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MINIREVIEW

Public Microbial Resource Centers: Key Hubs for Findable, Accessible, Interoperable, and Reusable (FAIR) Microorganisms and Genetic Materials

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ABSTRACT In the context of open science, the availability of research materials is essential for knowledge accumulation and to maximize the impact of scientific research. In microbiology, microbial domain biological resource centers (mBRCs) have long-standing experience in preserving and distributing authenticated microbial strains and genetic materials (e.g., recombinant plasmids and DNA libraries) to support new discoveries and follow-on studies. These culture collections play a central role in the conservation of microbial biodiversity and have expertise in cultivation, characterization, and taxonomy of microorganisms. Information associated with preserved biological resources is recorded in databases and is accessible through online catalogues. Legal expertise developed by mBRCs guarantees end users the traceability and legality of the acquired material, notably with respect to the Nagoya Protocol. However, awareness of the advantages of depositing biological materials in professional repositories remains low, and the necessity of securing strains and genetic resources for future research must be emphasized. This review describes the unique position of mBRCs in microbiology and molecular biology through their history, evolving roles, expertise, services, challenges, and international collaborations. It also calls for an increased deposit of strains and genetic resources, a responsibility shared by scientists, funding agencies, and publishers. Journal policies requesting a deposit during submission of a manuscript represent one of the measures to make more biological materials available to the broader community, hence fully releasing their potential and improving openness and reproducibility in scientific research.

KEYWORDS culture collection, FAIR, Nagoya Protocol, open access, mBRC

Open science includes a range of initiatives aimed at sharing scientific outputs, such as data sets (open data), source codes (open source), and publications (open access). The goal is to maximize scientific impact by making these outputs accessible to the research community (1). This availability allows future studies, facilitates new discoveries, and enables the verification and reproducibility of experiments and analyses (2). Open science generally focuses on data, a concept which received much interest from academia, industry, publishers, and funding agencies. This interest resulted notably in the development of guiding principles intending to make scientific data findable, accessible, interoperable, and reusable (FAIR) (3). In particular, these guidelines em-

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phasize the added value of reusing existing data in new concepts and new research questions (4). Noteworthy, the FAIR concept differs slightly from open science since it recognizes that accessibility can be restricted due to various factors, such as privacy, security, and competitiveness (5).

In this context, it is surprising that little attention is given to "open research materials," although their accessibility is equally important for reproducible science and to support future studies. In life sciences, public culture collections represent a historical example of open science, as they have a long-standing experience in the preservation of living microbial strains and genetic materials and their distribution for further scientific investigations. In addition, these collections have developed databases allowing users to benefit from a wealth of data related to the biological material. This review describes, from both historical and future perspectives, the active roles played by culture collections to sustain research and to disseminate scientific knowledge. It also calls for an increased deposit of biological resources in professional repositories.

EVOLVING ROLES OF CULTURE COLLECTIONS IN THEIR TRANSITION TO mBRCs

Microorganisms represent a huge biodiversity resulting from their adaptation to the extensive variety of ecological niches in which they have evolved during the past 3.5 billion years. They are an invaluable resource for fundamental research and for applications in bioindustry, agriculture, health care, and the environment. They also provide a range of genetic capacities that drive modern gene technologies, like recombinant plasmids or the bacterial CRISPR/Cas system for eukaryotic genome editing. However, contrary to common belief, this biodiversity is vulnerable to modifications and even extinction, and its preservation is therefore crucial more than ever. Some microorganisms are indeed restricted to particular environments or biogeographic regions and are threatened with extinction if their habitat is altered or destroyed (6). Many microbes live in intimate association with other organisms, and species-specific microbial symbionts can become extinct along with their host (6). At the level of the human body, the diversity of the gut microbiota is decreasing as a result of antimicrobial drug usage, changes in diet, agricultural practices, and sanitation (7, 8). This intestinal dysbiosis is suspected to play a role in health issues such as obesity, inflammatory bowel disease, asthma, depression, and neurodegenerative diseases (9, 10). Even in the agrifood industry, biodiversity is declining, notably by the uniform utilization of starters in food fermentation (11). From an evolutionary perspective, the analysis of bacterial extinction rates based on time-calibrated bacterial phylogenies has estimated that most bacterial lineages ever to have inhabited the Earth are extinct (12). These examples underline our current misconceptions about the lack of threat to microbial diversity by anthropogenic pressures or environmental changes (13).

