2030-FEDER-01909600), BACA is collaborating with a local feed-producing company to develop new microalgae-based supplements aimed at improving poultry fitness and animal welfare. These initiatives highlight the dual potential of microalgae for both human health and animal nutrition, reinforcing REBECA's role as a driver of blue biotechnology.

By integrating biodiversity conservation with applied research in health, environment, and nutrition, the REBECA network is establishing Macaronesia as a reference hub for sustainable biotechnology and innovation.

Session 8: Projects, networks and databases II

Multi-omics approaches built on the evolutionary treasure chest at SAG Culture Collection of Algae

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The SAG Culture Collection of Algae at Goettingen University is a large service culture collection and modern biological resource centre (BRC) holding over 2350 strains of algae and cyanobacteria in its public collection. More than 20% of these are type or authentic strains linked to types. SAG provides high quality reference material and metadata and adds its specific expertise to many fields of science, ranging from whole genome sequencing, functional genomics, ecotoxicology to biophysics. Resources and expertise at the SAG underpin species identification projects that cover classical metabarcoding to cutting-edge Artificial Intelligence (AI) for biodiversity research and protection. Over 65 % of SAG holdings already serve as molecular reference strains. 51 transcriptomes of SAG strains were published in the framework of the OneKP Project and 115 SAG strains of mainly chlorophytes add to the follow-up project 10KP (Cheng *et al.* 2018) sequencing genomes representing every major clade of plants and eukaryotic microbes. Phylogenomic studies based on the unique holdings of SAG and other Protist culture collections are key to understanding eukaryotic evolution (Bierenbroodspot *et al.* 2024). Multi-omics approaches of SAG strains underpin diverse research directions. For example, emerging model algae like SAG 12.97 *Mesotaenium endlicherianum* and SAG 698-1b *Zygnema circumcarinatum* help to unveil functional modules, including novel pathways and cascades playing a role in land plant terrestrialization and stress adaptation (Dadras *et al.* 2023, Kunz *et al.* 2025); using statistical modeling and AI, the assembly into regulatory networks akin to those of land plants has been inferred (Rieseberg *et al.* 2025). Comparative genomics of multiple holdings of Nostocales cyanobacteria will help reveal the symbiotic competence in cyanobacteria (de Vries *et al.* 2022).

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MIRRI-ERIC: Coordinating microbial resources for research, innovation, and a sustainable European bioeconomy

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Microbial resources are central to addressing challenges in health and food safety, agri-food, and environment and energy, yet access to high-quality resources and associated data in Europe is still fragmented. MIRRI-ERIC is the pan-European distributed Research Infrastructure established to consolidate and enhance access to microbial domain Biological Resource Centres (mBRCs) and foster research and innovation by academia and industry. MIRRI-ERIC has implemented a comprehensive service integration strategy through its National Nodes, including the development of the MIRRI catalogue of strains, harmonisation of best quality management practices, and the creation of a Collaborative Working Environment (CWE). Currently, the CWE enables access to over 180 000 microbial resources through the MIRRI catalogue of strains, plus 95 services. MIRRI-ERIC coordinates the MALDIBANK project, which focuses on advancing microbial identification and dereplication via an open source bank of microbial strains' MALDI-TOF spectra, and the MICROBES-4-CLIMATE project that provides services to enhance curiosity-driven research and innovation to mitigate climate change. MIRRI-ERIC is also participating in the ERIC Forum 2 to build shared services and strategies across European Research Infrastructures. These activities underline MIRRI-ERIC's role as a model for coordinated microbial resources provision in Europe, enhancing research efficiency, sustainability, and socio-economic impact, and positioning it as a driver of microbiology-based innovation to a prosperous European bioeconomy.

Join the Strain Discovery Database!
A community project for standardized data of cultured microbial strains

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Worldwide an unknown number of strains are deposited at culture collections and waiting to be discovered. The data about these microorganisms is not standardized, mostly unstructured and sometimes not even publicly available. This hinders the discovery of strains, diminishes the visibility of smaller collections and prevents larger analysis.

Our goal is to bring a strain discovery database into life, which includes not only the basic catalogue data, but also integrates the entirety of known resources and research results on the strains. Every collection that provides their data in the new microbial data standard and with the CC BY 4.0 license will be able to integrate their strains into the database. Strain data will be merged on strain level, but every datapoint will be traceable to its author. The database will cover a wide range of information, from basic data about growth conditions to detailed information on metabolism and also data on restrictions and safety will be included. This way the strain discovery database will serve like a super catalogue where you can search for a strain by its traits and regulations and follow the links to the respective collections.

To enable strain data search, comparison of strains and large-scale analysis across all the strains in culture, a new data standard is applied, which will lay the foundation for the easy exchange and updating of microbial strain related data. Through linking, strain data is automatically enriched with data from nomenclatural, sequence and literature resources. To further improve the handleability of data formatted in the new standard, tools will be established which will help with the transformation into the standard, ease data linking and automatically handle data validation. More than that, an ontology to explain the data will be published alongside the data standard and a SPARQL endpoint on the database will enable highly complex querying.

The format is developed by experts from DSMZ, Westerdijk and CECT (MIRRI-ES) within the Bioindustry 4.0 Project (Grant agreement ID: 101094287) and the biological data of the partners will be publicly available in the new standard.

Theme: Taxonomy and Phylogeny

Session 9: Taxonomy and phylogeny of eukaryotes

Genomic characterisation to decipher yeast taxonomy: the case of the *Metschnikowia pulcherrima* complex, and of several other yeast species

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Genome sequencing has become the gold standard for taxonomy, not only in bacteria but increasingly in fungi as well. However, unlike bacteria, fungi actively undergo recombination, hybridization, and exhibit variations in ploidy—factors that complicate phylogenetic analyses and may contribute to phenotypic differences observed among strains. In this study, we investigate how genomic data can enhance taxonomic resolution within the *Metschnikowia pulcherrima* clade. Our results show that several *M. pulcherrima*-related species can be classified into a unified group, with the notable exception of a distinct cluster of potential hybrids. We also report similar hybridization events in other genera, such as *Hanseniaspora* (Saubin *et al.* 2020), and *Pichia* underscoring the urgent need for systematic genomic characterization across eukaryotic lineages.

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Taxonomic updates and challenges in *Aspergillus*, *Penicillium* and *Talaromyces*

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Fungal spoilage and mycotoxin contamination continue to pose significant risks to global food safety, security, and public health. Accurate species identification is essential for understanding the unique properties of these fungi, such as antifungal resistance, mycotoxin production, and enzyme profiles. Specific *Aspergillus*, *Penicillium*, and *Talaromyces* species are consistently associated with particular food and feedstuffs due to biotic and abiotic factors, forming distinct mycobiota. While the mycobiota of various foods has been well studied, new species and associations are still being uncovered, emphasizing the need for ongoing taxonomic and ecological research.

Recent advances in the taxonomy of *Aspergillus* and *Penicillium* have resulted in the introduction of numerous new species and revisions of existing names. In *Penicillium*, species boundaries are relatively clear, whereas in *Aspergillus* increased variability has been observed, leading to refined and more robust delimitation. Complementing these developments, large-scale DNA barcoding efforts have significantly advanced the taxonomy of *Aspergillus*, *Penicillium*, and *Talaromyces*. Analysis of thousands of strains from the CBS biobank has led to the clarification of species boundaries and the discovery of numerous cryptic taxa, including more than 50 newly described species. These findings expand the available reference data for fungal systematics and enhance our understanding of the evolutionary diversity within *Eurotiales*.

Continuing studies that combine molecular and chemical methods are key to better define species in these genera, reduce food safety risks, and support their use in biotechnology and medicine.

Polyphasic identification and taxonomy of species within the dermatophyte genus *Arthroderma* including *A. fimbriatum* sp. nov. and *A. cellare* sp. nov.

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Arthroderma is a taxonomically diverse genus within the dermatophyte family (*Onygenales*, *Arthrodermataceae*) comprising primarily geophilic species typically found in animal burrows, where they feed on keratinous debris. In this study, species delineations within the genus were refined according to current taxonomic standards using the extensive array of *Arthroderma* strains of the BCCM/IHEM fungi collection. The methodology was based on a polyphasic approach including phenotypic analyses, multi-gene phylogenetic inference (comprising the internal transcribed spacer (ITS), β -tubulin (BT), and RNA polymerase II core subunit (RBP2) regions and MALDI-TOF mass spectrometry. Special attention was given to the highly diverse *A. quadrifidum* clade which contains both geophilic and potentially zoophilic species, assessing the phylogenetic position of recently described taxa within this group. In total, 77 strains from the BCCM/IHEM collection were (re-)examined. MALDI-TOF mass spectrometry was able to correctly identify 92% of the strains at species level. Additionally, certain isolates did not correspond to any previously described taxa, leading to the recognition, description and typification of two novel species.

