15TH INTERNATIONAL CONFERENCE ON CULTURE COLLECTIONS

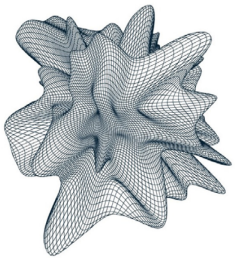
Exploiting Microbial Resources to Support Social Wellbeing

ICCC 15

Abstracts Book

Edited by:

Nelson Lima
Carla Santos
Célia Soares
Manuel G. Silva
Ana João Ferreira
Ricardo Meirelles Cruz



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12-16 JUNE **2023**

University of Minho, Campus Gualtar

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MUM MICOTECA DA UNIVERSIDADE DO MINHO

WFCC

15th International Conference on Culture Collections

Exploiting Microbial Resources to Support Social Wellbeing

Braga | University of Minho | Campus Gualtar
12 to 16 June 2023

Abstracts Book ICCC 15

Title:	15th International Conference on Culture Collections: Exploiting Microbial Resources to Support Social Wellbeing
Editors:	Lima N., Santos C., Soares C., Silva M. G., Ferreira A. J., Cruz R. M.
Cover, Graphic design & Text processing:	Manuel G. Silva, MUM - Micoteca da Universidade do Minho
Edition published by:	MUM - Micoteca da Universidade do Minho https://www.micoteca.deb.uminho.pt/
1st Edition:	November 2023
Place & Country:	Braga, Portugal
Digital publication:	PDF
ISBN:	978-972-97916-6-6

Scientific Program and Conference Committees

The Scientific Program and different Conference Committees are available on the ICCC15 webpage: www.iccc15.com.
During the meeting, a mobile app was also made available to the participants which comprised a Welcome Desk, Program, Abstracts, Exhibitors, Networking, Personal Area, Visit Braga, Digital Conference Bag, and Notifications.

Acknowledgments

The 15th International Conference on Culture Collections was organized by the MUM - Micoteca da Universidade do Minho, in collaboration with the Chilean Universidad de La Frontera (UFRO), the IS_MIRRI21 EU Horizon 2020 project (https://ismirri21.mirri.org/, grant agreement nº 871129), MIRRI-ERIC (https://www.mirri.org/), the Portuguese microBiological Resource Centre Network / MIRRI-PT Node (Pt-mBRCN, https://mbrcn.pt/), the Portuguese Society of Microbiology (SPM, https://spmicrobiologia.wordpress.com/) and the Portuguese Society of Biotechnology (SPBT, https://www.spbt.pt/), on behalf of the World Federation for Culture Collections (WFCC, https://www.wfcc.info/), with support of the following institutions, projects and enterprises, which are gratefully acknowledge.
The Local Organizing Committee (LOC) wishes also to acknowledge the "Leading Company" that with Micoteca da Universidade do Minho took care of the management and performance of the meeting with high professionalism and commitment.

Official Sponsors

The Local Organizing Committee (LOC) acknowledges the generous support of the following sponsors:

Abridge Scientific Program

DAY 1 MONDAY 12/06	
08:30 – 09:30	**Registration**
09:30 – 10:30	**Welcoming and Opening Ceremony**
10:30 – 11:00	Coffee Break Poster Session
11:00 – 12:30	**Opening Lectures** OL1.: Future needs for microbial diagnostics: tools and resources - Ellen Jo Baron, Stanford University (Retired), USA OL2.: MIRRI: The Strategic Research and Innovation Agenda for 2021-2030 - Rosa Aznar, CECT, Valencia University, ES
12:30 – 14:00	Lunch Poster Session
14:00 – 15:30	**Session 1: Circular Bioeconomy** S1.1.: Circular economy challenges in bioresources valorization – the role of microorganisms - Cristina M.R. Rocha, CEB/LABBELS, UMinho, PT S1.2.: Culture collections for bioprospecting in sustainability and innovation - Kevin McCluskey, Kansas State University (Retired), USA S1.3.: Cyanobacteria and microalgae culture collections and circular economy - Vitor Vasconcelos, CIIMAR-UP, PT S1.4.: UCCCB - Centre for microbial conservation and the development of bio-based solutions - Paula V. Morais, IAVT, PT
15:30 – 16:00	Coffee Break Poster Session
16:00 – 17:30	**Session 2: Legal & Policy Issues for Culture Collections** S2.1.: Restrictions placed on the distribution and utilization of biological material by Access and Benefit Sharing legislations - Manuela da Silva, FIOCRUZ, BR S2.2.: The COP15 DSI decision: what do scientists need to do now? - Amber Scholz, Leibniz-Institut DSMZ, DE

S2.3.: Pathogens infecting ABS implementation - Philippe Desmeth, BELSPO-Belgian Science Policy Office, BE

S2.4.: Development of the Budapest System: recent improvements and challenges ahead - Isabelle Chauvet, Patents and Treaties Law Section, WIPO, CH

DAY 2 TUESDAY 13/06	
08:30 – 10:30	**Session 3: Microbiomes** S3.1.: Bacterial diversity and culturable actinomycetes antimicrobial activity in tidal flats of southern China - Man Cai, IMCAS, CN S3.2.: Genome-resolved metagenomics provides novel insights into chitin turnover, metabolic specialization, and niche partitioning in the octocoral microbiome - Tina Keller-Costa, IBB-IST, PT S3.3.: A Treasure trove for future discoveries: the female urogenital bacterial collection (UroGenBC) - Teresa G. Ribeiro, i4HB, PT S3.4.: Where, when, and how environmental and food microbiomes meet each other - Luigi Chessa, Agris Sardegna, IT S3.5.: Unravelling the conundrum – preserving the microbiome for Phytobiomes research - Matthew Ryan, CABI, UK & The International Alliance for Phytobiomes Research
10:30 – 11:00	Coffee Break & Group Photo Poster Session
11:00 – 12:30	**Invited Lectures** IL1.: WFCC for wellbeing of the mankind and advancement of science and technology - Ipek Kurtboke, President of the WFCC, AU IL2.: Effects of long-term phosphorus fertilization on bacterial community structure and its potential gene function related to phosphorus mineralization in pastures, María de la Luz Mora, UFRO, CL
12:30 – 14:00	Lunch Poster Session + 13h30: remote presentations at A1 Auditorium
14:00 – 15:30	**Session 4: Overview on Microbial Preservation Techniques** S4.1.: Maintenance of microbial consortia from salami: a case study on the impact of cryopreservation - Giancarlo Perrone, CNR-ISPA, IT

S4.2.: CICC operation: discovery and application of industrial microorganisms resource - Yao Su, CICC, CN

S4.3.: Preserving viability and stabilizing properties of *Rhodococcus* biodegraders of pharma pollutants - Anastasiia Krivoruchko, IEGM, RU

S4.4.: Ensuring conservation of the diversity of *Leishmania* parasites available for scientific and technological development - Elisa Cupolillo, FIOCRUZ, BR

15:30 – 16:00 Coffee Break
Poster Session

16:00 – 17:30 **Session 5: Microbial Systematics**

S5.1.: Genotype-phenotype correlations with the Geodermatophilaceae - Maria del Carmen Montero-Calasanz, IFAPA/Las Torres, ES

S5.2.: Genome sequence data: the key driver in shaping prokaryotic systematics - Praveen Rahi, Institut Pasteur, FR

S5.3.: Collections, Cultures and the names of Fungi - Andrey Yurkov, DSMZ, DE

S5.4.: Phylogenomics of the genus *Alcaligenes*: proposal of *Alloalcaligenes* gen. nov. - Robert E. Durán, Lab Microbiol. Molecular y Biotec., CL

17:30 – 19:00 **Round Table: Cutting Edge Technologies In Microbial Culture Collection Services**

RT1.: Leverage and revolutionize the way you work with the newest Absolute Q Digital PCR System - Rui Batista, ThermoFisher Scientific

RT2.: MALDI Biotyper® - Recent Advances… - Rui Rocha, Portugal Bruker Director, PT

RT3.: Miniaturization of DNA analysis, a game changer for food safety and quality - Marta Prado, INL, PT

RT4.: The Italian network of culture collections: new cutting-edge technologies, new fields of research, new challenges to face - Cristina Giovanna Varese, JRU MIRRI-IT, IT

RT5.: Implementation of cutting-edge technologies for the benefit of culture collections - Carla Santos, MUM, CEB/LABBELS, UMinho, PT

DAY 3 WEDNESDAY 14/06		
08:30 – 10:30	**Session 6: Bioinformatics & Data Management in Culture Collections** S6.1.: DSMZ digital diversity: building a global biodata infrastructure - Lorenz Reimer, DSMZ, DE S6.2.: MSI-2 / An online identification tool for MALDI TOF Mass Spectra - Anne-Cécile Normand, Assistance Publique - Hôpitaux de Paris, FR S6.3.: The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics - Luc Cornet, BCCM/ULiège, BE S6.4.: The Westerdijk fungal data resources for fungal identification – Gerard Verkley, Westerdijk Institute, NL S6.5.: Culture collections data management, Vincent Robert, BioAware, BE S6.6.: WDCM serves as an information infrastructure for the exploration and utilization of microbial strains preserved worldwide - Linhuan Wu, WDCM, IMCAS, CN	
10:30 – 11:00	Coffee Break	
11:00 – 12:30	**Invited Lectures** IL3.: Fungal culture collections in 21st century, Wieland Meyer - Incoming Director of Westerdijk Institute, NL IL4.: The importance of bacteriophage collections for the development of phage therapy - Luís D.R. Melo, CEB/LABBELS, UMinho, PT	
12:30 – 14:00	Lunch Poster Session	
14:00 – 17:30	**Conference Tours**	**IS_MIRRI21 Final General Assembly** (close session)
17:30 – 19:00	**Free Time**	
19:00 – 22:00	Altogether Dinner at Restaurant Vila Galé Hotel	

DAY 4 THURSDAY 15/06	
08:30 – 10:30	**Session 7: National & Regional Network of Culture Collections** S7.1.: Microbiological collections of Paraná network (CMRP/Taxonline) - Vânia Vicente, UFPR, BR S7.2.: Moroccan Coordinated Collections of Microorganisms (CCMM): the first International Depositary Authority (IDA) in Africa and Nagoya Protocol implementation - Bahia Rached, CCMM, MA S7.3.: Virus collection of the new Fiocruz Covid-19 Biobank - Renata Campos Azevedo, FIOCRUZ, BR S7.4.: Biobank network in Korea - Tae-Eun Jin, KRIBB, KR S7.5.: The Norwegian Culture Collection of Algae (NORCCA): Diversity and Applications - Vladyslava Hostyeva, NIVA, NO S7.6.: Microbial Resource Center Network in ASEAN and along the Mekong River - Lily Eurwilaichitr, ENTEC/NSTDA, TH
10:30 – 11:00	Coffee Break Poster Session
11:00 – 12:30	**Session 8: ECCO Symposium - New services for public microbial collections** S8.1.: Welcome on behalf of the European Culture Collections' Organisation - Gerard Verkley, ECCO President, NL S8.2.: P-BIO: an overview of the Portuguese biotech ecosystem - Simão Soares, P- Bio/Portugal's Biotechnology Industry Organization, PT S8.3.: Driving innovation and pushing bioeconomy by offering smart scientific services - Mery Piña, EMBRC, FR S8.4.: The role of culture collections in clinical diagnostics and medical research - Wieland Meyer - Incoming Director of Westerdijk Institute, NL S8.5.: Discussion
12:30 – 14:00	Lunch Poster Session

14:00 – 15:30	**Session 9: IS_MIRRI_21 Symposium on Quality Management Systems - Global perspective** S9.1.: Welcome on behalf of the IS_MIRRI21 EU Project - Nelson Lima, Coordinator, MUM-UMinho, PT S9.2.: ISO 21710:2020 Specification on data management and publication in microbial resource centres - Linhuan Wu, IMCAS, CN S9.3.: ISO 20387:2018 How to implement? - Mieke De Wilde, Belgian Cancer Registry, BE S9.4.: Improvement of Quality Management System of Biological Resources at KCTC through Accreditation with ISO 20387 - Song-Gun Kim, KCTC, KR S9.5.: Supporting access and benefit-sharing by microbial collections for deposition of microbial strains and those deposited previously - Takahide Ishida, NIES, JP
15:30 – 16:00	Coffee Break Poster Session
16:00 – 17:30	**Session 10: IS_MIRRI21 Symposium on Quality Management Systems - Europe & the World** S10.1.: Multi-site ISO 9001 - Vincent Van de Perre, BCCM/CC, BE S10.2.: How to deal with multiple QMS? - Anabela Martins, MUM, CEB/LABBELS, UMinho, PT S10.3.: BBMRI-ERIC: how to provide quality/how to help as an infrastructure? - Andrea Wutte, BBMRI, CH S10.4.: Vision on quality within MIRRI-ERIC - Gerard Verkley, Westerdijk Institute, NL S10.5.: Round table and Conclusion
17:30 – 19:00	**IS_MIRRI21 Final General Assembly** (close session)
19:00 – 22:00	IS_MIRRI21 Dinner at UMinho Panorâmico Restaurant

DAY 5 FRIDAY 16/06	
08:30 – 09:30	**WFCC EB Meeting** (close session)
09:30 – 10:30	**WFCC General Assembly**

10:30 – 11:00	Coffee Break Poster Session
11:00 – 12:30	**Skerman Award Lecture** SAL1.: Advanced systematics of *Actinobacteria*: a key to exploiting their biotechnological potential - Imen Nouioui, DSMZ, DE Best Poster Prize ICCC15 Closure session
12:30 – 14:00	Lunch
14:00 – 15:30	**WDCM & MIRRI Joint Training Course for Big Data of Open Science in Microbiology** TC.1.: Welcome and presentation of the WDCM training courses - Juncai Ma, Director of the WDCM, IMCAS, CN TC.2.: Welcome and presentation of the MIRRI CWE and training courses - Nelson Lima, UMinho, PT TC.3.: Introduction to WDCM global collaborative work - Juncai Ma, WDCM Director, IMCAS, CN TC.4.: The WDCM 10K type strain sequencing project - Linhuan Wu, WDCM, IMCAS, CN TC.5.: YEASTRACT+ - Pedro Monteiro, INESC- ID, PT
15:30 – 16:00	Coffee Break
16:00 – 17:30	**WDCM & MIRRI Joint Training Course for Big Data of Open Science in Microbiology (cont.)** TC.6.: The UCCCB collection as a resource for bacteria PHA producers' genetic diversity assessment - Diogo Proença, UC, PT TC.7.: Research open data for use and reuse - Ana Alice Baptista, Centro ALGORITMI, Uminho, PT TC.8.: From compliance to capacity building: how European biological resource centres pave the way for benefit sharing - Anne Emmanuelle Kervella, EMBRC, FR TC.9.: Conclusion remarks - Biobanks' catalogues, open windows to the microbial realm - Philippe Desmeth, BELSPO-Belgian Science Policy Office, BE

ICCC15 - Group Photo

IS_MIRRI21 Final General Assembly - Group Photo

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Preface

The Local Organizing Committee (LOC) of the 15th International Conference on Culture Collections – ICCC15, an event organized every 3 years under the auspices of the World Federation of Culture Collections, was very proud to organize, in collaboration with the University of La Frontera (Chile), the hybrid conference last June at the University of Minho in Braga (Portugal). This year the ICCC15 had the *motto* of "Exploiting microbial resources to support social wellbeing" which involves harnessing the potential of microorganisms to improve various aspects of human life.

Microbes are tiny organisms that exist all around us, including in our bodies, soil, water, and air. The culture collections isolate, characterize, preserve, and distribute these microbial resources and associate data to the different user communities. The microbial culture collections are essential infrastructures to underpin the development of life and health sciences and the different biotechnologies.

During one week, the scientific community presented and discussed multiple ways in which microbial resources can be used to support social wellbeing connecting with environmental and economic developments. The United Nations Sustainable Development Goals and the European Green Deal paved the meeting too.

The ICCC15 was organized as a hybrid format that had a registration of 33 countries from the 5 continents with a total number of registrations of over 200. From this, the majority participated in face-to-face mode and 22% participated remotely. Ten sessions with a total of 46 talks, 2 opening lectures today, plus more 4 invited lectures; on the last day the "Skerman Award Lecture"; a round table on Cutting Edge Technologies in Microbial Culture Collection Services; a European Culture Collections' Organisation special session, and a post-conference World Data Centre of Microorganisms-MIRRI training course on Big Data of Open Science in Microbiology, plus 61 poster communications made ICCC15 unforgettable. The ICCC15 website (www.iccc15.com) was launched on 1st February 2023 and until the end of the event received 3,200 visits with an iteration time of 2:31 min on average. 6 Newsletters were produced to informe the scientific community and to give the relevant information, such as scientific program, deadlines and other praticalities. During the event, the mobile app got more than 1,700 clicks to get access to the different areas. All participants made this conference an intense and enlightening event.

The ICCC15 conference was also possible to the important connection and support with the European Microbial Resources Research Infrastructure – MIRRI -, which its headquarters is located on the University of Minho campus and the Implementation and Sustainability of MIRRI for the twenty-first century (IS_MIRRI21) European Horizon2020 project that also had its final General Assembly embedded in the event. This project was pivotal for remarkable achievements in the last 3 years to consolidate and operate the MIRRI-ERIC as a non-for-profit international legal organization.

The entire LOC is flattering for the support received from the WFCC Executive Board, the Sponsors, and the Leading Company that with many others, including all collaborators of the Micoteca da Universidade do Minho (MUM) fungal culture collection, to deliver an event with scientific, diverse and tackling emergent cross-cutting domains with outstanding quality.

This book covers the abstracts submitted by the contributors who, in a very short time, were able to respond to the invitation to participate in the ICCC15 and send their contributions to enrich the conference. The LOC hopes that you find the book comprehensive and that reinforces that the microBiological Resource Centres remain one of the cornerstones of Life Sciences, Biotechnology, and Bioeconomy to support social wellbeing.

The Local Organizing Committee

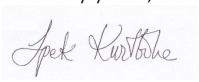
Nelson Lima
Carla Santos
Célia Soares
Manuel G. Silva
Ana João Ferreira
Ricardo Meirelles Cruz

Words from the President of WFCC

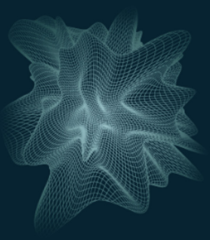
Dear Participants,

World Federation of Culture Collections (WFCC) is a multidisciplinary commission of the International Union of Biological Sciences (IUBS) and a Federation within the International Union of Microbiological Societies (IUMS). WFCC is the largest independent global organisation that represents culture collections concerned with the collection, authentication, maintenance, and distribution of cultures of microorganisms and cultured cells. WFCC runs International Culture Collections Conferences (ICCC) every 3 years and presents a Skerman Award to early career scientist for their achievements in microbial systematics. However, this conference chain has broken over the last 10 years due to unexpected man-made or natural disasters. We could not get together as planned face-to-face. In 2023, we got a kind offer from Professor Nelson Lima and Professor Cledir Santos to align the ICCC 15 with the final general Assembly of the IS_MIRRI21 (https://ismirri21.mirri.org/) EU Horizon2022 (grant agreement nº 871129) which paved the establishment and operation of MIRRI-ERIC as an international legal organisation (www.mirri.org/). With a very short time frame local organizers in Portugal, University of Minho, together with Universidad de La Frontera (Chile) put together an impressive program, capturing advances in the field and bringing the experts together. On behalf of the WFCC, I thank them immensely for the achievement of this conference and for the Abstract Book now published.

Sincerely yours,



İpek Kurtböke
President, WFCC



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Opening Lectures

Future needs for microbial diagnostics: tools and resources OL1

Baron E. J.

Prof. Emerita, Stanford University

Infectious disease diagnostics are entering a phase of rapid expansion based on development of new technologies, continually emerging antimicrobial resistance, and recognition of the role of microbial communities in disease. Examples of emerging diagnostic tools presented in this talk include invasive peptide nucleic acid target detection, enhanced Raman spectroscopy, colorimetric sensers of volatile products of microbial growth, genomics-based microbial identification, sequencing cell-free DNA, and characterizing host response markers. We are just beginning to understand and explore the role of the microbiome in autism, obesity, gastrointestinal disease, and other dysbiosis syndromes. How will we recognize and treat them? Of course, the microbes are fighting back: antimicrobial-resistant pathogens such as *Candida auris*, *Plasmodium falciparum*, *Acinetobacter baumannii*, pan-resistant *Klebsiella* and even *E. coli*, are gaining new ground. Finally, novel therapies such as bacteriophages, microbiota repopulation, repurposed human enzymes, and antibacterial peptides are entering our armamentarium. What biologics and resources should be created or archived, and thus be available to both developers (of therapeutics and diagnostics) and diagnostic laboratories in this new phase? This talk will suggest some possibilities.

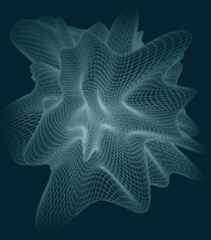
MIRRI: The Strategic Research and Innovation Agenda for 2021-2030 OL2

Aznar R.[1], Lima N.[2], Soares L.[2], Legras J.[3], IS_MIRRI21 Consortium[4]

[1]Spanish Type Culture Collection (CECT) - University of Valencia, [2]MUM, Universidade do Minho, [3]SPO, University Montpellier, INRAE, Institut Agro Montpellier - (CIRM - Levures), [4]IS_MIRRI21

The Microbial Resource Research Infrastructure (MIRRI) is the pan-European distributed Research Infrastructure for the preservation, systematic investigation, provision and valorisation of microbial resources and biodiversity. It currently brings together around 50 microbial domain Biological Resource Centres (mBRCs), culture collections and research institutes from ten European countries and one associated country. Among them an initial group of 14 partners and 8 third-parties have been involved in the IS_MIRRI21 H2020 project running from 2020-2023 which aims at consolidating MIRRI and securing its long-term sustainability. The MIRRI's Strategic Research & Innovation Agenda (SRIA) 2021-2030 is among the key results achieved in the project. With the motto "Microbial resources for a green, healthy and sustainable future" the SRIA is aligned with the most relevant global and European strategic agendas and the needs of user communities, to enable them to deliver the maximum value and impacts from their projects, technologies and products. It has been stablished following an exhaustive and comprehensive exercise of self-analysis, landscape analysis and horizon scanning, anticipating future trends and priorities for research and innovation in Health & Food, Agro-Food, and Environment & Energy, in line with the UN SDGs and the Horizon Europe. Seven strategic areas have been identified which are: Research on pathogenic microorganisms and human / human-animal infectious diseases; Research & Development of new (bio)pharmaceuticals / therapeutic solutions (including antimicrobials, vaccines, phage therapies and microbiome therapeutics – for human use); Research & Development of new, safe, healthy and sustainable food and feed products; Resources and methods for biological management of soils and crops; Resources and methods for biomonitoring and/or bioremediation of microbial pathogens, persistent organic pollutants and plastics in soils and waters; Research & Development of renewable biobased chemicals, materials and bioenergy sources; Rescuing and preserving microbial biodiversity. It is a "living document" to be revised and updated at the rhythm that the global challenges, the research and innovation landscape and the users' needs will dynamically change and evolve. MIRRI has since become involved in 13 high-level European projects (100% success rate), and its position in the European Research Area has also been consolidated since its recognition in 2021 as a 'Landmark' in the Health & Food domain of the European Strategy Forum on Research Infrastructures (ESFRI) Roadmap.

Acknowledgement:
This work was supported by the European Union's Horizon 2020 research and innovation programme under grant agreement nº 871129 - IS_MIRRI21 Project.



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Invited Lectures

WFCC For Wellbeing of Mankind and Advancement of Science and Technology IL1

Kurtböke I.

President, WFCC and Assoc. Prof. in Environmental Microbiology, University of the Sunshine Coast, Australia

Culture collections have evolved from their role as mostly providers of microbiological material for the society at large. While culture collections were essentially seen and run as centres of conservation and distribution of microbiological material in the past, transformed culture collection the Biological Resource Centres are now conceived as the source of all essential material for research and development in life sciences. To fulfil their role in basic infrastructure for knowledge-based bioeconomy, BRCs must implement "quality management systems, overcome legal and administrative obstacles, follow diverse international, supra-national and national laws and regulations and take extra appropriate precautions due to security concerns". The World Federation for Culture Collections (WFCC) play a major international role in all matters related to culture collections such as the operation and management of culture collections as well as addressing issues in a wider context such as the importance of (i) standardization and best practice guidelines, (ii) networking, capacity building and education, (iii) postal, quarantine and safety regulations (iv) IP, patent and commercialization, (v) access, policies and legal frameworks and (vi) sustainability of endangered collections. WFCC aligns with best practice guidelines and support its collections to achieve high standards. Moreover, WFCC in the era of molecular advancements places emphasis on genome level characterization of the microorganisms as well as defining criteria to ensure type strain integrity as well as its preservation in a genetically stable form. WFCC interacts with different global organizations to promote the importance of culture collections with emphasis placed on the contributions and the impact culture collections make on science, health, education, and society. This presentation will communicate WFCC's catalyst role for best practices in each member culture collections at four corners of the world where there may be legislative differences. It will also cover WFCC's importance for the well being of mankind, sustained global existence as well as timely delivery of the Sustainable Development Goals.

Effects of Long-Term Phosphorus Fertilization on Bacterial Community Structure and its Potential Gene Function Related to Phosphorus Mineralization in Pastures IL2

Mora M. L.[1], Leyton-Carcaman B.[1], Abanto M.[1], Demanet R.[1]

[1]*Universidad De La Frontera*

Phosphorus (P) is a crucial nutrient that limits the productivity of many agroecosystems worldwide. To maintain the productivity of these systems, continued inputs of P fertilizers are required. To assess the influence of different P fertilizers on microbial diversity and functionality in Andisol of Southern Chile, we conducted a pasture field trial for along six years to investigated the bacteria taxa changes related to sources of phosphorus amended including cattle dung and poultry manures and superphosphate as reference fertilizer. Our study revealed that bacterial abundance and composition were affected by the source of P applied. Furthermore, different P fertilizers were found to affect the expression of P-cycling-related bacterial genes such as phoD, phnK, pqqc, and gcd. Our analyses showed that diversity analysis involving similar conditions could minimize the differences between treatments. However, when treatments were grouped and analyzed according to their P source, they exhibited changes in microbial composition, highlighting certain taxa according to the treatment and doses applied. We observed a response in microbial diversity and abundance in response to contrasting fertilization schemes. We found that by the six year, there is an abundance of Acidobacteria, Verrucomicrobia and Proteobacteria. Moreover, organic fertilizer tends to inhibit the presence of ADE3, Bacteriordetes, Planctomycetes and Cloroflexi; and promote the predominance of Proteobacteria and Acidobacteria. According the functional evaluation, we found that the application of poultry manure fertilizer was associated with the most expressed phosphatase genes phoC and phoD in agree with the best dried matter production. Additionally, this response of microbial composition was related to variables of nutrition and plant growth. These preliminary findings suggest that it may be possible to identify the variables that affect plant growth and production, such as N, P, and C. By applying a multifactorial model for optimizing their turnover in pastures by controlling the "natural soil bioreactor", sustainable strategies for N fertilization can be developed.

Fungal culture collections in 21st century IL3

Meyer W.[1,2,3]

[1]Westerdijk Fungal Biodiversity Institute – KNAW, Utrecht, The Netherlands, [2]Curtin Medical School, Faculty of Health Sciences, Curtin University, Perth, WA, Australia, [3]Sydney School of Medical, Faculty of Medicine and Health, The University of Sydney, Sydney, NSW, Australia

With the increasing importance of fungi in bio conservation, waste recycling, agriculture, industry, and human, animal and plant health (One Health Concept), culture collections/biobanks holding fungal cultures and associated biological samples are becoming indispensable bioresource centres. Their main role is to collect, describe, store, and maintain fungal biodiversity and their associated metadate (strain information, DNA and protein data) for future generations, to provide, up to date taxonomical classifications, nomenclatural clarity and stability, supply fungal cultures for industrial applications, and as reference materials for fungal identification and antifungal susceptibility testing. They gain new importance in the 21st century as source of reference strains for fungal genomics, proteomics, and transcriptomics - forming the basis for product discovery, the search for new antimicrobials and drug development. Besides their enormous importance in all aspects of life they are often considers as a given and as such notoriously underappreciated and subsequently underfunded, while facing increasing energy and storage costs. New means of financial support are needed both from the public as well as the private sector to enable the establishment of next generation robotic storage, along with molecular (DNA sequencing) and proteomics (MALDI-TOF MS) based quality insurance. Changing country specific legal regulations and the increasing requirement for open access of biological material of publicly funded research while respecting the intellectual property rights of each source country calling for a global coordination and streamlining of the processes for the exchange of pure fungal cultures/biological materials between countries.

The importance of bacteriophage collection for the development of phage therapy IL4

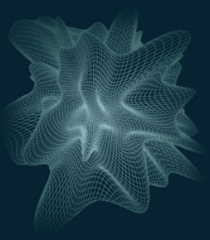
Melo L.[1,2], Azeredo J.[1,2]

[1]CEB - Centre of Biological Engineering, University of Minho, Braga, Portugal., [2]LABBELS –Associate Laboratory, Braga/Guimarães, Portugal

The World Health Organization (WHO) recently stated that for common bacterial infections, including urinary tract infections, sepsis, sexually transmitted infections, and gastrointestinal infections, high levels of resistance against antibiotics commonly used to treat them have been observed worldwide. This clearly indicates that we are running out of effective antibiotic and that antibiotic resistance is a very important global public health challenge, which consequences for global health might be devastating if novel antibacterial strategies are not quickly developed. Bacteriophages (phages) are viruses that specifically infect bacteria, being considered bacterial natural predators. The interest in using phages for therapy against bacterial infectious diseases re-emerged on the Western world over the last two decades.

The successful implementation of phage therapy relies in the existence of phage banks, with well characterized phages. Phages are isolated from environmental samples and their characterization includes transmission electron microscopy observation, genome sequencing and annotation and lytic spectra evaluation. Another important aspect is phage taxonomy; historically, phages have been classified according to their morphology, though the advances in sequencing technology boosted a genome-based classification. Indeed, over the last year, the International Committee on Taxonomy of Viruses (ICTV) reported several changes to virus taxonomy with 174 taxonomic proposals being changed and ratified.

In this talk we will describe the general procedures for generating a phage bank for the most important bacterial pathogens, including all steps from phage isolation to deep characterization. I will also discuss the importance of phage banks in a context of a global phage therapy and how the phage bank of the Centre of Biological Engineering has been used to treat national and international patients.