For research and applications in microbiology and molecular biology, the accessibility and valorization of living *ex situ* microbial strains and related genetic materials (e.g., recombinant plasmids and DNA libraries) through their long-term preservation and distribution by culture collections are indispensable. The Organisation for Economic Cooperation and Development (OECD) already recognized the role of culture collections in underpinning the future of life sciences and biotechnologies (14). The OECD emphasized that the sustainable access to biological resources requires professional repositories working under certified and/or accredited quality systems. Public culture collections that maintain a recognized quality management system were awarded the status of being a biological resource center (BRC). Among them, microbial domain BRCs (mBRCs) maintain and provide well-characterized and authenticated strains of microorganisms, as well as associated genetic materials and data (15). Specifically, mBRCs follow the best practice guidelines of the OECD to preserve biological resources. These guidelines include the validation of the taxonomy and properties of the preserved material, as well as quality controls to verify their viability, purity, and authenticity (16, 17). Moreover, at least two different preservation methods are used, including one long-term preservation technique, such as freeze-drying or cryo-

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preservation. These methods require specific equipment but ensure the best genetic stability of the material.

One role of the culture collections is indeed to limit the extent of genomic evolution of the maintained biological resources as much as possible, thanks to their preservation in an inactive state. In this regard, the long-term evolution experiment, started in 1988 in the laboratory of Richard E. Lenski, revealed that 12 *Escherichia coli* populations inoculated from a single ancestral clone and cultivated under identical culture conditions accumulated mutations to adapt to their environment and showed an increase in fitness that was rapid at the start and slowed down over time (18). The mutations were unique to each population, though sometimes affecting the same genes. Cells larger than the ancestor were also observed (19). In certain microorganisms, genomic changes can also be accelerated by lateral gene transfer. These genetic modifications also explain that strains with the same identifier but kept in different laboratories for many decades can become genomically different. The *Pseudomonas aeruginosa* strain PAO1, for instance, is one of the most commonly used research strains and is distributed worldwide since its isolation in 1954. Analysis of different representatives of this strain showed several genetic and phenotypic variations between settings, including inversions, duplications, and deletions of genomic regions, single-nucleotide substitutions, virulence capacities, and profiles of secreted molecular products (20–22). This resulted in diversity among sublines stored and handled in different laboratories and precluded the comparison and reproducibility of studies. Long-term preservation methods used by mBRCs intend to limit this microevolution. However, the extent of genomic variation of a same strain between collections or within a given mBRC through time cannot be excluded and needs to be evaluated.

The distribution of biological resources is essential in various domains, such as education and quality assurance (e.g., reference strains), but even more important to support basic and applied scientific research in life sciences. The access to biological materials in mBRCs indeed has an impact on knowledge accumulation by expanding follow-on studies, as demonstrated by the boost in citations of articles associated with strains after their deposit in public culture collections (23). Furthermore, it is important to secure biological materials for future utilizations that currently cannot be anticipated (24). On the one hand, new needs or challenges (e.g., biofuels, bioremediation, antibiotics, and genetic engineering) can be covered by properties of previously isolated microbes, notably through the screening of microbial collections. On the other hand, new technologies can reveal, in preserved biological materials, useful traits that were formerly hidden due to a lack of appropriate tools (e.g., high-throughput sequencing and omics-based approaches).

The contribution of mBRCs in the protection of intellectual property linked to biological resources having economic value or used in commercial applications is another way of making scientific outputs accessible. In total, 112 out of the 769 culture collections registered in the World Federation of Culture Collections (WFCC) obtained the status of international depositary authority according to the Budapest Treaty (https://www.wipo.int/treaties/en/registration/budapest). They offer the deposit of microbial strains, cell lines, or genetic materials for the purpose of a patent procedure, with this step being required if an invention involves a biological resource or its utilization.

Finally, mBRCs evolved into being multiservice centers (25) by providing training, consultancy, safe deposits, and expertise in various domains, such as the isolation, identification, and analysis of microorganisms, biosafety, biosecurity, or legal aspects of resource exchanges (see Accessibility and Utilization of Microbial Strains: the Nagoya Protocol on Access and Benefit Sharing, below).