Session 10: Taxonomy and phylogeny of prokaryotes

Are ITS rRNA thresholds robust in cyanobacteria? A case study in Pseudanabaenales

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The introduction of 16S rRNA gene phylogenetic analysis into the taxonomic studies of cyanobacteria towards the end of the 20th century led to large-scale classificatory changes. The taxonomic status of traditional genera such as *Synechococcus*, *Pseudanabaena*, *Nostoc* etc. was reevaluated, resulting in the descriptions of numerous cryptic genera and species. Over time, the limitations of 16S rRNA gene, particularly its inability to distinguish closely related species, became increasingly evident. As a result, the use of 16S-23S ITS rRNA region gained popularity for species-level delineation and is now widely used in cyanobacterial taxonomic studies. This study highlights the limitations of ITS rRNA region in the taxonomic investigations.

In this study, two strains – *Pseudanabaena* sp. PCC 7367 and *Pseudanabaena* sp. PCC 7403 – were reassessed using a polyphasic approach, as recent studies indicated that these strains do not belong to *Pseudanabaena*, but rather to the genera *Thalassoporum* and *Tumidithrix*, respectively (1, 2). Determining their correct taxonomic identity is important, as ultrastructural analyses of these strains have significantly contributed to our current understanding of *Pseudanabaena* morphology. Multilocus and 16S rRNA gene phylogenetic analyses conducted in this study confirmed that PCC 7367 and PCC 7403 belong to *Thalassoporum* and *Tumidithrix*, respectively. The ITS rRNA region effectively distinguished the closely related species of *Thalassoporum*, but failed in delineating the closely related species of *Tumidithrix*, that were effectively distinguished by genomic analyses. Notably, while the currently accepted threshold of the ITS rRNA region worked for species delineation in one genus of the order Pseudanabanales (*Thalassoporum*), it failed in another (*Tumidithrix*). This inconsistency highlights the need to revisit and refine ITS rRNA based species delineation thresholds to avoid underestimation of true species diversity.

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LEGE-CC: A key resource of the Portuguese Blue Biobank for cyanobacterial diversity, preservation, and taxonomic services

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The Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC), maintained at the Interdisciplinary Centre of Marine and Environmental Research (CIIMAR) in Matosinhos, Portugal, is a major resource for the preservation, study, and biotechnological application of cyanobacteria and microalgae. Established in 1991 with just 45 strains from Portuguese ecosystems, it has grown into the oldest and most diverse culture collection of its kind in Portugal, currently housing over 1,500 strains. These originate from various environments—freshwater, marine, brackish, and terrestrial—and from a wide geographical range, including Portugal (mainland, Azores, and Madeira), as well as Australia, Brazil, Bolivia, Chile, Colombia, Morocco, Mexico, the Dominican Republic, and Cape Verde. LEGE-CC is an integral part of the Portuguese Blue Biobank and collaborates with international networks such as WFCC, ECCO, EMBRC, and MIRRI.

The collection provides a wide range of services, including strain isolation and identification, culture distribution, deposit and curation, consultancy, and specialized training. It supports research focused on the development of bioactive compounds for use in health, food, cosmetics, and environmental applications—such as anti-cancer, anti-biofouling, anti-microbial, anti-biofilm, and anti-obesogenic agents. Even though only a fraction of its holdings has been thoroughly characterized, LEGE-CC demonstrates high potential for innovation in response to modern challenges, including the search for new antibiotics and sustainable biotechnological solutions.

Considering cyanobacteria, LEGE-CC houses approximately 1,500 strains across fourteen taxonomic orders. Through an integrated polyphasic approach—combining 16S rRNA phylogenetic analysis, ITS secondary structure characterization, and detailed morphological and ecological data—thirteen new genera and two new species have been formally described: *Geminobacterium*, *Lusitaniella*, *Calenema*, *Leptolyngbyopsis*, *Pseudoleptolyngbya*, *Eurychoronema*, *Ciimarium*, *Pseudolimnoccocus*, *Eucapsopsis*, *Acaryochloridopsis*, *Vasconcelosia*, *Zarconia*, *Romeriopsis* and *Vacuolonema* along with the species *Hyella patelloides* and *Jaaginema littorale*. Additionally, a new genus of microalgae, *Endolithella*, has also been identified. These ongoing discoveries highlight LEGE-CC's critical role in uncovering novel cyanobacterial diversity available to the scientific community and enriching the culture collection.

Poster Abstracts

Posters are here listed by registration number of the corresponding authors, which are placed in front of the abstract title of each poster, for example “[001]”.

In the poster exhibition, posters are placed by registration number.

Posters are arranged over Poster Session I-III. We ask poster presenters to be at their poster during their Poster Session, you can find an overview of all posters and their respective Poster Session in the table at the end of this booklet.

[004.2] *Arx*: A genome data management and comparative genomics platform for microbial strain collections

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Background

Driven by advances in sequencing technologies, many organizations and research groups have accumulated hundreds of genome sequences. While standardized data formats are widely used to store assemblies and annotations, only few attempts have been made to automate bioinformatic analyses to help non-programmers to explore the data. Furthermore, typical challenges of *digitalization* emerge as sequencing projects progress: storing data and metadata, tracking and denoting changes in assemblies or annotations, and enabling easy access.

Methods

Arx is an open-source Python/Django-based website that is designed to address these problems. We designed a simple folder structure to organize both the genomic data as well as metadata, as well as tools to help import new genomes into this system. *Arx* is distributed as a docker container, enabling a simple yet customizable setup.

Results

Arx allows users to easily filter and analyze genomes based on metadata, search for annotations, compare and navigate gene loci, browse pathway maps, perform gene trait matching, generate dot plots, execute BLAST searches, and access the raw data. We also have paid special attention to performance and user-friendliness during development.

Discussion

Arx is a value multiplier for genome databases as it helps to (i) organize large genome data sets, (ii) share data, and (iii) automate comparative genomics analyses. What sets *Arx* apart is that it is dataset independent and customizable. This means that it can be optimized, for example, for the study of antimicrobial resistance, as it is possible to annotate genomes with databases for resistance or virulence genes. Moreover, the gene trait matching tool can help researchers correlate resistance phenotypes to genes.

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[007]Can polluted urban wastewater sludges be a source of fungal biocatalysts? Insights from the SusWater project

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The increasing presence of Contaminants of Emerging Concern (CECs) in urban wastewater poses serious environmental threats, particularly due to the inefficiency of conventional wastewater treatment plants (WWTPs) in removing these micropollutants. Within the European SusWater project, this study explored the biotechnological potential of fungal communities naturally inhabiting activated sludge from a WWTP in Turin (Italy).

Using selective enrichment in the presence of four model CECs (carbamazepine, estriol, diclofenac, and ofloxacin), 104 fungal isolates were obtained and characterized morphologically and molecularly. The majority belonged to the Ascomycota phylum (78%), but Basidiomycota and Mucoromycota were also present, highlighting an unexpected fungal diversity.

Thirty-four isolates were selected for biodegradation assays. Results showed marked variability in CEC degradation capacity, both between and within genera. *Trichoderma*, *Mortierella*, and *Candida glabrata* were particularly promising, with *Fonsecaea pedrosoi* achieving 81.6% ofloxacin removal and *Trichoderma virens* reaching over 95% estriol degradation in 10 days. Conversely, carbamazepine remained the most recalcitrant compound. Surprisingly, laccase and peroxidase activity levels were negligible, suggesting alternative enzymatic pathways may be involved. The two best performing strains were selected for undergoing scale-up studies, due to their broad-spectrum degradation ability and robust growth under contaminant stress. These strains demonstrated high efficiency in reducing concentrations of multiple CECs—especially estriol, diclofenac, and ofloxacin—making them promising candidates for the development of sustainable, fungal-based wastewater treatment solutions. Future work will focus on optimizing culture conditions and reactor configurations to exploit their full biotechnological potential. These findings underline the potential of fungal consortia in the development of sustainable, bio-based strategies for advanced wastewater treatment.

[011] Utilization of VTTCC resources in biotechnology

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VTT Culture Collection (VTTCC) was established in 1959. Since that, microorganisms, isolated from diverse industrial and environmental samples, were deposited in the VTTCC making it a valuable recourse of microorganisms for various applications. Many of these organisms have been passively stored in the collection for many years. However, with developments of new high throughput technologies for screening and modelling, our collection is evolving from passive repository to active collection for discovering microbial strains with interesting properties.

With increasing pressure on environmental resources, bioeconomy and particularly microbial bioeconomy became important for ensuring a sustainable and resilient future. VTT is actively working on innovative solutions for the sustainable food and feed ingredients traditionally derived from animal or plant sources, as well as bulk ingredients for industry, application of microorganisms for transforming various underutilized resources such as industrial and agricultural side-streams into valuable products, and the production of biomaterial.

Generally, microbial culture collections serve as important infrastructures for biotechnology, offering access to quality-assured microbial strains. VTTCC exemplifies this role by supporting VTT's research in diverse biotechnology fields. The presentation will give an overview of the VTTCC's role in biotechnology research and give some examples of biotechnological applications.