ICCC 15

INTERNATIONAL CONFERENCE ON CULTURE COLLECTIONS

SKERMAN AWARD LECTURE

Sponsored by World Federation for Culture Collections

WFCC

Advanced systematics and Novel Bioactive Natural Products of Actinobacteria SAL1

Nouioui I. [1]

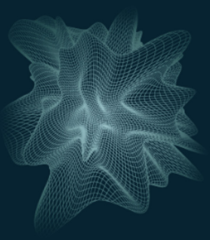
[1]*Leibniz-Institute DSMZ - German Collection of Microorganisms and Cell Cultures*

Actinobacteria are of great importance for agriculture, biotechnology, and medicine. Two-thirds of all clinically relevant antibiotics, as well as many anticancer, antifungal or immunosuppressive agents are derived from these organisms. Advanced prokaryotic systematics has greatly improved the classification of Actinobacteria and the understanding of their biodiversity in natural habitats. However, the phylogenetic relationships within some taxa still need to be revised and the genetic diversity of Actinobacteria has to be further explored. In this respect, 2 orders, 10 families, 17 genera, a reclassification of more than 100 species and the description of several new species of various taxa were introduced in this phylum [1]. Actinobacterial strains were screened for novel species on the premise that novel biology leads to novel chemical entities based on taxogenomic and genome mining approaches. Novel compounds with antimicrobial and anticancer activities were identified and characterised in the *Frankia* strains, nitrogen-fixing actinobacteria well known for their symbiotic interaction with a wide range of actinorhizal plants [2].

References:

[1]. Nouioui et al. 2018. Genome-Based Taxonomic Classification of the Phylum Actinobacteria. Front. Microbiol. Volume 9 - 2018

[2]. Nouioui et al. 2019. Genomic Insights Into Plant-Growth-Promoting Potentialities of the Genus *Frankia*. Front Microbiol. 2019; 10: 1457.



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Session 1: Circular Bioeconomy

Circular economy challenges in bioresources valorization- the role of microorganisms S1.1

Rocha C. M. R.[1,2]

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In a world that is expected to face acute resource shortage in the near future, exploring the possibility of fully using the available biomass and significantly improving the recovery of relevant nutrients/compounds are strategies of the utmost importance. Holistic strategies supporting a circular economy, enabling the sustainable and efficient use of available feedstocks, while targeting minimal environmental impact and zero wastes, are in order. In this context, selecting efficient strategies, aiming at recovering the maximum number of fractions while simultaneously allowing for high yields and functionality, economic feasibility, environmental sustainability, and holistic integration in biorefinery approaches, is a challenging task. Biorefineries were initially designed to provide energy and chemicals from lignocellulosic biomasses using fermentation processes. The concept can be extended to other types of under-used bioresources, including food wastes or marine biomasses. However, bottlenecks include the need for processes that can cope with different feedstocks and variable feedstock quality. In fact, improved enzymes and microorganisms are needed, resilient to these highly variable feedstocks and resistant to high(er) amounts of common inhibitors. Microorganisms capable of metabolizing specific compounds, such as oils or marine polysaccharides, into high-value products or ingredients would also allow broadening the range of biomasses that can be included in these circular economy approaches. Simpler valorisation strategies may include to enrich the biomass in different microbial metabolites or in single cell protein. Besides their role as high value commodities producer, microorganisms can also be an important processing aid. For instance, they may be used a stabilizing agent or to degrade packaging.

Summing up, microorganisms can be key players in adding value to under-used bioresources by providing feasible processes to convert these bioresources into different high-value products, thus increasing economy circularity.

Culture collections for bioprospecting in sustainability and innovation S1.2

McCluskey K.

Kansas State University (Retired), USA

Biomaterials and alternative food applications currently under development around the world depend on access to validated microbial genetic resources. Among these, strains of fungi, algae, and bacteria with clear provenance and defined rights are used for vegan leather, mushroom meat-replacement, and in GMO applications, cultured dairy products. Other applications include packaging, bioremediation, and a myriad of cell-factory processes. Among the approaches to utilizing microbial resources for novel sustainable products are the identification of novel characteristics, the development of novel processes to grow microbes in new formats, and the need to establish strain improvement programs to allow domestication of otherwise unimproved, wild strains. There are multiple barriers to using strains from established culture collections and these include high fees which limit the ability to do broad screening projects, undefined rights, and restrictive licensing requirements. By way of contrast, bioprospecting from nature faces resistance from landowners and even from public lands where clarity of rights is subject to debate. Moreover, it is difficult to access biodiversity using only locally isolated strains. Similarly, strain improvement practices that depend on access to genetic sequence resources are increasingly facing scrutiny as the rights under the Nagoya Protocol surrounding access to digital sequence information are elucidated. The role of a global leader in access and utilization of microbial resources, such as the World Federation for Culture Collections in facilitating the development of novel sustainable food and fiber alternatives depends on continued support and recognition of the WFCC. It is for this reason that the WFCC, in recognition of over 70 years of service and on behalf of over 600 registered collections, should have a Nobel Prize.

Cyanobacteria and microalgae culture collections and circular economy: the example of Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC) S1.3

Vasconcelos V.[1,2], Silva R.[1], Oliveira F.[1,2], Cruz P.[1,2], Moreira G.[1], Scotta Hentschke G.[1], Morais J.[1,2]

[1]CIIMAR, [2]University of Porto

The European Green Deal and the Recovery Plan for Europe will define the European economy for many years, or even decades. This has several important implications as the blue economy contributes to climate change mitigation by developing offshore renewable energy, decarbonizing maritime transport and greening ports making the economy more circular by renewing the standards for fishing gear design, for ship recycling and for the decommissioning of offshore platforms and contribute for the developing of green infrastructures in coastal areas will help preserve biodiversity and landscapes, while benefitting tourism and the coastal economy. New products such as pharmaceuticals, nutraceuticals, food and feed items as well as molecules for industrial processes may come from the aquatic environment helping these actions. Microorganisms play an important role in this process since they can be produced in a sustainable way in controlled environments using a biorefinery approach. Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC, https://lege.ciimar.up.pt/), is a biological resource centre located at Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), Matosinhos, Portugal, that comprises more than 1100 different cyanobacterial and microalgae strains. LEGE-CC strains are mostly obtained from Portuguese ecosystems, including the Azores and Madeira archipelagos, which gives the collection a unique richness from a geographical and phylogenetic point of view. We have been using microorganisms from this culture collection to produce a wide array of new molecules with applications such as pigments, antiobesity, anticancer, antibiotic, antifouling to name a few. The possibility of sequential extractions allows us to take advantage of the whole biomass, with the final residues with applications ion feed for agriculture as biofertilizers. In this talk, we will provide few examples of these applications and the way the concept of circular bioeconomy can be applied.

UCCCB- Centre for Microbial Conservation and the Development of Bio-based Solutions S1.4

Morais P.[1,2], Henriques T.[2,3], Proença D. A. N.[1,2]

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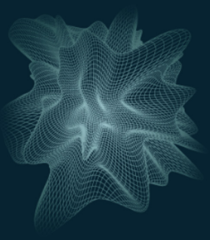
Microorganisms are indispensable for solving the problems faced by today's society. They are key tools for obtaining innovative bio-based solutions to address the challenges we face in many areas, such as the environment, food, health, energy, and more. Microorganisms are, therefore, essential to achieve the UN Sustainable Development Goals. Simultaneously, they play an essential role in the transition towards a bio-economy, serving as a driving force for the development of a circular and environmentally sustainable economy. In this context, the University of Coimbra Bacteria Culture Collection (UCCCB) was created, constituting a reliable and relevant microbiological resource for both scientific and industrial communities. UCCCB, registered as collection No. 1179 (WDCM), was the first culture collection dedicated to bacteria in Portugal registered and recognized by the World Federation of Culture Collections. In addition, UCCCB is also part of the Portuguese microBiological Resource Centre Network (Pt-mBRCN/MIRRI-PT), which is, in turn, part of the pan-European distributed Microbial Resource Research Infrastructure (MIRRI). In this way, UCCCB extends its outreach to national and international communities while contributing to safeguarding the Portuguese microbiological heritage and the implementation of the United Nations Convention on Biological Diversity.

UCCCB's mission is to acquire, identify, characterize, and conserve microbial strains and genetic resources, while simultaneously offering access to microbiological cultures, supplying biological materials, and providing customer-focused services. Being a culture collection, UCCCB ensures continuity with the past by preserving and distributing microbial strains described or cited in publications, while it also keeps novel microorganisms awaiting future exploitation by biotechnology. UCCCB's services include, among others, cell and microbial culturing and identification, development and production of controls and derivatives, proficiency testing, and biomaterial banking. Thus, UCCCB is positioned as a centre for attracting and fostering partnerships between academia, research, companies, and developers, serving as a driving force for the bio-development of the economy and society. UCCCB's primary socio-economic contributions stem from its provision of services, which generate value for its users and potentiate the creation of start-ups and spin-offs. UCCCB's additional contributions encompass income generated from intellectual property rights, commercialization of new products and instruments, the economic value of scientific research outcomes such as publications, organization of scientific events, and promotion of R&D.

Sustainable development can only be achieved with the contribution of microorganisms. Thus, UCCCB, by preserving and distributing microbiological resources, services, and knowledge, is a driving force of bio-development



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Session 2: Legal & Policy Issues for Culture Collections

Restrictions placed on the distribution and utilization of microorganisms by Access and Benefit Sharing legislations S2.1

da Silva M.[1]

[1]*General Manager of Fiocruz Covid-19 Biobank, Fundação Oswaldo Cruz (Fiocruz), Rio de Janeiro, Brazil.*

In 1992 in Rio de Janeiro, Brazil, during the United Nations Conference on Environment and Development (the Rio "Earth Summit"), the Convention on Biological Diversity (CBD) was opened for signature and in 1993 entered into force. The objectives of the Convention are the conservation of biological diversity, the sustainable use of its components and the fair and equitable sharing of the benefits arising out of the utilization of genetic resources. Based on this third objective, the CBD established the concept of Access and Benefit Sharing (ABS), which defines how genetic resources can be accessed and how the benefits resulting from their use are shared between users and providers. In 2014 entered into force the Nagoya Protocol (NP) on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity, which is the international framework for ABS. Therefore, Parties to the CBD and NP have sovereign rights over their genetic resources, have the authority to determine access to these resources and to implement the prior and informed consent and the mutually agreed terms. Currently, 139 countries are Parties to NP, so there are a wide range of different rules and requirements regarding the activities of depositing, sharing and utilizing genetic resources, which are common activities in biological collections. This means that curators must be aware of these requirements on genetic resources from different countries maintained by the collection. Many countries with great biodiversity, the so-called megadiverse countries, have opted for tight control and restrictions for accessing and sharing their genetic resources, which are set out in documents such as material transfer agreement (MTA) and mutually agreed terms (MAT). Consequently, international cultures collections are having difficulties in distributing microorganisms from these countries, which has resulted in some cases their removal from microbial catalogs and even the exclusion of strains coming from Brazil, India and South Africa to serve as type material for the validation of species names, as well described in the article How legislations affect new taxonomic descriptions by Manuela da Silva, Philippe Desmeth, Stephanus N Venter, Yogesh Shouche and Andrey Yurkov published in Trends Microbiology in 2023 (https://doi.org/10.1016/j.tim.2022.10.010)

Pathogens Infecting ABS Implementation: At the crossroad of different regulatory frameworks S2.3

Philippe Desmeth

Belgian Coordinated Collections of Micro-organisms - Belgian Science Policy Office
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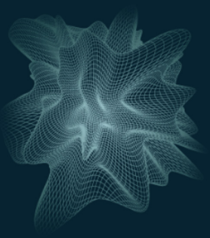
The genomes that constitute the human microbiome represent a remarkably diverse array of microorganisms that includes bacteria, archaea, fungi, and viruses. The total of microbial cells is estimated at around 40 trillion, while the entire human body consists of about 30 trillion cells. By some estimates, the human microbiota may consist of a total of 900 or 1,000 different species of microorganisms, making for an extraordinarily diverse collection of microbial genomes. The sheer microbial abundance suggests that the human body is in fact a collection of human and microbial cells and genes.

When we explore and study this host-resident complex, in addition to the technical and scientific difficulties, we are confronted with a series of laws which legislate the proper exploitation of scientific results in compliance with human rights, national and international laws and the rights and duties of all stakeholders. In particular, human pathogens are subject to numerous and specific ethical, legal and social considerations. This legislative framework is complex and sometimes subject to contradictory interpretation, hence the difficulty for operators such as cultural collections to operate in a legal and optimal manner. Moreover, ABS regulations under the Nagoya Protocol add a layer of complexity that can sometimes undermine the effectiveness of the scientific process.

Likewise, there are multiple operators, from civil society, lawyers, officials, authorities, entrepreneurs to scientists.

Microbial culture collections, also called nowadays microbiological resources centres and microbial biobanks, are essential research and innovation infrastructures for life sciences and biotechnology. Their mission is to provide -Fit for Purpose- solutions adapted to the needs of research and innovation in an efficient and affordable manner, whether in terms of relevant and reliable microbiological materials, expertise or data, and this in a complex legal, ethical and social environment.

Catalogues are the primary mean of communication for microbial culture collections to their users. These catalogues are the sum of multiple efforts and constitute open doors to the microbial world, helping users to get legal access to microbial R&I resources that are fit-for-purpose.



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Session 3: Microbiomes

Bacterial diversity and culturable actinomycetes antimicrobial activity in tidal flats of southern China S3.1

Li B.[1], Wu D.[1], Fang B.[2], Zhou Y.[1], Li W.[3], **Cai M.[1]**

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Tidal flats are globally distributed coastal ecosystems that occur at the interface between land and sea. They support biodiversity and maintain the ecosystem by offering services including storm protection, shoreline stabilization, and food production. Although marine ecosystems have become hotspots in recent decades, little attention was given to the microbial diversity and resources of coastal tidal flats. Using high-throughput sequencing of 16S rRNA gene, this study examined the bacterial diversity and community structure of tidal flats in southern China with coastlines exceeding 10,000 kilometers. Combining the co-occurrence network analysis, was used culturomics approach to acquire tidal flat bacterial resources, especially for actinomyces, to discover more antibiotics that held medical and industrial potential. The research suggested that bacterial communities varied with distinct latitude and longitude, as well as the texture of tidal flats. Pseudomonadota, Chloroflexota, Acidobacteriota, and Bacteroidota were the dominating bacterial phyla, at the genus level, unassigned operational taxonomic units were most prevalent. Additionally, network analysis indicated that the top 20 percent of core taxa were all uncultured bacteria, which might be keystone taxa during tidal flat microbial community construction. Microbial functions predicted based on phylogenetic investigation of communities by reconstruction of unobserved states (PICRUSt2) demonstrated that terpenoids and polyketide metabolism genes were abundant. To get more antibiotic producing bacteria, 15 types of isolate media were used, and a total of 629 actinomycete strains belonging to 35 genera, including *Micromonospora*, *Streptomyces*, *Agromyces*, *Rhodococcus*, and *Micrococcus*, were isolated, of which 45 novel species candidates were discovered. 56 isolates were found to contain at least one of the three biosynthetic gene clusters (PKS-I, PKS-II, and NRPS), taking into account their biosynthetic potential. Furthermore, six human opportunistic pathogens (*Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, *Aeromonas veronii*, and *Aeromonas hydrophila*) were used to assay their antimicrobial activity. Out of the 56 strains, 31 exhibited positive resistance against at least one of the six test pathogens. All our preliminary results highlight the diversity and composition of the microbiome in underexplored habitats such as tidal flats. In addition, this work also advanced the understanding of tidal flats as a treasury of antibacterial compounds that may be with uncommon resistance mechanisms for human pathogens.

Genome-resolved metagenomics provides novel insights into chitin turnover, metabolic specialization, and niche partitioning in the octocoral microbiome S3.2

Keller-Costa T.[1,2], Kozma L.[1], Silva S.[1,2], Toscan R.[3], Gonçalves J.[4], Lago-Lestón A.[5], Kyrpides N.[6], Nunes da Rocha U.[3], Costa R.[1,2]

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Octocorals (Octocorallia, Cnidaria) are an integral part of benthic marine ecosystems. They increase habitat complexity and biodiversity and play key roles in coastal food chains. They are found in association with various microorganisms. Our previous work showed that the octocoral microbiome is distinct from the environmental surroundings, host genus-specific, and undergoes complex structural changes in the transition to the dysbiotic state [1]. However, the role of bacterial symbionts that populate octocorals is still poorly understood. To shed light on their metabolic capacities, we examined 66 high-quality metagenome-assembled genomes (MAGs) spanning 30 prokaryotic species, retrieved from microbial metagenomes of three octocoral species and seawater [2].

Symbionts of healthy octocorals were affiliated with the taxa Endozoicomonadaceae, Candidatus Thioglobaceae, Metamycoplasmataceae, unclassified Pseudomonadales, Rhodobacteraceae, unclassified Alphaproteobacteria and Candidatus Rhabdochlamydiaceae. Phylogenomics inference revealed that the Endozoicomonadaceae symbionts uncovered here represent two species of a novel genus unique to temperate octocorals, here denoted Candidatus Gorgonimonas eunicellae and Candidatus Gorgonimonas leptogorgiae. Their genomes revealed metabolic capacities to thrive under suboxic conditions and high gene copy numbers of serine-threonine protein kinases, type III-secretion system, type IV-pili, and ankyrin-repeat proteins, suggesting excellent capabilities to colonize, aggregate, and persist inside their host. Contrarily, MAGs obtained from seawater frequently lacked symbiosis-related genes.

All Endozoicomonadaceae symbionts harbored endo-chitinase and chitin-binging protein-encoding genes, indicating that they can hydrolyze the most abundant polysaccharide in the oceans. Other symbionts, including Metamycoplasmataceae and Candidatus Thioglobaceae, may assimilate the smaller chitin-oligosaccharides resulting from chitin breakdown and engage in chitin deacetylation, respectively, suggesting possibilities for substrate cross-feeding and a role for the coral microbiome in overall chitin turnover. We also observed sharp differences in secondary metabolite production potential between symbiotic lineages. Specific Proteobacteria taxa may specialize in chemical defense and guard other symbionts, including Endozoicomonadaceae, which lack such capacity.

We identify a thus-far unanticipated, global role for Endozoicomonadaceae symbionts of corals in the processing of chitin, a major component of the natural zoo- and phytoplankton

feed of octocorals. We conclude that niche partitioning, metabolic specialization, and adaptation to low oxygen conditions among prokaryotic symbionts likely contribute to the plasticity and adaptability of the octocoral holobiont in changing marine environments. These findings bear implications for our understanding of symbiotic relationships in marine environments and benthic ecosystem functioning. They may further guide the formulation of new culture media, targeting elusive symbionts of marine animals.

[1] Keller-Costa et al., 2021, Microbiome, 9, 1-21
[2] Keller-Costa et al., 2022, Microbiome 10, 151

A Treasure Trove for Future Discoveries: The Female Urogenital Bacterial Collection (UroGenBC) S3.3

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The female urogenital microbiome (FUM) harbours a unique and dynamic microbial community that can impact human biology and health. Whole-genome shotgun metagenomics is the most advantageous method to provide a complete picture of the genome content of FUM and achieve accurate functional assignments. This can only be warranted if metagenome sequences can be interpreted to reveal all the species and strains present, and a positive control (mock community with a known polymicrobial profile) is included to assess biases and accuracy of the experimental and computational procedure from low microbial biomass samples (urinary microbiome). Thus, understanding FUM functions requires cultivated bacteria for experimental validation, and reference bacterial genome sequences to interpret metagenome datasets and guide functional analyses. Currently, none of the recognized culture collections has devoted time and effort to advancing FUM's research and innovation.

Under the UroGenBC project, CCP aims to: i) present the first female urogenital bacteria culture collection, a comprehensive set of complete bacterial genome sequences from female midstream urine and vaginal samples; ii) develop DNA and whole-cell mock communities; and iii) build a consortium for a Horizon Europe project.

The Culture Collection of Porto-Faculty of Pharmacy, University of Porto (CCP; https://ccp.ff.up.pt/) holds a private collection of almost 2000 bacterial strains isolated from midstream urine and vaginal samples, at two distant time points (within 2.5-year interval), from 20 reproductive-age asymptomatic women (DOI: 10.1186/s12866-021-02123-3, DOI: 10.1128/spectrum.01308-22). The strains were previously identified by MALDI-TOF MS and gene markers sequencing, and represented almost 50 genera (mostly belonging to Bacillota and Actinobacteria phyla, followed by less prevalent Proteobacteria, Bacteroidetes, and Fusobacteria). The focus on high-resolution identification of Lactobacillaceae family, *Corynebacterium* and *Gardnerella* genera allowed our group to unveil 13 new bacterial species (3, 8 submitted to IJSEM for validation, and 2 under review, respectively) (DOI: 10.1099/ijsem.0.003901, DOI: 10.1099/ijsem.0.004726, DOI: 10.3390/microorganisms 11020388). CCP believes that further exploration of the remaining genera will depict new species inhabiting the urogenital sites of female body. Moreover, we revealed that the healthy FUM is a source of potentially pathogenic and antibiotic resistant *Escherichia coli* strains, including those causing urinary tract infections, and diverse *E. coli* lineages were observed per individual and urogenital sample type (DOI: 10.3390/microorganisms

10010027). The future strategy of CCP is to achieve the proposed goals, crucial for fully understand the association of urogenital microbiome with urinary/vaginal diseases and disorder, underpinned by the United Nations for Sustainable Development Goal 3, in partnership with other European culture collections.

Where, when, and how environmental and food microbiomes meet each other S3.4

Chessa L.[1], Daga E.[1], Comunian R.[1]

[1]*Agris Sardegna - Associated Member of the JRU MIRRI-IT, Località Bonassai SS 291 km 18.6, 07100*

The microbiome can be considered a network of interactions in a contiguous environment among living microorganisms (constituting the microbiota), structural elements, metabolites, and the habitat. The characterisation, preservation, and reproduction of in toto microbiomes of different origins (such as terrestrial, aquatic, atmospheric, food, and living host) is one of the most current challenges for scientists to face. The complexity of these interactions can make it difficult to understand several biological processes in the microbiome, assess the composition of alive microorganisms able to make activities, and realise what they are acting, at the time of the investigation. Among microbiomes, those of soil origin can include microorganisms having a crucial role in nutrient cycling, maintenance of soil fertility, and carbon sequestration, whereas, among those of food origin, starter cultures contain microorganisms added to raw food matrices, normally already colonised by resident microbiota, to achieve an attractive and durable product with peculiar characteristics. While there is great awareness of the high level of complexity of soil microbiomes, it is commonly argued that those of food origin are generally considered less complex, though there is still a great unknown in understanding the microbial composition and the interactions among the players involved even in this type of microbiome. In this context of complexity, scientists investigating microbiomes of different origins generally follow distinct approaches and techniques, culture-dependent and –independent, and multi-omics (i.e. metagenomic, metatranscriptomic, metaproteomic, and metabolomics). The improvement of culturing strategies to recover as much as possible of the microbial biodiversity composing the microbiomes, as well as the enhancement of genomics approaches to a better understanding of the role of horizontal gene transfer and viruses in microbiome evolution would be valuable. But above, greater and more cohesive interaction among scientists from different research fields could help a faster and more accurate characterisation of microbiomes. Indeed, normally, scientists involved in a specific research field read papers, attend conferences, and interact mainly with scientists in the same field. This presentation aims to be a stimulus for scientists investigating different research fields to collaborate, exchange knowledge and ideas, and use their skills to better unravel the complexity of the different matrices that teem with the invisible world of microbial communities.

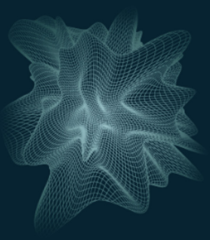
Unravelling the conundrum – preserving the microbiome for Phytobiomes research S3.5

Ryan M.[1], Gallagher D.[2], Eversole K.[2]

[1]CAB International, UK, [2]The International Alliance for Phytobiomes Research

Culture Collections have a long history of supporting microbiological research, primarily through the accession, preservation and supply of axenically cultured microorganisms. However, in nature microbes do not exist on their own, they interact with many millions of other microbes, many of which are either difficult to culture or cannot be cultured at all. With developments in technology, microbiome research is changing the way culture collections and biobanks need to support their user communities. Phytobiomes consist of plants, their environment, and their associated communities of organisms and there is a fundamental need to underpin phytobiomes research through the provision of a supporting infrastructure. The EU Microbiome Support CSA has defined key requirements, including the development of standards; the need to deposit material and supply cultures, samples and associated data for future research in both academia and industry. Importantly this will also provide a mechanism to protect intellectual property, and help researchers adhere to legislative and regulatory requirements including the Nagoya Protocol of the CBD. Integral to the above is the need to preserve soil and plant samples and their microbiota.

Historically, culture collections have used cryopreservation at ultra-low temperature and freeze-drying protocols to preserve microbes. However, the microbiome presents a more challenging conundrum – how do we translate the methodology to complex samples that may contain many thousands of different species? The answer lies in our understanding of how microbial cells respond to the stresses encountered during freezing, thawing and recovery and how methods can be optmised to retain physiological and genomic integrity for different taxa and cell types. Using this approach, we can start to predict the components of the microbiome that may retain viability and, importantly, retain their functional potential. In this talk an overview will be provided of how 'state-of-the-art; technologies are being developed, adapted and applied to complex microbial samples and synthetic consortia through two ongoing projects, the EU Microbiome Biobanking Enabler and the UK Crop Microbiome Cryobank. We will explore how biobanking, culture collection and data networks can come together, working with Industry/academic collaboratives such as the International Alliance for Phytobiomes Research, to support the needs of the academic and industrial research community.



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Session 4: Overview on Microbial Preservation Techniques

Maintenance of microbial consortia from salami: a case study on the impact of cryopreservation S4.1

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In recent years, the importance of the conservation of microbial biodiversity has achieved high awareness. Conservation biologists have highlighted that weaknesses in microbial preservation can lead to the loss of valuable bio-resources and gene pools that provide high levels of resistance against changing environmental conditions and adaptation to novel production processes. Community, habitat and intact microbial communites preservation are promising solutions to mitigate and counteract these emerging problems, favouring the biotechnological valorisation of microbiomes. Generally, microbiologists focus their consideration only on culturable microbes and on pure cultures, thus preserving only a tiny fraction of microbial diversity and functional potential of that microbiota. Besides, very few studies have been conducted to study the optimal conditions of storage of microbial consortia and their effect on microbial community structure and the related functional potential. An efficient storing method must be able to maintain microbial strains in a viable state to protect their morphological and genetic stability for a long time under laboratory conditions. Several methods are used for the preservation and maintenance of microorganisms. Usually, lyophilisation and cryopreservation are versatile and widely applicable for a large number of microorganisms. Moreover, the presence of cryoprotectants often increases the survival of microorganisms, and in particular, glycerol and DMSO were shown to protect microbial cells against freezing damage. This study aimed to evaluate the effectiveness of freezing procedures to cryopreserve the microbiota isolated from the surface of an Apulian cured sausage, using glycerol or DMSO as cryoprotectants and two different storing temperatures (-80 °C and -135 °C) for the short and mid-term period. The microbial population of the sausage was studied by culture-dependent method and metagenomic analysis comparing analyses before and after storing period. Results indicated that after 1 and 8 months of cryopreservation, the viability of the bacterial population of microbial consortium decreased at the same rate for both cryoprotectants and storing temperatures. A similar trend was also observed for fungi and yeasts with the exception of storage conditions that include glycerol and temperature of -135°C, which better preserve the viability of yeasts and fungi after eight months. This study pointed out the first scientific evidence on the effect of cryopreservation of the whole microbial consortia collected from the surface of cured sausages.

Part of this work was granted by the European Commission – NextGenerationEU, Project "Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy", code n. IR0000005.

CICC Operation: Discovery and Application of Industrial Microorganisms Resource S4.2

Su Y.

China Center of Industrial Culture Collection

China Center of Industrial Culture Collection (CICC) was founded in 1930, which is the the industrial microorganism sub-center of the National Microbiology Resource Center of China and is a member of the World Federation for Culture Collections (WFCC). CICC is responsible for the conservation and sharing, research and development, scientific and technological services, and international exchange of industrial microbial resources in China. CICC carries out various microorganism conservation of more than 13,000 strains, the development of more than 300 microbial standard products, and more than 230 microbial technical services, and has been accredited to ISO 9001, ISO 17034, ISO 17025, and China Inspection Body and Laboratory Mandatory Approval (CMA). Every year, more than 60,000 strains and 8,000 technical services were provided by CICC for food, pharmaceutical, feed, daily chemical, and other industrial field practitioners.

The research direction of CICC covers microbial resource center construction, operation, and resource sharing; the research of microbial precise identification and evaluation technology; the discovery and evaluation of traditional fermented food cultures; microorganism mutagenesis and molecular selection; and the research in key technologies of production cultures and standard product creation, etc. In traditional fermented foods, CICC was the first to propose an Inventory of Chinese Traditional Fermented Food Cultures and establish a systematic evaluation technology system for culture functionality, resistance, and safety. At the same time, China's first traditional fermented food culture database was built and systematically collected and organized 4839 strains of fermented cultures from 124 species, which were used for 13 types of traditional fermented foods, including Baijiu, Paocai, tea, sufu, vinegar, ham, dairy products, etc. The construction of a traditional fermented food culture database strongly supported the innovative development of China's traditional fermented food industry.

Preserving Viability and Stabilizing Properties of *Rhodococcus* Biodegraders of Pharma Pollutants S4.3

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Methods of short- and long-term storage of *Rhodococcus* biodegraders of NSAID-based pharma pollutants (diclofenac, drotaverine, ibuprofen, ketoprofen, meloxicam, and naproxen) maintained in the Regional Specialized Collection of Alkanotrophic Microorganisms (acronym IEGM, WFCC # 285, http://www.iegmcol.ru) were developed. For preserving live cultures, subculturing from minimal agar, water and 0.5% NaCl was most appropriate and guaranteed 30–74% survival rates and maintenance of cell metabolic activities for 2–10 years. Preservation of non-dividing vegetative Rhodococcus cells on membrane filters applied to the surface of nutrient agar or mineral agar with n-hexadecane and followed by removal of filters with grown cells and storage in sealed sterile test tubes at 4 °C guaranteed survival and unchanged phenotypic properties of strains within 2–3 years. The most reliable methods of long-term storage were lyophilization and low temperature freezing. To increase viability of cells during storage and at the rehydration-reactivation step, rhodococci at the concentration of 10^8–10^9 cells/mL with induced alkanotrophic metabolism and upon transition to the stationary phase were used. Transiting cells realized "self-preservation" processes, such as the formation of capsule-like structures, cyst-like cells and carotenoid pigments, synthesis of protective compounds (trehalose, biosurfactants, and amino acids), cell aggregation and immobilization. A protective mechanism of alkanotrophy was related with endogenous respiration, accumulation of poly-β-oxybutyrate granules, increased amounts of odd-numbered fatty acids, and enhanced synthesis of biosurfactants and amino acids. It was advisable to pre-grow rhodococci on liquid n-alkanes rather than gaseous ones for a higher proportion of unsaturated fatty acids. To prevent their oxidation, 1 mM α-tocopherol acetate was added to the cell suspension before storage. To store frozen Rhodococcus cells, they were immobilized in the growth medium on paper disks, dried at 28 °C, frozen and stored at -85 °C. To cryopreserve Rhodococcus cell suspensions at lower (4.3×10^7 cells/mL) concentration, 5% dimethyl sulfoxide and 10% glycerol were added. However, for certain strains, cryopreservation without a protective agent was more effective. The approximate time for *Rhodococcus* spp. to preserve viability in the lyophilized state was estimated at 5.9–43.9 years. According to the control testing the 64 lyophilized Rhodococcus cultures stored for 15 years, 73% were successfully recovered and retained cell integrity, main morphological and cultural properties. Low temperature freezing provided 45–94% viability of rhodococci by the end of the first storage year and resulted in the average survival rate of 77%.