EXPERTISE IN MICROBIAL TAXONOMY, CULTIVATION, AND ANNOTATION

Species concepts in microbiology are more complex than in animals or plants due to high mutation rates and high intraspecific genetic variations encountered in microorganisms (24). Historically, microorganisms were described and delimited according to

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their phenotypic features. However, molecular phylogenies based on gene or whole-genome sequences revealed a higher species diversity and the evolutionary relationships between taxa. This resulted in important revisions of microbial taxonomies with the description of new taxa and nomenclature changes. A robust taxonomic framework is much more than "putting a name." It allows the identification of isolates and the detection of new species. Microbial taxonomy represents a key activity of mBRCs which, by characterizing microbiological materials, are on the front line to propose new taxonomies. mBRCs also support studies on microbial systematics and taxonomy by distributing strains or their DNA. In particular, they are able to provide standardized and high-quality genomic DNA for whole-genome sequencing, hence supporting *in silico* taxonomic works (26). Moreover, geographical, ecological, and temporal distributions of a species can be assessed by exploring the origins of their representatives in the different collections. Similarly, population dynamics can be analyzed by genotyping strains of a given species archived in one or several collections. As an example, the analysis of 93 *Bacillus anthracis* strains preserved by the Kazakhstan National Culture Collection and covering a 53-year period revealed the epidemiology of the genetic clusters circulating in the country and responsible for historical anthrax outbreaks (27).

Another important element covered by the mBRCs is the deposit, for each described species, of a type strain, considered to be a reference point for the classification and identification of isolates. According to the International Code of Nomenclature of Prokaryotes, the description of new species of *Bacteria* or *Archaea* requires the deposit of a living type strain in two members of the WFCC, located in different countries (28). For the other microorganisms, the International Code of Nomenclature of algae, fungi, and plants stipulates that type specimens must be preserved permanently and recommends depositing living cultures in at least two institutional culture collections (29). mBRCs preserving plasmids focus on the annotation of the biological material, which is essential to spot the resources via common identifiers such as gene identifiers (IDs), EMBL/GenBank accession numbers, gene symbols, and PubMed IDs. Also, searches on Gene Ontology terms, which are structured, controlled vocabularies and classifications covering key domains of molecular and cell biology (30), as well as BLAST searches, are important to find sets of plasmids containing defined sequence strings or carrying genes belonging to specific research domains.

Culture-independent approaches have revealed the huge gap between the existing microbial diversity and its cultivated representatives (31). For bacteria and archaea, about 15,000 species have been published so far, but they represent only 0.001 to 0.1% of the estimated global species number (32). Moreover, operational taxonomic units detected by high-throughput sequencing are recognized at a rate that exceeds almost 100 times the rate of species description (32). In mycology, the number of described fungal species is currently around 120,000, but estimations range between 500,000 and 10 million species (33). In the case of protists, the number of described species reaches about 74,400, while the predicted species richness ranges from 0.15 and 1.66 million (34, 35). However, if the information obtained with omics-based approaches can be fruitfully exploited to design better isolation strategies (36), the physiology and metabolic capabilities can only be verified in studies of cultivated organisms (11, 31). In particular, the fraction of genes that can be annotated for a given genome is positively correlated with the proportion of cultivated representatives in the corresponding phylum (37). A recent proposal to describe species based solely on the detection of new DNA sequences in environmental samples (32) is therefore disputable, since it prevents phenotypic studies of the species. Cultivation of microorganisms is important to exploit their potential, and improvement in this field notably requires better simulations of natural growth conditions, adaptations of culture media, and technical advances (31). An example is the development of high-throughput culturomics approaches for the human gut microbiome (38, 39). Nevertheless, such necessary but fastidious developments would not make sense without the preservation of the cultures. To this end, mBRCs developed and maintain the infrastructure and the necessary expertise for the conservation and cultivation of the microorganisms in which they are specialized.

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DATA NETWORKS

Biological materials entering mBRCs receive a unique identifier (i.e., accession number), consisting of the collection acronym and a number, which are registered in a database together with metadata like the provenance (e.g., substrate, date, location, depositor, and parental clones), history, phenotypic characteristics (e.g., morphology, physiology, biochemistry, and resistance to antimicrobial drugs), genetic information (e.g., genotype, nucleotide or genome sequences, and plasmid features), possible applications, bibliography, and growth conditions. Depending on the mBRC, all or part of these data is available and searchable through their online catalogues and websites. Some collections also valorized their databases by offering online tools for specific purposes. For instance, the Westerdijk Fungal Biodiversity Institute provides an online polyphasic identification tool for the identification of yeasts based on their morphology, physiology, sexuality, and DNA sequences (http://www.westerdijkinstitute.nl/Collections/BiolomicsID.aspx?IdentScenario=Yeast2011ID). A Web application was developed in collaboration with the BCCM/IHEM fungal collection for the identification of medical and veterinary mold isolates using matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry (40, 41). The German Collection of Microorganisms and Cell Cultures (DSMZ) elaborated a range of publicly available online tools for prokaryotic research, including genome-based species delineation or up-to-date bacterial nomenclature listings (https://www.dsmz.de/services/online-tools). Moreover, since the development of technologies such as DNA sequencing, microbiology also became a data science, and culture collections have increasing responsibility in (big) data and information storage.