[012] Optimizing ITS metabarcoding for fungal identification: Impacts of ITS region, database choice, and bioinformatics tools on taxonomic accuracy

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Classical morphological identification of fungi involves culturing on selective media, isolating pure cultures, and analyzing macro- and micromorphological features, but it is labor-intensive, time-consuming, and limited by difficulties in distinguishing closely related species, competition on media, and the inability to culture some fungi. To overcome these challenges, ITS metabarcoding has become a widely adopted approach for identifying fungal species in mixed samples. However, identification accuracy is affected by variations in ITS subregions, database quality, and bioinformatics tools.

This study evaluates key factors affecting molecular identification accuracy, including the choice of ITS region (ITS1 and/or ITS2), reference database (UNITE versus BCCM/IHEM), bioinformatics software (BLAST versus mothur), and taxonomic resolution (species versus genus level).

To investigate these variables, we constructed 37 Defined Mock Communities (DMCs) containing DNA from 51 fungal species across 35 genera from the BCCM/IHEM collection in Brussels. Each DMC included DNA from five distinct fungal species in equal proportions. Illumina MiSeq technology was used to target the ITS1 and ITS2 regions, and the resulting sequences were classified with both the UNITE and in-house BCCM/IHEM databases using BLAST and mothur. BLAST was tested with strict (single top hit) and loose (multiple target hits) approaches, while in mothur the Wang (k-mer) method and k-nearest neighbors (knn) were used.

The results demonstrated that classification performance varied depending on sequencing technology, taxonomic level, ITS region, software, and database. Genus-level classification was effective, although species-level accuracy was limited, especially within genera such as *Aspergillus*, *Penicillium*, *Cladosporium*, *Aureobasidium*, *Cephalotrichum*, and *Fusarium*. In these cases, subgeneric levels (e.g., series and section) partially compensated for species-level limitations. Notably, ITS2 showed slightly better precision than ITS1. The choice of database had a strong impact, with BCCM/IHEM outperforming UNITE, most likely due to its greater size and taxonomic coverage. BLAST provided greater accuracy when results were manually curated, whereas mothur was better suited for automated, high-throughput workflows.

In summary, Illumina-based ITS metabarcoding is a powerful tool for analyzing fungal diversity in complex samples, with results typically accurate at the genus level due to ITS's limited species-level resolution in some fungal groups. Manual curation enhances identification by supporting classification to subgeneric levels, thereby improving the depth of analysis. Overall, our findings offer practical guidance for selecting optimal metabarcoding workflows and maximizing taxonomic accuracy in fungal community studies.

[018] Seven novel *Blastobotrys* species described from various substrates and proposing three new combinations

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Blastobotrys species are known for their diverse origin as they can be found in numerous locations worldwide and on various types of substrates. *Blastobotrys* are yeast mostly known by their asexual form. Nonetheless, for some species, a sexual form is also reported and included in *Trichomonascus*. Through different independent investigations several isolates were recovered from basidiomata, decaying wood, and insects. After a combination of phylogenetic analysis, using the ITS regions (ITS 1, ITS 2 and the intervening 5S rRNA gene) and the D1/D2 domain of the large-subunit (LSU) rRNA gene, and physiological characteristics, seven novel species were identified, named *B. bolitointerruptus*, *B. dehoogii*, *B. hennebertii*, *B. jacksonii*, *B. larixii*, *B. plurivora* and *B. pulvis*. Sexual reproduction was only observed in *B. bolitointerruptus* and *B. pulvis*. Additionally, *T. apis*, *T. ciferrii*, and *T. petasosporus* are transferred to *Blastobotrys*. The currently known distribution and substrate range of *Blastobotrys* spp. is recorded using the Globalfungi database as well as data available from the CBS yeast collection. Both sources indicated that *Blastobotrys* spp. have been mostly found in North and South America, Asia, and Europe, and less frequently in Africa, Australia, and Antarctic. The natural environment of *Blastobotrys* species consists mainly of insects, soil, deadwood, other fungi, anthropogenic sources, but eventually can cause infections in humans, and are rarely found in water.

[020] Microbial Diversity of CIIMAR Microbial Culture Collection (CM2C) and its potential for biotechnological applications

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CIIMAR Microbial Culture Collection (CM2C) is a biobank of non-photosynthetic marine microorganisms located at Interdisciplinary Centre of Marine and Environmental Research (CIIMAR). CM2C collection comprises bacteria and fungi retrieved from different aquatic samples (seawater, freshwater, sediment, salterns, macroalgae, sponges, corals), collected in sampling campaigns in the Atlantic coast, deep-sea and inland waters from Portugal, including Azores and Madeira. The microbial strains from CM2C are being explored for their biotechnological potential, especially for bioprospecting new bioactive compounds with medical or industrial applications, and for the development of bioremediation tools for the degradation of different pollutants. For instance, several CM2C strains belonging to the phyla Actinomycetota and Planctomycetota showed capacity to produce bioactive compounds with antimicrobial, anti-inflammatory, anticancer, antifungal, anti-obesity and pro-osteogenic activity (Girão *et al.* 2019; Ribeiro *et al.* 2020; Vitorino *et al.* 2022). Furthermore, several CM2C strains from the Pseudomonadota, Actinomycetota and Bacteroidota phyla have been associated with the degradation of pesticides, pharmaceuticals and hydrocarbons (Alexandrino *et al.* 2020; Fernandes *et al.* 2020; Perdigão *et al.* 2020). CM2C is registered in the World Federation for Culture Collections (WFCC) and in the World Data Centre for Microorganisms (WDCM). In addition, this collection ensures full traceability of the samples in compliance with the Access and Benefit Sharing regulation (Nagoya Protocol).

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[021] From StrainRegistry to StrainInfo: tracking microbial strains through a FAIR deposition system

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In scientific literature and databases, different strain identifiers can be used to describe the same microbial strain, which significantly impedes the findability, reusability and integration of published information, and thus also the reproducibility of research results. In order to ensure the traceability of microbial strains, the StrainInfo database collects and matches all their known strain identifiers. To additionally improve and encourage the referencing and linking of microbial strain data, StrainInfo has introduced the DOI as a persistent identifier for strains.

When researchers isolate and describe large sets of strains from microbiome studies they need persistent identifiers early on to keep track of them throughout the deposition process in culture collections as well as in publications and sequence submissions. The DSMZ has developed a bulk submission procedure for strain collections that greatly simplifies the deposition of large sets of strains and provides StrainInfo DOIs early in the process. This allows the tracking of the deposition statuses of strains and improves the traceability by their DOI throughout literature and databases.

A new deposition management system, called StrainRegistry, will further ease the process in the future. It will allow microbiologists to register strains, that they wish to deposit in a culture collection, with meta- and deposition data. This ensures that FAIR strain data is available from the outset. While the data will initially be kept private, it will be possible to directly submit it to one or more participating culture collections for deposition. Later, it can easily be integrated into StrainInfo and other databases. StrainRegistry will visualize the deposition status of each strain and facilitate communication between the depositors and the responsible culture collection curators and thus assist researchers in managing the deposition of strains.

[023] A novel collection of viable human endometriosis-associated bacteria in HUMB collection: a valuable microbial resource for reproductive health research

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Endometriosis is a chronic inflammatory disease with a complex and largely unknown etiology (Ata et al., 2019). Although DNA-based studies suggest a potential role for the microbes, they cannot confirm the viability of the detected bacteria (Altmäe et al., 2021). Culturomics has recently emerged as a promising approach for identifying viable endometrial microbes (Vanstokstraeten et al., 2023).

The primary objective was to characterize the endometrial microbiota in women with and without untreated endometriosis.

Materials and methods. Study group consisted of 10 patients with untreated endometriosis and 10 controls (male-factor infertility), all sampled during the receptive phase of the cycle. Endometrial biopsies were quantitatively cultured under aerobic, microaerobic and anaerobic conditions. In parallel, next-generation sequencing (NGS) was applied.

Results. More than 2,500 cultured colonies were identified, resulting in 22 genera and 40 species, mostly Gram-positive bacteria. Nine genera were detected by both methods, 13 genera by culturomics only while 44 genera by sequencing only (incl. mycoplasmas). *Lactobacillus crispatus* was the most common species, found in 50% of both groups, followed by *Cutibacterium acnes* (detected in 45%). Nine species were exclusive to endometriosis patients and 15 were unique to controls.

Conclusions. Our findings highlight the utility of culturomics in detecting viable bacterial species associated with endometriosis and demonstrate its complementarity to sequencing-based approaches. The strains have been deposited in the Human Microbiota Biobank (HUMB), providing a valuable resource for studying host–microbe interactions and identifying potential endometriosis-associated biomarkers. All deposited strains are available for future research.