The study was fulfilled under the State Assignment (AAAA-A19-119112290008-4) and the Russian Science Foundation grant (21-14-00132).

The CLIOC Workflow: Ensuring Conservation of the Diversity of *Leishmania* Parasites Available for Scientific and Technological Development S4.4

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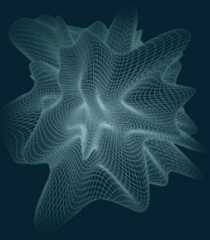
Microbial collections of pathogens are essential for the advance of research in different areas, development of diagnostic methods, treatments, and vaccines. They are of great importance for the understanding and control of the diseases they cause. They are also used to detect the emergence of new strains of pathogens and to monitor the evolution of existing ones. The Leishmania Collection from Oswaldo Cruz Foundation (CLIOC) is an important repository of strains of *Leishmania* parasites serving for these purposes. CLIOC includes different Leishmania strains from all over the world, mainly from American countries, endemic regions for leishmaniasis, a serious and neglected global public health threat. Isolation and cultivation of *Leishmania* spp., followed by correct identification, storage - employing appropriated methods - and associating to clinical and epidemiological information, are essential to preserve the diversity of natural population of these parasites, a source for the development of researchers in different subject. Here we'll outline the complex workflow that was implemented for 1670 *Leishmania* spp. strains available for donation for different purposes, which represent about 40% of the strains already deposited at CLIOC. These strains correspond to 34 species, classified into five subgenera, representing the taxonomic groups of *Leishmania* worldwide distributed, some of them responsible for causing leishmaniasis. From their reception, through species identification by different biochemical (multilocus enzyme electrophoresis) and molecular (partial sequencing of different genes) approaches, followed by cryopreservation, quality control checks, and ultimately, the transfer of the associated data to an online catalogue, all procedures are conducted in accordance with the quality management system, adhering to the ABNT NBR ISO/IEC 17025:2017 (General requirements for the competence of testing and calibration Laboratories) standards. Furthermore, we will also present all services incorporated into the routine of CLIOC, which comprises, in addition to the aforementioned: distribution of strains, human resources training, provision of information and procedures, scientific-technical consulting, development and supervision of research projects. We aim to bring to the light the need of accurately describe the information associated with Leishmania spp in scientific publications, in order to ensure reproducibility of research. Finally, we will highlight the importance of depositing *Leishmania* spp. strains in institutional collections to ensure their availability for future research and promote scientific rigor, since the deposit of *Leishmania* spp. parasites in microbiological collections is not commonly adopted by the scientific community and is not mandatory even for new species description.



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Session 5: Microbial Systematics

Genotype-phenotype correlations with the Geodermatophilaceae S5.1

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The integration of genomic information into microbial systematics along with physiological and chemotaxonomic parameters provides for a reliable classification of prokaryotes. The use of in silico analysis Laboratory-based DNA-DNA hybridisation methods have routinely been replaced by ANI and in silico DNA-DNA analysis. In silico analysis for phenotypic traits are now being introduced to replace characteristics traditionally determined in the laboratory with the dual goal of increasing the speed of the description of taxa and the accuracy and consistency of taxonomic reports. In conjunction with the taxonomic characterisation of four strains phylogenetically located within the Geodermatophilaceae, we conducted a phylogenetic analysis of the whole proteomes of the sequenced type strains and established genotype–phenotype correlations for traits related to chemotaxonomy, cell morphology and metabolism. Results indicated that the four isolates under study represent four novel species within the genus *Blastococcus*. In silico chemotaxonomic results were overall consistent with wet-lab results. Even though in silico discriminatory levels varied depending on the respective chemotaxonomic trait, this approach is promising for effectively replacing and/or complementing chemotaxonomic analyses at taxonomic ranks above the species level. Finally, interesting but previously overlooked insights regarding morphology and ecology were revealed by the presence of a repertoire of genes related to flagellum synthesis, chemotaxis, spore production and pilus assembly in all representatives of the family. A rich carbon metabolism including four different CO_2 fixation pathways and a battery of enzymes able to degrade complex carbohydrates were also identified in *Blastococcus* genomes.

Funding:
MdCMC is grateful for funding received from the Ramón y Cajal Research Grant (RYC2019-028468-I) from the Spanish Ministry of Economy, Industry and Competitiveness (MINECO).

Genome sequence data: the key driver in shaping prokaryotic systematics S5.2

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Names are important for all organisms, including bacteria and archaea. It is often the first thing we want to know and form judgments instantly once the name is known. The description of a taxon of bacteria and archaea requires several experiments. Traditionally, microbial classification was based on the physical and biochemical characteristics of organisms, such as their morphology, physiology, and metabolism. However, these methods were often subjective and unreliable, which lead to the misclassification of several prokaryotes. Microbial biological resource centres (mBRCs) ensure access to authenticated and quality-controlled microbial resources. Therefore, ensuring the correct taxonomy of microbial strains is a must for an mBRC, as its resources are often used to support new discoveries and follow-up studies. With the advent of high-throughput sequencing technologies, it is now possible to obtain a comprehensive and objective view of the genetic makeup and evolutionary relationships of microorganisms, allowing a more accurate and systematic classification. At the Collection of Institut Pasteur (CIP), we are using genome sequencing data for the accurate identification of bacterial strains. Based on the core-gene phylogeny inference, organisms with shared evolutionary histories were accurately placed into monophyletic clades. Monophyletic clades were also found for the members of complex groups, for which the 16S rRNA gene-based identification was inconclusive and 16S rRNA gene phylogeny resulted in polyphyletic clades. Genome sequencing data has therefore led to the description of many new bacterial taxa, which were previously misclassified. Additionally, the genome sequence-based analyses, such as phylogenomics, average nucleotide identity, and average amino acid identity helped resolve the taxonomic conflicts and provided evidence for several reclassifications. All these advanced bioinformatics are accessible to everyone. At Institut Pasteur, we host BIGSdb-Pasteur, a genomic taxonomy and nomenclature platform for bacterial strains available at bigsdb.pasteur.fr. This system allows non-bioinformatician users to perform species identification and whole genome typing based on (ribosomal, core genome) multilocus sequence typing (MLST) scheme, in addition to antimicrobial resistance or virulence characterization. In conclusion, genome sequencing and analysis have become an essential tool for prokaryotic systematics (providing a more accurate, objective, and comprehensive view of microbial diversity and evolution) and can be easily accessed by the scientific community through dedicated service platforms.

Collections, Cultures and the names of Fungi S5.3

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Names of Fungi are critical for communicating scientific findings, but also for clinical diagnostics, legal compliance, and regulatory controls, such as biosafety, food security, quarantine regulations, and industrial applications. The stability of the taxonomic system and the traceability of nomenclatural changes is crucial for a broad range of users and taxonomists. The unambiguous application of names is assured by the preservation of nomenclatural history and the physical material of the organism representing a name. The International Code of Nomenclature for Algae, Fungi, and Plants (ICNafp) permits cultures to represent a type if they are stored in a metabolically inactive state. The collections ensure safe preservation of the type material and collection numbers are the unique identifiers to be cited in a taxonomic description. The current edition of the ICNafp allows culture collection acronyms to be used in the protologue, and the Code refers to the World directory of collections of cultures of microorganisms (Art. 40.7, Note 4), the discontinued service of the WFCC and WDCM.
Mycologists working with yeasts campaign for using viable cultures as nomenclatural types under the ICNafp. Nowadays, many collections employ modern preservation techniques and management practices to ensure safe preservation of the material and the associated information. A number of already existing mechanisms, including mandatory authentication of deposited cultures, deposition certificates and registration in electronic nomenclature repositories can help to create a transparent system for tracking viable type material. The WFCC collections can play an important role in the process by creating common standards and certificates, and by reviving the World directory of collections as a voluntary register of collections accepting type viable material under common quality standards.

Phylogenomics of the genus *Alcaligenes*: proposal of *Alloalcaligenes* gen. nov. S5.4

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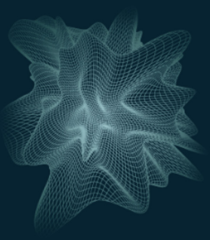
The genus *Alcaligenes* (sensu lato) is comprised by 17 species validly published under the ICNP, with 7 effectively (not validly) published species, albeit many of them reclassified into other or novel genera. In contrast, *Alcaligenes* (sensu stricto) is currently comprised of four validly published species (viz. *A. faecalis*, *A. aquatilis*, *A. pakistanensis* and *A. endophyticus*) predominantly represented by *A. faecalis* in public genome sequence databases (> 70%). Strains identified as species of *Alcaligenes* (sensu stricto) have been isolated from human clinical samples, insect gut, agricultural soil, phyllosphere, rhizosphere, marine sediment, marine and fresh water, polluted ecosystems, and industrial sites, showing a ubiquitous presence. *Alcaligenes* (sensu stricto) spp. strains are halotolerant (NaCl tolerance up to 8% w/v), and others able to degrade aromatic compounds (e.g. phenol, etc.). Direct ammonia oxidation (Dirammox) discovery under aerobic conditions in strains of *Alcaligenes* spp. suggests its implication and relevance for the global nitrogen cycle. In this study, a detailed analysis of the *Alcaligenes* genus based on phylogenomics was conducted to understand the genus and species boundaries within *Alcaligenes*, with a special focus on osmoprotective capabilities, aromatic catabolism and Dirammox metabolism. *Alcaligenes* (sensu stricto) genome sequences (n = 73) were retrieved from the NCBI database, including an additional 29 genome sequences from the species type strains of *Alcaligenes* (sensu lato) and Alcaligenaceae genera, as outgroups. Three missing genome sequences of type strains of Alcaligenes were determined and assembled. Quality assessment of the assemblies were evaluated, using CheckM, admitting a total of 94 genomes for further analysis. Based on whole-genome comparison, using a core genome tree, obtained by PhyloPhlan3.0, average nucleotide identity (ANIb) and digital DNA-DNA hybridization (dDDH), using the TYGS server, we showed that eight species-clusters comprise the diversity of *Alcaligenes* (sensu stricto), supporting the reclassification of *Alcaligenes faecalis* subsp. *parafaecalis* and *Alcaligenes faecalis* subsp. *phenolicus* to the species level. Genomic context analysis showed that the dnfABCD gene cluster associated with Dirammox, the ectoine-hydroxyectoine biosynthetic gene cluster (ectABCD) and the phenol hydroxylase encoding gene cluster dmpKLMNOP, were conserved in the *Alcaligenes* (senso stricto). Average amino acid identity (AAI), GC content, and the lack of distinctive metabolic traits for *Alcaligenes* (sensu stricto) confirmed

that *Alcaligenes endophyticus* represents a novel genus of the *Alcaligenes* (sensu lato) complex, proposed as *Alloalcaligenes* gen. nov.

Funding: This work was supported by FONDECYT 1200756 (MS, RED), USM grants PI_M_43_2020 and PI_M_23_02 (RED, MS, VSU, CBA).



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Session 6: Bioinformatics & Data Management in Culture Collections

DSMZ Digital Diversity: Building a global biodata infrastructure S6.1

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For over a decade the DSMZ has been developing and providing biodata webservices for the wider microbial research community, such as the Bacterial Diversity Metadatabase BacDive or the "Prokaryotic Names Up-to-date" (PNU) database, which was combined with the List of Prokaryotic Names with Standing in Nomenclature (LPSN) in 2019. More recent developments are the Type Strain Genome Server (TYGS), a high-throughput database-driven platform for state-of-the-art genome-based taxonomy of prokaryotes and MediaDive, the largest database for standardized cultivation media for microorganisms.

Here we present the development of the new IT platform DSMZ Digital Diversity, that integrates the two renowned databases BRENDA and SILVA into the DSMZ database portfolio, with the aim to build a global biodata infrastructure. BRENDA is the world's most comprehensive enzyme database, providing enzyme and enzyme-ligand related data. SILVA is a sequence database specialized on providing high-quality ribosomal RNA sequence data for identification of microorganisms. Together this database consortium covers the fields taxonomy, nomenclature, metabolism, phenotypic and environmental data, as well as high quality ribosomal and genomic sequence data. The goal is to establish an all-encompassing platform for standardized and integrated data and state-of-the-art analysis tools. The DSMZ Digital Diversity (https://stb.dsmz.de) will serve researchers as a one-stop-shop for connecting, retrieving and analyzing data and thereby will pave the way for large scale high-throughput analyses.

MSI-2 / An online identification tool for MALDI TOF Mass Spectra S6.2

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MSI-2 is an online platform built in collaboration with the BCCM/IHEM in Brussels. MSI-2 is accessible online since 2019. The platform hosts six databases 1) *Leishmania*, with all species represented, 2) Fungi, with more than 1600 species of yeasts, molds and dermatophytes, 3) *Enterobacter cloacae* complex, 4) *Amanita* genus, 5) Dipters (with mostly Anopheles species) and *Phlebotomus*. MSI-2 platform places much emphasis on the references spectra belonging to *Aspergillus*, *Penicillium*, *Fusarium* and *Trichophyton* genera in order to meet the main clinical users' expectations.

The MSI-2 platform can be accessed for free at the address https://msi.happy-dev.fr/. Today, it is compatible with Bruker (fid files) and with BioMérieux (.mzml or .txt) spectra as long as they are compressed as .zip files. There are currently 381 active registered users on the application in 39 countries (20 of which are outside Europe and correspond to 60 users), and 19 in European countries (188 users). Each user possess a free account that is protected by a login and a password. A submitted project can contain several spectra and results are expressed as three best species identified with a score ranging from 0 to 100. A threshold of 20 is considered as correct for an identification. The BCCM-IHEM collection number of each of the references can be recovered from the application and each user can compare individual spectra they obtain to all spectra they already submitted through their login and password. Identification results are stored in the application for future accession. A study assessing the reliability of the application for the identification of molds was published in the journal JCM and another, focusing on dermatophytes, in J. Fungi.

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The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics S6.3

Cornet L.[1], Durieu B.[4], Baert F.[1], D'hooge E.[1], Colignon D.[7], Meunier L.[2], Lupo V.[2], Cleenwerck I.[6], Heide-Marie D.[5], Rigouts L.[3], Sirjacobs D.[2], Declerck S.[5], Vandamme P.[6], Wilmotte A.[4], Baurain D.[2], Becker P.[1]

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Microbial culture collections play a key role in taxonomy by studying the diversity of their strains and providing well-characterized biological material to the scientific community for fundamental and applied research. These microbial resource centers thus need to implement new standards in species delineation, including whole-genome sequencing and phylogenomics. In this context, the genomic needs of the Belgian Coordinated Collections of Microorganisms (BCCM) were studied, resulting in the GEN-ERA toolbox, a unified cluster of bioinformatic workflows dedicated to both bacteria and small eukaryotes (e.g., yeasts). This public toolbox is designed for researchers without a specific training in bioinformatics (launched by a single command line). Hence, it facilitates all steps from genome downloading and quality assessment, including genomic contamination estimation, to tree reconstruction. It also offers workflows for average nucleotide identity comparisons and metabolic modeling. All the workflows are based on Singularity containers and Nextflow to increase reproducibility. The GEN-ERA toolbox can be used to infer completely reproducible comparative genomic and metabolic analyses on prokaryotes and small eukaryotes. Although designed for routine bioinformatics of culture collections, it can also be used by all researchers interested in microbial taxonomy, as exemplified by our case study on Gloeobacterales (Cyanobacteria).
This study is published at https://doi.org/10.1093/gigascience/giad022.

The Westerdijk fungal data resources for fungal identification S6.4

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At the Westerdijk Fungal Biodiversity Institute, we maintain a world-renowned microbial genetic resource, the CBS collection with more than 100K living strains of micro-organisms, representing a large percentage of the species in the fungal kingdom that have been cultured to date. In the WI-DNA barcoding project, we have generated more than 200,000 DNA barcode sequences (ITS and LSU), for fungal identification. Two large barcode datasets were released to GenBank in 2016 and 2019 as reference sequences for yeast and filamentous fungal identification respectively, an unprecedented data release event in global fungal barcoding efforts to date (Vu et al 2016, 2019). Both datasets are globally used for describing new fungal species, for taxonomic reclassification, and for the identification of mycobiota from environmental samples (eDNA). They were integrated into ARISE, an Authoritative and Rapid Identification System for Essential biodiversity information, for species identification and for monitoring biodiversity in the Netherlands. The datasets were also used for identifying mycobiota from the gardens around the Netherlands in Citizen Science projects. The filamentous fungi dataset was awarded the Dutch Data Prize 2022.
Based on our barcode datasets, we were able to develop a number of bioinformatics tools to improve accuracy, precision, and speed of fungal identification (Vu et al. 2012, 2014, 2018, 2020). In most ecological studies, only one single similarity cut-off such as 97% is used for species identification. As more and more barcodes were generated, it gradually became clear that the use of single, static threshold for identification is problematic. We demonstrated in our recent study (Vu et al. 2022) that metabarcoding loses resolution and scientific explanatory power by relying on a single similarity cut-off for taxonomic assignment. We introduced dnabarcoder, a software tool to compute dynamic similarity cut-offs for different clades for fungal identification. It was shown that dynamic similarity cut-offs assigned fewer sequences than the traditional similarity cut-offs, but the accuracy and precision were significantly improved.

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Culture collections data management S6.5

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Over the past 30-40 years, many new technologies have emerged that have revolutionized the way we work, and the tools available to us are so advanced that they would have been unimaginable just a few decades ago.
The rapid development of new technologies in the fields of DNA, RNA, and protein analysis has revolutionized biological research and generated huge amounts of complex data. However, managing and analyzing these data sets is not easy and requires sophisticated information technologies and algorithms. Many scientists face difficulties in understanding and applying these tools effectively. To overcome these challenges, new approaches and collaborations are needed between research groups and private companies. Artificial intelligence is one of the promising avenues in this domain. Our group has been working for more than 30 years to develop tools that can handle any data that culture collections need to manage. Our BioloMICS software is now used worldwide by the largest public collections, many private companies as well as international initiatives like MIRRI, MycoBank, Q-Bank, and many others. We are looking forward to tackling new and exciting challenges that will require dedicated, professional and large teams of software developers.

WDCM serves as an information infrastructure for the exploration and utilization of microbial strains preserved worldwide S6.6

Wu L.

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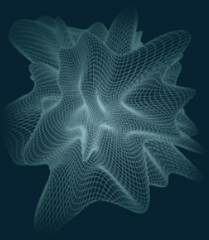
The World Data Centre for Microorganisms (WDCM) aims to provide integrated information services by fully utilizing hyperlinked big data technology for microbial resource centers and microbiologists all over the world. In this report, we provide an overview of WDCM information platform and services. CCINFO (Culture Collections Information Worldwide) provides metadata information on 834 culture collections from 78 countries and regions. The GCM (Global Catalogue of Microorganism) gathers strain catalogue information and provides a data retrieval, analysis, and visualization system for microbial resources. Now it includes more than 520,000 strains from 151 culture collections in 48 countries and regions. The gcType database provides the most comprehensive genomic information on type strains together with user friendly genomic analysis pipelines. The ABC (Analyzer of Bio-resource Citation) is a data mining tool extracting strain related publications, patents, nucleotide sequences and genomes information from public data sources to form a knowledge base. The RSC (Reference Strain Catalogue) maintains an online database of strains listed in ISO and other international or regional standards. It allocates a unique identifier to strains recommended for use in diagnosis and quality control and hence serves as a valuable cross-platform reference. WDCM hope to further develop these platforms to be an integrated data server by cutting-edge information technology for culture collections and microbiologists all over the world.



ICCC 15
INTERNATIONAL CONFERENCE
ON CULTURE COLLECTIONS

Session 7: National & Regional Network of Culture Collections

Microbiological Collections of Paraná Network (CMRP/Taxonline) S7.1

Bittencourt J.[2], **Vicente V. A.[1]**, Panagio L.[3], Svidzinski T.[4], Marinoni L.[1]

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The Center of Microbiological Collections of Paraná Network Taxonline (CMRP/Taxonline) was created in 2012 as part of the Network of Biological Collections of Paraná - Taxonline (http://taxonline.bio.br), with financial support from the Fundação Araucária agency of Parana State (FA), Ministry of Science, Technology and Innovations (MCTI) and National Council for Scientific and Technological Development (CNPq). The CMRP/Taxonline concentrates the microbiological collections from the Federal University of Paraná (UFPR) and associated laboratories from the State University of Maringá/PR (UEM), Federal Technological University of Paraná (UTFPR) and State University of Londrina/PR (UEL), under unified operational protocols for biosafety and collection management, with head laboratory housed at the UFPR. The center acts as depository for academic and research collections in the Parana and several institutions in other Brazilian regions, providing services on conservation of clinical and environmental species strains (types and references) of bacteria, filamentous fungi and yeasts for academic and biotechnological applications. In a recent expansion the center incorporated the collections of mammalian cells and plasmid DNA. The CMRP/Taxonline was created with the aim of ensuring the preservation of microbiological material from academic activities, attending the governmental goals for the preservation of Brazilian biodiversity and current legislation regarding compliance with the Nagoya protocol (https://www.cbd.int/abs/nagoya protocol/signatories /default.shtml - Law nº 13.123, "Biodiversity Law"). The CMRP/Taxonline follow the minimum organizational criteria for preservation, identification and cataloging of microbial cultures in accordance with the recommendations of the General Coordination of Accreditation of Inmetro (Cgcre) (http://www.inmetro.gov.br/credenciamento). Through the Taxonline Network (http://taxonline.bio.br), the CMRP collections became part of the Brazilian Biodiversity Information System /SIBBR (http://www.sibbr.gov.br) and of Global Biodiversity Information Facility (http://www.gbif.org), with databases implemented in SpeciesLink (splink.cria.org.br). The CMRP/Taxonline is a member of the World Federation for Culture Collections - WFCC (https://wfcc.info/home_view) and brings together species of clinical and biotechnological interest with access to databases such as Mycobank to deposit fungal types of strains, it offers open and restricted deposits, with molecular ID of strains. In early 2020, the Taxonline Network has been recognized as a NAPI (New Research and Innovation Arrangement) inside the system of the Science and Technology in Paraná characterized by a new incentive provided by the state development agency, Fundação Araucária (FA). In this way, the CMRP/Taxonline became a consolidated network as a reference collection which has been attracting resources, providing unified infrastructure and protocols among

associated laboratories, and offering courses and training in taxonomy and cultures conservation.

Moroccan Coordinated Collections of Microorganisms (CCMM): The first International Depositary Authority (IDA) in Africa and Nagoya Protocol implementation

S7.2

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For the first time, in 1998, a focal point was created in Morocco, where national microbiological resources were collected and preserved with related information and data, namely the Moroccan Coordinated Collections of Microorganisms (CCMM). CCMM intend to maintain and enhance national microbial genetic resources and is hosted by the National Center for Scientific and Technical Research (CNRST) in Rabat. The CCMM is the unique culture collection in North Africa and the second in Africa. In 2018, it was designated as an International Depositary Authority for the deposit of microorganisms for patent purposes. In addition, the CCMM serves as the focal point for implementing the Nagoya Protocol in Morocco for microbial genetic resources. The organization, purposes, and innovative actions of the CCMM, and the services it provides through the CNRST technical platforms to the scientific and industrial communities, are described in this presentation.

Virus Collection of the new Fiocruz Covid-19 Biobank S7.3

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Viral emergencies have become increasingly frequent, with significant repercussions on public health. Epidemics caused by the viruses SARS-CoV, MERS-CoV, Ebola, Chikungunya, Zika, SARS-CoV-2, and, most recently, Monkeypox marked the beginning of the 21st century. The Oswaldo Cruz Foundation (Fiocruz) coordinates, as part of the Ministry of Health, a well-structured network of epidemiological control and public health, in assistance of the Brazilian Unified Health System (SUS). Numerous national and international reference laboratories and research laboratories in virology were consolidated over the 100 years of the Fiocruz activities. Driven by the Covid-19 pandemic, Fiocruz created the Covid-19 Biobank (BC19-Fiocruz), which has the infrastructure to safely, reliably, ethically, legally, and traceably store human and non-human biological material (viruses), according to quality standards. The area dedicated to the virus collection has infrastructure for isolation, quantification, and molecular and antigenic characterization, compatible with several viral species. In addition to providing reference viral strains and their derivatives, BC19-Fiocruz aims to offer viral isolation and characterization services to different research groups, boosting viral prospecting in Brazil. The architectural design of BC19-Fiocruz, as well as the implementation of its procedures, were planned based on the general requirements for biobanking specified in the ISO 20387:2018, aiming at its accreditation. This initiative is a milestone for establishing Fiocruz's first collection of human pathogenic viruses. One objective of BC19-Fiocruz is to reduce the vast disparity between laboratories holding virus isolates by offering a high-quality facility, staff, and financial support to preserve and distribute viruses. Having accessible reference material at an affordable price in the national market brings democracy, reliability to national research, and the possibility of assertive responses during health public emergencies. In addition to intramural efforts, Fiocruz for the last 15 years supported the consolidation of the Brazilian Network of Biological Resource Centers (BRC-Br Network), whose compliance system was designed following the structure recommended by the OECD Best Practice Guidelines for BRCs and currently is involved with the consolidation of the Brazilian Biological Collections Network, to which the new virus collection will be linked together the other Fiocruz Biological Collections.

Biobank network in Korea S7.4

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'The 3rd master plan for management and utilization of national bio-resources' was established to promote the user-friendly utilization environment of bio-resources in 2020. By 3rd master plan, South Korea's 274 bio-resource banks have been organized into 14 themed clusters, each led by central banks. The 14 clusters include human-derived material, cell lines, animal model, microoragnisms, etc. Each cluster is composed of central banks and branch banks. The central banks, as leader which would be more than one, support and manage branch banks in their cluster. Each spoke bank collects and manages its own resource for supplying to research and industry fields. The central banks collect the data of their branch banks for the integrated system for public service and manage the projects of their branch banks. The branch bank collects and manages its own resource for supplying to research and industry fields.

To promote collaboration between clusters and biobanks in cluster, the Office for Bio-Resource Planning (OBRP) at Korea Bioinformation Center (KOBIC) in Korea Research Institute for Bioscience and Biotechnology (KRIBB) is designated as a secretary of 14 clusters network. The OBRP supports a bio-resource bank management, studies for strategies to utilized bio-resources, and manage the bio-resource information system. It will response national issues and promote collaboration between domestic and global networks.

The Norwegian Culture Collection of Algae (NORCCA): Diversity and Applications S7.5

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The Norwegian Culture Collection of Algae, NORCCA, is the largest algal culture collection in the Nordic countries, with more than 2000 prokaryotic and eukaryotic microalgae strains. NORCCA gives access to an essential asset for research and industries in various fields. The available microalgae are biologically and chemically diverse and can be used for different applications, such as nutritional supplements, feed ingredients, wastewater management, and pharmaceutical or cosmetic industries.

In the past few years, NORCCA became a key player in several projects focusing on strains valorization, linking NORCCA's biological diversity, and the implemented effective and reliable high throughput screening platform, with industries in different fields of algae application. Urban wastewater bioremediation is being explored under ALGECO project. This project is funded by the Research Council of Norway, and aims to promote a green shift into the sector using filamentous green algae co-culture. Other application sectors are currently explored, such as the development of microalgae-based functional aquafeeds to improve fish health and resilience to pathogens (MICROBOOST, funded by the EEA Grants), or lipid-rich diet formulations for larvae scallops (MARBLE, Vestland Regional Research Fund).

NORCCA represents a great resource for researchers around the globe, as well as for industrially and commercial exploitation. The collection intends to keep the work on utilising the algal strains stored and is actively working on expanding the range of applications.

Microbial Resource Center Network in ASEAN and along the Mekong River S7.6

Eurwilaichitr L.[1], Ingsriswang S.[2]

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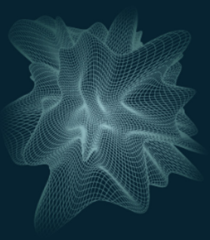
ASEAN member countries are located on the 4 biodiversity hotspots, "Indo-Burma, Sundaland, Wallacea, and the Philippines". This rich natural environment enables ASEAN member countries to generate economic value from its biological resources and enhance its competitiveness in emerging biotechnological fields such as green and clean technologies through research and development. Recognizing the potential application of microorganisms, every ASEAN member country is engaging in research into microbial utilization in various degree, some looking into the development of biopesticide, while others exploring the potential of microorganisms in pharmaceutical or green industrial applications. ASEAN member countries therefore are in a unique position and have high potential to develop bioeconomy to improve the livelihood of their populations.

An ASEAN Network on Microbial Utilization (AnMicro) http://www.anmicro.org was established in 2014 under the auspices of ASEAN Sub Committee on Biotechnology to foster scientific collaboration and strengthen research and human capacity in the field of microbial utilization among academic and research institutes in ASEAN, as well as facilitating dialogues and joint activities between ASEAN and other international organizations. Since its inception, AnMicro has made considerable progress, with the membership has grown to 21 organizations from 8 countries in ASEAN (as of May 2023). AnMicro has been actively promoting the practice of Microbial resource management through training of iCollect (a software uniquely designed for the management of biological collections) which is directly linked to World Data Center of Microorganisms (WDCM). AnMicro and ASEAN Center on Biodiversity (ACB) also launched a project led to an establishment and maintenance of microbial data collection in each ASEAN country, so-called AmiBase (http://Amibase.org). This will enable access to a larger pool of microbial data which were previously kept individually in different formats, subsequently accelerating discoveries and innovations to underpin the development of bioeconomy. AnMicro has established a linkage with other international networks including Asian Consortium for the conservation and sustainable use of Microbial resources (ACM), Asian Network of Research Resource Centers (ANRRC), World Data Center for Microorganisms (WDCM) and World Federation for Culture Collections (WFCC).

In this talk, one of the international scientific networks in the region extended from the ACM and AnMicro will be presented. This network has focused on the exploration of the diversity of microorganisms in the area of the Mekong River. The River covers a distance of approximately 5000 Km from the Tibetan Plateau where it originates to Mekong Delta, and flows through six countries, namely China, Myanmar, Thailand, Lao PDR, Cambodia and

Vietnam. Funded by the Lancang Mekong Cooperation (LMC), the project has joined by Institute of Microbiology, Chinese Academy of Science (IMCAS), China, National Center for Genetic Engineering and Biotechnology (BIOTEC), Thailand and Vietnam National University, Ho Chi Minh (VNUHCM) University of Science, Vietnam. This project aims to use metabarcoding to assess taxonomic richness and abundance of microorganisms and their related ecological communities in the Lancang-Mekong River. The metabarcoding methods has been used to analyze the microbial community (or microbiome) composition at three different areas of the Lancang-Mekong River: the upstream of the river in China, the central part of the river in Thailand, and the downstream area in Vietnam before entering the South China Sea. The data and analysis results contribute to an establishment of biodiversity knowledgebase and new ecological molecular indices for Mekong river ecosystem. The project has been successful mainly due to a collaboration between governmental sector, academic scientists, and citizen-scientists living in the Lancang-Mekong basin. The project has also set up the “Citizen Science” program to raise awareness of science-driven and ecologically-sustainable conservation of Mekong biodiversity.