Historically, the computerization of metadata stimulated European culture collections to launch networking initiatives in order to make their databases interoperable. The Microbial Information Network Europe (MINE) project was performed in the late 1980s by major European culture collections in order to adopt a uniform format for the computer storage and retrieval of strain data (42, 43). A key element was the definition of a common minimal data set comprising a list of essential characteristics (42, 43). This facilitated the exchange of data between collections and the production of integrated catalogues. The Common Access to Biological Resources and Information (CABRI) project elaborated the first common catalogue (http://www.cabri.org/). CABRI is a network service for the distribution of more than 150,000 biological resources and related data from 28 European collections, representing about half of the total deposits in Europe (44). Linking information from culture collections to bioinformatic and bibliographic databases is also essential to enhance research. The European BRCs Network (EBRCN) project was therefore conducted in the early 2000s to develop cross-references between the CABRI catalogue and other databases, such as EMBL or Medline (44). Later on, the StrainInfo initiative was developed as a virtual, integrated online catalogue of the microorganisms preserved by mBRCs (45). These good practices in data resource management were also part of the Microbial Resource Research Infrastructure (MIRRI) preparatory phase project. MIRRI aimed at coordinating mBRCs in a multidisciplinary pan-European platform, notably by developing further the interoperability and accessibility of resources and data (46–48). MIRRI will be further developed into a pan-European Research Infrastructure with the status of European Research Infrastructure Consortium (ERIC).

Based upon these initiatives and the OECD best practice guidelines for BRCs, the WFCC developed similar worldwide initiatives through its World Data Centre for Microorganisms (WDCM) (http://www.wdcm.org/). The WDCM was created in 1966 and initially aimed at providing information on the WFCC member collections (e.g., scope, provided services, scientific interests, and type of organization) (49). In 2012, the WDCM launched the Global Catalogue of Microorganisms (GCM) to gather collection catalogues and biological resource-related information (50). The GCM currently includes more than 420,000 records from 126 collections in 47 countries and regions. The GCM also contains a data mining tool called the Analyser of Bioresource Citation that extracts

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biological material-related publications, patents, nucleotide sequences, and genome information from public sources (e.g., PubMed, NCBI, WIPO, and Genome Online) (51). Similarly, the NCBI established its BioCollections Database that aims at linking the sequence data deposited in GenBank with the culture collection that holds the corresponding strain (52). It is thus possible to provide the URL of a catalogue page to link the sequence entries to the strain of the relevant collection, hence simplifying the search for microbial resources on the basis of their deposited sequence data.

New challenges in database accessibility and interoperability are anticipated for the future. Surveys performed in the frame of the MIRRI project indeed revealed that users of collections request improvement of the quality and diversity of possible searches in databases. Users also look for the possibility to make these searches simultaneously in catalogues of different collections (53). These demands will require the collections to continue investing in common data management standards and information systems.

ACCESSIBILITY AND UTILIZATION OF MICROBIAL STRAINS: THE NAGOYA PROTOCOL ON ACCESS AND BENEFIT SHARING

The basic principle of the Convention on Biological Diversity (CBD) (54), signed in 1992, is to recognize the sovereignty of countries over their biological resources (and associated genetic resources), hence counteracting one-sided exploitation or biopiracy. The CBD has three main objectives, as follows: (i) conservation of biological diversity, (ii) sustainable use of biological resources, and (iii) fair and equitable sharing of benefits arising from the utilization of genetic resources. The Nagoya Protocol (NP) was adopted in 2010 and came into force in October 2014 mainly to address this third objective and to guide the implementation of access and benefit sharing (ABS) into national laws (55). In practice, signatory countries are obliged to ensure the legal use of foreign resources and the benefit sharing within their jurisdiction. It is notably based on prior informed consent (PIC) and mutually agreed terms (MAT), both of these concepts being introduced by the CBD. Users of a biological resource are indeed required to obtain a PIC issued by the competent national authority (CNA) of the country of origin and explaining the particular purpose of the resource. They also need to settle MAT with the providing country, including details on the sharing of benefits (monetary and other) arising from its utilization. Once a permit to collect the material is granted, an internationally recognized certificate of compliance (IRCC) is issued by the CNA to facilitate its transfer to third parties for further use.