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[026] The SUS-MIRRI.IT project: research, services, and training for sustainable bioscience and bioeconomy by the MIRRI-IT Research Infrastructure

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SUS-MIRRI.IT, funded by the NextGenerationEU programme with a total budget of about € 17,000,000, is a project coordinated by the University of Turin and involves 24 Italian Operative Units. The mission is to strengthen the Italian Microbial Resource Research Infrastructure (MIRRI-IT) by the acquisition of cutting-edge equipment, infrastructural improvements, recruitment of high-qualified staff, to valorize preserved microbial resources with associated (meta)data, and to implement top-level services for academia and industry. The project consists of 6 Work Packages (WPs): WP1 drives management, governance, and sustainability; WP2 is involved in microbial Culture Collections consolidation; WP3 focuses on digital activities for the creation of the single-entry point to the National Database of microbial resources and services; WP4 aims to study the biotechnological valorization of microbiomes; WP5 deals with the implementation of offered services and training courses; WP6 is dedicated to communication and dissemination actions. The strategic impact of SUS-MIRRI.IT is to promote partnerships, to encourage aggregation of skills, structures, and bioresources, promoting the transition towards the green economy, and contributing to the sustainability and safety of the environment.

To date, 50 researchers, PhD students, and technicians have been hired; about 80% of the funds for innovative technologies have been used. The online platform with the catalogue of Italian microbial resources holding 37,000 strains of bacteria, filamentous fungi, yeasts, microalgae and viruses has been launched; 29 advanced Training courses have been delivered; 56 new services ranging from microbiological analyses to user-tailored consultancies have been set up; 55 scientific papers have been published. All project updates are communicated by SUS-MIRRI.IT website and social media. An important recently achieved goal is the creation of Italian National Node of the European consortium MIRRI-ERIC, MIRRI-IT.

[041] LAB from Sardinian PDO cheeses: Vitality of twenty-years old freeze-dried cultures

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The conservation of microbial agrobiodiversity, especially lactic acid bacteria (LAB), is essential for the development of biotechnological applications in the food industry. LAB are crucial in producing fermented foods, contributing to preservation, digestibility, sensory qualities, and improved nutritional value through the formation of essential compounds. Maintaining LAB diversity in cheese is vital for the quality of traditional and PDO products. Freeze-drying, involving suspending cells in cryoprotective agents before freezing and dehydration, is widely used for long-term strain preservation. The success of this method depends on cultivation conditions and the type of cryoprotectant, whose effectiveness can vary among strains. A total of 66 LAB strains isolated from PDO cheeses in the 1990s belonging to *Lactococcus lactis* (N. 39), *Lactiplantibacillus plantarum* (N. 10), *Lacticaseibacillus paracasei* (N. 17) were freeze-dried in 2003. After overnight incubation in appropriate broth media (in M17 at 30°C for *L. lactis*, and MRS at 37°C for *L. plantarum* and *L. paracasei*) cultures were centrifuged and resuspended in a cryoprotectant composed of 100 g/L skim milk, 30g/L lactose, 3g/L yeast extract. Suspensions were frozen at -40°C, freeze-dried, and stored at ambient temperature with wide daily and seasonal fluctuations, for more than twenty years. Upon rehydration and inoculation in MRS broth (for *L. plantarum* and *L. paracasei*) incubated at 37°C, and in M17 broth, with 1% of lactose added after autoclaving, (for *L. lactis*) at 30°C, most strains (51 out of 66) exhibited growth overnight while 14 *L. paracasei* grew after a 48-hour incubation. Only one strain belonging to *L. plantarum* was not viable. Therefore, 98% of strains preserved their viability despite the suboptimal storage conditions (significant fluctuations in room temperature). The cryoprotective agent and freeze-drying conditions used proved effective for the long-term preservation of nearly all different strains tested.

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[049] Biodiversity and plant growth-promoting traits of yeasts from alpine peatlands

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Peatlands are waterlogged areas where the rate of biomass production is greater than the rate of decomposition, thus resulting in the formation of peat, a complex material that consists of partly fossilized plant residues. Peatlands can be found in the arctic, boreal, temperate and tropical zones, and support a unique biodiversity in terms of plants, animals and microorganisms (bacteria, filamentous fungi and yeasts). Fungi are mainly responsible for the degradation of peat, as a result of their ability to degrade lignin. On the opposite, yeasts are involved in the utilization of simple carbon compounds and are generally considered secondary saprotrophs; however, their ecological roles in this ecosystem still need to be clarified (Thormann 2007, Juan-Ovejero *et al.* 2020). In recent years, investigations on yeasts as plant growth promoters (PGP) have significantly increased, stimulating studies on yeasts isolated from this habitat (Jaiboon *et al.* 2017). The aim of this work was to isolate and identify yeasts from peat samples, and to screen them for PGP traits. Peat samples were collected from two alpine peatlands (Northern Italy) at different depths, diluted 1:10 and plated on YM agar supplemented with sodium propionate to inhibit filamentous fungi growth. A total of 12 strains were analyzed. Most of them belonged to taxa previously identified in peatland environments (e.g., *Candida vartiovaarae*). Conversely, *Solicoccozyma aquatica* and *Phaeotremella ovata* were new records for this ecosystem. Furthermore, based on phylogenetic analysis, two isolates (*Halobasidium* sp. and *Sterigmatospora* sp.) could not be assigned to any recognized species. The PGP traits of strains were evaluated by screening for phosphate solubilization, ammonia production, indole-3-acetic acid (IAA) production, 1-aminocyclopropane-1-carboxylate (ACC) deaminase activity, and siderophore production. This study investigated, for the first time, the yeast biodiversity using culturable methods, and PGP traits of selected strains, suggesting their potential application as biofertilizers or regulators in sustainable agriculture.

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[051] Collection of Industrial Microorganisms (KKP) as a source of beneficial strains for sustainable agriculture and biotechnology

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The Collection of Industrial Microorganisms (KKP) is one of Poland's leading microbiological resource centers, housing around 3000 strains of bacteria, yeasts, filamentous fungi, and bacteriophages. More than 98% of these isolates originate from Poland, making the collection a unique national repository of microbial diversity. These strains, classified primarily within risk groups 1 and 2, are provided to science and industry to support applications in agriculture, food production, pharmaceuticals, biotechnology, and environmental protection.

In the field of sustainable agriculture, KKP serves as a platform for identifying and developing beneficial strains. Research on several *Bacillus subtilis* isolates from the collection, including KKP 3905, KKP 3901, and KKP 3894, has shown that optimized cultivation strategies can enhance biomass yields, supporting the cost-effective production of biological plant protection agents. Similarly, multiple *Trichoderma* strains, such as KKP 4166, KKP 4180, and KKP 788, demonstrated antagonistic activity against important phytopathogens including *Fusarium*, *Botrytis*, and *Alternaria*, with some isolates exhibiting broad-spectrum biocontrol potential. Newly isolated lactic acid bacteria, encompassing species such as *Limosilactobacillus reuteri* KKP 4201, *Lactococcus garvieae* KKP 4205, and *Lactobacillus delbrueckii* KKP 3514, were assessed for traits of probiotic potential, such as survival under acidic and bile salt conditions. At the same time, observations of antibiotic resistance in certain isolates highlight the importance of rigorous evaluation before agricultural or biotechnological use.

To bridge research with practice, KKP is supported by semi-technical infrastructure equipped with bioreactors ranging from 50 to 1500 liters. This facility allows scaling of laboratory findings, optimization of microbial stability, and development of industrial processes. By combining preservation of microbial resources with applied research and technological capacity, KKP acts as both a guardian of biodiversity and a driver of innovation.

Altogether, KKP demonstrates how a national collection can become a source of beneficial strains for sustainable agriculture and biotechnology, while also emphasizing the responsibility of ensuring safety and environmental compatibility in their use.

[052] BCCM/ULC: A public culture collection for *ex situ* conservation of cyanobacterial diversity and support of taxonomic and genomic studies

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Cyanobacteria are a phylum of morphologically diverse photosynthetic bacteria. During their long and complex evolutionary history, they successfully colonized a wide range of habitats from polar to temperate and tropical regions. They also show interesting adaptations to extreme habitats (e.g. high salinity, high or low temperature, light intensity, exposure to UV, freezing, desiccation) but their diversity is still insufficiently studied.

BCCM/ULC is a young public collection, currently hosting more than 500 cyanobacterial strains, of which approximately 140 derive from (sub)polar and alpine environments, followed by tropical, subtropical and Mediterranean biotopes as well as strains of Belgian origin. An ISO 9001 certificate covers the public deposition and distribution of strains, as part of a multi-site certification for the BCCM consortium.

All strains are studied by applying a polyphasic approach workflow (i.e., morphological, molecular, and ecological data). Furthermore, the collection includes more than 20 strains that are the reference (or ‘type’) for newly described taxa including *Plectolyngbya*, *Shackletoniella*, *Timaviella*, *Parakomarekiella*, *Petrachloros*, *Leptochromothrix*, *Vermifilum*, *Tigrinifilum*, *Affixifilum*, *Sirenicapillaria*, *Ophiophycus* and *Floridanema*. Recently, a set of taxonomically interesting strains of rock-inhabiting cyanobacteria from Finland as well as strains from freshwater, marine and terrestrial habitats from Florida, USA (Berthold–Laughinghouse Culture Collection) have been deposited into the collection.