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INTERNATIONAL CONFERENCE ON CULTURE COLLECTIONS

SESSION 8: ECCO SYMPOSIUM - NEW SERVICES FOR PUBLIC MICROBIAL COLLECTIONS

Sponsored by European Culture Collections' Organization

ECCO

Driving innovation and pushing bioeconomy by offering smart scientific services S8.3

PIÑA M.

European Marine Biological Resource Centre

"Data is the new oil"1. As days go by, this phrase describes more and more accurately the reality we live in. The European Marine Biological Resource Center - European Research Infrastructure Consortium (EMBRC-ERIC) is a pan-European Research Infrastructure dedicated to marine biology and ecology, with a special focus on understanding their function for societal benefit. EMBRC-ERIC is stepping forward to position itself in the bieconomy as a reference for blue data access and coordination by creating a European-scale, omics-based, marine observation network, the European Marine Omics Biodiversity Observation Network (EMO BON) in 2021. Fully funded by the ERIC, EMO BON, is a long-term, sustainable initiative that seeks to contribute towards globally coordinated research in marine biodiversity, encompassing microbial communities to macro-organisms, by applying environmental omics approaches and integrating other forthcoming technologies2. Novel ecosystem services, offered thanks to EMO BON's data analysis, could have several applications for fisheries, such as defining indicators on ecological pressures, water quality monitoring, migratory patterns in a changing environment, amongst others. Data collection and processing is helping aquaculture companies to better integrate ecosystem interactions, like boat traffic and ocean currents, and improve the mesocosm's design for more sustainable and profitable systems. An example is integrated multi tropic aquaculture, or IMTA, an evolving approach for seafood production where multiple aquatic species are farmed together with the objective that the byproduct of one species is the input for another circular economy at its apex! EMBRC-ERIC is starting to contribute actively to achieve UNESCO's Sustainable Development Goal 7, affordable and clean energy, by placing its infrastructure at the service of offshore wind farms and floating solar panels. We support our users in measuring the environmental impacts of novel sites, while in construction or in operation. Moreover, we are able to compare their ecological impact with regional data and data around Europe to determine the collective effect of the turbines in a global level. Data are the means for the marine sector to leverage challenges imposed by climate change and a growing biodiversity crisis and EMO BON is the tool EMBRC-ERIC offers to face these challenges and promote a sustainable management of marine natural resources.

1 Clive Humby, British matematician and entrepreneur.
2 Santi I, et al. 2023; Front. Mar. Sci. 10:1118120. doi: 10.3389/fmars.2023.1118120

The role of culture collections in clinical diagnostics and medical research S8.4

Meyer W.[1,2,3]

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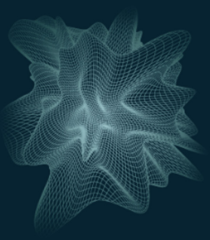
Invasive fungal infections (IFIs) cause 1.6 million deaths/year globally and account for 10% of all hospital-acquired infections. At least 15-25% of pneumonia, 40-60% of meningitis/ encephalitis and 20% of fever/sepsis cases are due to unknown causes, with IFIs suspected in many instances. Transplant, haematology, cancer, immunocompromised and cystic fibroses patients are at a particular risk. Recently pulmonary aspergillosis and mucormycoses have risen dramatically in COVID-19 ICU patients. New IFIs are emerging, e.g., candidemia due to multidrug-resistant *Candida auris*, spreading rapidly and persisting in health care environments. If diagnosed in a timely manner, IFIs are treatable. However, despite available effective antifungal therapies, the death rate from IFIs still can reach 50%, largely because fungal infections are under-recognized and conventional techniques currently used for diagnosis take days to weeks for results and lack specificity and sensitivity. Antifungal sensitivity testing is equally cumbersome. Unacceptable treatment delays, sub-optimal therapy, increased morbidity and mortality, prolonged hospitalisation, productivity loss, and sky-rocketing healthcare costs (e.g., $11.5 billion/year in the US) are common. With this background in mind fungal culture collections are an indispensable bioresource, having a critical role in providing quality-controlled reference strains for the clinical microbiology diagnostics laboratories as well as for development of new diagnostic methods, such as next generation sequencing and metagenomics, antifungal susceptibility testing, and medical research aimed to gain a better understating of mycoses. They are also the fundamental basis for the establishment of reference databases of fungal DNA barcode e.g. the (ISHAM)-ITS database for human/animal pathogenic fungi, http://its.mycologylab.org containing ITS1/2 and TF1alfa reference sequences and in the future whole genome sequences or protein spectra. Their major role is to provide an accurate taxonomy and maintaining nomenclature stability in view of clinical relevance. Increasingly it is also important to maintain not only fungal strains (culture collections) but also store associated clinical samples (e.g. sputum, blood, tissue, faces) (Biobank/Bioresource Centre) to conduct retro- and prospective clinical studies, including epidemiology, molecular and metagenomics research to understand the biological interactions between fungi and with other microorganism (bacteria parasites, viruses, etc.) and to establish the source and the spread of particular genetic clones , caring either high virulence/pathogenicity treats or antifungal resistance markers. They form a basic role in understanding links between the environment, agriculture, and human health (One Health Concept).



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INTERNATIONAL CONFERENCE ON CULTURE COLLECTIONS

SESSION 9: IS_MIRRI_21 SYMPOSIUM ON QUALITY MANAGEMENT SYSTEMS - GLOBAL PERSPECTIVE

Sponsored by the Horizon2020 project "Implementation and Sustainability of Microbial Resource Research Infrastructure for the 21st century (Grant Agreement no 871129)

MIRRI IS21

ISO 21710:2020 Specification on data management and publication in microbial resource centres. S9.2

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Different culture collections use their own data form for in-house data management and also online data sharing, which greatly hinder the further data exchange and integration globally. As a result, it is difficult for all the clients and potential users to access the information of microbes preserved in mBRCs, which severely impedes the further exploitation of the microbial resources in academia and bioindustries. This is especially true for the biotechnology companies focusing on microbial resource development that depend to a great part on the deep utilization of their own and external resources by tapping into the huge body of data.

Therefore, the ISO 21710: Specification on data management and publication in microbial resource centres, which was published in 2020 by ISO technical committee 276 Biotechnology, aiming at realize accurate, reliable and cost-efficiency data access, exchanges and integrations between mBRCs and between mBRCs and the users. It specifies requirements for the data management workflow and information which should be recorded in the in-house database of a microbial resource centre, and also specifies criteria for the data sharing of online catalogue, including minimum dataset and recommended dataset which will be used for the data publication.

High Quality BioBanking in Belgium: the Road towards ISO20387 Accreditation (B3-ISO) S9.3

de Wilde A.[1], Debucquoy A.[1], Guns J.[2], Merhi A.[3], Linsen L.[4], Moons P.[5], Van Rossen E.[6], Huizing M.[5], Emmerechts K.[1], Smits E.[5]

[1]BBMRI.be - Belgian Cancer Registry, [2]Central Biobank, UZBrussel, [3]IPG BioBank and Laboratory of Translational Oncology, Institut de Pathologie et de Génétique, [4]AC Biobanking, University Hospitals Leuven, [5]Biobank Antwerp, Antwerp University Hospital, [6]BELAC, Federal Public Service Economy, SME, Self-employed and Energy

A large part of the irreproducibility of research on human body material originates from the biospecimens used and has been identified as a major undermining factor regarding the translation of research results into clinical applications. As, since the new Royal Decree on the biobanks in 2018, all human body material used for research, has to pass via a Belgian biobank, such biobanks can play an important role in reducing research variation by providing high quality, fit-for-purpose samples and associated data.
The European infrastructure for biobanking BBMRI-ERIC is reflected in the National Node BBMRI.be, established in 2013 at the Belgian Cancer Registry and connects 20 Belgian biobanks. Many of these biobanks arose from existing sample collections, sometimes with limited quality management systems (QMS). The biobank standard (ISO 20387), which was recently published and will be included in the portfolio of the Belgian accreditation organization BELAC, will allow biobanks to formalize their competences and because of its international recognition will allow the Belgian biobanks to demonstrate their readiness to support (inter)national translational research.
To harmonize and enhance the quality management activities of the BBMRI.be biobanks, BBMRI.be develops a stepwise quality improvement program that can be implemented at the individual biobanks.
A kickoff survey elucidated that the starting positions of the Belgian biobanks are diverse. The ambitions of the participating biobanks are in line with the goals of the project and will support substantial quality improvement. ISO20387 implementation support is needed in diverse domains. In cooperation with the participating biobanks, BBMRI.be coordinates the development of guidelines, templates and policies, the organization of webinars, and the development of an interactive FAQ tool. Templates are being harmonized and integrated in the domains of IT, ELSI and sustainability. Self-assessment tools and a stepwise auditing program is developed. At the same time, an accreditation program is being established together with BELAC, ultimately leading to ISO accreditation.
The setup of this program and the implementation of the ISO 20387 standard will substantially contribute to (inter)national translational research and foster collaborations between industry and academia in the biomedical sector.

Acknowledgements: The B3-ISO project is financed by BELSPO in the framework of the ESFRI-FED call.

Improvement of Quality Management System of Biological Resources at KCTC through Accreditation with ISO 20387 S9.4

Song-Gun Kim

KCTC, Korea Research Institute of Bioscience and Biotechnology

Korean Collection for Type Cultures (KCTC) was established in the Korea Research Institute of Bioscience and Biotechnology (KRIBB) in 1985. KCTC joined the World Federation of Culture Collections (WFCC) in 1985 and the World Data Center for Microorganisms (WDCM) in 1986. It has also gained the status of an International Depositary Authority (IDA) from the World Intellectual Property Organization (WIPO) in 1990 under the Budapest Treaty. KCTC has obtained and maintained the certification of ISO 9001: 2015 for its quality management system since 2019.

To improve the quality management system to an international standard, KCTC has been accredited in accordance with the recognized International Standard ISO 20387:2018. KCTC staff has completed the required training courses. The procedures of the detailed steps of accession, cultivation, preservation, and distribution of biological resources have been documented. During the application of ISO 20387 accreditation, a group of auditors visited KCTC for three days and carefully checked all documents, equipment, facilities, and procedures. The auditors checked the competency of KCTC staff by in person interviews. The auditors made a list of nonconformities that required corrective action. KCTC submitted the corrections in documents and the documents were finally accepted. This accreditation of ISO 20387:2018 demonstrates technical competence for a defined scope and the operation of the KCTC quality management system.

Supporting access and benefit-sharing by microbial collections for deposition of microbial strains and those deposited previously S9.5

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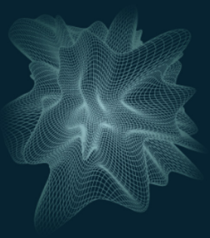
Under the growing awareness and legislation about access and benefit-sharing (ABS), it has become standard procedure to obtain prior informed consent (PIC) and mutually agreed terms (MAT) from the country of origin when conducting biological research in other countries. While these documents, where required by law, are necessary to ensure legislative access to genetic resources, they may not always provide the necessary approvals for all biological research activities. Specifically, third-party transfer of genetic resources is often not approved, which is critical for taxonomists and microbiologists who need to deposit specimens in ex situ collections. This lack of consent from the country of origin can lead to legal ambiguity for deposited strains, which may also be a concern for subsequent users and further undermine the social role of public microbial collections in transferring strains with scientific significance and legal certainty.

To encourage researchers to obtain appropriate approval for depositing strains from their studies, the Microbial Culture Collection (MCC) at the National Institute for Environmental Studies (NIES) has been offering ABS consultation prior to the commencement of overseas microbial research. In order to enhance ABS support, NIES is now working on agreements with public microbial collections in other countries to cooperatively support ABS for collaborative research between Japan and the country, enabling lawful deposition of strains in both collections. To address concerns about traceability when strains are distributed by the country of non-origin, the agreement stipulates reporting distribution records by the collection in the country of non-origin. This agreement is open to the public and is expected to be referenced in international collaborative research proposals as a reliable measure to deposit strains, which facilitate government understanding on scientific practices.

In addition to supporting the future deposition of strains, the agreement also focuses on ABS of strains deposited previously, although not in a legal sense. For these strains, NIES promotes deposition to the collection in the country of origin (repatriation) so that the country of origin has access and control of their genetic resources. NIES also offers reports of distribution record from NIES. The details of these agreements will be presented.



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INTERNATIONAL CONFERENCE ON CULTURE COLLECTIONS

SESSION 10: IS_MIRRI21 SYMPOSIUM ON QUALITY MANAGEMENT SYSTEMS - EUROPE & THE WORLD

Sponsored by the Horizon2020 project "Implementation and Sustainability of Microbial Resource Research Infrastructure for the 21st century (Grant Agreement no 871129)

MIRRI IS21

Multi-site ISO 9001 S10.1

Van De Perre V.[1], Desmeth P.[1], Bosschaerts M.[1]

[1]*Belgian Coordinated Collections of Microorganisms/Coordination Cell (BCCM/CC), Belgian Science Policy Office (BELSPO)*

The working context of microbial biobanks is continuously evolving due to: Biotechnological evolution, new/updated legislation, new/updated policies, participation to national or international infrastructures/organizations… Additionally, customers expect high quality materials and services at low prices. All these requirements result in extra administration for the culture collections.
International standards can guide microbial biobanks in coping with evolving requirements imposed on them by their customers and stakeholders and complying with regulatory issues. Both elements are essential for the sustainability of culture collections. Unfortunately, working with standards can have a negative effect on the administrative workload, when inefficiently implemented.
Multiple international standards are applicable for microbial biobanks: ISO 9001, ISO 15189, ISO/IEC 17025, ISO 17034, ISO 20387, ISO 24088-1... However, what are good strategies to assure a certain quality level in a culture collection or in a network of culture collections, in a given context, on an efficient manner? This lecture will give more information on the multi-site quality management system of the BCCM consortium, ISO 9001 certificated since 2005.

Acknowledgements:
The symposium on quality management systems (sessions 9 & 10) is possible through the IS_MIRRI21 project, financed by H2020 (grant agreement nº 871129), and the support of MIRRI-ERIC.

How to deal with multiple quality management systems S10.2

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International standards and best practice documents, play a crucial role in culture collections (CC) by establishing provisions (such as recommendations, rules and specifications) for various aspects of CC operation. Some key elements for which standards are of utmost importance are: quality assurance, as they provide the framework for standardised processes and protocols conducting to consistent and reliable results as well as compatibility across culture collections; validity and traceability of results, ensuring they are accurate, reliable, and comparable providing confidence to all interested parties; competence assurance; designing mechanisms for ongoing monitoring, managing safety, security, and risk. Adherence to different standards increases the CC robustness and may expand the range of services. Also enhances market force because users/clients are loyal to organizations that are competent and supply high-quality biological material. Different standards may be implemented in culture collections, according to the CC's goals. The challenge of implementing multiple standards requires strategies to provide a unified framework – an integrated management system - to address the requirements of each standard while ensuring consistency and efficiency in operation. It requires accurate planning and coordination. The implementation may include several stages such as conducting a gap analysis, outlining tasks, timelines, responsibilities, and resources, providing training, building awareness, establishing a cross-functional team, monitoring the progress towards the objectives, and performing the review of the integrated system. Implementation of several standards is a challenge requiring careful planning although, the resulting integrated management system provides the culture collections with a comprehensive quality system, contributing to the overall reliability, accuracy, and credibility of the CC operation.

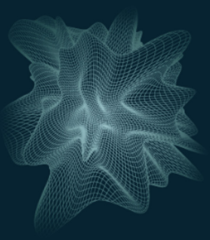
Acknowledgments: This research had the partial financial support of the European Union's Horizon 2020 research and innovation programme under grant agreement nº 871129 - IS_MIRRI21 Project and of "MIRRI-PT (Polo Norte)" project (PINFRA04/84445/2020) funded by the ERDF under the scope of Norte2020 Programa Operacional Regional do Norte.

BBMRI-ERIC- Development of a quality management service for a consortium of biobanks, a nine-year review and outlook S10.3

Wutte A.

BBMRI, AT

The implementation of comprehensive quality measures in biobanks is crucial for ensuring reliable and reproducible research on biological material. Additionally, it plays a vital role in promoting sustainable biobanking and contributes significantly to society's healthcare mission. Hence, it is imperative for biobankers and biomedical researchers to adopt standardized practices, including international standards where applicable, in order to enhance biobanking activities and align them with the latest advancements in research.
In this presentation, you will gain insight into the BBMRI-ERIC Quality Management Services, which have been providing support to biobanks and biomedical researchers across 24 Member and Observer countries since their inauguration in 2013.



ICCC 15
INTERNATIONAL CONFERENCE
ON CULTURE COLLECTIONS

Round Table: Cutting Edge Technologies In Microbial Culture Collection Services

Leverage and revolutionize the way you work with the newest Absolute Q Digital PCR System

RT1

Batista R.

ThermoFisher Scientific

Digital PCR is a robust technique that overcomes variability and low accuracy by allowing absolute quantification of DNA/RNA targets without the need for a standard curve. Dividing the bulk reaction into thousands of smaller independent reactions (micro-chambers) is the basis of dPCR and allows numerous advantages such as high resistance to inhibitors present in particularly difficult samples.

The Applied Biosystems QuantStudio Absolute Q Digital PCR System is a plate-based digital PCR (dPCR) platform powered by proprietary microfluidic array plate (MAP) technology that allows to deliver highly accurate dPCR results. The MAP has 16 dPCR reaction units, made up of 20,480 fixed array microchambers. Once the reagents have been compartmentalized into the microchambers, PCR amplification then proceeds, and the number of microchambers with successful DNA amplification are counted.
This state-of-the-art technology allowed to overcome most of the main limitations of other existing digital PCR platforms. With this technology there is:

- less sample/reagent waste (95% of the sample is effectively analyzed)
- high consistency in the analysis (a minimum of 20000 independent reactions are analyzed per array)
- high confidence (through an auto false-positive rejection algorithm).
- MAP technology enables all the necessary steps for dPCR—compartmentalizing, thermal cycling, and data acquisition to be conducted on a single instrument.
- The QuantStudio Absolute Q dPCR workflow is identical to the qPCR workflow to improve ease of use, minimize hands on steps, and maximize consistency
- Fast time-to-results in just 90 minutes.
- Multiplexing capabilities with up to 4 targets being amplified in the same Array.
- High flexibility allowing from 4 to 16 samples per run

The QuantStudio Absolute Q Digital PCR System advantages make it the ideal platform when quick and reliable absolute quantification, rare target detection/quantification and SNP discrimination, high confidence copy number variation or very sensitive gene expression are needed. Come learn more about this technology and be part of the (R)evolution.

E MALDI Biotyper® – Recent Advances… RT2

Rocha R.

Portugal Bruker Director, PT

Classical biochemical techniques that detect different metabolic properties of microorganisms typically take hours or even days and often lack specificity.
Using the MALDI Biotyper, you can go from sample to result within minutes.
MALDI Biotyper systems provide high-speed, high-confidence identification and taxonomical classification of bacteria, yeasts, and fungi.
Classification and identification are based on proteomic fingerprinting using high-throughput MALDI-TOF mass spectrometry.
Bruker leading this technology since 2010, continuously improve this solution, and develop easy workflows and other techniques around to go further than the simple identification…

Miniaturization of DNA analysis, a game changer for food safety and quality RT3

Prado M.

International Iberian Nanotechnology Laboratory (INL)

The main objective of the Food & Quality Research Group is the development of analytical approaches based on the combination of molecular biology (mainly DNA based methodology) and nano and microfabrication technology in order to provide the food industry and control laboratories with reliable analytical tools.
Following this objective, the methodology is based on working on very specific analytical needs and on using a modular approach for each of the steps of the analytical process. This approach, help us to evaluate and to choose the best method in each case, to have a sound integrated final product, and at the same time a wide-range of intermediate products that can be used by themselves to solve specific analytical challenges.
Figure 1 summarizes the overall approach and research lines. Our topics of interest involve the detection of foodborne pathogens, the detection of allergenic ingredients in food products and food authenticity.

Research Lines:
Sample preparation

Sample preparation is the series of steps required to transform a sample to a form suitable for analysis, the reliability of the conclusions drawn from food analysis greatly depends upon on this step. We work on: (i) the development of pre-treatment steps in order to overcome some of the limitations associated with food analysis and (ii) on the development of tailored, miniaturized, automatized and faster sample preparation techniques. Microscale solid phase extraction (μSPE) is used for on-chip DNA extraction and purification, being possible to put in contact a higher volume of initial binding material with the solid phase and recover the DNA in a lower volume during the elution phase. This feature allows to concentrate the DNA when minute amounts are present in the sample (e.g. olive oil, wine), for complex matrixes such as processed foodstuff and for environmental samples (e.g. water samples).

Alternative DNA amplification methods:

Food & Quality Safety Research Group is working on new amplification techniques, in their combination with NPs and on the evaluation of DNA based analytical methods for food analysis. We work on isothermal amplification techniques, such as Loop-Mediated Isothermal Amplification (LAMP), and Recombinase Polymerase Amplification (RPA), specially interesting for miniaturization purposes. Other alternative techniques currently being used include Ligation Chain Reaction (LCR) which allows to distinguish very closely related organisms and high similar DNA sequences.

Nanoparticle-assisted DNA analysis:

The use of nanomaterials for DNA analysis has the potential of providing increased sensitivity, multiplexing capabilities, and reduced costs. Exploiting the features of

nanoparticles (NPs) is considered to be a good alternative to foster the potential of diagnostics and analytical method development. NPs, such as gold NPs (AuNPs) and gold nanorods (AuNRs) are being used for DNA detection taking advantage of their optical properties.

The Italian network of culture collections: new cutting-edge technologies, new fields of research, new challenges to face

RT4

Varese C. G.[1], JRU MIRRI-IT

[1]*University of Torino*

The JRU MIRRI-IT (www.mirri-it.it) is the Italian network of microbial culture collections which currently includes 24 partners operating in various sectors (clinical, food, environmental, agricultural, cultural heritage, etc.). The network includes collections of viruses, microalgae, bacteria and fungi distributed throughout the national territory; 8 of its partners work under a certification and accreditation scheme.

Thanks to the funding of the PNRR project SUS-MIRRI-IT, the Italian network wants to focus on the new opportunities that microbiology poses to the civil society to face challenges such as improving human well-being and food quality, facing the climate change and environmental pollution.

From the last 6 months (and for the next two years) the JRU has focused its interest on some activities under the umbrella of those carried out by MIRRI-ERIC:

- development of Standard Operation Procedures (SOPs) for sampling, characterization, conservation and processing of microbiomes in several sectors i.e. fermented foods, clinical samples, soil, plants, insect;
- development of a national network of laboratories to implement the use of MALDI-TOF as a gold standard for the rapid identification of microorganisms in other fields of application besides the clinic;
- set up of a national plan for whole genome sequencing (WGS) of microorganisms;
- creation of a national database of microbial resources according to FAIR criteria;
- creation of new pipelines for microbiomes' description and genomes' annotation.

In addition, experts of JRU MIRRI-IT are engaged in the activity of Ministerial technical boards to raise awareness of national Policy on the conservation, protection, and enhancement of microbial resources biodiversity. A brief overview on the preliminary results obtained by the JRU, and an excursus on the different foreseen activities and potentiality of the network will be discussed and presented.

Implementation of cutting-edge technologies for the benefit of culture collections: the case of Micoteca da Universidade do Minho

RT5

Carla Santos[1,2], Soares C.[1,2], Venâncio A.[1,2], Lima N.[1,2]

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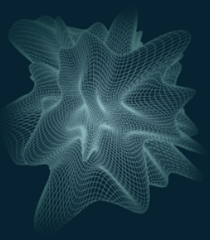
[2]LABBELS - Associate Laboratory

Since 1890, microbial culture collections (CCs) have been providing services to the scientific community, acting as reservoirs and providers of microorganisms, including their living cells, genomes, and information, being key players for the development of new and more sustainable products, compounds, and practices. For this reason, the Organisation for Economic Cooperation and Development (OECD) recognized CCs as "a key component of the scientific and technological infrastructure of the life sciences and biotechnology". Along with preservation, deposit, and transfer of microorganisms, CCs can provide additional services such as strain identification and characterization, consulting, patent deposit, and training. Through these activities, CCs play a fundamental role in different fields, including agriculture, food security and safety, genetics, industrial and medical microbiology.

However, to increase knowledge and maximise the benefits of their holdings for biotechnological applications, CCs must face new challenges and embrace the cutting-edge technologies that allow them to better characterize the microbial strains in their possession. CCs must thoroughly study strain capabilities, dedicating time and resources to the research and characterization of promising strains for biotechnological applications. Furthermore, the generated information regarding function, biosafety, taxonomy, and application, among others, must be made publicly available in CCs catalogues to promote the extensive use of such promising strains.

This work will present the example of Micoteca da Universidade do Minho (MUM) and how it is implementing several cutting-edge technologies for the benefit of biotechnology and to respond to client demands, following a strategy integrated in a coordinated effort inside the MIRRI-ERIC Portuguese node. By installing several technological platforms, including cryopreservation in liquid nitrogen, ultra-performance liquid chromatography-mass spectrometry (UPLC-MS), matrix-assisted laser desorption ionization–time-of-flight mass spectrometry (MALDI-TOF MS), and next generation sequencing (NGS), MUM will advance and improve the conservation, biochemical, physiological, and genetic characterisation of more than 1,000 strains it has available in its catalogue, while also assuming a leading role in the microbiome revolution that we are currently living.

This study partially supported by the Portuguese Foundation for Science and Technology (FCT) under the scope of the strategic funding of UIDB/04469/2020 unit and LABBELS – Associate Laboratory in Biotechnology, Bioengineering and Microelectromechanical Systems (LA/P/0029/2020); and by "MIRRI-PT (Pólo Norte)" project (PINFRA04/84445/2020) funded by the European Regional Development Fund under Norte2020-Programa Operacional Regional do Norte, and by IS_MIRRI21 project (grant agreement nº 871129) funded by the EU H2020 research and innovation programme.



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WDCM & MIRRI Joint Training Course for Big Data of Open Science in Microbiology

Sponsored by World Data Centre of Microorganisms and IS_MIRRI21 (Grant Agreement nº 871129)

WDCM WORLD DATA CENTRE FOR MICROORGANISMS

MIRRI IS21

Introduction to WDCM global collaborative work TC3

Ma J.

WFCC-MIRCEN World Data Centre for Microorganisms, Institute of Microbiology, Chinese Academy of Sciences, China

WFCC-MIRCEN World Data Centre for Microorganisms (WDCM, http://www.wdcm.org/) has long been committed to facilitating the application of cutting-edge information technology to improve the interoperability of microbial data, promote the access and use of data and information, and coordinate international open science and cooperation between culture collections, scientists and other user communities.

To help plenty of culture collections that cannot make their data available online as well as advocate open science and global cooperation, WDCM launched the Global Catalogue of Microorganisms (GCM) (http://gcm.wdcm.org/) project in 2012. Up to now, GCM (http://gcm.wdcm.org/) has become one of the largest data portals for public service microbial collections and several international culture collection networks, providing data retrieval, analysis, and visualization system for microbial resources. Furthermore, GCM gradually developed into a knowledge base linking taxonomy, phenotype, omics data as well as relative scientific papers and patents with its catalogue information, which currently has aggregated 525,563 strains and other holdings (plasmids and antibodys) deposited in 151 collections from 51countries and regions.

WDCM announced the launching of Global Microbial Type Strain Genome and Microbiome Sequencing Project in 2017, marking the GCM project has begun to enter a new stage (GCM 2.0). Focused on exploring the genomic information of microorganisms, this project has planned to sequence all uncovered prokaryotic type strains together with select eukaryotic type strains, construct a database for genomics data sharing based on open science, and also provide online data mining environment. Working groups responsible for selecting bacterial and fungal strains, drafting SOP, managing intellectual property right and legal issues and constructing database have already embarked on the pioneer stage of GCM 2.0. The project will establish an open science network for type strain sequencing and functional mining, and complete genome sequencing of over 10000 species of microbial type strains in five years.

The WDCM 10K type strain sequencing project TC4

Wu L.

WFCC-MIRCEN World Data Centre for Microorganisms, Institute of Microbiology, Chinese Academy of Sciences, China

The global catalogue of microorganisms 10K type strain sequencing project focuses on closing the genomic gaps for the validly published prokaryotic and fungi species1, which including two core subprojects, sequencing 10,000 bacterial and archaeal type strains and sequencing of some of the fungal type strains. Outcomes of the project will ensure to close currently existing large gaps in the available genomic sequencing information published for bacterial and archaeal species. This gap is even larger for fungal type strains. GCM lead and internationally coordinated effort will facilitate generation of more comprehensive genomic information platform to be used for research via in-depth genome mining. Information to be generated on the taxonomic, phylogenetic, functional existence and functional genes of microorganisms will be of immense value for advancement of biological sciences and biotechnology.

In this project, 10,000 type strains will be genome sequenced (http://gcm.wdcm.org/typestrain/) and the WDCM will cover the costs for sequencing services, database system and data analysis. Upon completion raw data and analysis results will also be published online for free access. So far 25 collections from 16 different countries have accepted to take part in the project.

The project has established standard operational procedures for DNA extraction, sample submission, sequencing, and data processing to ensure that all genetic resources, data, and metadata associated with type strains are appropriately obtained, recorded, and stored. A project proposed by the WDCM, “CD 20170: Specification on Data Integration and Publication in Microbial Resource Centers,” which would meet International Organization for Standardization standards, is under development.

The GCM type strain sequencing project encourages all culture collections to participate in this international collaborative project. Interested parties should be willing to provide DNA for type strains held in their collections. All microbiologists and institutions from related fields are welcome to submit subprojects for genomic data-related research questions. In addition, the WDCM has established a MOU with the International Journal of Systematic and Evolutionary Microbiology and Bergey's Manual Trust in March 2019 and will provide free services for genome sequencing and annotation required for description of new species and publication.

The YEASTRACT+ database to explore the transcription regulation and metabolic model data in yeasts

TC5

Teixeira M.C., Viana R., Palma M., Oliveira J., Galocha M., Mota M.N., Couceiro D., Pereira M.G., Antunes M., Costa I.V., Pais P., Parada C., Chaouiya C., Sá-Correia I., **Monteiro P.T.**

YEASTRACT+ (http://yeastract-plus.org/), created and maintained for more than 15 years [1,2], is a database on yeast transcriptional regulation, including more than 300.000 transcription regulatory associations between transcription factors (TFs) and target genes in 11 yeast species.

These species are grouped into thematic clusters: YEASTRACT, the original database focusing on *Saccharomyces cerevisiae;* PathoYeastract focusing on pathogenic yeasts of the Candida genus; and NCYeastract focusing on non-conventional yeasts of biotechnological relevance. These upgrades accompanied the more recent notion of the importance of exploring yeast biodiversity and the consequent reinforcement of scientific research and technological development dedicated to non-Saccharomyces yeasts.