The application of the NP on microorganisms has been questioned by several authors, as it would threaten basic research in microbiology (56–58). Overrestrictive access laws in providing countries could indeed reduce exchanges of biological resources and decrease scientific activities in different fields, such as taxonomy, ecology, and biodiversity. In recipient countries, complex regulations and unclear definitions in legal documents could have the same effect. Moreover, the varied temporal scope and laws across countries further complicate the situation (58). In this context, culture collections may experience a decrease in the deposit of biological materials by researchers due to these legal complexities (59). However, the available information on relevant national legislations of each country that signed the CBD can be found in the ABS Clearing House (ABSCH) database (https://absch.cbd.int/). This database also publishes IRCCs and provides contact details of the ABS national focal points that can be consulted for more specific questions (60).

Additionally, mBRCs, through their legal expertise, can guide depositors and help researchers access microbial materials lawfully. Any deposit in public collections is indeed verified by curators for its compliance with the NP, and, if applicable, required documents (e.g., PIC, MAT, and IRCC) are requested to accompany the biological material. A material deposit agreement (MDA) including the legal terms of the deposit is also signed between the depositor and the mBRC. For their distribution, biological resources are supplied by mBRCs with a material transfer agreement (MTA) describing the conditions and limitations of their utilization (60). Combined, all these legal

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procedures and documents ensure traceable and legitimate exchanges of microbial and genetic resources.

For the deposit and distribution of biological resources, the transport to or from a collection can be performed in different forms depending on the type of material. Depositors can provide strains to collections in any viable form, including active cultures in test tubes or petri dishes, in freeze-dried form, or as a suspension in microtubes. Similarly, genetic materials (e.g., genomic DNA and plasmids) can be provided in suspension or lyophilized, as well as precipitated or evaporated. Shipment in a frozen form is also an option and is even mandatory for cell lines and hybridomas. This requires the use of dry ice, resulting in additional safety measures and higher shipment costs. Collections generally distribute biological material in freeze-dried form or as active cultures. In addition, the shipment of microorganisms that are harmful for humans, animals, or plants must comply with the dangerous goods regulations, such as those defined by the International Air Transport Association (IATA) or the European agreement concerning the international carriage of dangerous goods by road (ADR). These regulations include multiple layers of packaging to avoid breakage and spillage during transport, necessary labels on the outer package, and additional accompanying documents. For the transportation itself, the use of a professional courier with experience in the shipment of dangerous goods is recommended. Of note, shipments to certain countries can be restricted by specific national laws. All of these transportation regulations increase the safety and traceability when shipping biological resources.

Several coordinated initiatives were conducted by mBRCs to develop harmonized best practices for ABS. The European Culture Collections Organisation (ECCO) developed a harmonized "core-MTA" that raised awareness on ABS (61). The Microorganisms Sustainable use and Access regulation International Code of Conduct (MOSAICC) project started in 1997 and was the first effort to support the implementation of the CBD for microorganisms. It provided model clauses for legal documents, such as PIC and MAT, while combining the need for easy transfers of biological resources with the necessity to monitor these transfers (16). In 2012, the TRansparent User-friendly System of Transfer (TRUST) initiative revisited MOSAICC to answer efficiently the NP technical challenges. Its goal was to further implement the NP in the scientific, technical, and administrative activities of mBRCs (62). In the future, the European Union plans to establish a registry of European mBRCs that can demonstrate full compliance with the NP and the European regulation 511/2014 (73) on compliance measure for users from the NP. The advantage of accessing biological resources from mBRCs with the status of "registered collection" is that users will be considered as having exercised due diligence regarding ABS and thus would benefit from less administrative workload to access resources in legal certainty (63, 64).