Additionally, an integrated approach that combines whole-genome sequencing, metagenomics, phylogenomics and phylogenetic placement is applied to study taxonomically interesting morphotypes and bioactive metabolite-producing strains. Genome sequencing has already been performed for 25 strains, 10 of them being currently analysed within the collection. Recently, the collection has developed a suite of highly reproducible genomic workflows (GEN-ERA; <https://github.com/Lcornet/GENERA>), coded in Nextflow and based on Singularity containers, that meet the requirements of open science and FAIR practices.

[056] From culture to control: BACA toxic strains as a resource for environmental assessment and monitoring

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Harmful algal blooms (HABs), including cyanobacteria harmful blooms (CHABs) pose a threat to public and environmental health. They often result in biodiversity loss and ecosystem disruption. HABs are caused by various microalgae, including diatoms and dinoflagellates, which are known to produce potent toxins such as domoic acid and okadaic acid. Toxic cyanobacteria produce a diverse array of toxins, including microcystins (MC), cylindrospermopsins (CYN), anatoxins (ATX) and saxitoxins (STX). The Bank of Algae and Cyanobacteria of the Azores (BACA) is a unique culture collection with over 800 strains of microalgae and cyanobacteria, isolated from all nine of the Azores' islands. It has played a central role in cyanotoxin monitoring in the Azores, with over ten toxic strains fully characterized by PCR, genomics, ELISA and HRLC-MS/MS. These include known toxin-producing species, such as MC-producers *Microcystis aeruginosa* BACA0148 (Cordeiro et al. 2021) and *Neowestielloopsis persica* BACA0089 (Luz et al. 2024); STX-producer *Aphanizomenon gracile* (BACA0809), ATX-producers *Kamptonema* sp. (BACA0007) and *Tychonema* sp. (BACA0570, BACA0575); CYN-producers *Kamptonema* sp. (BACA0671, BACA0763) and Aphanizomenaceae strains (BACA0025, BACA0031, BACA0109) (Cordeiro et al. 2021). The marine dinoflagellate *Amphidinium carterae* BACA0621 has been recently identified as a novel STX-producing strain. BACA strains have supported mainly PCR and ELISA methodologies, and have directly contributed to the inclusion of new cyanotoxins in the official Azores lake monitoring program. As the risk of HABs increases due to climate change, culture collections such as BACA will become even more critical resources. Ongoing studies aim to characterize more strains, explore their genomes, and improve molecular tools for early detection.

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**[057] Strategies for *ex-situ* conservation of cold soil microbiomes:
monitoring biodiversity and function**

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Cold soils of both polar and non-polar regions harbor unique microbiomes that play essential roles in ecosystem processes and offer significant biotechnological promises. Due to global warming progressively altering these environments, cold soils have become critical hotspots of climate change. They support psychrophilic (cold-adapted) microbial communities that are highly sensitive to increasing temperatures. Therefore, protecting these microbiomes is essential, not only to enhance our ecological understanding but also to unlock new environmental and biotechnological insights.

This study investigated the performance of commonly used preservation methods over a 180-day period, focusing on how these techniques can affect microbial composition, functionality, and overall stability. To identify the most effective conservation strategies, the research involved: (i) profiling community structure and quantifying microbial abundance, (ii) assessing taxonomic diversity across both total and actively transcribing populations, and (iii) evaluating metabolic activity and functional capabilities.

By correlating preservation methods with microbiome resilience and function, the study pinpointed the most robust approach for *ex-situ* conservation. These findings aim to provide standardized microbiome preservation protocols, enhancing the reproducibility of microbial research across diverse settings while supporting long-term biodiversity conservation efforts.

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[060] Culture collections of microorganisms in the Czech Republic – overview of the current situation

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There are currently 15 institutions in the Czech Republic that own collections of microorganisms providing microbial strains. The collections have different sizes and most of these collections are at public research institutions and universities, but some are owned by private companies. Five of them (CAPM, CCF, CCM, CNCTC, VURV) are members of ECCO, and five of them (CCALA, CCDM, CCM, CNCTC, VURV) are members of WFCC. Fourteen collections are registered in WDCM, but more than 70% of them updated their information on the WDCM website more than nine years ago, and three of them are in the process of being removed from the WDCM database. Twelve collections participate in the Czech "National programme for the conservation and utilisation of microbial genetic resources of importance to agriculture" (NPMGR), which was established by the Ministry of Agriculture of the Czech Republic and information about strains maintained with the support of NPMGR is available in the NPMGR online database. Five smaller collections in Biology Centre CAS are not registered with WDCM and do not participate in NPMGR. Nine collections preserve bacteria (and archaea), 14 collections preserve fungi (and fungus-like organisms), eight collections preserve viruses, and four collections preserve algae (and cyanobacteria). Two collections preserve, among other things, biotrophic fungi (rusts, powdery mildews, and biotrophic Oomycota), which are less frequently preserved in culture collections. Preservation at ultra-low temperatures (especially in liquid nitrogen) and / or lyophilization are used in most collections for organisms that can be preserved by these methods. Five years ago, six small collections of cultures were merged into the Culture collection of microorganisms of CARC (VURV), and at the beginning of 2025, the Collection of industrially utilizable microorganisms (RIFIS) of the Food Research Institute in Prague was merged with the VURV collection. The collections of three institutions (Biology Centre CAS, Silva Tarouca research institute for landscape and ornamental gardening, Palacký University in Olomouc) own interesting sets of microbial strains, and it would be sensible and meaningful that these collections be registered with the WDCM. For the past seven years, a one-day seminar focusing on the issue of cultural collections of microorganisms has been held annually in Prague, attended by collection staff from the Czech Republic and Slovakia. This is a continuation of the traditionally rich relations between collections in the Czech Republic and Slovakia.

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[076] Biodiversity of yeasts isolated from vineyards of Qartli region of Georgia

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Georgia is one of the oldest countries of vine and wine culture, where the number of endemic grape varieties is more than 500. Nowadays it is confirmed that Grape (*Vitis vinifera*) wine has been produced in Georgia since BC. 6000-5800 (McGovern *et al.* 2017). Wine fermentation is a complex multispecies process and many bacteria and fungi influence on wine chemical composition and sensory properties (Capece & Romano, 2019). The diversity of Georgian endemic vine varieties may be responsible for the diversity of yeasts present on grape. Therefore, the aim of the presented work was to investigate the biodiversity of yeasts spread on the grape of the vine varieties common for the Qartli region of Georgia.

78 Samples were taken from 29 different endemic vine varieties characteristic for Qartli region of Georgia, especially: *Aladasturi*, *Atenis Saperavi*, *Black Chinuri*, *Black Rkatsiteli*, *Borchalo*, *Budeshuri*, *Buza*, *Cardinali*, *Cheishvili*, *Chinuri*, *Chkapa*, *Danakhariuli*, *Dirbula*, *Goruli Mtsvane*, *Jvari*, *Kapita*, *Qartlis Kharistvala*, *Qartula*, *Kharistvala*, *Kharistvala Basha*, *Kishuri*, *Kvishkhuri*, *Pink Rkatsiteli*, *Sabatone*, *Saperavi* *Budeshuri-like*, *Shavkapito*, *Shavtita*, *Supris Gorula*, *Tavkveri*, as well as from endemic (*Rkatsiteli*, *Saperavi*) and imported vine varieties (*Pinot white*) and hybrid (*Isabella*) cultivated in all of Georgia.

253 yeast isolates were obtained representing 36 different species belonging to 18 genera, identified by MALDI-TOF MS and qPCR analysis. *Hanseniaspora uvarum* (28.4%), *Metschnikowia pulcherrima* (16.6%), and *Starmerella bacillaris* (9.9%) were the dominant yeasts found on grapes; The highest species diversity was found for the genus *Pichia*: *P. terricola* (4.3%), *P. kudriavzevii* (3.6%), *P. kluyveri* (1.6%), *P. membranifaciens* (1.6%), *P. sporocuriosa* (1.2%), *P. californica* (0.8%), *P. garciniae* (0.4%), *P. manshurica* (0.4%), *P. occidentalis* (0.4%), but some of these species are represented by only one strain. *Saccharomyces cerevisiae* (5.1%) was represented by 13 isolates. Most of the other species were rendered by 1-3 isolates. The yeast collection is maintained in 30% glycerol at -20 °C and in YPD broth at +4 °C.

The observed biodiversity of *Saccharomyces* and non-*Saccharomyces* yeasts could explain regional differences of wine features and can be applied to promote obtaining wines of local origin with high quality and unique degustation indices.