The genomic data from each species is obtained from the corresponding reference genome retrieved from GenBank. Regulatory associations are manually curated and based on published data. For each species, these regulatory associations form a network where each node represents a transcription factor and/or a gene, and the edges their associations. Each edge is associated with the corresponding experimental setup and environmental conditions in which the regulatory association was experimentally characterized.

By computing the homology between genes of different species, YEASTRACT+ builds a multilayer network to offer functionalities and visualization tools for cross-species comparative genomics of transcription regulation in yeasts. These tools, include network comparison between a species, or the homologous network, i.e, the projection of regulatory associations of a more studied species over genes of a less studied species.

Also, YEASTRACT+ provides visualization tools to map transcription factor binding sites on the promoter of target genes, as well as search capabilities of novel binding sites on the promoter of all YEASTRACT+ genes, or the search of YEASTRACT+ binding sites on user provided promoters.

Lately, a new set of tools, currently implemented for *S. cerevisiae* and *C. albicans*, is offered combining regulatory information with genome-scale metabolic models to provide predictions on the most promising transcription factors to be exploited in cell factory optimization or to be used as novel drug targets.

The YEASTRACT+ team aims to include genome-scale metabolic models for the remaining species, as well as to expand the set of network modeling tools and the number of options offered in this context, particularly the possibility to predict synthetic lethality as a means to identify possible targets for combination therapy.

In addition to the 7 articles published to date in the Database issue of Nucleic Acids Research describing the regular updates and improvements to the initial database on *S. cerevisiae*

(YEASTRACT), the yeast research community has, at disposal, guidelines and relevant examples on how to fully explore this bioinformatics tool [3,4].

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[2] Teixeira et al. NAR 51:D785-D791, 2023
[3] Godinho et al. FEMS Yeast Res 21(6):foab045, 2021
[4] Monteiro et al. NAR 45(D1):D597-D603, 2017

Acknowledgements
We acknowledge project LISBOA-01-0145-FEDER-022231 - Biodata.pt Research Infrastructure, and national funds through Fundação para a Ciência e a Tecnologia (FCT) for projects 2022.01501.PTDC and PTDC/BII-BIO/28216/2017, multi-anual funding of iBB (UIDB/04565/2020 and UIDP/04565/2020), i4HB (LA/P/0140/2020), and INESC-ID (UID/CEC/50021/2020), and PhD fellowships to RV, MG, MNM, MA and IVC.

The UCCCB collection as a resource for bacteria PHA producers' genetic diversity assessment

TC6

Proença D.[1,2], Henriques T.[1,3], Morais P.[1,2]

[1]University of Coimbra, Centre for Mechanical Engineering, Materials and Processes, UCCCB, Department Of Life Sciences, [2]UCCCB – University of Coimbra Bacteria Culture Collection, Department of Life Science, University of Coimbra, [3]IATV – Instituto do Ambiente Tecnologia e Vida

The University of Coimbra Bacteria Culture Collection (UCCCB) is the Portuguese bacterial culture collection that integrates the World Federation of Culture Collections the Portuguese microBiological Resource Centre Network (Pt-mBRCN/MIRRI-PT). The collection includes 3 sub-collections according to the origin of isolation:
i) Environmental collection with isolates from water and sediments from hydrothermal zones on the ocean floor, hospital environments with different levels of antibiotic resistance, metal-contaminated environments, river sediments, and from soil; ii) Human host collection with isolates from hospital inpatient samples; iii) Host-interaction collection with isolates from plants, endophytic or plant pathogens, frog and nematodes.
In order to find not yet described bacterial polyhydroxyalkanoates (PHA) producers, 110 strains from the 3 sub-collections, belonging to 5 different phyla, 11 classes, 24 orders, and 50 families were screened. The 33 selected polymers-producing strains belonged to 5 different classes. A deep characterization of the producers revealed four strains belonging to genera that have never been reported as PHA producers. The genomic analysis of these strains revealed the presence of phaC gene in all strains, although belonging to different phylogenetic classes, with a diversity in the organization and the number of additional genes. The chemical characterization of the polymers revealed structural differences when comparing polymers produced by strains belonging to different genera.
The work performed at UCCCB highlighted the relevance of this culture collection as a valuable source of novel and unique strains that are an important resource for the discovery of new compounds with biotechnological applications. UCCCB is funded by National and European projects and works as a technical platform to support research in UC and abroad, and will maintain novel microorganisms awaiting future exploitation by biotechnology.

Open research data for use and re-use TC7

Ana Alice Baptista

ALGORITMI Center, University of Minho

Open Research Data (ORD) “refers to the data underpinning scientific research results that has no restrictions on its access, enabling anyone to access it” (European Commission, Directorate-General for Research and Innovation, n.d.). Researchers open their data for various reasons, including for: transparency, public scrutiny, and for use & re-use.

For these reasons, especially use & re-use, the data has to be made available the right way: richly described using metadata, with an appropriate license, with detailed provenance information and meeting relevant community standards (Wilkinson et al., 2016). The Data on the Web Best Practices (Lóscio et al., 2017) presents 35 detailed best practices for publishing data on the web.

Although still more concerned with the publication of data, its re-use is beginning to gain ground in studies and funding programs. Paradigmatic examples of data re-use were clearly visible during the SARS-Cov-2 pandemic, which allowed to accelerate drug and vaccine development, as well as public health decision-making. The "Citizen science in the surveillance and monitoring of mosquito-borne diseases" (European Commission. Directorate-General for Research and Innovation. et al., 2019) is also a good example of re-use with an impact on the quality of human life. Another prominent example, is FishBase, a digital catalogue of fishes that collects a variety of data on 34,300 fish species (Pavone, 2020).

Re-use of ORD opens doors to re-analysis, re-interpretation, and relation with other data from other sources (including own). It provides ground for new advances, new theories, contributing to accelerate scientific progress. Researchers should therefore not only endeavour to make good data available, but also re-use data provided by other researchers.

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From compliance to capacity building: how European biological resource centres pave the way for benefit sharing

TC8

Anne Emmanuelle Kervella

EMBRC-ERIC

As custodian of biodiversity, biological resource centres are essential services to foster scientific research In the European Union, these facilities have been structured around the concept of research infrastructures, which was promoted from the noughties by the European institutions and member states as a means to mutualize, monitor and combine national research efforts, in the roadmap of the European Strategic Forum for Research Infrastructures (ESFRI).

ESFRI biological resource centres abide by the overarching European Open science policy and provide interoperable and standardised trusted data. They process large datasets of sequences, metadata, historical time series and literature resources, curated and stored in European open access data centres. By cooperating with the ESFRI digital research infrastructures, they feed the European Open Science Cloud, a centralized European gateway to open data supported by the European institutions.

EMBRC is on the ESFRI roadmap since 2008, it launched its negotiation in 2013, and has been granted an ERIC in 2018. EMBRC is governed by 9 countries, with a statutory seat in Paris, and is the single entry-point to a wide range of scientific facilities placed in biological marine stations along the European coasts: coastal observatories, in-situ coastal resource centres, about 10 biobanks and more than 30 culture collections. EMBRC provides access to genetic resources from 119 countries, 118 parties to the Convention on Biological Diversity and thus having endorsed the principle of fair and equitable sharing of benefits for the use of genetic resources.

As a research infrastructure whose mission depends strongly on access to and supply of bioresources and biodiversity, EMBRC is constantly improving its activities and standards *"from sampling to data"*. In 2021, EMBRC has adopted best practices for stewardship of bioresources, to guide ABS compliance and is developping a centralized catalogue of bioresources (TRACE) with a resource passport attached to each biological material.

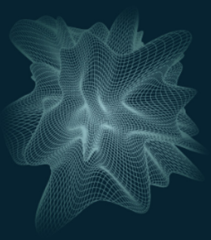
The European biological resource centres serve the structuring effort of the European Research Area, are European based but global by nature (hosting non-EU samples, strains and sequences) and by design (providing services outside of the EU), and help make science more globally accessible, inclusive and equitable for the benefit of all. Their challenge is now to build strong synergies with large biodata infrastructures to foster European capacity in life sciences.

E Culture Collections catalogues are open doors to the microbial world. Closing remark of the WDCM-MIRRI Joint Training Course for Big Data of Open Science in Microbiology TC9

Philippe Desmeth

Belgian Coordinated Collections of Micro-organisms - Belgian Science Policy Office
WTC III Simon Bolivar boulevard, 30 Box 7, 1000 Brussels, Belgium

When users search through biobank catalogues, it is like looking through open windows and discovering what the microbial world has to offer. Yet scientists are rarely aware of the enormous work behind the list of strains they consult. The biobank catalogues are the sum of many efforts.
Culture collections use the most advanced conservation techniques to ensure the long-term preservation of the living material they provide. They manage stock optimally by operating within a quality management system. Culture collections use state-of-the-art technologies to characterize the microbiological material they collect or receive in deposit.
The information system stores and processes not only scientific and technical information, but also administrative and clerical data to ensure that the material provided is fit-for-purpose from both a scientific and legal perspective.
The material is well identified and named according to the updated nomenclature, has the characteristics expected both for trials and for standardized industrial production under safe conditions and respecting the intellectual property rights of each.
When scientists and technicians eventually receive the microorganisms, they receive the keys to exploring and exploiting the microbial world through the professional dedication of the door openers that are culture collections.
As demonstrated again at the 15th International Conference on Culture Collections organized and hosted by one of them at the University of Minho in Braga, it is by working together and jointly improving their skills that culture collections, biobanks, will be able to collectively face the scientific, technical, legal and social challenges they face daily.



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INTERNATIONAL CONFERENCE
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Posters

The Czech National Collection of Type Cultures (CNCTC), its history and present P4

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This year marks the 76th anniversary of the founding of the Czech National Collection of Type Cultures (CNCTC), which operates within the Centre of Epidemiology and Microbiology at the National Institute of Public Health (NIPH) in Prague, Czech Republic. The CNCTC was officially established in 1947 as a central collection of local culture collections managed by individual national reference laboratories. The first curator was Dr. Juraj Strauss, during whose tenure the collection gained type strains from foreign collections, he introduced uniform documentation and registration of cultures of bacteria and applied modern method of strain preservation like lyophilization. The next curator of the collection was Dr. Jiří Šourek, who led the collection for over 40 years and significantly expanded it to 5000 strains. Under his leadership, the collection was already registered with the acronym CNCTC in the World Federation of Culture Collections (WFCC) and in the European Culture Collections Organisation (ECCO). Since 1999 the collection was managed by M.D. Helena Žemličková, Ph. D., and the collection was granted the status of a National Reference Laboratory. She was responsible for an extensive revision of the collection (biochemical methods). In 2014 (till now), the collection was handed over to Dr. R. Šafránková, PhD. Revision of microorganisms in the collection is based on the usage of modern molecular methods including matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) identification, 16S rDNA gene sequencing analysis, and the whole genome sequencing. In this symposium, we would like to present the activities of CNCTC, which are dedicated not only to the preservation of cultures of microorganisms, and their distribution (sale), but also to the preparation of External Quality Assessment in bacteriology in the Czech Republic, revision and publication activities

Korean Gut Microbiome Bank (KGMB) P5

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The human gut is colonized by billions of commensal microbes, which make up a complex and diverse community known as the gut microbiota. Physiological and omics-based studies to date have shown that the potential exists for human health and disease risk to be mediated or modulated by the gut microbial community. Until now, many microbiome studies have focused on metagenomic analyses, which has resulted in insufficient availability of gut microbes, making it difficult to conduct follow-up studies utilizing microbial resources. To study the relationship between the gut microbiome and disease, it is necessary to study the characteristics and functions of different strains that show distinct differences in population in healthy and diseased individuals. Therefore, collecting gut microbiota strains is essential to study the gut microbiome. We started the Korean Gut Microbiome Bank (KGMB) project to overcome these limitations in microbiome research and to conduct research on the Korean gut microbiome in 2016. So far, we have isolated and preserved 13,066 strains belonging to 457 species from 835 healthy Koreans. Now, we distribute the gut microbiota that we have isolated and preserved on our website (https://www.kobic.re.kr/kgmb_dist). We also provide the results of metagenomic analyses of gut microbial community and the coding sequences (CDSs) in whole genome sequences of each isolate to help recipients to select strains for the purpose (https://www.kobic.kr/kgmb). In addition, we are conducting multi-omics analyses, such as transcriptomics, proteomics, and metabolomics of the isolated strains and will also disclose these data. For those who want to use resources that are not currently distributed, we will support recipients through consultation. We hope to activate microbiome research and industry through the utilization of KGMB resources.

This work was supported by the National Research Foundation of Korea (NRF) funded by the Ministry of Science and ICT (NRF-2016M3A9F3947962) and Korea Research Institute of Bioscience and Biotechnology (KRIBB) Research Initiative Program.

Functional differences driven by evolutionary and competitive strategies of *Akkermansia muciniphila* in gut

P7

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Akkermansia muciniphila is a commensal bacterium using mucin as its sole carbon and nitrogen source. A. muciniphila is a promising candidate for next-generation probiotics to prevent inflammatory and metabolic disorders, including diabetes and obesity, and to increase the response to cancer immunotherapy. We started the Korean Gut Microbiome Bank (KGMB) project to conduct research on the Korean gut microbiome in 2016. In this study, a comparative pan-genome analysis was conducted to investigate the genomic diversity and evolutionary relationships between complete genomes of 27 *A. muciniphila* strains, including KGMB strains isolated from healthy Koreans. The analysis showed that A. muciniphila strains formed two clades of group A and B in a phylogenetic tree constructed using 1,219 orthologous single-copy core genes. Interestingly, group A comprised of strains from human feces in Korea, whereas most of group B comprised of strains from human feces in Europe and China, and from mouse feces. As group A and B branched, mucin hydrolysis played an important role in the stability of the core genome and drove evolution in the direction of defense against invading pathogens, survival in, and colonization in the mucus layer. In addition, WapA and anSME, which function in competition and post-translational modification of sulfatase, respectively, have been a particularly important selective pressure in the evolution of group A. KGMB strains in group A with anSME gene showed sulfatase activity, but KCTC 15667T in group B without anSME did not. Our findings revealed that KGMB strains evolved to gain an edge in the competition with other gut bacteria by increasing the utilization of sulfated mucin, which will allow it to become highly colonized in the gut environment. Furthermore, we are studying how differences in the genomes of these *A. muciniphila* strains along their evolutionary pathways have influenced their characteristics and functions in gut.

This work was supported by the National Research Foundation of Korea (NRF) funded by the Ministry of Science and ICT (NRF-2016M3A9F3947962) and Korea Research Institute of Bioscience and Biotechnology (KRIBB) Research Initiative Program.

Comparative genomics reveals the adaptive evolution to temperature of genus *Cryobacterium* and proposal of 19 novel species isolated from glaciers P9

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The bacterial genus *Cryobacterium* includes at present 14 species that live in cryospheric environments. We analyzed 101 genomes of *Cryobacterium* with pure cultures obtained from Genbank. They could be classified into 44 species based on average nucleotide identity (ANI) analysis, showing the diversity of Cryobacterium. Among these, 19 strains in our laboratory were isolated from the glacier samples in China. The pairwise ANI values of these 19 strains and known species were less than 95%, indicating that they represented 19 novel species. The comparative genomic analysis showed significant differences in gene content between the two groups with maximum growth temperature (Tmax) ≤20°C and Tmax >20°C. A comprehensive and robust phylogenetic tree, including 14 known species and 19 novel species, was constructed and showed five phylogenetic branches based on 265 concatenated single-copy gene sequences. The Tmax parameter had a strong phylogenetic signal, indicating that the temperature adaptation of Cryobacterium was largely through vertical transfer rather than from horizontal gene transfer and was affected by selection. Further, using polyphasic taxonomy combined with phylogenomic analysis, we proposed 19 novel species of the genus *Cryobacterium* by the following 19 names: *Cryobacterium serini* sp. nov., *C. lactosi* sp. nov., *C. gelidum* sp. nov., *C. suzukii* sp. nov., *C. fucosi* sp. nov., *C. frigoriphilum* sp. nov., *C. cryoconiti* sp. nov., *C. lyxosi* sp. nov., *C. sinapicolor* sp. nov., *C. sandaracinum* sp. nov., *C. cheniae* sp. nov., *C. shii* sp. nov., *C. glucosi* sp. nov., *C. algoritolerans* sp. nov., *C. mannosilyticum* sp. nov., *C. adonitolivorans* sp. nov., *C. algoricola* sp. nov., *C. tagatosivorans* sp. nov., and *C. glaciale* sp. nov. Overall, the taxonomy and genomic analysis can improve our knowledge of phenotypic diversity, genetic diversity, and evolutionary characteristics of *Cryobacterium*.

Microbiological Resource Unit (Urmicro) of the Federal University of Lavras-Minas Gerais/Brasil P11

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The Collection of Cultures of Microorganisms of the Department of Food Science (CCDCA) of the Federal University of Lavras (UFLA) was created in 2010 with the mission of maintaining representatives of the Brazilian microbial biodiversity, being representative of the Genetic Heritage Management Council of the Ministry of Environment. Since then, the collection has been modernized, monitored and funded through research projects and funding agencies. Due to the demand for the deposit of isolates of filamentous fungi, yeasts and bacteria, as well as the need for preservation and adequate maintenance of these microorganisms, the constant updating of the collection and the guarantee of availability of reliable and quality data, a process of restructuring and adaptation of the collection began in 2020 for the implementation of the Microbiological Resources Unit (URMICRO) through the Taxonomy Training Program, funded by the National Council for Scientific and Technological Development (CNPq). Currently, URMICRO has a collection of approximately 1650 isolates of filamentous fungi and 250 yeasts from several substrates, such as soil from native areas (Atlantic Forest, Cerrado and Caatinga), soil from agricultural areas (coffee and wine grapes), agricultural products (coffee, wine grapes) and food (cheese, sausages, nuts and grains). Some of the genera that compose the collection are *Aspergillus*, *Penicillium*, *Talaromyces*, *Cladosporium*, *Mucor*, *Geotrichum*, *Paecilomyces*, *Candida*, *Kluyveromyces*, *Yarrowia*, *Debaromyces*, *Trichosporon*, and *Pichia*. URMICRO currently uses three preservation methods (cryopreservation at -80 ºC, Castellani and filter paper) to maintain the viability and morphological, physiological and genetic integrity of the cultures over time. Besides the preservation and maintenance of the Brazilian genetic heritage, URMICRO also aims to provide pure cultures that can be used in several biotechnological applications (production of enzymes, biological control), teaching and research. URMICRO allows the preservation and proper cataloging of the isolates, generating a database accessible to the scientific community in general, thus integrating part of a country's genetic heritage.

Microbial Terroir in Artisan Cheeses Produced in Minas Gerais, Brazil P12

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Artisnal Minas Cheese (AMC) is a product of historical and cultural heritage, produced in different regions of the state of Minas Gerais, Brazil. This cheese carries with it unique attributes, specific to each location, culture, and tradition where it is produced. Its production is made with raw milk, by means of artisanal techniques, meeting the current good agricultural practices, being the main source of income for several producers in the family agribusiness. Even though it is a regional product, AMC has been gaining prominence since 2017, especially after several producers had their cheeses awarded in important international competitions such as the "Mondial du Fromage et des Produits Laitiers" held in Tour, France. The composition of the microbiota of the AMC from a particular region is extremely important, as it contributes to the unique quality and safety characteristics of the food. However, this type of cheese still remained informal in Minas Gerias State because there was no research on the identification of the predominant fungi on its surface. Based on the request of producers, the project Microbial terroir of Artisanal Minas Cheese was started at the Federal University of Lavras. The microbial terroir, so called, is closely related to the natural factors observed (geography, geology, climate and human work), the raw materials used, the breed of dairy cows, animal feed, and the human influence on the manufacturing stages. Thus, the mycobiota of each artisanal producer was studied and considered specific to each of the following producing regions in Minas Gerais: Serro, Serra da Canastra, Campo das Vertentes, Cerrado, Diamantina, and Araxá. So far, a complex diversity of microorganisms has been identified showing the presence of *Geotrichum candidum*, *Candida catenulata*, *Debaryomyces hansenii*, *Yarrowia lipolytica*, *Candida zeylanoides*, *Kluyveromyces lactis*, *Trichosporon coremiiforme*, *Trichosporon japonicum*, *Aspergillus* spp., *Torulaspora* spp., *Paecilomyces* spp., *Cladosporium* spp., and *Penicillium roqueforti*. The fungal community found on the surface of these cheeses is dominantly constituted by the species Geotrichum candidum. The dynamics of microbial interactions are especially complex in traditional cheeses. However, the potential impact of microbial terroir on the composition of artisanal cheese contributes to the regional identity and authenticity of cheeses, considering indigenous microorganisms, adding value to the product and reinforcing its identity as a historical and cultural heritage. This research on microbial terroir allowed the regulation of AMC, leaving the informality and being legally recognized as a specific type of cheese in the state of Minas Gerais, Brazil.

Unlocking the Potential of KCTC Microalgal Resources: Taxonomy and Application Perspectives

P13

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Microalgal resources have the potential to address a variety of global challenges, including climate change, food security, and renewable energy. At the Korean Collection for Type Cultures (KCTC), 1,544 microalgal strains belonging to 10 phyla and 274 species are currently cultivated. Chlorophyta is the most abundant class, accounting for 72% of all strains, followed by Cyanobacteria (18%), Bacillariophyta (2%), Charophyta (2%), Euglenozoa (1%), Miozoa (1%), Haptista (1%), Ochrophyta (1%), Rhodophyta (1%) and Cryptophyta (1%). Most of these strains (95%) were isolated from freshwater environments, while 3% and 2% were of marine and brackish water origin, respectively. To improve the availability of KCTC resources, we recently focused on analyzing the classification and functional characteristics of some potentially useful resources. As an example, we investigated the morphology, molecular phylogeny, and fatty acid composition of an euglenoid strain (KCTC 19016P) isolated from Korean coastal waters. Phylogenetic analyses based on nuclear SSU (nSSU) and chloroplast SSU (cpSSU) rRNA sequences revealed that Eutreptiella sp. (KCTC 19016P) was nested within the genus Eutreptiella and closely related to E. pomquetensis (AJ532398). The total fatty acid content of major omega-3 fatty acids was 37.61 ± 1.27%, of which alpha-linolenic acid (ALA), eicosapentaenoic acid (EPA), and docosahexaenoic acid (DHA) were 4.07 ± 2.01%, 19.29 ± 0.63%, and 11.5 ± 0.12%, respectively. This result indicates that strain KCTC 19016P has a high potential as a feed in aquaculture.

Learning through digital media for introducing scientific and student communities to the world of Biobanks

P14

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Nowadays, technology brings the necessary tools to facilitate knowledge and make it reach many people. MOOCs (Massive Open Online Courses), as examples of e-learning, are courses accessible via the web and are open for registration, generally with no limits on the number of learners or prerequisites. Registration for these courses is free, although in some cases a payment must be made if a certificate is required. These courses are available on pre-defined dates, with a start and end date, but allow learners to complete each section or module at their own pace. The Institut Pasteur develops digital educational courses, through the production and the replay of MOOCs, as part of its strategic plan, focusing on the development of courses targeted to strategic scientific priorities.

General information about biobanking can be easily found online. However, there are only few available online courses that can give the scientific and student communities more practical information on biobanking. The MOOC on Biobanking organised by the Biological Resource Centre of the Institut Pasteur (CRBIP) aims to confront the scientific and student communities to the daily work of a biobank, giving examples related to the application of legislation, the characterization of samples, and the organization of a biobank.

The MOOC on Biobanking was offered for the first time in 2021, with 2,319 participants from 101 countries having registered in a first season and 1,829 participants from 97 countries in the second season. Participants had access to expert videos, quizzes and a forum animated by community managers. In addition, a webinar was organised with a live Q&A session. Registered participants had the possibility to obtain an authenticated certificate upon a successful MCQ exam. In 2023, the MOOC will be available again from March 15 to May 18.

In conclusion, the format of this course allows a wide audience to benefit from it regardless of the place where participants are located. Also, the content and the way of presentation was satisfactory to the great majority of the participants. We intend to significantly expand the contents of this MOOC in the coming years.

Establishing the Andalusian Culture Collection of Microorganisms for Agricultural and Environmental Sustainability

P16

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Microbial Resource Centres are essential infrastructures for the preservation and provision of microbial biodiversity whose importance has been recognized by the OECD and the Commission on Genetic Resources of the Food and Agriculture Organization of the United Nations (FAO). Throughout four decades, researchers from the Department of Inoculants at the Andalusian Institute of Agricultural and Fisheries Research and Training (IFAPA) have portrayed the microbial diversity associated with the main agricultural crops in Andalusia (Spain), selecting more than 2,600 microorganisms with agriculture and environmental applications. However, the preservation and the biotechnological exploitation of those resources have been limited for a long time by the lack of a specific management infrastructure. Since 2022, our research group carries out a global action focused on developing a proper infrastructure that allows the maintenance and management of IFAPA's collections, and the provision of the associated information and genetic material to the scientific community, technicians, farmers and companies. This action aims at the creation in IFAPA of a permanent and unique infrastructure in Andalusia focused on promoting the development of bio-based agro-solutions in a context of Global Change, knowledge transfer between the public and private sectors and on the preservation of Andalusian microbial resources.

Funding: MdCMC is grateful for funding received from the Ramón y Cajal Research Grant (RYC2019-028468-I) from the Spanish Ministry of Economy, Industry and Competitiveness (MINECO).

CGMCC: Promoting the Utilization of Microbial Resources P19

Song L.

China General Microbiological Culture Collection Center (cgmcc)

China General Microbiological Culture Collection Center (CGMCC) is a non-profit organization financed by the Chinese Academy of Sciences. The main focus of CGMCC is to preserve, supply and maintain living microbial resources and aims to contribute to scientific communities by serving high quality microbial resources useful for various research fields. CGMCC is exploiting new microbial resources from various natural environments, describing novel microbial taxa, and accepting potential useful microorganisms from researchers in academic and applied sectors.

Exploring the Diverse Applications of Fungal Resources: A Comprehensive Study of KCTC Strains

P20

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Fungi are important organisms that play a crucial role in ecosystems around the world. They can produce a wide range of useful compounds, such as antibiotics, enzymes and pigments, which have numerous applications in agriculture, food and pharmaceuticals. In these areas, fungi have been recognized as useful microorganisms that can control environmental pollution. KCTC currently has the technology to preserve and cultivate more than 8,530 strains of potentially valuable resources. Recently, plastic pollution has become a major environmental, economic and social problem. To address this issue, we aimed to investigate the biodegradation of LDPE plastic by microorganisms to elucidate the process. We isolated and identified A. nidulans from agricultural waste and tested its ability to biodegrade LDPE. Our results showed that A. nidulans was able to grow on LDPE as a sole carbon source. Fourier transform infrared spectroscopy analysis confirmed the formation of hydroxyl and other chemical bonding groups on the oxidized LDPE film. GC-MS and XPS analysis identified intermediate metabolites that appear during biodegradation. This study contributes to the discovery of new functions of *A. nidulans* and provides valuable information for the development of strategies to combat plastic pollution.

Using artificial intelligence and a novel media database to predict cultivation conditions for bacteria P21

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Growing new types of bacteria in the laboratory is a basis for their biochemical and physiological characterization but to date the design of appropriate cultivation conditions remains a challenge.
As a basis for the prediction of suitable cultivation media from genome information, we developed MediaDive (https://mediadive.dsmz.de), a comprehensive and expert-curated cultivation media database, which comprises recipes, instructions and molecular compositions of more than 3,200 standardized cultivation media for more than 45,000 microbial strains from all domains of life, including media and strains from the collections of DSMZ, JCM and CCAP. MediaDive is designed to enable broad range applications ranging from every-day-use in research and diagnostic laboratories to knowledge-driven support of new media design and artificial intelligence-driven data mining. It offers a number of intuitive search and comparison tools, as for example the identification of media from related taxonomic groups and the integration of strain-specific requirements. Besides classical PDF archiving and printing, the state-of-the-art website allows paperless use of media recipes on mobile devices. External user engagement is enabled by a dedicated media builder tool.
The standardized and programmatically accessible data of MediaDive open new avenues for the rational design of cultivation media, especially when targeting the vast majority of uncultured microorganisms. Based on the genome information of more than 16,000 microbial strains, we developed an AI-guided approach for the prediction of cultivation media. Users will be able to upload a (meta-)genome sequence and retrieve suggestions on medium compositions based on a k-Nearest-Neighbor (kNN)-based algorithm. Additionally, predictions of relevant phenotypes such as optimal temperature, pH and the ability to utilize various carbon and nitrogen sources are available. Thereby, MediaDive in combination with AI will be able to guide the future design of cultivation media for microbial dark matter.

Microbiology education: The case of the SARS-CoV-2 and Covid-19 pandemic in didactic transposition P22

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The school constitutes a privileged setting for learning international scientific knowledge and local socio-economic and political context knowledge. Selecting content to be learned in school is a permanent tension matter of great social and political relevance. The didactic transposition looks at how and when scientific contents ("International scientific knowledge") are selected to be taught in school ("Knowledge to be taught") in the External Didactic Transposition (EDT) process and how this knowledge is taught and learned at school ("Learned knowledge") in the Internal Didactic Transposition (IDT). In the EDT process, policymakers select the knowledge to be taught in schools from international scientific knowledge, creating national school programmes that also serve as textbook guidelines to be used as pedagogical resources in the classroom. These decisions are subject to the influences of several sectors of society, such as politicians, agencies, educators and other stakeholders, and so they take a long time to be established.
This work shows how critical social issues such as the SARS-CoV-2 and Covid-19 pandemic could disturb the usual process of didactic transposition. Indeed, usually, there is a considerable period between the emergence of a scientific concept and its appearance in the national curriculum called Didactic Transposition Delay (DTD). Therefore, it was expected that the SARS-CoV-2 and Covid-19 pandemic topics would be added, in the future, to the national curricula and textbooks of most countries. However, being a matter of great social interest, the SARS-CoV-2 and Covid-19 pandemic topic, which emerged in late 2019 and had a massive social impact on the whole planet in 2020, started almost immediately to be a matter of classroom discussions between teachers and students ("learned knowledge"), much time before textbooks were available to support the teaching and learning process and national programmes would be published even much later. Therefore, in this process, there was a shortcut where the SARS-CoV-2 and Covid-19 pandemic topic ("International scientific knowledge") surpassed the curriculum step ("Knowledge to be taught") to be taught in school ("Learned knowledge") at once.

Acknowledgements: This research had partial financial support from Portuguese national funds through the FCT (Foundation for Science and Technology) within the framework of the CIEC project UIDB/00317/2020 and CEB project UIDB/04469/2020. It also had the partial support of the European Union's Horizon 2020 research and innovation programme under grant agreement nº 871129 - IS_MIRRI21 Project.