ENHANCING THE DEPOSIT OF MICROBIAL STRAINS AND GENETIC RESOURCES

Networking among mBRCs is essential, not only for data sharing but also for the distribution and exchange of microorganisms and genetic resources. Indeed, the largest public culture collection holds less than 2% of the total strains gathered by the WFCC members (65). This illustrates the high level of interdependency and the necessary collaboration between repositories. Globalization of efforts through organizations such as the WFCC, ECCO, U.S. Culture Collection Network (USCCN), and Asian Consortium for the Conservation and Sustainable Use of Microbial Resources (ACM) therefore facilitates the access to a wider range of resources, expertise and services. This was also the purpose of international initiatives such as the European Consortium of Microbial Resources Centres (EMbaRC) (http://www.embarc.eu/ and https://cordis.europa.eu/project/rcn/90998/reporting/en) and Global BRC Network (GBRCN) projects (66). Besides these networks, mBRCs are connected to academia, industry, governmental, and higher education institutions. They are also linked to providers and users of microbial materials, originating from both the public and private sectors and having diverse profiles. Based on this unique position, mBRCs are considered knowledge hubs

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in life sciences, supporting innovation by offering access to quality-controlled microorganisms and genetic resources (24).

As with open data, the responsibility to make biological materials available for future research is shared by researchers, funding agencies, and publishers (67). Governmental funding policies should not focus solely on data sharing to valorize important public research investments (68). They should also consider the access to physical outputs and require the deposit of microbial strains and genetic resources obtained and/or studied during financed projects. Regarding publications, most journal policies encourage authors to make biological materials used in publications available to the scientific community. However, the majority of strains appearing in articles are not deposited in public culture collections. In 2008, a survey that screened 835 articles from eight European microbiology journals revealed that less than 1% of the strains were deposited (69). Moreover, in an anonymous request to obtain strains from 100 randomly selected authors, only 5% confirmed deposit, and 19% indicated their willingness to deposit, while 61% did not respond at all, and 15% responded that the material was dead or unavailable (69). This illustrates the lack of awareness by many microbiologists of the importance and advantages of depositing their biological material in order to make it available to the broader community, hence fully releasing its potential.

However, considering the current limited capacities and funding of mBRCs, it might be impossible to preserve all biological resources appearing in published articles in a quality-assured manner. Consequently, the concept of "key strains" was introduced to prioritize strains for acquisition by mBRCs (26, 68). For prokaryotes, the selection criteria include phylogenetic, metabolic, and genomic uniqueness, strains with a whole-genome sequence, additional strains of species for which only the type strain is available, strains associated with significant plant or animal diseases, and strains from unexplored environments. In mycology and algology, the criteria also cover type strains of novel taxa given that fungi and algae may be validly described using dried herbarium specimens as types. For phylogenetically highly diverse but understudied groups of protists, such criteria need to be developed and may need to be adapted to the particularities of each group's biology. Nevertheless, a survey on author opinions regarding the deposit of key strains revealed that most of them agree that journal guidelines should ask for their deposit in culture collections for further research (70). Editors and publishers should therefore require authors to deposit key strains in mBRCs before submission or acceptance of an article. This could be linked to transparency and openness promotion (TOP) guidelines for journals formulated by the TOP committee (71). These guidelines combine eight standards, including research material transparency. Three levels of stringency are proposed, out of which the first two are applicable to the deposit of microorganisms. The first one stipulates that the article has to state whether materials are available and, if so, where to access them. According to the second level, materials must be deposited to a trusted repository (71). The adoption of such guidelines for microbial key strains would be a step forward toward greater openness in microbial research.

Another important element to ensure the conservation of the microbial diversity is the transfer of vulnerable research collections to mBRCs. Indeed, many laboratories assembled valuable collections in the frame of their activities or research projects. However, these collections are at risk of loss following retirement or departure of the principal investigator, lack of funding, or termination of research programs. The incorporation of all or part of these collections into mBRCs is therefore necessary for their long-term preservation and availability, with large mBRCs generally receiving better financial support through long-term public funding, project grants, and end-user fees (59, 72). However, maintaining and building a culture collection with high quality standards have an enormous cost, and mBRCs are regularly asked to adapt their business plan and/or to diversify their activities in order to ensure sustainable financing (59, 72). This strategy requires collections' staff to divert their efforts away from core operations, while its efficiency remains to be proven. It is therefore essential to

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highlight the uniqueness of the biological patrimony preserved in collections and the support it should receive.