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[077] Genome mining of the Fraunhofer strain collection

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In 2020, Fraunhofer IME took over one of the world's largest microbial strain collections (over 110.000 strains, 79% bacteria, 21% fungi) from Sanofi (Fox 2014). This collection is the legacy of decades of committed industrial efforts towards collecting, cultivating, and preserving microbes following the mission to use their evolved features as starting points for product developments. This unique FHG collection is well-curated and consists of various functional subcollections. Besides the soil collection which has historically been used to explore novel pharmaceutical drugs we have a food collection consisting of qualified presumption of safety (QPS) listed strains and edible mushrooms (basidiomycetes), a biocontrol and plant growth promoting collection (e.g. entomopathogenic fungi, *Pseudomonas* spp., *Arthrobacter* sp.), a marine collection consisting of microbes isolated from marine algae, invertebrates, coral reefs and marine sediments, and an arthropod collection consisting of gut-related microorganism. In addition, we also explore the under-investigated bacterial space and provide access to very rare phylogenetic branches, such as *Acidobacteria* (Oberpaul *et al.* 2020).

Despite its potential, managing the collection's biodiversity is complex and requires tailored client solutions. Nowadays, to meet industry standards, clients often request genomic data - digital sequence information (DSI) and compliance with access and benefit sharing (ABS) regulations. Although less than 1% of the FHG collection is genome sequenced, the collection includes several hundred genomes and an extensive amount of data (e.g., metabolomics) available for the discovery of novel natural products relevant to the pharmaceutical, veterinary, agricultural, and food industries. Our excellence in applying OMICS data for the discovery of novel natural products is exemplified by Brinkmann *et al.* (2022).

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[085] Advancing yeast identification using high-throughput DNA barcode data from a curated culture collection

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Accurate yeast identification is essential in fields ranging from microbiology and biotechnology to food science and medicine. While DNA barcoding has become the standard for identifying cultured strains, environmental DNA (eDNA) metabarcoding has revolutionized microbial community profiling, providing deeper insights into yeast populations across diverse ecosystems.

A major challenge in DNA (meta)barcoding remains the limited availability of high-quality reference sequences, which are critical for accurate species identification and comprehensive taxonomic profiling of both environmental and clinical samples.

To address this gap, the Westerdijk Fungal Biodiversity Institute (WI) launched a DNA barcoding initiative in 2006 to generate high-quality, often type-derived ITS and LSU barcodes for all ~100,000 strains preserved in the CBS culture collection. Building on the yeast barcode dataset released in 2016, we now present an expanded set of 2,856 ITS and 3,815 LSU sequences, representing 911 and 1,137 yeast species, respectively. Notably, 27–29% of these sequences are derived from ex-type cultures.

Using both newly generated and previously published barcodes, we assess the taxonomic resolution of commonly used yeast metabarcoding markers (ITS, ITS1, ITS2, and LSU) and propose marker-specific similarity cut-offs for different yeast clades. These results provide actionable guidance for marker selection and improve the interpretation of metabarcoding data. We further demonstrate the impact of well-curated reference databases with up-to-date taxonomy by reanalyzing Human Microbiome Project data, revealing how diet and environment shape the gut mycobiota.

[086] How *Aspergillus fumigatus* studies can benefit from MALDIBANK project

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The *Aspergillus fumigatus* species complex poses a major threat to human and agricultural health, as the primary cause of pulmonary aspergillosis, a potentially fatal infection, which can affect both immunocompetent and immunocompromised individuals. A growing concern in managing this infection is the rise of azole resistance, largely due to the extensive use of azole-based fungicides in environmental and agricultural contexts. Current methods to distinguish azole-resistant from susceptible strains rely on genotypic analyses (e.g., *cyp51A* mutations or WGS) and phenotypic antifungal susceptibility testing. While effective, these approaches are often time-consuming and not easily implemented in routine clinical or environmental surveillance. The MALDIBANK project proposes a faster alternative using MALDI-TOF MS, combined with advanced spectral analysis and AI tools, to differentiate resistant from susceptible strains. In addition to the conventional positive ion mode (used for protein profiling), the project explores negative ion mode to detect lipidomic features potentially linked to resistance. To develop and test these methods, 23 *A. fumigatus* Brazilian strains originated from the city of São Paulo (urban) and the city of Ribeirão Preto (rural), previously characterised for azole resistance, were selected. Spectral data in positive ion mode have been collected, and the IR Biotyper (based on FTIR spectroscopy) was evaluated as a complementary tool. Although IR Biotyper does not detect resistance genes directly, it may identify biochemical changes. However, due to the small dataset and its reliance on machine learning, the method showed limited discriminatory power in this case. With continued development of MALDI-TOF MS databases, refined analysis techniques, and AI integration, the MALDIBANK project will enhance the rapid detection of azole-resistant *A. fumigatus* strains. This approach could complement existing molecular diagnostics and improve surveillance in clinical and environmental settings.

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[087] Bioprospection of psychrotolerant bacteria for regenerative agriculture

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Regenerative agriculture is a modern farming approach that blends sustainable innovation with tradition. It focuses on restoring and improving the health of the soil, ecosystem, and overall farm environment by implementing innovative technologies. Instead of relying heavily on chemical inputs, regenerative agriculture emphasises practices that promote soil health, biodiversity, and resilience. Some common regenerative practices include cover cropping, crop rotation, reduced tillage, integrating livestock into farming systems, and biocomposting. One of the advantageous approaches in regenerative agriculture could be the introduction of cold-active bacteria and their enzymes which efficiently accelerate (bio)chemical processes of choice at comparatively low temperatures, e.g. enhance biocomposting of postharvest or remaining plant residues on fields. These psychrotolerant bacteria and their enzymes function at lower temperatures, making them valuable for agricultural applications in diverse climates. Amongst cold-active (but also generally) enzymes, those processing polysaccharides, i.e. cellulases, pectinases, amylases, and glycosidases, play a crucial role in regenerative agriculture by facilitating the breakdown of complex plant organic macromolecules, improving nutrient availability, and promoting overall soil health. In the RegAgro project, we utilise the microbiological resources of Arctic and Antarctic soils to identify novel psychrotolerant bacteria and novel cold-active enzymes that may be exploited in regenerative agriculture.

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[091] Tolerance and degradation of plant phytohormones by soil and phyllosphere yeasts

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Phytohormones are the most important substances produced by plants, being involved in plant reproduction and growth, development of organs, and tolerance to biotic and abiotic stress. However, some members of the microbiota naturally inhabiting plants have been found to produce phytohormones and, in addition, degrade them in excess (Nascimento *et al.* 2019). Various studies have shown that some soil and phyllosphere yeasts are capable of producing plant phytohormones, such as IAA and ACC (Carvajal *et al.* 2024). However, little is known about the ability of yeasts to tolerate and/or degrade phytohormones.

In total, 13 ascomycetous and 20 basidiomycetous yeast species were tested for their tolerance or utilization of plant phytohormones. All yeast species grew at the presence of 100 mM gamma-butyric acid (10 g/L) and 25 mM gibberellic acid (8.7 mg/L), respectively. In particular, species commonly found in soil, such as *Galactomyces* spp., *Barnettozyma californica*, *Debaryomyces* spp. and *Trichosporon asahii*, as well as red yeast species of the genera *Sporobolomyces* and *Rhodotorula*, widely inhabiting phyllosphere, showed the highest tolerance to indole acetic acid (IAA) (10 mM = 1.75 mg/L). However, none of the tested species were able to utilize the aforementioned phytohormones as a carbon source. The *Rhodotorula* species together with *Mycosarcoma maydis*, *Heterocephalacria lusitanica* and *Aureobasidium* spp. were able to degrade salicylic acid in a concentration of 4 mM (0.56 g/L). Our results also showed that the yeast species tested were able to tolerate or degrade phytohormones only in the presence of glucose which is the dominant sugar on the leaf surface and in the soil environment (Mercier & Lindow 2000; Gunina & Kuzyakov 2015).

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[093] A microbial repository of extremophiles: Unlocking novel metabolic potential for environmental and biotechnological research

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Microorganisms, microbiomes, and their products (e.g., enzymes, metabolites, antibiotics) are key players in the functioning of Earth ecosystems (Moretti *et al* 2024). Microbial culture collections play a crucial role in preserving bacterial biodiversity, using microbial resources and fostering the sustainable development of novel biotechnologies (Daniel & Prasad 2010). The collections serve as invaluable repositories of genetic and functional diversity, provide biological material for high quality research as reference strain or quality control (Smith *et al* 2003), addressing key research priorities of our era ranging from biotechnology to environmental science, fighting the biodiversity loss due to global changes. The advent of modern molecular technologies, and the advances in fieldwork, has increased our potential to discover new species and isolate little-known biodiversity. This contribution reports the isolation of bacterial banks sourced from extreme environments (including deep-sea marine habitats, hydrothermal vents, polar regions), with the aim of establishing a curated collection of strains. The work presents standardized protocols for bacterial isolation, cultivation, and preservation to ensure the viability and authenticity of the strains. The bacterial bank is divided in special panels including: thermophiles, cold-adapted and piezophilic microbes, to explore novel metabolic pathways and develop biotechnological applications suited to extreme conditions; luminous bacteria, of particular interest for their applications in biosensing and bioimaging; bacterial strains resistant to pollutants (i.e. heavy metals, pesticides, hydrocarbons), crucial for advancing bioremediation strategies; antibiotic-resistant bacteria, essential for monitoring the spread of resistance, understanding its mechanisms, and developing new strategies to combat antimicrobial threats. Overall, the collection not only safeguards microbial heritage but also provides a strategic resource for biotechnological innovation and sustainable scientific development. Further efforts will be spent to attract the necessary resources and funding to establish a formally recognized microbial strain collection.