Diversity of thraustochytrid in marine wetland from Taiwan P23

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Wetlands are crucial ecosystems that are inundated with water. In these wetlands, marine thraustochytrids play a vital role in the organic matter cycle and have significant biological functions as saprobes, parasites, and commensals. This research project aims to examine the diversity and community structure of thraustochytrids in wetlands using isolation and culture techniques. A total of 192 isolates were obtained, including 18 different species such as *Aurantiochytrium acetophilum*, *Botryochytrium* sp., *Corallochytrium* spp., *Parietichytrium sarkarianum*, *Ulkenia visurgensis*, *Ulkenia* sp., *Thraustochytrium aureum*, *Thraustochytrium* spp., *Thraustochytriaceae* spp., *Sicyoidochytrium minutum* and *Schizochytrium* spp. We found that the communities of marine thraustochytrids showed seasonal variations. Additionally, the differences in thraustochytrids isolated from each monitoring site and season were linked to differences in environmental factors, such as water temperature, salinity, and nutrient sources.

From biochemical and immunological techniques to the genomic era: achievements on the systematics of protozoan parasites classified as *Leishmania* spp. P24

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Leishmaniasis is a complex disease that is endemic in several regions of the World, affecting more than 98 countries, caused by different Leishmania species, a protistan parasite. The transmission cycles involve diverse vertebrate and sandfly species. There are three main forms of this disease: visceral (VL), cutaneous (CL), and mucosal (ML). Despite taxonomic controversies, more than 30 *Leishmania* species are recognized that can be found in sandflies, mammals and reptiles, and some seem to be geographically restricted to certain endemic areas, but others are dispersed along different regions. The first species to be described was *Leishmania donovani* Laveran & Mesnil 1903, a parasite causing human VL, followed by L. tropica, causative agent of CL, both from the Old World. Many species were described considering eco-epidemiological characteristics, including disease manifestation and geographic origin. In the 70's, Multilocus Enzyme Electrophoresis (MLEE) was described as a useful method for *Leishmania* species identification and detection of genetic variability. A decade later, monoclonal antibodies were also developed with this purpose, and both became gold standard methods for *Leishmania* typing. The genomic era started with the possibility of sequencing specific regions of the DNA to identify *Leishmania* species and to understand its genetic diversity, with the advantage of evaluating both cultured and non-cultured parasites. More recently, Whole Genome Sequencing brought new insights on *Leishmania* species. Our intention is to show and discuss the limitations and advantages of old approaches, like MLEE and single locus sequence typing, to evidence the contributions of multilocus sequence analyses and conclude with the aftermath of whole genome deep sequencing. With these objectives in mind, we will draw on samples maintained by the Leishmania Collection of the Oswaldo Cruz Foundation (CLIOC) and, therefore, will focus on the *Leishmania* species that circulate in the Americas. One of our goals will center on establishing the case of taxonomic synonymia of *Leishmania infantum*, named as *L. chagasi* when referring to American parasites. All steps taken to prove the hypothesis of colonization during the invasion of the American Continent by Europeans will be reported, ultimately describing the findings that point to fitness gain during the parasites' adaptation to a new environment. Moreover, the discovery of a diversity of species and strains autochthonous

to American regions, classified as *Leishmania* (*Viannia*), bearing or not RNA virus, will also be taken into account when discussing new advances in the knowledge of systematics of these parasites.

Preservation strategies of marine thraustochytrids P27

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Thraustochytrids are marine protists and they play important biological roles as saprobes, parasites and commensals. They produced lots of bio-actives and attracted attentions. Currently, most marine eukaryotes are maintained by serially subculturing, an extremely labour intensive procedure which repeatedly exposes the culture to contamination and handling error. Having a cryopreservation technique will be useful for the long-term storage of thraustochytrid cultures. In this study, we develop cryopreservation techniques to preserve 10 thraustochytrid isolates, including *Ulkenia visurgensis*, *Ulkenia* sp., *Thraustochytrium aureum*, *Botryochytrium radiatum*, *Parietichytrium sarkarianum*, *Thraustochytriaceae* sp., *Sicyoidochytrium minutum* and *U. profunda*. Three cryopreservative combinations containing dimethylsulfide, glycerol and trehalose dihydrate. Results indicated that a combination of glycerol and trehalose dihydrate were the most effective cryoprotectants for each of the strains tested. The cells stored in a mechanical freezer had a relatively constant growth rate up to 6 months of storage. The protocols developed and tested in this study may have further application for cryopreserving other thraustochytrids.

MALDI-TOF MS to detect *Fusarium* spp. susceptibility to amphotericin B P31

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Fusarium genus is composed by fungal species capable of infecting plants, humans, and animals, a phenomenon known as trans-kingdom pathogenicity. The increase of fusariosis in recent decades and high mortality rates due to *Fusarium* spp. intrinsic resistance to antifungals, especially among immunocompromised patients, is drawing the attention of the medical community. The gold-standard method to determine the in vitro susceptibility of clinical fungal isolates to antifungals is the broth microdilution method from Clinical and Laboratory Standards Institute (CLSI). The Minimum Profile Change Concentration (MPCC) is a fast antimicrobial susceptibility mass spectral test based on analysis of matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF-MS) that showed full agreement with results obtained from the reference CLSI method for different fungi as *Candida* spp. and *Aspergillus* spp. Thus, the present study aimed to evaluate the feasibility of using MPCC by MALDI-TOF MS as a rapid method to determine the susceptibility of *Fusarium* spp. to amphotericin B. Thirteen clinical isolates of *F. oxysporum*, *F. solani*, *F. fujikuroi*, and *F. dimerum* species complex and two reference strains were analysed. The data were evaluated by both direct visual inspection of the mass spectra and pearson correlation index (PCI) matrix analysis. For the gold-standard method (M38-A2 protocol), all but one *Fusarium* spp. strains (93.3% n=14/15) presented the AMB minimum inhibitory concentrations (MICs) range of 1 to 4 µg/ml. The clinical isolate LMC7108.01 (*F. keratoplasticum*) (6.7% n=1/15) presented AMB MIC of >32 µg/ml. The AMB MPCC range of 1 to 8 µg/ml was observed to 86.7% (n=13/15) of *Fusarium* spp. strains. The LMC7108.01 (*F. keratoplasticum*) and LMC7163.01 (*F. solani*) clinical isolate presented AMB MPCC of >32 µg/ml and <0.06 µg/ml, respectively. Thus, AMB MPCCs and MICs values were identical or with 1-fold dilution diference to 80% (n=12/15) of the *Fusarium* spp. strains. Two clinical isolates (13.3% n=2/15) presented two-fold dilution diference between both methods. Finally, the correlation between MIC and MPCC indicated a significant linear regression correlation ($P<0.000000042$) and a regression coefficient of 0.97, indicating a linear association between MPCC and MIC. Here we show MALDI-TOF MS as a prominent tool to determine MPCCs in a faster, cost-effective, and accurate way for antifungal susceptibility determination of *Fusarium* spp. However, further validations with additional *Fusarium* spp. strains are recommended.

Iodidimonas denitrificans sp. nov., an aerobic nitrate-reducing bacterium isolated from iodide-rich brine and inducing iron corrosion concomitant with nitrate reduction

P32

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Microbially influenced corrosion (MIC) may contribute significantly to a major cause of corrosion-related failures in injection wells and iron pipes of the iodine production facilities. In this study, we isolated *Iodidimonas* sp. strain Q-1^T from iodide-rich brine associated with natural gas in Miyazaki, Japan, and investigated the iron (Fe^0) corroding activity of *Iodidimonas* strains under a variety of culture conditions and characterized taxonomic status of the Fe^0-corroding Iodidimonas strain Q-1^T revealed to be a new species. Under aerobic condition, *Iodidimonas* sp. Q-1^T oxidized the Fe^0 foil in the presence of nitrate and yeast extract, while the other two strains did not. The amount of dissolved iron in this culture was six times higher than that in the aseptic control. The oxidation of Fe^0 in the aerobic cultures of nitrate-reducing *Iodidimonas* sp. Q-1^T occurred concomitantly with the formation of nitrite from nitrate. This Fe^0-corrosion by the nitrate-reducing *Iodidimonas* sp. Q-1^T was supported by the decline of nitrite produced until day 4 and the lack of genes for nitrite reductase in the genome sequence of strain Q-1^T, followed by the chemical oxidation of Fe^0 coupled to the reduction of nitrite. Cells of strain Q-1^T are Gram-negative rods, aerobic, motile, and non-sporulating. Catalase-positive and oxidase-positive. Oxidizes iodide on a marine agar. Mesophilic with the optimum at 30 ºC, neutrophilic with the optimum around 7.5 and moderately halophilic with an optimum at 3% (w/v) NaCl. Nitrate reduction of strain Q-1^T is a unique trait differed from two known species of *Iodidimonas*. The hydrolysis of aesculin and gelatin, the cellular fatty acids profiling also distinguished strain Q-1^T from two known species. The 16S rRNA gene sequence similarity was less than 96.1% sequence similarity to two known *Iodidimonas* species. Digital DNA-DNA hybridization (dDDH) value and average nucleotide identity (ANI) values were lower than the threshold used for prokaryotic species delineation with 17.2–19.3% and 73.4–73.7%, respectively. Consequently, a novel species with the name *Iodidimonas denitrificans* sp. nov., is proposed for nitrate-reducing Fe^0-corroding strain Q-1^T.

Automated high-throughput strain purification using a Hamilton liquid handling robot P33

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Chr. Hansen

Chr. Hansen is one of the leading companies providing natural solutions and ingredients within the food, nutritional, pharma and agricultural industries. Our culture collection constitutes a cornerstone in the company as the point of origin for numerous R&D activities. To ensure the quality of in-sourced strains, the Culture Collection Department routinely perform automated high-throughput purification campaigns. Here, we present a state-of-the-art workflow for an almost fully automated strain purification process utilizing a Hamilton Star liquid handling robot.

Spanning a full week, the automated purification pipeline can process up to 96 strains per run. The process consists of four separate Hamilton methods covering two consecutive single colony picking events from agar media, an enrichment step in liquid media as well as final aliquoting method where various plate and tube formats are prepared for downstream analysis or storage.

The first step in the process is drop plating using 24 well agar plates. In short, the liquid source material is loaded onto the Hamilton robot in either cryotubes or a 96-well plate, serially diluted and subsequently drop plated onto 24-well agar plates. After overnight incubation, a second drop plating event is performed. However, the dilution series are made from single colonies detected from the first outgrowth on agar. This is automatically carried out by the Hamilton robot as it is scanning the agar plates and detecting suitable colonies from which a new dilution series is made. After overnight incubation, the same scanning procedure is utilized to pick single colonies for liquid propagation. Each selected colony is picked with a Hamilton tip and transferred to a 50 mL centrifuge tube containing liquid media. After overnight incubation, the 50 mL tubes are centrifuged, and supernatants are manually decanted followed by addition of fresh media with 20% glycerol in which the cultures are whirl mixed. A Hamilton method is run to aliquot purified strains to various 96-well plates and cryotubes for downstream analysis or storage. It should be highlighted that all the strains processed in the pipeline are tracked throughput the entire process as all tubes and plates utilized are labeled with barcodes read by the Hamilton robot.

National Infectious Diseases Bank P34

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The COVID-19 pandemic caused serious damage in human health and economy. The government of Taiwan realized that it is essential to establish a National Infectious Diseases Bank (NIDB) for facing emerging and reemerging global infectious diseases. Therefore, the government supports and encourags National Health Research Institutes to establish NIDB to collect and provide biological materials to academia and industry for developing diagnosis kits, drugs, and vaccines for future pandemic and epidemic. The NIDB establishment program was started in 2022 and the new building is expected to be completed in 2025. While conducting the establishment program, NIDB started collecting important pathogens, including bacteria, fungi, and viruses. NIDB coordinates with Taiwan CDC and FDA to prepare various standard strains for the research community and industrial needs. In addition, NIDB also established a service platform, providing pathogen-related investigation, whole genome sequencing and animal models for researches on infectious diseases or efficacy of new compounds. For the preparedness for future pandemics, we look forward to establishing international collaborations.

Photobacterium- Bioluminescent Bacteria of Marine Origin- Occurrence in Food P37

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Photobacterium is a gram-negative, relatively aerobic, motile bacteria of the Vibrionaceae family that exhibit bioluminescence. These bacteria are associated with the marine ecosystem and until now were considered to spoil the meat of fish, as well as to cause food poisoning, due to their ability to produce biogenic amines. Implementing molecular biology methods for food research enables a better understanding of the diversity of microorganisms present in food, including those that cause its spoilage. Since 2011, scientific reports have begun to appear on the presence of *Photobacterium* DNA in beef, pork, ostrich, and raw meat, regardless of how it was packaged and stored. *Photobacterium* was isolated from pork meat by the culture method in 2016.

The subject of our study was an attempt to isolate *Photobacterium* by conventional cultural methods along with next-generation sequencing (NGS) analysis from food samples. First, the conventional culture method used Marine Agar (Difco) culture medium with meat extract and vancomycin (incubation at 15 °C for 5 days) to isolate microorganisms from food samples. The NGS analysis demonstrated that *Photobacterium* was the dominant microbiota in samples of ostrich fillets and steaks vacuum-packed, reaching from 47.2% to 91.8% after 14 days of storage. In turn, in samples of raw salmon fillets packaged in a modified atmosphere, *Photobacterium* reached from 90.7 to 95.8% after 6 days of storage. Finally, in cold-smoked and vacuum-packaged salmon, *Photobacterium* ranged from 2.8% to 45.1% after 33 days of storage.

The abundance of presumed *Photobacterium* in the tested samples was approximately 7 log [CFU/g]. Based on the 16S rDNA analysis in bioluminescence samples, most sequences were assigned to *Photobacterium phosphoreum* and *Photobacterium kishitanii*, *Aliivibrio logei*/*Aliivibrio salmonicida*. At the same time, isolates not bioluminescent were identified as *Serratia*, *Pseudomonas*, *Brochotrix*, and occasionally *Acinetobacter*. These studies indicate that *Photobacterium* contamination is a common problem in fish processing and the meat industry.

Isolation and identification of new acetic bacteria of the genus *Asaia* resources of the IAFB Collection of Industrial Microorganisms. P38

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The genus *Asaia* was established in 2000 as the fifth genus of acetic bacteria. The name of the genus comes from the Japanese bacteriologist Toshinobu Asai, who focused on the systematics of acetic bacteria. Bacteria of the *Asia* genus were initially isolated from the flowers of the orchid tree (*Bauhinia purpurea*) and plumbago (*Plumbago*), which are tropical plants. The natural habitat of *Asaia* sp. is tropical flowers, fruits, and insects of Southeast Asia. However, there have been reports of their occurrence in Europe in drinks with natural juices and flavorings. Asaia sp. bacteria are gram-negative, aerobic rods measuring 0.4 – 1.0 × 0.8 – 2.5 µm. Most species do not produce acid from ethanol, and their growth is inhibited or very weak in the presence of 0.35 % (v/v) acetic acid. In plate cultures, they usually form small, light pink to pink colonies measuring 1 to 3 mm.

This study aimed to identify and characterize gram-negative rods isolated from a sports drink with visual flocks as a defect, bottled water, and a strawberry drink. Molecular identification through PCR amplification of a partial region of the 16S rRNA gene allowed the classification of these bacteria as *Asaia lannensis*, *Asaia bogorensis*, and *Asaia* sp. This is the second reported case of isolation of these bacteria in Poland. Phylogenetic analysis based on the 16S rDNA gene sequence showed that the tested isolates formed distinct, independent clusters, assigning *Asaia lannensis* to one group and *Asaia* sp. and *Asaia bogorensis* to the other group, while also showing the distance of the tested strains to the sequences taken from the NCBI database. The strains were deposited in the Culture Collection of Industrial Microorganisms - Microbiological Resource Center, Institute of Agricultural and Food Biotechnology - State Research Institute (IAFB), Poland.

Disclosure of patents- 30 years of storage and beyond P39

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A patentable invention must be new or novel and non-obvious, it must have a useful purpose (industrial applicability) and it must be disclosed in the application in such a clear and complete manner that a person skilled in the art can carry it out. Disclosure of the invention is thus a prerequisite for the grant of patents. If an invention involves a microorganism or the use of a microorganism, disclosure is not readily possible in writing, but can only be made by deposit with a specialised institution. The DSMZ has acted as such a patent depository for more than 45 years. Since 1981, the DSMZ has been recognised as an International Depositary Agency (IDA) under the Budapest Treaty. In total, the DSMZ holds over 9,000 items of biological material, including bacteria and archaea, fungi and yeasts, plasmids, bacteriophages, human, animal and plant cell lines and plant viruses. Rule 9.1 of the Budapest Treaty states that " Any microorganism deposited with an international depositary authority shall be stored by such authority, with all the care necessary to keep it viable and uncontaminated, for a period of at least five years after the most recent request for the furnishing of a sample of the deposited microorganism was received by the said authority and, in any case, for a period of at least 30 years after the date of the deposit." In the meantime, more than 30 years have passed and the question arises as to what should be done with these deposits after the described storage period, considering various aspects such as disclosure of patents, free availability of the material and feasibility for IDA collections. Since the stored material could be important for both scientific research and new biotechnological applications, the various stakeholders (including IDAs, the World Intellectual Property Organisation) are discussing solutions that meet all requirements.

Diversity in the DSMZ microorganisms culture collection: A resource for science and research P41

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The culture collection at the Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Culture GmbH contains four departments: Microorganisms, Bioresources for Bioeconomy and Health Research, Human and Animal Cell Lines, and Plant Viruses and Antisera. In the Department of Microorganisms, we currently hold > 26.000 bacterial and archaeal strains listed in the online catalogue. This represents the world's most diverse collection of archaea and bacteria, which is currently growing steadily with 500-1.000 new strain deposits every year, and for which long term availability and authenticity is ensured by cultivation experts.

Our culture collection and expertise provide researchers with an outstanding taxonomic and functional diversity for research, not to mention knowledge exchange and consulting service. Environmental and phenotypical metadata, including growth characteristics of our strains form the basis for different databases, such as BacDive (https://bacdive.dsmz.de/) and MediaDive (https://mediadive.dsmz.de/). Further, many of our strains have been included in The Genomic Encyclopedia of Bacteria and Archaea (GEBA), a project aimed at systematically filling in the gaps of genomes from bacterial and archaeal type strains throughout the tree of life.

The more than 700 archaeal stains, representing >400 species complement our large collection of bacterial strains (>25.000, >12.000 species in almost all bacterial phyla), which are representing the full variety of microbial metabolic and phenotypic diversity. More than 1.800 different medium recipes in combination with a variety of different cultivation conditions, as well as the experience and expertise of our staff, allows the growth of very different microorgansims: psychrophiles and extremely thermophiles, acidophiles and alkaliphiles, strictly non-halophiles and extremely halophiles, while they all include strictly anaerobic, microaerobic, as well as facultative and obligately aerobic organisms.

In addition to chemohetero- and chemoautotrophic organisms, our collection covers aerobic and anaerobic, oxygenic and anoxygenic phototrophic bacteria. Other functional groups represented include ammonium oxidizing bacteria and archaea, nitrite oxidizing bacteria, nitrogen fixing bacteria, xenobiotics degrading bacteria, methanogens, methano- and methylotrophs, as well as sulphur oxidizing and sulphate reducing organisms. Further, special collections, such as the European Space Agency (ESA) strain collection, the Reichenbach collection of Myxobacteria, teaching strains for schools and universities, as well as reference strains for industrial applications and water quality control are included. We are now in the process of expanding our special collections by including strains from selected microbiomes, and to become a digital repository.

Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC): A Valuable Resource for Bioprospection P42

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Microbial culture collections are important resources that support a wide range of scientific, industrial and educational activities. Their continued maintenance and development are essential for advancement of various fields of study. Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC) is a biological resource centre located at Interdisciplinary Centre of Marine and Environmental Research (CIIMAR) that comprises more than 1100 cyanobacterial and microalgae strains. LEGE-CC strains have been isolated since 1991 and are mostly obtained from Portuguese ecosystems, including the Azores and Madeira, which gives the collection a unique richness from a geographical and phylogenetic point of view. LEGE culture collection includes strains obtained from different environments (freshwater, marine, brackish and terrestrial) and collected in different countries around the world. LEGE-CC has been doing a great effort in sampling both nationally and internationally (focusing in underexplored environments and locations) with the aim of isolating different microorganisms to increase the available diversity and thus enhance our biotechnology pipeline. Over the past few decades, there has been a growing focus on cyanobacteria and microalgae due the capacity these microorganisms have to produce a wide range of chemical compounds, such as toxins or other bioactive molecules that could have valuable biotechnological, health and food applications. LEGE-CC is the basis for several studies over the years and strains have been screened for a diverse range of purposes such as anti-cancer, anti-biofouling, anti-microbial, anti-biofilm, anti-obesogenic and related diseases, cosmetics, and food. Many studies have demonstrated that our LEGE-CC strains have the potential and capacity to produce a wide array of metabolites, including toxins as well as newly discovered molecules like Portoamides, Hierridin B and C, Bartolosides, Nocuolin A, Chlorosphaerolactylates A–D, and Desmamides A-C. LEGE-CC is member of the World Federation for Culture Collections (WFCC), the European Culture Collections Organisation (ECCO), and is also part of different infrastructures (EMBRC and MIRRI). LEGE-CC aims to provide various services such as the provision of starter cultures for different purposes, isolation and identification of strains, deposit, consultancy and training courses. Although only a small percentage of strains have been explored, based on potential demonstrated in previous studies, we believe that LEGE-CC is an excellent source for addressing current problems such as the lack of new antibiotics, incorporation of new eco-friendly compounds in anti-biofouling paints, discovery of new drugs for cancer, obesity and related diseases,

food and also provision of reference materials for quality control and standardization purposes.

LEGE-CC from 8 to 80: The importance of sampling campaigns P43

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Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC) is a biological resource centre located at Interdisciplinary Centre of Marine and Environmental Research (CIIMAR). LEGE-CC is member of World Federation for Culture Collections (WFCC), European Culture Collections' Organization (ECCO) and it is also part of the research infrastructures such as EMBRC and MIRRI. With the aim of being considered one of the top culture collections worldwide, LEGE-CC seeks to hold a unique diversity in cyanobacteria as well as in microalgae. For that matter, sampling campaigns have a huge contribute, allowing the culture collection to grow in numbers and in variety of strains with the capacity to produce a wide range of chemical compounds, such as cyanotoxins or other bioactive molecules that could have valuable biotechnological, health and food applications. Over the past four years we were able to conclude eight sampling campaigns, five of them in Portuguese territory (Caramulo, Alentejo, Algarve and Azores and Madeira Archipelagos) and three that took abroad along the Atlantic coast of Morocco, Cape Verde archipelago and in Mexico, around Chichonal volcano area. The criteria to select these sampling locations was based on diverse habitats (freshwater, marine, brackish and terrestrial), ongoing projects at nationally and internationally level and focusing on underexplored locations with the aim of isolating different microorganisms. In total, 248 environmental samples were collected from the eight sampling sites, 150 of them still in isolation process. From these, until today more than 500 strains were isolated and in the end of this effort the isolation and identification of more than 700 new strains is expected which will confer a boost not only for LEGE-CC but also for all associated research. New diversity not only represents quantity of strains for LEGE-CC, but also could be a new and unexplored chemical diversity that can be used for different purposes. Furthermore, LEGE-CC provides several services such as provision of starter cultures for diverse purposes, isolation and identification of strains, cryopreservation, training courses, and at the same time increase the available diversity of microorganisms enhancing our biotechnology pipeline.

The Path Followed by the Le*ishmania* Collection to be Incorporated into Fiocruz's Biobank: Beginning of a New Journey P44

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Biological collections are crucial for preserving and studying biological diversity, but they are susceptible to damage from natural disasters and human activities. To mitigate these risks, the Collection of Leishmania of Oswaldo Cruz Foundation (CLIOC) is planning to back up its collection at Fiocruz's biobank (BC19 - FIOCRUZ, Rio de Janeiro, Brazil), created to save biological material related to SARS-COV pandemic, but now organized for receiving other type of samples. The CLIOC collection is the pioneering culture collection of *Leishmania* species at the foundation and contains 1670 available *Leishmania* specimens, each with essential information about, provided by rigorous scientific research. The aim of this study is to demonstrate the logistics of sending material to the biobank, following the ABNT NBR ISO/IEC 17025:2017 (General requirements for the competence of testing and calibration Laboratories) and ABNT NBR ISO 20387:2020 (Biotechnology — Biobanking — General requirements for biobanking). For this purpose, it was established a quality management system workflow in order to ensure the long-term maintenance of these samples in liquid nitrogen, along with safeguarding the data associated with each sample. The priority for Leishmania spp. strain transfer will follow specific criteria: 1) reference strains; 2) strains used for biotechnological development and production of inputs; 3) strains with complete genome sequenced (around 250 so far, but constantly increasing) and 4) strains of importance for epidemiological and ecological studies. All data associated with each strain will be informed to BC19-Fiocruz following the recommendation in ABNT NBR ISO/IEC 27001:2013 (Information technology-Security thecniques-Information security manegement systems-Requirements). The proposal workflow for transferring strains from CLIOC to BC19-Fiocruz is being tested with 16 *Leishmania* strains, representing the most commonly used reference strains, classified as different species. This criterion was based on internal reports from CLIOC considering requested strains in the last 16 years. The viability and purity of each sample was assessed by tripan blue assay, and cryopreservation was carried out. Each strain is being characterized again by multilocus enzyme electrophoresis (still the gold standard for *Leishmania* typing) and PCR followed by sequencing of specific regions, standardized methods provided as service by CLIOC. All steps were registered to ensure the authenticity and traceability of the preparation all biological materials from CLIOC that now will be part of BC19-Fiocruz.

Marine Sponge and Octocoral-Associated Bacteria Show Versatile Secondary Metabolite Biosynthesis Potential and Antimicrobial Activities against Human Pathogens

P47

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Marine microbiomes are prolific sources of bioactive natural products of potential pharmaceutical value. This study inspected two culture collections comprising 919 host-associated marine bacteria belonging to 55 genera and several thus-far unclassified lineages to identify isolates with potentially rich secondary metabolism and antimicrobial activities [1]. The first collection was established between 2010 and 2020 during multiple sampling events of temperate marine sponges, octocorals and fish larvae in Portugal, while the second collection comprises bacterial isolates from 14 tropical marine sponge species collected in Taiwan. Seventy representative isolates of the two culture collections had their genomes sequenced and mined for secondary metabolite biosynthetic gene clusters (BGCs). These isolates were further screened for antimicrobial activities against four canonical human-pathogenic bacteria (*Staphylococcus aureus*, methicillin-resistant *S. aureus*, *Salmonella enterica* serovar *Typhimurium*, *Vibrio parahaemolyticus*) and five pathogenic *Candida* strains (*C. albicans*, *C. auris*, *C. parapsilosis*, *C. glabrata* wildtype, *C. glabrata* Δpdr1 deletion mutant). To obtain slow growing, rarely isolated bacteria, a series of low-carbon media, prolonged incubation times and lower incubation temperatures were employed, allowing for the isolation of difficult-to-cultivate marine taxa, such as *Anderseniella*, *Lentilitoribacter*, *Pelagibius*, *Tateyamaria*, *Marinicauda* and *Parendozoicomonas*, with a limited number of known species and genomes available. Among 70 sequenced genomes, 466 BGCs were identified and antimicrobial peptide- and polyketide synthase-related BGCs were frequently detected. The Bacteroidetes genus *Aquimarina* and unclassified Flavobacteriaceae strain RHTr2 were enriched for polyketide BGCs, and three largely unknown genera, *Grimontia*, *Enterovibrio* and *Thalassomonas*, for non-ribosomal peptides. Only 38 of the 466 BGCs had similarities greater than 70% to BGCs encoding known compounds, highlighting the potential biosynthetic novelty encoded in these genomes. Cross-streak assays showed that 33 of the 70 genome-sequenced isolates were active against at least one *Candida* species, while 44 isolates showed activity against at least one bacterial pathogen. Taxon-specific differences in antimicrobial activity among isolates suggested distinct molecules involved in antagonism against bacterial versus *Candida* pathogens. The here reported culture collections and genome-sequenced isolates constitute a valuable resource of understudied marine bacteria

displaying antimicrobial activities and potential for the biosynthesis of novel secondary metabolites, holding promise for a future sustainable production of marine drug leads.

[1] Almeida, J.F., Marques, M., Oliveira, V., Egas, C., Mil-Homens, D., Viana, R., Cleary, D., Huang, Y.M., Fialho, A.M., Teixeira, M.C., Gomes, N.C.M., Costa, R., Keller-Costa, T. Marine sponge and octocoral-associated bacteria show versatile secondary metabolite biosynthesis capacities and antimicrobial activities against human pathogens. Marine Drugs 21(1), 34.

Mycobiota of São Jorge Cheeses with different ripening periods P48

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The growth of filamentous fungi in the cheese surface makes the product undesirable (and therefore disposable) and can even present a health risk due to the production of secondary metabolites, such as mycotoxins. The São Jorge cheese is a highly appreciated product from São Jorge Island, Azores, Portugal. It is made with raw cow milk and has long ripening periods, up to 36 months. This product obtained the Protected Designation of Origin (PDO) certification in 1986.

Considering that the mycobiota of traditional Portuguese cheeses is understudied, the main goal of this work was to unveil the mycobiota of three São Jorge cheeses with different ripening periods (five, nine and thirty months). Direct inoculation of the cheese in three different culture media was used and the isolates were identified through molecular methods (analysis of ITS and/or partial benA). A total of 32 isolates were identified from the cheese with the lowest period of ripening, mainly *Penicillium* spp. ser. *Camembertiorum* (23 isolates), but also *Aspergillus* sp. (1 isolates), *Scopulariopsis* sp. (1 isolate), and several yeasts (7 isolates). The mycobiota of cheese with the seven months of ripening was mostly composed of *Penicillium* spp. ser. *Camembertiorum* and *Saccharomyces cerevisiae*, with 8 and 9 isolates, respectively. In the 30 months cheese *Penicillium* spp. ser. *Camembertiorum* were also isolated, but *Scopulariopsis* spp. was predominant, with 20 out of 24 isolates. Although the mycobiota was largely composed of Ascomycota, two Basidiomycota were found in the cheeses with the longest periods of ripening.

Future studies will be conducted using metabarcoding techniques to disclose the uncultured mycobiota. These culture-independent techniques are less time consuming and more sensitive. They have shown to be a powerful tool to gain a better and faster understanding of the influence of the microorganisms in the cheese ripening process.

Acknowledgements: Teresa Vale Dias thanks for the Ph.D. scholarship given by the Foundation for Science and Technology (FCT) - 2020.05849.BD. This study was also supported by FCT under the scope of the strategic funding of CEB (UIDB/04469/2020), LABBELS – Associate Laboratory in Biotechnology, Bioengineering and Microelectromechanical Systems, LA/P/0029/2020, CIMO (UIDB/00690/2020) and SusTEC (LA/P/0007/2020).

Novel halotolerant bacteria isolated from salt lake in Tibet and their biomanufacturing potential for producing different metabolic targets

P50

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Halophilic and halotolerant microorganisms are a heterogeneous group of extremophilic organisms able to survive and even thrive in highly saline environments. Among them, the moderately halophilic and halotolerant bacteria are spread over a large number of phylogenetic branches, most species being grouped in the Proteobacteria (γ- and α-Proteobacteria), Firmicutes and Actinobacteria.