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[097] Towards a national framework for Microbial Resource Centres in France

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Microbial Resource Centres (mBRCs) or microbial biobanks play a central role in advancing research and innovation but remain insufficiently acknowledged within the scientific landscape. The European initiative MIRRI has laid the foundation for greater visibility, yet this recognition must also be consolidated at the national level, where their operational activities take place. National funding of mBRCs is therefore essential to enhance their standing, ensure long-term sustainability, and maximise their scientific and societal impact.

In France, a first step forward was the integration of mBRCs into the national infrastructure RARE (Resources for research in Biology, Agronomy and Environment) and its microbial pillar⁵, which positioned the network on the national roadmap of research infrastructures. The 10 French mBRCs currently involved cover a wide range of fields, including human and veterinary health, plant health, food fermentation and biotechnology. Together, they conserve more than 62,000 pure strains of bacteria, cyanobacteria, yeasts, filamentous fungi and microbiota of human, animal, plant, environmental, and food origins. The network brings together around 60 staff members across 8 sites in France. All mBRCs operate under a quality management system and are ISO 9001:2015 certified for the acquisition, preservation, characterisation, and distribution of microbial resources. They also implement Data Management Plans (DMPs) and comply with FAIR principles as well as GDPR requirements.

A key challenge is to bring together mBRCs belonging to different institutions, each with its own strategy and objectives. To achieve this, the network has been established as a contractual vehicle under the status of a Scientific Interest Group (Groupement d'Intérêt Scientifique, GIS), providing flexible yet robust governance. The GIS has no legal status but serves as a contractual framework between three founding institutions — INRAE, Institut Pasteur, and Université de Bretagne Occidentale — which assume binding legal commitments. The objective of this national organisation is to strengthen cooperation between mBRCs, while ensuring alignment between the national MIRRI node and the microbial pillar of RARE. The GIS MIRRI-France is designed to remain open to all public collections meeting service quality requirements and wishing to join.

This collaborative approach aims to provide mBRCs with the means to act in a coordinated manner, to better communicate the value of their microbial resources and to raise funds to enhance their characterisation and to develop innovative services — ultimately fostering scientific excellence, supporting innovation, and maximising the benefits of microbial resources for research and society.

[098] Industrial Biotechnology Algal Bank (IBAB): The biobank for industrial production, adding a new feature for the development of new products

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The microalgae production industry has experienced significant growth, driven by its potential to address global food and environmental challenges. Central to this expansion is the role of robust culture collections. On this view, the Industrial Biotechnology Algal Bank (IBAB) by Greencolab was created to ensure industrial partners and associates have rapid access to production-ready strains, reducing downtime from months to days. IBAB provides a comprehensive suite of services, including bioprospection, strain isolation and optimisation, taxonomic classification, and biochemical analysis, supported by facilities capable of scaling from 1L to 100L bioreactors. This new approach to culture collection presents a fresh perspective on biobanks, involving the maintenance of a small number of strains in various growth stages, ranging from cryopreservation to solid media, stagnant cultures in low volumes, and bubbling columns with cultures in the exponential growth phase. However, a significant threat to industrial-scale production is culture collapse caused by Harmful Biological Contaminants (HBCs), which can destroy cultures within days and lead to significant economic losses. Understanding the biology of these contaminants is crucial for developing effective mitigation strategies, yet challenges have hindered their study in maintaining and preserving them over the long term in a laboratory setting. To address this critical gap, the Contaminants Working Group from Greencolab is collaborating with the IBAB on the development of a dedicated HBC biobank by creating tailored cryopreservation protocols. This initiative focuses on optimising methods for the long-term storage of contaminants using different cryoprotectants. The goal is to develop standardised, species-specific protocols that ensure the viability and purity of HBCs without the need for continuous subculturing. This enters on the subject of the ParAqua COST ACTION by studying and tackling the conservation and research on zoospore parasites that can be contaminants in microalgae production. By establishing a cryopreserved HBC biobank, IBAB will provide an invaluable resource for the research community and industry partners. This will facilitate the molecular and biological characterisation of contaminants, accelerating the development of early detection methods and effective mitigation strategies. This strategic expansion of our services will not only enhance the robustness of industrial microalgae production but also solidify IBAB's role as a key facilitator for innovation and sustainability in the blue biotechnology sector.

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[099] *Bacillus licheniformis*: Challenges in food safety and biocontrol through bacteriophages

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Bacillus licheniformis is a spore-forming Gram-positive bacterium commonly found in soil, water, and food processing environments. It is widely exploited in biotechnology for the production of enzymes, antibiotics, and biosurfactants, but at the same time it is known as a frequent contaminant in food and beverage industries, where its ability to survive pasteurization, form biofilms, and produce spoilage metabolites makes it a significant concern for food safety and quality. The dual nature of *B. licheniformis*—as both a useful industrial organism and a problematic contaminant—creates a need for effective control strategies that are sustainable and targeted. Conventional chemical or thermal treatments often fail to fully eliminate spores and may negatively affect product quality, which highlights the potential of bacteriophages as a natural and highly specific biocontrol solution.

In this study, virulent bacteriophages infecting *B. licheniformis* were isolated and systematically characterized in terms of their biological properties and genomic features. Host range assays confirmed that the phages could effectively lyse multiple strains of *B. licheniformis*, while infection dynamics identified an optimal multiplicity of infection (MOI) that achieved efficient growth inhibition, including in juice-based food models. Whole-genome sequencing revealed double-stranded DNA genomes devoid of lysogeny-associated genes or virulence factors, confirming their strictly lytic nature and safety for application.

These results demonstrate that *B. licheniformis*-targeting phages are promising candidates for food biocontrol, offering a precise and eco-friendly tool to reduce contamination risks. Beyond their applied value, their preservation in microbial collections provides an important resource for future research, standardization, and biotechnology. Integrating such phages into biological resource centers contributes to global efforts in food safety, sustainable microbial management, and aligns with One Health strategies by reducing reliance on chemical interventions.

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[100] Providing Safe Storage and Controlled Access – The DSMZ as Patent Depositary and “Safe” for Microorganisms

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Biological resource centers are instrumental for the future advancement of science, public health and bioeconomy. Therefore, the high-quality long-term storage of the valuable living materials is essential. To avoid the loss of material via staff shortage, supply problems and disasters, spatially separated back-up solutions are strongly recommended and often mandatory for biobanks. Therefore, the DSMZ offers the safe deposit as a special service for the long-term preservation and safe storage of biological material, which is not included in the DSMZ catalogue or passed on to third parties without a written request by the depositor. Furthermore, the DSMZ has served as a depositary of microorganisms for patent purposes since 1974. Since 1981, the DSMZ has been recognised as an International Depositary Authority (IDA) under the Budapest Treaty. According to the Budapest Treaty, all biological material must be tested for viability and purity. Successfully deposited cultures are kept for at least 30 years under the terms of the Budapest Treaty. To enable that the biological material is stored in a genetically unchanged way, cryostorage in the vapor or liquid nitrogen (LN) phase at temperatures below -150 °C is used. Additionally, microorganisms are maintained as dried lyophilisates, if possible. As a quality measure, LN tanks are cleaned at certain intervals. To evaluate the potential risk of microbial cross-contaminations during cryostorage, LN tanks in different biobank facilities have been systematically examined for the presence of bacteria, fungi, plant, and human cells at different phases of LN storage in the framework of the GDK (Association of German Cryobanks) “Hygiene-Project” (Bajerski *et al.*, 2020). In identifying potential contaminants, their sources, and evaluating their potential harms, it was found that the samples themselves, the LN, the human microbiome, and the environment are all potential routes of contamination (Bajerski *et al.*, 2021). The freshly produced LN is usually not the source of contamination.