The isolation and taxonomic characterization of halophilic and halotolerant bacteria have allowed us to learn more about their heterogeneity, their metabolic and physiological characteristics. Omics studies are providing valuable information regarding their diversity and biotechnological potential. Over recent decades, they have been studied mainly for their adaptation mechanisms to extreme conditions and the different molecules that they are able to produce (enzymes, polysaccharides, etc.), and for their biotechnological applications.

During the investigate of bacterial diversity of salt lakes in Tibet, many halotolerant bacteria were isolated from water, soil and sediment samples of Longmu Co lake, which was formed 50 thousand years ago, with an altitude of 5100m. In this research, 56 *Halomonas* strains and 39 *Lysobacter* strains were isolated and identified as 7 novel species of *Halomonas* and 9 novel species of *Lysobacter* respectively. According to genome analysis, the group of *Halomonas* strains contained a gene cluster for ectoine production, including gene ectA, ectB and ectC. Ectoine produced by these strains were extracted and confirmed by HPLC-MS, and the conditions for ectoine producing were further optimized. The key gene for protease synthesis was found in *Lysobacter* strains, and the physiological characteristics of protease produced by *Lysobacter* strains was analyzed. Based on the genomic and physiological research, both strains of the *Halomonas* and *Lysobacter* showed the potential on biomanufacturing.

Estimating the age of divergence date by constructing a large-scale genome phylogenetic tree P51

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The last universal common ancestor (LUCA) emerged 4.1 billion years ago (Ga) and branched into Bacteria and Archaea (later Eukarya), but, in the phylogenetic diversification thereafter, how life metabolically diversified and how these related chronologically with the Earth's history remains unclear. Here, we estimated divergence dates across a "three-domain" tree (eukaryotes, bacteria, and archaea) and examined their metabolic diversity.
All genomes included in the genome taxonomy database (GTDB r95) [Eukaryotes (43 species), Archaea (147 species), and Bacteria (146 species)] were annotated using Prokka and all the protein-coding genes were predicted. A concatenated alignment of 29 universally conserved ribosomal proteins was used for constructing a tree through a maximum-likelihood estimation Molecular clock analysis was performed using BEAST v.2.6.6, using Relaxed Clock Log Normal and a Yule model, with topology fixed based on the tree constructed through a maximum likelihood estimation. Molecular clock analyses were calibrated using 11 geological records based on isotopic and fossil evidence. The presence of respiratory pathways was examined against 19,000 bacterial and archaeal genomes based on eggnog-mapper annotations and/or BLAST search.
Archaeal supergroups were estimated to have emerged earlier or around the same period as the last common ancestor of Bacteria (Euryarchaeota at 3.27-2.83 Ga and DPANN, TACK, and Asgardarchaea at 3.5-3.3 Ga vs Bacteria at 2.97-2.58 Ga). Of the 19,000 genomes targeted in the study for metabolic analysis, 80.3% retained terminal oxidase, suggesting that oxygen can be used in respiration. On the other hand, 19.7% were suggested to obtain energy through fermentation. Among the relatively lately diverged bacterial lineages after the Great Oxidation Events, we observed some conservation/clustering of respiratory metabolisms (e.g., aerobic respiration). This is the foundation for studying how microorganisms have adapted and how respiration became the dominant process on the early Earth.

Strengthening the MIRRI Italian Research Infrastructure for Sustainable Bioscience and Bioeconomy: The SUS-MIRRI.IT Project

P54

de Vero L.

University of Modena and Reggio Emilia. On the behalf of the SUS-MIRRI.IT Partners (PNRR project code n. IR0000005)

SUS-MIRRI.IT (www.sus-mirri.it/it/) is a project funded by the National Recovery and Resilience Plan (PNRR) and granted by the European Commission's NextGenerationEU programme, with a total budget of about €17.000.000.
The project is coordinated by the University of Turin and involves 15 institutions with 24 operative units (UOs). The culture collections of all UOs hold different microbial resources, including bacteria, filamentous fungi, yeasts, microalgae and viruses, which can be exploited in the Health, Agro-Food and Environment domains. Moreover, they collect and store data associated with microorganisms, carry out research and provide external users with support and services related to microbial resources.
SUS-MIRRI.IT aims to develop Research, Services and Training in tight collaboration with the Italian network of culture collections MIRRI-IT. Through the project the bioresources stored at the MIRRI-IT RI will be increased, improving their characterization and optimising their management, thus unlocking their genomic and metabolic potential. The optimised management of the resources coupled with the digital platform and data handling/sharing strategy will lead to further discoveries and the establishment of innovative solutions and products of biotechnological interest, stimulating the bio- and circular economy.
The strategic impact of the project will be:

- Promotion of partnerships on the territory to enhance the synergies and favouring the aggregation of skills, structures and bioresources;
- Promotion of the development of the bio-based economy, contributing to the sustainability and safety of the environment and industrial processes;
- Targeted initiatives and stakeholder-oriented actions will assure that all the results produced by SUS-MIRRI.IT will be disseminated, and, when possible, transferred to industry, promoting the contribution to the bioeconomy.

Coimbra Collection of Algae (ACOI): enhancing microalgae research and innovation through a living collection

P55

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The Coimbra Collection of Algae (ACOI) is a biological resource center that provides access to one of the world's largest collections of living microalgae and cyanobacteria. It is a unique, nationally, and internationally significant collection of more than 4.000 native Portuguese strains. ACOI mission is to promote sustainability and improve the quality of life through microalgae by developing fundamental and applied research and providing high-quality products and services. It contributes as resource and service platform for two national infrastructures MIRRI.PT and EMBRC.PT and is also a member of the World Federation for Culture Collections (WFCC). As a nationally and internationally recognized resource center ACOI strains have been the basis of several research and innovation projects. Although algal culture collections provide an enormous diversity of microorganisms, until now only a very minor fraction of the available strain diversity has been exploited for biotechnological purposes. Despite all the diversity, only a small percentage of ACOI strains has been screened, however demonstrating the potential and effective capacity of the strains to produce a diverse array of metabolites with different applications and activities (e.g. anticancer, antibacterial, antibiofilm, remediation, cosmetics, food, etc.). The ACOI collection is a resource center capable of providing solutions that we believe strongly impact the sustainable development goals (SDG)

Marine Microbial Resources: Paving the Way for a Blue Bioeconomy P57

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The marine environment is still an underexplored source of biodiversity. The vast range of ecosystems in this environment with various salinities, pressures, temperatures, and nutrient availabilities has led to the evolution of complex and diverse microbial communities. As a result, marine microorganisms can present unique metabolic pathways and biochemical adaptations, becoming relevant targets for the bioprospection of novel bioactive compounds.

Within the scope of the River2Ocean project, we have established a microbial biobank of marine microorganisms that will be explored for the production of value-added products and processes with high biotechnological potential, such as antimicrobials, enzymes, carboxylic acids, biosurfactants, and bioremediation strategies.

The microbial isolates obtained from environmental marine samples collected on the northern coast of Portugal include gram-positive and gram-negative bacteria, actinobacteria, yeasts, and filamentous fungi. Currently, the isolates are being identified by ribosomal RNA sequencing, using the 16S rRNA gene for Bacteria and Archaea, and the ITS region for Fungi. The results obtained so far indicate the presence of the genera of bacteria *Pseudomonas* (5%), *Pseudoalteromonas* (7%), *Cobetia* (10%) and *Vibrio* (17%), the yeasts *Debaryomyces* (5%) and *Rhodotorula* (15%), as well as different bacteria belonging to the group of actinomycetes (10%), among others.

It is expected that this marine microbial biobank will offer a range of benefits to the industrial and entrepreneurial ecosystems, leading to the development of innovative research and innovation strategies. For instance, by supporting the development of sustainable biotechnological value-added products, contributing to a circular bioeconomy. Moreover, marine microbial resources have great potential for the implementation of bioremediation strategies targeting the decontamination of polluted sites, which can benefit local communities by improving environmental quality and supporting public health. Indeed, we have already isolated and identified several marine bacteria from our biobank with the ability to consume hydrocarbons (32%), which are promising for the bioremediation of oil spills and restoration of contaminated environments.

The establishment of a marine microbial biobank provides a biotechnological platform with high innovation potential to promote bilateral cooperation between academy and industry, and pushing forward the transition to a blue bioeconomy.

Acknowledgements: This work was supported by project River2Ocean – Socio-ecological and biotechnological solutions for the conservation and valorization of aquatic biodiversity in the Minho

Region, with reference NORTE-01-0145-FEDER-000068, co-financed by the European Regional Development Fund (ERDF), through Programa Operacional Regional do Norte (NORTE 2020).

The importance of culture collections for biodiversity assessment, conservation, and biotechnological applications: The case of the BACA culture collection

P61

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Culture collections hold a high diversity of microorganisms that can be used for biodiversity assessment, ecological and conservation studies, and to search for pharmaceutical compounds or biotechnological applications. The BACA culture collection (Bank of Algae and Cyanobacteria of the Azores) was created in 2018 to gather several small culture collections held at the University of the Azores in a single infrastructure and to preserve and increase this collected biodiversity for future research. Recently it was integrated as a member of the ECCO and PT-mBRCN. Since then, it has expanded its collection, holding presently 811 strains, 406 cyanobacteria, 318 green microalgae, 85 diatoms, and one dinoflagellate, with more than 600 strains genetically characterized (e.g. 16S rRNA, 18S rRNA, rbcl). The genetic analysis has allowed the identification of a unique cyanobacteria diversity in the collection and the Azores, with several new taxa to be described based on the strains present in BACA. The prospection of toxins and their biosynthesis genes in cyanobacteria strains allowed the identification of several cyanotoxins (e.g., microcystin, saxitoxin, cylindrospermopsin and anatoxin) from different strains and habitats (freshwater and brackish) in several Azorean islands, contributing to a better knowledge of the distribution of cyanotoxin producers in the Azores and worldwide. The BACA culture collection has also been used for the search for new bioactive compounds from well-characterized strains, allowing the identification of new secondary metabolite-rich genera and species to search for new bioactive compounds. These results highlight the need to promote and support culture collections, such as BACA, that have contributed to the knowledge of diversity, toxicology, and biotechnological applications of algae present in the Azores, allowing a better understanding of the opportunities and problems that might come from the presence of such taxa in the Azores.

The CCM- 60 years as a public service collection P62

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The Czech Collection of Microorganisms (CCM) was founded as a specialized research and service institution in 1963 at the Faculty of Science of Masaryk University. The main activities of the CCM focus on the deposition, preservation and distribution of cultures of bacteria, archaea, filamentous fungi, yeasts and staphylococcal bacteriophages. The CCM represents biological ressource centre now - continuously replenishes its bioresources and actively contributes to the preservation of the gene pool and the protection of the biodiversity of microorganisms ex situ. Long-term maintenance of viable cultures is ensured for most strains by freeze-drying, storage in liquid nitrogen (at -196 °C), and in a deep-freeze box (at -70 °C). The services offered by the CCM support basic and applied research, industrial/commercial applications, biotechnology, and education. The research activities of the CCM focus mainly on the taxonomy of bacteria of the phyla Bacillota, Pseudomonadota and Bacteroidota isolated from the environment, plants, animals and human clinical material, as well as on aquatic hyphomycetes and melanised fungi of the class Dothideomycetes. Since 2008, the CCM has been an active member of Masaryk University's polar research program and the collected Antarctic microbiota represent an incredible source of new properties for potential industrial, biotechnological and pharmaceutical applications as well as an attractive material for educational purposes and student research activities.

With all its activities, the CCM has become an internationally recognized repository for microbial resources, providing high-quality expertise in microbial taxonomy, cultivation and characterization for 60 years already.

Massilia pseudviolaceinigra sp. nov and *Massilia scottii* sp. nov. have the ability to inhibit Gram-positive bacteria. P63

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Three bacterial strains producing blue-violet pigmented colonies on R2A agar were isolated from wet rock wall and lakes located in a deglaciated northern part of James Ross Island, Antarctica. The isolated strains inhibited various phytopathogenic as well as medically important Gram-positive bacteria (e.g. *Clavibacter* spp., *Curtobacterium* spp., *Staphylococcus* spp.). Phylogenetic analysis based on the 16S rRNA gene indicated that the isolates belonged to the genus *Massilia* and the closest relatives were *Massilia violaceinigra* B2T, *Massilia rubra* CCM 8692T, *Massilia frigida* CCM 8695T, *Massilia antarctica* CCM 8941T, and *Massilia aquatica* CCM 8693T. A polyphasic taxonomic study based on gyrB and lepA genes sequencing, automated ribotyping, MALDI-TOF MS, chemotaxonomy analyses, extensive biotyping and average nucleotide identity and digital DNA-DNA hybridization calculations based on whole-genome sequences clearly proved that the isolates represent two novel *Massilia* species. Based on all the obtained results, we propose a novel species for which the names *Massilia pseudviolaceinigra* sp. nov. and *Massilia scottii* sp. nov. are suggested, with the type strains P3689T (= CCM 9206T) and P5043T (= CCM 9029T), respectively. Those two-novel bioactive-substances-producing species may play a role in shaping the composition of the fresh-water Antarctic microbiomes due to the inhibition of Gram-positive bacteria.

Effect of increased CO_2 on biomass production and protein content in naturally tolerant microalgae and cyanobacteria from Azorean volcanic environments P64

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Climate change has been discussed worldwide and rising awareness to this problematic has inspired several new studies to find ways to mitigate this environmental crisis. Microalgae biomass production for CO_2 sequestration has been pointed out as one of the ways to mitigate climate change and to develop a sustainable blue bioeconomy (e.g., biofuel, supplements, fishmeal). Included in the Microalgae in IT project (ERA-NET BlueBio COFUND), this study aimed to search microalgae and cyanobacteria strains naturally tolerant to elevated CO_2 concentration and assess the effect of increased levels of CO_2 injection on biomass production and protein content. For this purpose, a bioprospection of microalgae and cyanobacteria on naturally CO_2-enriched aquatic vents in São Miguel Island (Azores) was carried out. Twelve samples were obtained and put to grown in enriched media (e.g., BG-11, Waris-H). A total of four cyanobacteria and eight microalgae strains were isolated and maintained in the BACA culture collection (Bank of Algae and Cyanobacteria of the Azores). Six of those strains, including two commercially valued species (*Chlorella vulgaris* BACA0162 and *Haematococcus pluvialis* BACA0702), were produced in 1L bioreactors at 25ºC with a 16h:10h light/dark photoperiod and two aeration conditions: i) simple aeration at 1L/min, and ii) aeration at 1L/min with 10% CO_2. After 28 days, biomass production was quantified as freeze-dried biomass. Protein content was determined by the microbiuret method. Preliminary results show that BACA0801 produced the highest biomass with 1.7 g/L/28 days, up to three times more of *Chlorella vulgaris* BACA0162, and has the best protein/biomass ratio. Increased CO_2 did not affect the biomass production of these strains at 10% CO_2 intake. Further tests with different CO_2 intake levels and their effect on protein and other nutrients (carbohydrates and lipids) will enable us to select suitable strains for biomass production with CO_2 rich flue gas that can be used to produce microalgae pellets for feeding or downstream valued products.

New Anatoxin producing cyanobacteria: the importance of culture collection on cyanotoxin research P66

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Cyanobacteria are well known for toxin production and their impacts on public and environmental health. Although cyanotoxins have been deeply studied, with the identification of several producers and their biosynthesis gene clusters, the phylogenetic distribution of these genes and the ability to produce toxins is still relatively unknown, as demonstrated by the increased number of recently reported cyanotoxin-producing species and toxin gene-clusters variability.

This study focused on finding new Anatoxin-a-producing cyanobacteria by screening nine cyanobacteria cultured strains from the BACA culture collection. Anatoxin-a biosynthesis genes (anaC and anaF) and partial 16S rRNA were targeted by conventional PCR. Toxin production was confirmed by ELISA and HRLC-MS/MS. Phylogenetic analysis was made using cyanotoxins biosynthesis genes and partial 16S rRNA sequences.

Anatoxin-a genes were amplified in three cultured strains, identified morphologically and by 16S rRNA phylogeny as *Kamptonema* and *Tychonema*. Anatoxin production was confirmed by ELISA in three strains *Kamptonema* sp. BACA0007 and *Tychonema* sp. BACA0570, BACA0575. HRLC-MS/MS identified the production of 4R-Hydroxyhomoanatoxin-a or 4S-Hydroxyhomoanatoxin-a and Homoanatoxin-a in *Kamptonema* sp. BACA0007. Our results highlight the need to increase cyanotoxins bioprospection as there is still many unknown producing-taxa and emphasize the importance of culture collections in cyanotoxins research and mitigation.

Evaluation of lipid extraction methods from Antarctic filamentous fungi P68

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Purpose: The benefits of natural compounds have been studied for decades for the development of new technologies to answer the global change challenges. In order to develop these new technologies, lipids represent a great class of bioactive molecules. However, the research on lipids and their applications still present gaps about new sources as well as on the extraction methods. Filamentous fungi found in Antarctic territory could represent a new source of novel bioactive lipids. Currently Folch, Bligh & Dyer and Lewis methods are the most widely employed for extraction of lipid from different sample types. Nonetheless, choosing a single extraction method as the gold standard could represent a limitation, especially when the microorganism has not been studied yet. Taking the above into consideration, the main objective of the present study was to evaluate the best extraction method to obtain lipids from different Antarctic filamentous fungal genera.
Material and methods: Three isolates of Antarctic fungi belonging to each genus: *Mucor*, *Mortierella*, *Cladosporium*, *Penicillium* and *Pseudogymnoascus* isolates from Fildes Bay, Antarctica, were evaluated. A total of 15 isolates were assessed. Folch, Bligh & Dyer and Lewis extraction method were performed. Extraction was monitored by recording spectra of FT-IR spectroscopy of the biomass before and after lipid extraction.
Results: Folch was the best method to obtain lipids from filamentous Antarctic fungi, followed by Lewis extraction. Among the three extraction methods evaluated, Bligh & Dyer was the method that presented the lowest yield, compared to Folch and Lewis for each genus and strain. Strains of the genera *Mortierella* and *Mucor* were the ones that showed the best performance for the Folch and Lewis methods. The three *Penicillium* isolates were the third group with the best lipids' yield for the Folch method. The strains of genera *Cladosporium* and *Pseudogymnoascus* showed better yields for the Lewis method.
Conclusions: In this study it was observed that the lipids' yield varies according to the extraction methods, as well as both the fungal isolate and fungal genus. Depending on the purpose and fungi taxa, to obtain lipids from Antarctic fungi Folch or Lewis extraction methods are recommended.

Acknowledgments for partial funding: This work was funded by the Chilean Antarctic Institute through the INACH Regular project RT_16_20, and partially funded by the Universidad de La Frontera (Chile). Authors thank to the InES19-FRO19001 project, funded by the Ministerio de Educación (Chile) and executed by the Universidad de La Frontera.

Viability and Identification of *Penicillium spp.* associated with *Arrabidaea chica* deposited in the Central Microbiological Collection of Amazonas State University P69

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The Central Microbiological Collection (CCM) of the Amazonas State University (UEA) aims to maintain the preservation of ex situ specimens, as well as to provide information regarding the taxonomy and biogeography of the preserved specimens. Among the diverse group of fungi deposited in the CCM/UEA, there are endophytes isolates from the medicinal plant *Arrabidaea chica* (Bignoniaceae), known as crajiru. The objective of this research was to evaluate the physiological viability of *A. chica* endophytic fungi isolated in 2019, which are deposited in the CCM/UEA, and to identify the isolates of the genus *Penicillium*. The fungi preserved in Castellani and mineral oil were reactivated in Potato Dextrose Agar. Cell viability was verified by the growth of the pure seeded colonies. The observed macromorphological characteristics was mycelium textures, colony coloration, presence of exudates and pigments. The micromorphological characteristics were confirmed from the preparation of microculture slides, which was stained with lactophenol blue to verify the reproductive structures and compared with identification keys. From the strains identified as Penicillium, DNA extraction was performed by the CTAB method, with adaptations, followed by amplification using the Polymerase Chain Reaction (PCR) technique, with the primers Its1-Its4, Btub3-Btub4r and Calm228f-Calm737r. The PCR product was purified with PureLinkTM PCR Purification Kit (Invitrogen). Sequencing was performed using the Sanger technique, and sequences were checked (Bioedit 7.2.6) using as standard sequences acquired from the GenBank of BLASTN at NCBI. The sequences were aligned (MAFFT) and the phylogenetic analyses were conducted by the MEGA X program using the Maximum Likelihood method, with 1000 bootstrap replicates. 176 fungi were reactivated, of which 138 (78.40%) were considered viable, due to pure growth and because they presented macromorphological characteristics that was similar to the deposit records from 2019. On the other hand, only 5 (3.6%) species were identified as *Penicillium* spp. from the micromorphology analyses, namely: CG1-1, CF2-17, CG2-5, CG4-5, CF4-22. According to the molecular identification, 3 species were authenticated: *Penicillium expansum* CG2-5, *Penicillium* sp. CF2 -17 and *Penicillium* sp. CG1-11. *Penicillium* species have already been reported in the literature as endophytes and are known as potential biotechnological resources, since they are producers of bioactive compounds. Antimicrobial, cytotoxic and antioxidant activities are interesting to the pharmaceutical and cosmetic industries, and *Penicillium* spp. can produce metabolites

with these effects. Our results pointed out that Castellani and mineral oil preservation methods were efficient to preserve endophytic fungi, and was possible to identify 3 *Penicillium* specimens.

Characterisation of different Chilean *Capsicum* spp. varieties and the antifungal activity of their aqueous extracts P71

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The increase in fungal resistance to synthetic antifungals used in agrifood production has brought the need to develop new technologies based on an eco-friendly approach. The main aim of this work was to evaluate the antifungal potential of Chilean *Capsicum* spp. extracts against plant pathogens and mycotoxigenic fungi found in agrifood production.
Five different varieties of Chilean *Capsicum* spp. were obtained from both farmers and local markets in the city of Temuco, Chile. A specialist Botanist at the Universidad de La Frontera (Chile) confirmed the identification of pepper species and varieties. Fresh samples were grounded with a blender and freeze-dried for 7 days in the dark. After that, dry powder samples were stored at -20 °C in the dark until use. Pepper pod aqueous extracts were obtained by blending the freeze-dried puree from *Capsicum* spp. with 300 mL distilled water. Samples were incubated at 90°C for 20 minutes in a water bath with intermittent cycles of manual stirring every 2 minutes. The determination of capsaicinoid content was performed on an HPLC-FD system and the total polyphenols content was performed on an HPLC-DAD system. The antioxidant activity was carried out in a microplate reader using the DPPH and CUPRAC method. Reference strains of *Alternaria*, *Aspergillus*, *Fusarium*, *Penicillium* and *Rhizopus* were subjected to susceptibility tests (disc and culture media diffusion methods and MIC assay) against different concentrations of each pepper pod extract. Pure capsaicin, dihydrocapsaicin, nordihydrocapsaicin and amphotericin B were used as standard in the susceptibility tests.
Significant differences in the concentration of capsaicinoids were found among the different varieties of the same *Capsicum* species. The pepper pod extracts affected the macro- and micro-morphological features of the analysed filamentous fungal strains. Fungal strains belonging to the genera *Alternaria*, *Aspergillus*, *Fusarium*, *Penicillium* and *Rhizopus* produced mycelium with thinning, fragile and easily-break structure. In addition, their conidiophores became fragile presenting easily-break structures. Regarding other fungal genera (data not shown), the main alteration was the absence of conidiophore formation in some strains.
The morphological changes observed in the filamentous fungi strains suggest the fungistatic potential of pepper pod extracts. Results suggest pepper pod extracts could not kill non-

target fungal biodiversity but could control the growth and reproduction of some fungal plant pathogens. Inhibition of mycotoxin production is now under evaluation. Additional work is being developed in the field to validate the in vitro results.

Acknowledgments: ANID (Agencia Nacional de Investigación y Desarrollo, Chile) through the ANID/FONDECYT/1221024 project. This work was partially funded by the Universidad de La Frontera (Chile). Authors thank the InES19-FRO19001 project, funded by the Ministerio de Educación (Chile) and executed by the Universidad de La Frontera. The authors thank Professor Ruben Carrillo (UFRO) for his support in confirming the pepper species and varieties identification.

Physiological viability and occurrence of *Penicillium* spp. endophytic from the Central of Microbiological Collections of the UEA P73

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Endophytic fungi are organisms that live inside plants without causing damage. The Microbiological Collections Center of the University of the State of Amazonas (CCM/UEA) has in its collection, several endophytic fungi, at the moment, 1318 fungi are deposited in the CCM/UEA, of which 837 are fungi isolated from associations with plants. In this sense, the objective of this research was to evaluate the physiological viability and occurrence of fungi of the genus *Penicillium* associated with Amazonian plants deposited in the CCM/UEA. The specimens preserved in Castellani and mineral oil were reactivated in Potato Dextrose Agar (PDA), incubated in a microbiological oven at 28 ºC in the absence of light, after 7 days the cell viability was verified by the pure growth of the colonies and with similar aspects to the records of the deposited culture, the observed macromorphological characteristics were: textures of the mycelium, relief, coloring of the colonies, presence of exudates and pigments, the micromorphological characteristics were confirmed from the preparation of slides derived from microculture and stained with lactophenol blue to verify the reproductive structures, comparing them with identification keys, in order to quantify fungi identified as Penicillium sp. 449 specimens preserved in Castellani and Mineral Oil isolated from Amazonian plants (*Piper hispidum*: 86 isolates; *Myrcia guianensis*: 123 isolates; *Aniba canelilla*: 62 isolates; *Euterpe precatoria*: 40 isolates; *Arrabidaea chica*: 138 isolates), 81.74% were reactivated were identified as viable, due to pure growth and because they present macromorphological characteristics similar to the deposit records made between 2018 and 2019, of this total, fungi isolated from *A. chica* were considered the most viable (37.6%). On the other hand, only 24 specimens were identified as *Penicillium* spp. from micromorphology. Data reported in this work reaffirms the need for maintenance of microorganisms deposited in culture collections, on the other hand, the index of viable individuals indicates the Castellani method and Mineral Oil as efficient methods of preservation of microorganisms associated with plants. Fungi that were not recognized as from the original culture were isolated as airborne, opportunistic organisms. The maintenance of these organisms is important, since they are reported in the literature as potential biotechnological resources, such as antimicrobial, cytotoxic, antioxidant and other biological activities of metabolic extracts of these species and/or their molecules that can help in the pharmaceutical and cosmetic industry.

The challenges of a small culture collection toward accreditation P76

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Culture collections (CCs) provide authentic biological materials, having a public service role dedicated to support a variety of microbiological work, providing solid assurance of continuity through preservation and delivery of strains described or cited in publications. Moreover, CCs often maintain novel microorganisms awaiting future exploitation by biotechnology, guaranteeing an active role in R&D activities. The size and complexity of CCs can differ greatly, ranging from private to public, from basic operational resources to high-quality standard conditions, with either certification, accreditation or both in place.
The case of Micoteca da Universidade do Minho (MUM) is rather unique – it operates under high-quality standards and has its Quality Management System (QMS) certified under the ISO 9001 norm. Nevertheless, it is a small collection that continues to grow due to the efforts of a reduced multitasking team dedicated to continuous improvement through new deposits, services, and projects.
To be certified, CCs need to demonstrate to a third party that they have an effective QMS in place. The process conformity is monitored to prevent deviations in the final product and to ensure client satisfaction. Critical points identified in the risk analysis must be addressed and preventive measures put in place.
In an accreditation system, other challenges arise. CCs must provide evidence of competence and impartiality to perform specific technical activities. Therefore, CCs must follow a series of actions to guarantee the quality and validity of the measurements, including equipment calibration, environmental monitoring, technical validation of the methodology, and trained and qualified staff for such activities, which has severe financial implications for CCs activities. In small collections like MUM, this is a challenge that should not be underestimated. The lack of human resources prevents quicker growth and new revenues, creating a classic vicious cycle that can only be broken with full access to external funding that would allow the pursuit of accreditation.

Acknowledgments: This study was partially supported by the Portuguese Foundation for Science and Technology (FCT) under the scope of strategic funding of UIDB/04469/2020 unit and LABBELS (LA/P/0029/2020); and by "MIRRI-PT (Pólo Norte)" project (PINFRA04/84445/2020) funded by European Regional Development Fund under Norte2020—Programa Operacional Regional do Norte, and by IS_MIRRI21 project (grant agreement nº 871129) funded by EU Horizon 2020 research and innovation programme.

BCCM/ULC: a Public Culture Collection to conserve ex situ the cyanobacterial diversity and taxonomic reference strains P80

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The BCCM/ULC public collection (https://bccm.belspo.be/about-us/bccm-ulc) aims to gather a representative portion of terrestrial, freshwater, and marine cyanobacterial strains from different ecosystems with a focus on the polar diversity (140/283 strains). Amongst the 243 strains, for which the 16S rRNA gene sequence was determined, 93 OTU's (99% 16S rRNA similarity) were recognized. To distinguish closely related strains, the ITS are also sequenced. A dozen genomes are presently being sequenced, a.o. in the frame of the BRAIN-BE project GEN-ERA. The collection's aim is to preserve the deposited biological material, to valorize it by performing research on it, to provide it to interested parties for fundamental and applied research, and to provide services linked to the identification of the Cyanobacteria for the scientific community. An ISO 9001 certificate was obtained for the public deposition and distribution of strains, as part of the multi-site certification for the BCCM consortium. Several strains are the reference (or 'type') for newly described taxa. They include *Plectolyngbya hodgsonii* (ULC009), which is an endemic taxon from Antarctic continental lakes, *Shackletoniella antarctica* (ULC037) that has a bipolar distribution, *Timaviella circinata* and *T. karstica* (ULC401, ULC402), isolated from the Lampenflora of the Giant Cave in Italy and *Parakomarekiella sesnandensis* (ULC591), isolated from the biodeteriorated walls of the Old Cathedral of Coimbra, an UNESCO World Heritage Site. Recently, the BLCC (Berthold-Laughinghouse Culture Collection) deposited 196 strains with several new taxa. The goal of these isolations was to describe and characterize novel cyanobacteria from different ecosystems in Florida, a subtropical to tropical climate region. These deposits include newly described genera and species including *Johannesbaptistia floridana*, *Iningainema tapete*, *Brasilonema fioreae*, and *Neolyngbya biscaynensis* sp. The diversity of cyanobacteria in these mats is huge and still largely unexplored. Moreover, these ecosystems are a potential source of novel secondary compounds. For example, species of *Neolyngbya* and *Brasilonema* have been shown to produce compounds with antibiotic and antifungal properties.

Cotton Textile with Antimicrobial Activity and Enhanced Durability Produced by L-Cysteine-Capped Silver Nanoparticles P81

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In this study, L-cysteine-capped silver nanoparticles (Cys-AgNPs) were successfully linked in a cotton textile, being attached in a covalent way to the cotton fibers via esterification with the hydroxyl groups from the cellulose. The AgNPs were strongly adhered to the fiber surface through coordination bonds with the thiol groups from the L-cys. In addition, they were compared with biogenic silver nanoparticles produced from fungi (bio-AgNPs). Materials and methods: The characterization of the Cys-AgNP and the bio-AgNP solutions were accomplished by UV–visible (UV–Vis), Z-potential, and X-ray diffraction (XRD). After the attachment of the Cys- AgNPs and the bio-AgNPs to the raw cotton, the textile surface was characterized by variable pressure scanning electron microscopy (VP-SEM), energy dispersive X-ray (EDX), and Fourier transform infrared spectroscopy (FT-IR). The antibacterial activity was performed by disk diffusion analysis. Results: The results of the UV–Vis analysis showed the presence of AgNPs in the Cys-AgNPs and the bio-AgNPs solutions, showing the Surface Plasmon resonance (SPR) for the AgNPs among 380–420 nm. In addition, they exhibited a Z-potential of −27 and −24 mV, respectively, with the presence of elemental silver shown by the XRD analysis. The VP-SEM images from the cotton fabrics covered in Cys-AgNPs and bio-AgNPs showed the presence of spherical AgNPs on their surface, and EDX analysis revealed the presence of peaks associated with the presence of Ag, C, and O. Furthermore, FT-IR analysis exhibited peaks associated with the presence of L-cysteine (SH-) and carboxylic acid arising from the esterification reaction among the cellulose from cotton and the carboxylic acid in the L-Cys molecules. Finally, the cotton textile exhibited antibacterial activity against Escherichia coli and Staphylococcus aureus. Conclusions: This study demonstrates the ability of Cys-AgNPs to bind to the cellulose from cotton fabric so as to produce antibacterial fabrics with enhanced durability, opening a wide range of options to be further used in healthcare and other industries.

Creating community of microbiology-related professionals through the MIRRI Collaborative Working Environment (CWE) P82

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MIRRI-ERIC supports the biosciences scientific community and bioindustries by providing a single point of access to microbial related services, the MIRRI Collaborative Working Environment (CWE, www.mirri.org). The CWE facilitates the access to the broadest range of high-quality microorganisms, their derivatives, associated data and services, and it is complemented with a forum of experts created to share and generate knowledge within the MIRRI stakeholder community (culture collections, policy makers, scientists, bioindustry, etc.). The clusters covered by the platform will be:

- Legal/Regulatory Issues & Standards (e.g. ABS, Biosafety, Budapest Treaty)
- Applications in Biotechnology & Bioindustries (topics aligned with the MIRRI Research & Innovation Agenda)
- Taxonomy (microbial groups in the scope of MIRRI expertise)
- Bioprospection, Cultivation & Preservation (microbial groups and samples in the scope of MIRRI expertise)
- High-end Technologies & Platforms (e.g. MALDI-TOF, Genome analysis, Culturomics, Digital Technologies & FAIR data)

The forum is being implemented in the frame of the project IS_MIRRI21 (H2020 GA nº 871129). As a pilot, the cluster on Legal/Regulatory Issues & Standards is available to be used for the community. Consultation of the forum is open to everybody through the public site of the CWE. However, use of the forum (add new topics or reply to posts) requires registration into the platform.

With this tool, MIRRI aims to foster innovation within science, research and development, bringing together students and professionals working in cross disciplinary aspects in the microbial-related value chain.

Identification and reclassification of *Pseudomonas* strains deposited in the NCCB Collection using 16S rRNA, gyrB and rpoD sequence analysis. P83

Figge M.

Westerdijk Instute

The Netherlands Culture Collection of Bacteria (NCCB) was formed by the merger of the collection of the Kluyver Institute for Biotechnology (LMD, formerly Laboratory of Microbiology, Delft) and Phabagen. M.W. Beijerinck and A.J. Kluyver initiated the LMD collection in 1922. At present the NCCB collection is incorporated in the Westerdijk Fungal Biodiversity Institute.
During the past century over 300 *Pseudomonas* strains have been deposited in the NCCB collection, most of which were mainly identified with primary and phenotypic tests. In this study, many *Pseudomonas* strains that previously were only characterized with phenotypic methods were identified to the species level with 16S rRNA, gyrB and rpoD sequence analysis. Results obtained indicated several possible new *Pseudomonas* species. Furthermore, several strains were re-identified as recently described species. Among these, were also old reference strains that were thus far incompletely described *Pseudomonas* species, for example NCCB 22037 (=ATCC 19373=NCIB 9031) "*Pseudomonas caryocyanea*" Dupaix 1933 isolated by M.W. Beijerinck. The latter strain was identified belonging to one of the recently described and close related species *P. lactis* or *P. salmasensis* based on rpoD sequence analysis but this gene does not discriminate these two species.

Bioprospection of antibiotics and biofilm inhibitors from under-exploited filamentous fungi

P85

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In the past century, millions of lives were saved by antibiotics, which treat some of the historically more deadly diseases. However, bacteria may quickly develop antibiotic resistance and the speed of development of new drugs has decreased significantly in the last decades. Filamentous fungi have a great potential for novel antibiotic discovery, given their vast, largely unexplored metabolome. The One Strain MAny Compounds (OSMAC) approach serves as a tool to obtain a wide range of metabolites by varying various culture conditions. In this study, eight under-explored fungal species from Micoteca da Universidade do Minho (MUM) were used, aiming to identify compounds with antibiotic or antibiofilm properties produced by them: *Coprinopsis spilospora*, *Penicillium tunisiense*, *Trichoderma aestuarinum*, *Colletotrichum coccodes*, *Talaromyces saxoxalicus*, *Diaporthe phillipsii*, *Cladosporium rubrum*, and *Neopestalotiopsis scalabiensis*. They grew in different culture media, under submerged fermentation for 7 and 14 days under varying conditions of agitation and aeration, and the resulting supernatants were tested for their antimicrobial activity against *Staphylococcus aureus* and *Escherichia coli* using the disk diffusion method. Almost all fungi grew on the different media and under the diverse process conditions. It was found that *Coprinopsis spilospora* metabolites inhibited *S. aureus* growth and demonstrated antibiofilm properties. They reduced the biofilm by 74% in crystal violet staining, metabolic activity by 100% in Alamar blue test, and viable cell counts by 98% in CFU counting. The effect against E. coli was more modest, although still reduced CFU counts by 96%. High-pressure liquid chromatography/high-resolution mass spectrometry (HPLC/HRMS) showed that these results are likely due to the presence of compounds in the illudin family. The pioneer results obtained in the present study highlight the potential of filamentous fungi for bioprospection for antibiotic discovery.

The Collection of Marine Microorganisms (CoSMi), a valuable bio-resource for scientific innovation, sustainable economy and conservation of environmental biodiversity P86

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The Collection of Sea Microorganisms (CoSMi), maintained at the National Institute of Oceanography and Applied Geophysics (OGS) in Trieste, is an infrastructure that is part of the WFCC - World Federation for Culture Collections and linked to national and international research infrastructures such as MIRRI.IT, LifeWatch, ECCSEL and EMBRC ERIC in addition to be an integral part of the BioMarine Lab and of the Gulf of Trieste observatory system.
CoSMi is a bioresource center comprising many species of autotrophic unicellular eukaryotes mostly isolated from the Gulf of Trieste (Northern Adriatic Sea, Mediterranean Sea), such as potentially toxic and non-toxic dinoflagellates, diatoms responsible for blooms, coccolithophores, and flagellates, which may represent a source of genetic diversity to be studied and preserved.
The main task of CoSMi is to isolate microalgae primarily from the North Adriatic Sea, maintain them in culture and identify them at species level using morphological and genetic methods. In many cases a definitive taxonomic determination is exclusively possible on cultured material and several species have already been newly described or redescribed using CoSMi cultures. To date, CoSMi includes about 200 strains of phytoplanktonic organisms available for scientific purposes to enhance collaborations and networking at regional and international scale. The presence of two refrigerated cells equipped with photobioreactors allows conducting experiments at controlled conditions of pH, temperature, light, O2 and CO2 to study the response of microorganisms in different environmental conditions and explore potential biotechnological applications of microalgae. Moreover, cultures are made available for different industry sectors: aquaculture, pharmaceutical, nutraceutical, energy and for ecotoxicology.
CoSMi's team is active in outreach and communication regarding the topic of biodiversity of microorganism - mainly microalgae - and their importance in the marine food web, climate change studies and in other environmental dynamics.
More recently, in the framework of the Italian PNRR project, SUS-MIRRI.IT, promoted by JRU MIRRI.IT, the Italian network of the microbial culture collection, CoSMi collection will be strengthened through the improvement of technological equipment and scientific instrumentation and better characterization of microbial biodiversity using different tools (morphological, physiological and molecular). Additionally, the implementation of the operative culturing procedures and the development of standard operation procedures for sampling, characterization, and conservation will be adopted. Finally, resources, services, skills, and innovation will be promoted and the cooperation with stakeholders will be strengthened.

CIIMAR Microbial Culture Collection (CM2C) – unravelling biological marine resources for the blue biotechnology P87

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CIIMAR Microbial Culture Collection (CM2C) is a biobank located at CIIMAR - Interdisciplinary Centre of Marine and Environmental Research – created with the purpose to gather marine microbial strains with different biotechnological applications. This biobank will comprise different microbial strains, mainly Bacteria and Fungi, retrieved from marine and environmental sources (seawater, freshwater, sediment, salterns, macroalgae, sponges, corals and other organisms), obtained from Atlantic coast, deep-sea and inland waters from Portugal, including Azores and Madeira. CM2C collection gathers a great diversity of marine microbial strains, that are being explored for health, industrial and environmental applications. CM2C will serve as a supplier of marine biological resources for academia and industrial researchers.

This collection is being explored by different researchers for the bioprospection of new bioactive compounds with health or industrial applications and for the development of bioremediation tools for environmental recovery. For example, several microbial strains belonging to the phyla Actinomycetota and Planctomycetota showed capacity to produce bioactive molecules with anticancer, antimicrobial, anti-inflammatory, antifungal and anti-obesity activity [1-4]. Moreover, CM2C collection holds a great diversity of microbial strains, mainly from the phyla Pseudomonadota, Bacteroidota and Actinomycetota, that are being explored for their capacity to degrade persistent and emerging pollutants (e.g. Hydrocarbons, Pesticides, Pharmaceuticals) [5-7].

CM2C will be soon registered in the world federation for culture collections (WFCC) and in the World Data Centre for Microorganisms (WDCM). In addition, this collection will ensure full traceability of the samples in compliance with the Access and Benefit Sharing regulation associated with the Nagoya Protocol.

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Acknowledgments: This work is a result of the project ATLANTIDA (ref. NORTE-01-0145-FEDER-000040), supported by the Norte Portugal Regional Operational Programme (NORTE 2020), under the PORTUGAL 2020 Partnership Agreement and through the European Regional Development Fund (ERDF).

Taxonomically unique actinomycetes isolated from chilean environments: *Corynebacterium alimapuensis* sp. nov., and *Spiractinospora alimapuensis* gen. nov., sp. nov. P88

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Actinomycetes are a group of Gram-positive bacteria in the order Actinomycetales, known for producing secondary metabolites with a wide range of biological activities. In fact, actinomycetes are responsible for producing over 70% of known antibiotics. The initial stages of bioprospecting depend on the taxonomic classification of the microorganisms being studied. This is based on the theory that taxonomic diversity is related to chemical diversity, and on the concept that new species may produce unique compounds due to the role that the evolution of secondary metabolites plays in bacterial speciation.

Our research group focuses on the bioprospecting of actinomycetes from marine environments from Chile. In this study, we examined strains of actinomycetes isolated by our group from Chile that may represent new taxa. We identified five potential new taxa, including three belonging to the genus *Streptomyces* (VB1, VS4-2, and Vc67-4), one to the genus *Corynebacterium* (VA37-3), and one to the family Nocardiopsaceae (VN6-2). The taxonomic position of two of these strains was studied.

Strain VA37-3(T) was found to be an aerobic, non-motile, non-spore-forming, and coccobacilli-shaped actinomycete. The strain grew optimally at 30 °C and in the presence of 3-4 % NaCl. Strain VA37-3(T) requires seawater or a sodium-enriched medium for growth. Strain VA37-3(T) formed a distinct phyletic line within the genus *Corynebacterium* and shared the highest sequence similarity with *Corynebacterium marinum* D7015(T) (97.6%). Based on the data from the polyphasic study, we propose the name *Corynebacterium alimapuense* sp. nov., with the type strain being VA37-3(T).

The strain VN6-2(T) was found to be aerobic, non-motile, alkaliphilic, halotolerant, and filamentous actinomycete. Substrate mycelium is extensively branched with non-fragmenting hyphae. Aerial mycelium forms short and wavy or spiral spore chains. The strain grew optimally at 30°C, pH 9-10, and in the presence of 3-4 % NaCl. Both the phylogenetic analyses, based on 16S rRNA gene sequences, and the phylogenomic study revealed that strain VN6- 2(T) formed a distinct monophyletic clade within the family Nocardiopsaceae, and exhibited the highest 16S rRNA gene sequence similarity with Salinactinospora qingdaonensis CXB832(T) (93.9 %). Based on the data from the polyphasic study, we propose the name *Spiractinospora alimapuensis* gen. nov., sp. nov., with the type strain being VN6-2(T).

This study shows that Chile's natural environments are a rich source of new actinomycete and potential producers of bioactive compounds.

Exploiting microbial diversity from estuarine sediments for bioremediation of two pharmaceutical compounds P89

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Pharmaceuticals are crucial to our society to prevent and treat several diseases. However, their intensive consumption has led to their presence in the environment, affecting the living organisms that inhabits these ecosystems and the ecosystems functioning. Solutions are needed to remove pharmaceuticals from natural environments as most emerging technologies are designed to be applied in wastewater treatments plants, one of the major sources of pharmaceuticals in the environment. Microorganisms holds a metabolic capacity to degrade a wide range of pollutants and can be a powerful tool for the development of bioremediation tools to respond to pollution incidents. Thus, this work seeks to study the biodegradation potential of microorganisms to remove pharmaceuticals (paroxetine and bezafibrate), combining culture-dependent and -independent methods. For that, an enrichment process was assembled by exposing estuarine sediment of Lima River Estuary to 1 mgL-1 of paroxetine or bezafibrate, for 20 weeks (10 cycles). Enriched cultures were plated in different culture media and colonies with different morphologies were purified, preserved at -80°C and identified through 16S rRNA gene sequencing. At the end of each cycle, samples were collected for microbial community characterization by next-generation sequencing (V4-V5 hypervariable region of the 16S rRNA gene) and to evaluate the removal of bezafibrate and paroxetine by liquid chromatography analysis. Preliminary results showed that both pharmaceuticals were not detected until the 6th cycle (removal efficiency > 80%). Moreover, community analysis showed changes in the community structure throughout time, although a high removal efficiency was attained during the six cycles analysed. In addition, 12 different bacterial genera were obtained through culture dependent methods, in which 6 of those 12 bacterial genera had a relative abundance greater than 2% in the enriched microbial cultures. This study will contribute to better understand the microbial community involved in the degradation of paroxetine and bezafibrate, and the microbial strains isolated will be deposit in the CIIMAR Microbial Culture Collection (CM2C), for further development of bioremediation strategies to recover polluted environments, contributing to the Zero pollution action plan and to the EU Mission: Restore our Ocean and Waters.

Acknowledgments: This work was partially funded by the project Ocean3R (NORTE-01-0145-FEDER-000064), supported by the North Portugal Regional Operational Programme (NORTE2020), under the PORTUGAL 2020 Partnership Agreement and through the European Regional Development Fund (ERDF), and by the project BIOSYSMO funded the European Union under the GA no 101060211.

Aflatoxins and ochratoxin A contamination during Merkén Pepper Powder Production in Chile

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Berry fruits of *Capsicum annuum* L. cv. "Cacho de Cabra" are used for the manufacture of a traditional pepper powder known as Merkén, which is a Chilean spicy widely consumed at national level in Chile and also exported to different countries. Merkén contamination with Aflatoxins (AFs) and Ochratoxin A (OTA) is a main concerning for local producers and national and worldwide consumers. In the present study, AFs and OTA contamination in berry fruits of C. annuum L. cv. "Cacho de Cabra" was determined at (1) harvest, (2) dried and (3) smoked stages of Merkén production, in (4) cumin and coriander seeds, used as Merkén ingredients, and in (5) the final packed Merkén produced by local farmers. In addition, Merkén obtained from local markets in the Region of La Araucanía (Chile), where obtained and evaluated. Aflatoxigenic and ochratoxigenic potential of fungal strains isolated from the above-mentioned substrates were also assessed. There was no detection of AFs nor OTA on pepper pods and seeds used as Merkén ingredients. In contrast, co-occurrence of aflatoxin B1 (AFB1) and OTA were detected in c.a. 57% of final packed Merkén samples (12 out of 21 samples). Regarding AFB1, Merkén samples produced by local farmers presented contamination level from 0.19±0.26 to 1.44±0.10 µg/kg; while Merkén sample purchased from local markets presented contamination level from 0.29±0.37 to 1.67±0.32 µg/kg. For these samples, no AFB2, AFG1, and AFG2 were detected. Ochratoxin A contamination was detected for 100% of Merkén samples from both local producers (0.79±0.05 to 5.99±0.68 µg/kg) and local markets (0.83±0.83-19.81±0.70 µg/kg). There was no detection of AFs and OTA on Petri plate for *Aspergillus* (n=52) and *Penicillium* (n=129) strains isolated from pepper pods, cumin and coriander seeds and Merkén. The lack of high AFs/OTA-producer among the isolated fungal species can explain and support the absence of contamination in pepper pods. In Merkén production chain the harvest and primary processing of post-harvest (dried and smoking of pepper pods) is a key point to fungal grow but are not critical for AFs and OTA production. In contrast, the second phase of post-harvest (milling, storage) are critical points for AFs and OTA contamination. Prolonged storage under poor hygienic conditions, oscillation in the water activity, and temperature can provide suitable conditions for mycotoxins production. In addition, NaCl and capsaicinoids compounds present on pepper pods and Merkén can act as intrinsic factor up-/downregulation AFs and OTA biosynthesis in this type of substrate.

Phenolic compounds, antioxidant analysis, and lipids and ribosomal protein profiles of fungi specimens collected from Brazilian and Chilean environments P91

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The Fungi Kingdom comprises about 100,000 species currently described, being considered one of the most diverse groups of organisms on the planet (Watkinson et al. 2015). Fungi are widely used in research and biotechnological applications. Brazil and Chile are countries with high mycological diversity. To know their fungi biotechnological capacity, research is often developed in both countries (Arrieche et al. 2023, Costa et al. 2023). The main aim of this work was to characterize fungi specimens collected from Brazilian and Chilean environments regarding their phenolic compounds profile, antioxidant activity, and lipids and ribosomal protein profiles. Sixteen fungi specimens were collected from different locations in Brazil and in Chile. Fungi were isolated on PDA, and the ascomata and basidiomata were deposited in both the Herbarium URM (Brazil) and the Herbarium UFRO-H (Chile). Fungi belonging to the Ascomycota division were assessed: *Aspergillus* (1070), *Nemania* (51), and *Pestalotiopsis* (A1); and Basidiomycota were found: Deconica (V11), Hexagonia (8114), Perenniporia (8352), *Pycnoporus* (A3), *Schizophyllum* (V63, 177, 8112, AS172) and *Trametes* (1064, 8350, 8354, 1001, 3231). The phenolic compounds profile was determined by the Folin-Ciocalteu method, and the antioxidant activity was determined by the ABTS, DPPH and CUPRAC methods, according to Nahuelcura et al. (2021), with modifications. MALDI-TOF/TOF MS was used for fungal species classification and characterization based on both ribosomal proteins and lipids profiles following the methodology of Paziani et al. (2020) and Puttaraju et al. (2006), respectively, with modifications. For the Folin-Ciocalteu method, specimens 1064 and V11 showed the best results, while 177 and 8112 showed the lowest results regarding total phenolic compounds production. In the DPPH method, V11, 1070 and 8352 presented the best results, while A1, V63 and 8351 presented the lowest results regarding antioxidant activity. Similarly, in the TEAC method, 1064, 1070 and V11 had the best results, while 177 and 8112 had the lowest results regarding antioxidant activity. Finally, for the CUPRAC method, specimens 1064, 71, 8352 and V11 showed the best results, while 177 and A3 presented the lowest results regarding antioxidant activity. The MALDI-TOF/TOF MS proteins and lipids profiles were useful for the previous fungal classification. The results suggest that the analyzed fungal genera are good producers of antioxidant substances. However, additional analyzes are necessary for better optimization of the extraction of the compounds. Both the proteins and lipids profiles by MALDI-TOF/TOF MS are useful strategy for previous classification of these fungal asset.

Filamentous fungi isolated and identified from Antarctic soil (Fildes Bay, Antarctica) P92

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Purpose: Antarctica is a unique place with extreme environmental conditions, including low temperature, high solar radiation, low nutrient availability and strong winds. This different environment represents a gateway to studies on the taxonomy, ecology, and biotechnology of organisms under extreme conditions. Fungi are ubiquitous and diverse organisms in Antarctica and have been described as growing in different substrates such as plants, soil, rocks, ice, snow, and animals. To survive in such extreme conditions' fungi might display unusual biochemical pathways able to generate specific or novel compounds with biotechnological relevance. Before accessing the fungal biotechnological potential, knowing the fungal species is mandatory. The main aim of this study was to isolate and identify fungal strains from Antarctic soil (Fildes Bay, Antarctica).
Material and methods: Soil samples were collected using a 4x25 m transect at a depth of 0-20 cm in different geographic areas of Fildes Bay (Antarctica). A total of 13 composed soil samples were collected. Composed soil aqueous suspensions were incubated on Potato Dextrose Agar (PDA), Dichloran Glycerol Agar 18% (DG18) and Dichloran Rose Bengal Chloramphenicol Agar (DRBC) media at 10 ºC for 21 days in the dark. Subsequently, filamentous fungi were isolated and cultured on PDA. The morphological identification of the isolated strains was carried out according to the classic macro- and micromorphological taxonomy.
Results: A set of c.a. 1600 fungal strains belonging to the genera *Acremonium*, *Aspergillus*, *Cladosporium*, *Mortierella*, *Mucor*, *Penicillium*, *Psudogymnoascus* and other four non-identified fungal genera were isolated. In addition, a relationship between the geographical area of the soil sample and the fungal genera was observed.
Conclusions: Despite both the adverse environmental conditions and Antarctic soils that are not completely devoid of life, it was possible to observe a great diversity of filamentous fungi in some assessed soil samples. This indicates the ability of filamentous fungi in adapting to and survive in extreme conditions such as some of those found in Antarctica. This work represents the first report of large-scale fungal isolation in Fildes Bay, Antarctica. Molecular biology identification is being developed for isolated fungal strains.

Acknowledgments: This research was funded by the Instituto Antártico Chileno (INACH, Chile) through the Project INACH Regular RT_16_20, and partially funded by the Universidad de La Frontera (Chile). Authors thank to the InES19-FRO19001 project, funded by the Ministerio de Educación (Chile) and executed by the Universidad de La Frontera.

Capsicum spp. and the antifungal potential of capsaicinoids as safeguards for agri-food production P95

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In recent years, cases of pathogenic fungi in agricultural crops and in animals, including humans, are growing (Paziani et al., 2020; Costa et al., 2022). Many of these pathogenic fungi are resistant to the commonly used antifungals. This scenario has created a need for new effective antifungals, particularly those based on eco-friendly approaches, such as plant secondary metabolites (e.g. capsaicinoids from *Capsicum* species) (Costa et al., 2022).

The American Phytopathological Society recognises a biofungicide as a naturally based biochemical product that must contain naturally-occurring substances (McGrath, 2004). The use of pepper pod extracts for the production of biofungicide has been proposed in the literature (Costa et al., 2022). As a natural compound, capsaicinoids and their analogues are much less dangerous than commercial synthetic fungicides.

Biofungicides present a low risk for environmental health. They could be applied in different stages of agricultural production without putting workers and the environment at health risk. In addition, since biofungicides are based on non-recalcitrant molecules, there is expected no risk of contaminating soil and groundwater. In this context, the use of natural compounds is directly related with the One Health approach, which tries to find a balance among people, animals and the environment's health (World Health Organization, 2023).

In fact, capsaicinoids compounds has been characterised as antifungal molecules. Capsaicinoids-based biofungicides could have the potential to improve food safety, nutritional value and overcome antimicrobial resistance, with less associated health risk. Beneficial characteristics of capsaicinoids include the demonstrated fungicidal and fungistatic activities of pure *Capsicum* extracts and purified capsaicinoids (Soumya and Nair, 2012; Costa et al., 2022). These molecules can be used to control the growth of pathogenic fungi in plant crops and as ecological alternatives for pest management. This work aims to review the use of pepper pod extracts, rich in capsaicinoid compounds, as a strategy for safeguarding of agrifood production. The advantages and limitations, for environmental health, of using capsaicinoids-based biofungicides will be presented and discussed in this work.

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The phylogenetic diversity of some isolates from the Freshwater Microalgae Culture Collection (CCMA-UFSCar) P100

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The Freshwater Microalgae Culture Collection of the Federal University of São Carlos (CCMA-UFSCar) present a huge diversity of Brazilian isolates, being a potencial source of interesting biomolecules. On the last decade, the phylogenetic studies on some of these isolates have started, by acquiring the 18S rDNA, ITS, rbcL and tufA genes. Thus, the observations on life cycle and morphology have also been covered. According to the applied polyphasic studies, with morphological and molecular taxonomy, the green microalgae isolates studied until now belong to the Phyla Chlorophyta and are distributed in the families Chlorococcaceae, Scenedesmaceae, Botryococcaceae, Hydrodictyaceae, Oocystaceae, Radiococcaceae, Sphaerocystidaceae and Volvocaceae, in addition to some still undefined orders and families. Furthermore, the phylogeny of Euastrum and Micrasterias is being untangled, using Brazilian and European strains, revealing new genera and species to be described. For the Ochrophyta, five new lineages are being described. In summary, the studies on the CCMA-UFSCar strains reveals how diverse the Brazilian microalgae are and emphasizes the importance of microalgae culture collections in diferent areas of the globe.

Diversity and Bioactive Potential of Marine Actinobacteria Integrating CIIMAR Microbial Culture Collection (CM2C) P103

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The CIIMAR Microbial Culture Collection (CM2C) is a biobank situated at CIIMAR, which integrates a wide range of bacterial and fungal strains with several biotechnological applications. Among Bacteria, the biobank comprises a collection of actinobacteria isolated from coastal and deep-sea sediments, macroalgae, sponges, fish and ascidia, from the Portuguese Atlantic Coast, Arctic Ocean and Portuguese Archipelagos (Azores and Madeira). This collection includes 107 actinobacterial strains distributed by 21 genera (from the most to the least abundant): Streptomyces, Micromonospora, Nocardiopsis, Rhodococcus, Brevibacterium, Microbacterium, Tsukamurella, Brachybacterium, Micrococcus, Gordonia, Nocardioides, Arthrobacter. Mycolicibacterium, Saccharomonospora, Cellulosimicrobium, Actinomadura, Paenarthrobacter, Herbiconiux, Isoptericola, Polymorphospora and Glutamicibacter. Some of these strains showed antimicrobial activity against Candida albicans and anticancer activity against the cancer cell lines T-47D (breast ductal carcinoma), HepG2 (liver cancer) and/or SH-SY5Y (neuroblastoma cancer) and can be a promising source of new molecules with biotechnological importance [1-3].
CM2C is on the verge of being officially registered with the World Federation for Culture Collections (WFCC) and the World Data Centre for Microorganisms (WDCM).

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Acknowledgments: This work is a result of the project ATLANTIDA (ref. NORTE-01-0145-FEDER-000040), supported by the Norte Portugal Regional Operational Programme (NORTE 2020), under the PORTUGAL 2020 Partnership Agreement and through the European Regional Development Fund (ERDF)

Unraveling microbial diversity of CM2C (CIIMAR Microbial Culture Collection) for bioremediation applications P104

Fernandes J.[1,2], Perdigão R.[1,3], Alexandrino D. A. M.[1], Bôto M. L.[1,3], Ribeiro I.[1,3], Carvalho M. F.[1,3], Mucha A. P.[1,2]

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CIIMAR Microbial Culture Collection (CM2C), a georeferenced biobank of microorganisms, is being created at CIIMAR, to provide marine biological resources for academia and industrial researchers. CM2C will comprise a wide diversity of microbial strains which are being explored for different environmental and industrial applications. CM2C xenobiotic degraders have been associated with the degradation of hydrocarbons [1], pesticides [2] and pharmaceuticals [3] and were isolated from several environmental samples such as seawater or sediments, to create sustainable bioremediation technologies to recover contaminated environments [1,2,3]. Additionally, microbial communities associated to plastics and marine litter are also being explored as a source of potential plastic degraders. Most xenobiotic degraders of CM2C collection belongs to the Pseudomonadota phylum, in which species from the genera *Pseudomonas*, *Acinetobacter*, *Ochrobactrum* and *Hydrogenophaga* have been associated with the degradation of pesticides, pharmaceuticals and hydrocarbons. The collection also holds xenobiotic degraders from Bacteroidota and Actinomycetota phyla, that have been associated with the degradation of pesticides and pharmaceuticals (e.g genus *Microbacterium*) and hydrocarbons (e.g. genus *Rhodococcus*).
CM2C will provide access to marine bioresources and serve as a tool for the development of bioremediation technologies to recover contaminated environments, contributing to the Zero pollution action plan and to the EU Mission: Restore our Ocean and Waters.

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Acknowledgments: This work is a result of the project ATLANTIDA (ref. NORTE-01-0145-FEDER-000040), supported by the Norte Portugal Regional Operational Programme (NORTE 2020), under the PORTUGAL 2020 Partnership Agreement and through the European Regional Development Fund (ERDF).

How are the carcasses from the turkey production industry eliminated? A potential environmental problem P117

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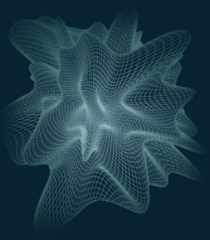
The Americas is the world's largest turkey region, producing over 60% of the world's total. After the US, Brazil is the region's second largest producer with over 390,000 tonnes per year. Then, the European Union is the third world producer. For various reasons, turkey production is subject to losing large numbers of herds, particularly young turkeys are vulnerable to respiratory diseases, outbreaks, including salmonellosis, which make them listless and ultimately die. Production plants dispose of turkey carcasses through composting, but when the composting facility is full or many turkeys have died, disposal can be done by burying them anywhere without any technical assistance. The main objective of this work is to study the practical conditions used by production plants to landfill turkey carcasses. To carry out the study, a qualitative methodology was used, combining document analysis, including the legal framework and company records, and fieldwork to make observations and interview the owner. The company chosen for this case study operated in the municipality of Carlos Barbosa (RS) with 3 employees and 17 years of uninterrupted activity, and capacity for 34,000 turkeys. On average, the company loses about 8% of turkeys per month due to death or illness and uses 4 composters, each measuring 3x2x2 m, to dispose of carcasses. However, the company makes a landfill next to the dead turkeys on its premises without any control of the aquifer or the soil's waterproofing capacity, where it has been noticed and photographed that the manure that comes out of the composters goes directly to the soil. In conclusion, burying turkey carcasses requires an environmental impact assessment and incineration is not an economically viable treatment for this activity.



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