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[101] Bringing the CoSMi collection to the next level: cryopreservation and molecular profiling of marine microalgae

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CoSMi (Collection of Sea Microorganisms) is a collection of marine microalgae, unicellular photosynthetic organisms that are characterised by great diversity. They play a crucial role in the marine environment due to their oxygen production and carbon dioxide removal and are essential for life in the oceans as the basis of the marine food web. In addition, they represent a strategic biological resource for scientific research and industrial applications in biotechnology, due to their extraordinary metabolic versatility, rapid growth and ability to produce compounds with high added value. CoSMi maintains a great variety of marine algal strains that can be utilised in different fields, from the production of biopharmaceuticals, food supplements and natural cosmetics to the development of biofuels and environmental remediation solutions. To strengthen this heritage and support its use by scientists and industry, it is vital to maintain and preserve the collection diversity, to provide a complete and integrated characterisation on each strain, and to improve the accessibility of the available information for the users. As part of the Italian PNRR project SUS-MIRRI.IT, promoted by JRU MIRRI.IT, the CoSMi collection has committed to strengthening the strategies for the long-term conservation of its strains through cryopreservation. This approach allows to maintain the genetic and physiological integrity of the strains over time, reducing the risk of mutations due to repeated subcultures and ensuring a stable and reliable biological resource for research and industry. At the same time, the ongoing genetic characterization of the strains will provide users of the collection with accurate and up-to-date documentation. These improvements will raise the scientific standards of the collection and increase the reliability, traceability and added value of the strains, contributing to make CoSMi an international reference for marine microalgae.

[103] Advancing microbial diversity characterization for ecological innovation: bifidobacteria from pre-weaning calves

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The gut microbiota of neonatal ruminants plays a pivotal role in animal health, productivity, and environmental sustainability (Amin & Seifert 2021). Among early colonizers, *Bifidobacterium* species represent promising candidates for the development of eco-friendly probiotic strategies in livestock management. In this study, approximately 150 bifidobacterial strains were isolated from ten pre-weaning dairy calves. Species identification was performed using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS, Liu *et al.* 2023) and confirmed through whole-genome sequencing and repetitive sequence-based PCR (rep-PCR) fingerprinting (Masco *et al.* 2003). The isolates were mainly identified as *Bifidobacterium longum* (n=127), followed by *Bifidobacterium bifidum* (n=20), *Bifidobacterium animalis* (n=2), *Bifidobacterium pseudocatenulatum* (n=1), and *Bifidobacterium pseudolongum* (n=1). The combined use of phenotypic and genotypic methods allowed for accurate identification of *Bifidobacterium* species. These results contribute to our better understanding of the gut microbiota in young ruminants and may support future strategies promoting sustainable livestock farming through the use of beneficial microbes.

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[106] Phages at the DSMZ – from fundamental research to applicative projects

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The DSMZ Phage Bank, the largest phage bank service registered in the WFCC Directory, has been preserving bacteriophages since 1986. Initially focused on phages for biotechnological applications, the collection has expanded significantly to include phages of therapeutic relevance, particularly following rising global concern over multidrug-resistant (MDR) bacteria and the WHO's survey on antimicrobial resistance. As of January 2025, the bank contains approximately 1,500 phages, covering more than 150 bacterial species, with a particular emphasis on ESKAPE pathogens. The DSMZ Phage Bank continues to grow through in-house isolation efforts and external deposits from laboratories worldwide wishing to secure and, if desired, share their phage resources.

The DSMZ Phage Bank contributes directly to major translational and therapeutic phage projects, including:

- Phage4Cure (Federal Ministry of Education and Research BMBF), Germany's first clinical trial of a pathogen-targeted phage medicinal product (PTMP) for inhalable phage therapy targeting *Pseudomonas aeruginosa* lung infections.
- EVREA-Phage (German Center for Infection research DZIF), development of a phage cocktail to decolonize vancomycin-resistant *Enterococcus faecium* (VRE) in immunocompromised patients.
- Further projects, studies on predicting *Pseudomonas aeruginosa* phage–host interactions and phage–antibiotic combinations for *Stenotrophomonas maltophilia*.

Beyond applications, the DSMZ Phage Bank also supports fundamental phage biology, backed by the DFG-funded SPP2330 Z project. Key activities include:

- Phage isolation, deposition, and characterization.
- Integration of consortium phages and hosts into the DSMZ Phage Bank.
- Development of PhageDive, a comprehensive and searchable database for prokaryotic viruses, consolidating data from diverse sources.
- Research on phage genomics, diversity, host–phage interactions, and taxonomy, including classification efforts within the ICTV (e.g., the *Schitoviridae* family).

Together with the DSMZ extensive bacterial strain collection, the Phage Bank provides critical infrastructure for both translational medicine and basic phage biology. Enabling safeguarding phages of medical importance, facilitating collaborative international projects and driving innovation in combating antimicrobial resistance. The DSMZ Phage Bank thus represents one of the world's most comprehensive resources for phage research, advancing both clinical applications and fundamental discoveries.

[107] Native soilborne fungi to improve vineyard production: the experience of the RAISE project

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In recent years, agricultural enterprises have increasingly adopted intensive production practices to remain competitive, often overlooking the environmental sustainability. In response, the RAISE project (funded by the Italian Ministry of University and Research) aims to develop advanced, eco-compatible technologies for precision agriculture, with a focus on the Ligurian region in Northwest Italy.

As part of SPOKE 3 - Project 5 (<https://www.raiseliguria.it/en/spoke-3-raise/>), the CoLD-UNIGE microbial collection has formulated a tailored microbial biostimulant for a Ligurian vineyard. The initial phase was the isolation and characterization of fungal taxa from the local agroecosystem. A total of 29 strains from 13 genera with several showing promising plant growth-promoting activity, have been preserved in the CoLD-UNIGE collection.

For field phase, three fungal strains (*Penicillium pinophilum*, *P. citrinum*, *Trichoderma harzianum*) and two bacterial strains (genus *Agrobacterium*) were selected. The biostimulant was applied also via terrestrial drones, and an IoT-based sensor network was installed to monitor environmental conditions and support microbial viability.

Preliminary data from July 2025 have indicated successful colonization and persistence of the inoculated strains under challenging climatic conditions. Ongoing monitoring will guide optimization strategies, contributing to resilient and sustainable viticultural practices.

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[113] Towards a comprehensive Decision Support System (DSS) for strain discovery

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The field of biotechnology is experiencing exponential growth in data, creating a significant bottleneck for researchers. Structured databases like GenBank are expanding at unprecedented rates, with over 25 trillion bases and 3.7 billion records (NCBI 2025). Simultaneously, unstructured scientific literature on platforms such as PubMed is accumulating at approximately two publications per minute (Chen et al. 2024). The effective discovery of microbial strains for bioindustry applications now depends on integrating and querying these vast and heterogeneous data sources.

We are developing a comprehensive Decision Support System (DSS) designed to democratize data access for researchers. Our system leverages modern Large Language Models (LLMs) to create a seamless, natural language interface for complex biological data queries. The core of the DSS is an NLP-driven engine, built upon transformer architecture, which translates user prompts written in plain English into optimized, machine-readable queries, such as SPARQL. This enables real-time interrogation of an integrated knowledge graph that unifies information from strain databases (e.g., BacDive) with insights extracted from scientific literature (Reimer et al. 2025).

A functional prototype has been developed to validate this approach. The system successfully translates complex queries, such as "Give me all strains of the genus *Bacillus* that were isolated from soil in Germany," into correct SPARQL syntax, demonstrating the feasibility of using LLMs as an intuitive front-end for biological data exploration (Liu et al. 2025). Future work focuses on enhancing system capabilities by developing a custom, domain-specific model. By employing advanced techniques such as fine-tuning on curated datasets, we aim to improve query accuracy, ensure data privacy, and create a cost-effective alternative to general-purpose APIs. This will ultimately provide the bioindustry with a powerful tool to accelerate strain discovery and streamline research workflows.

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[114] Antagonistic activity of *Streptomyces* spp. against plant fungal pathogens

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Temporal broadleaf forests are essential for ecosystems, with trees like European ash and oak being associated with biodiversity due to their role in nutrient cycling, impact on soil health, as well as association with higher species richness due to the habitat they provide. Changes in climate and increased anthropogenic activity have a direct effect on forest health and survival, leading to more disturbances and broader spread of pathogens.

Ash dieback, caused by the pathogenic fungus *Hymenoscyphus fraxineus* poses a serious threat to broadleaf tree stands in Europe. Numerous studies have been conducted on the impact, mechanisms and possible antagonists of the disease. However, there are no biological control agents that could successfully eliminate or restrict the spread of the disease.

Using strains of underexplored *Streptomyces* spp., we performed a series of in-vitro experiments to explore the antimicrobial efficiency and antagonistic mechanisms, including experiments with other plant fungal pathogens – *Botrytis cinerea*, *Mycosphaerella* sp., *Fusarium oxysporum* and *F. graminearum*. The most effective bacterial strains belonged almost exclusively to the genus *Streptomyces*, with *Streptomyces* sp. MSCL 350, MSCL 1739 and MSCL 1720 ranking among the top performers based on mean inhibition across all fungi. These findings support the hypothesis that selected *Streptomyces* spp. possess broad-spectrum antifungal activity and could serve as promising candidates for the development of biological control agents against *H. fraxineus* and other plant pathogens.