CONCLUSION

The FAIR principle described for data sharing can be applied to microbiological resources provided that they are preserved in mBRCs. Indeed, each deposit is findable through the allocation of a unique accession number and is accessible via mBRCs online catalogues and distribution. Living materials are not interoperable *per se,* but associated data are recorded in databases that are increasingly interoperable following international efforts, such as MIRRI and the WDCM. Thanks to the expertise of mBRCs, microbiological resources are maintained viably for long periods and are authenticated, well characterized, NP compliant, and quality controlled. They are therefore reusable for future studies and to support cumulative knowledge in life sciences. Similar to FAIR data, the concept of FAIR microorganisms and genetic materials recognizes that the access to certain resources can be restricted for security or commercialization reasons. However, an increase in deposits is needed and requires the awareness and implication of all stakeholders, including researchers, funding agencies, and publishers.

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P. Becker obtained his PhD in Biological Science at the University of Mons (Belgium) in 2007. His thesis investigated bacterial diseases affecting marine invertebrates. He then pursued an academic career as a postdoctoral researcher at the University of Mons and the Free University of Brussels, working on different projects in the fields of environmental microbiology and biochemistry of bioadhesives. In 2012, he joined the Mycology and Aerobiology laboratory of Sciensano (formerly Belgian Scientific Institute of Public Health) where he became the head of research of the BCCM/IHEM fungal collection, a position that he still occupies today. His research interests focus on medical mycology and include antifungal drug resistance and consumption and the phylogeny and taxonomy of fungal pathogens, as well as the identification of fungal isolates by MALDI-TOF mass spectrometry.

M. Bosschaerts graduated as a bioengineer from the Katholieke Universiteit Leuven (Belgium). In 1995, she joined the Belgian Science Policy Office (BELSPO) as the first member of the coordination cell for the Belgian Coordinated Collections of Microorganisms (BCCM). During her career, she has focused on quality management and external communication; she has managed scientific programs related to BCCM and was involved in several European projects with other European biological resource centers. She was a member of the OECD Task Force on biological resource centers and has worked with WIPO on harmonized practices for "International Depositary Authorities" under the Budapest Treaty (patent procedure). She is now the manager of the BCCM coordination cell and deputy director of BELSPO's Research Programs department. In the frame of the construction of the European Research Infrastructure Consortium for the Microbial Resource Research Infrastructure (MIRRI-ERIC), she is the chair of the Assembly of prospective Members.

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P. Chaerle has worked since 2017 as a scientist, curator, and manager for BCCM/DCG diatom collection. He obtained his PhD in 2006 from the University of Ghent (Belgium) and continued to work at UGent as a researcher and lecturer. In 2008, he accepted a job as a scientist at the R&D department of SBAE Industries, and in 2011 became group leader of the Seed Evaluation Group at BASF. His main research interests are systematics and evolution of vascular plants and protists (microalgae in particular); anatomy of archaeological plant findings; identification of recent pollen; microscopy, biometry, and image processing; and cultivation of various microalgae (including large-volume setups of 75,000 liters) and the study of their reproductive behavior.

H.-M. Daniel started her academic education at the Humboldt University of Berlin in food science and technology and has a PhD in Biotechnology from the Technical University of Berlin, Germany. She serves as yeast curator, deputy BRC manager, and responsible for yeast-related services including public, safe, and patent deposits at BCCM/MUCL, the Agro-food & Environmental Fungal culture collection hosted by the Laboratory of Mycology, Earth and Life Institute, Pole of Applied Microbiology of the Université catholique de Louvain (UCLouvain), Louvain-la-Neuve, Belgium. The study of the molecular phylogeny of Candida species and related ascomycetous yeasts during her MSc and PhD projects at Westmead Hospital in Sydney, Australia, shaped her interest and 23 years' experience in the diversity, cultivation, molecular identification, and systematics of yeasts.

A. Hellemans obtained her PhD in Veterinary Medicine at the University of Ghent (UGent, Belgium). During her PhD thesis work, she studied bacterial infections in pigs in a search for new antimicrobial therapy, by which her interest in isolating, growing, and preserving bacteria, especially Helicobacter species, was raised. She worked as a preclinical project manager in the private sector for several years, where she managed different discovery projects and learned that a link between research institutes and private companies is an important means to valorize scientific results. Since 2013, she has managed the BCCM/LMG bacterial collection, a public collection of more than 25,000 bacterial strains containing large subcollections of several taxa. In this function, she uses her management skills to valorize the potential of the diverse bacterial strain collection and the expertise of the BCCM/LMG team working together with nonprofit and for-profit organizations.

A. Olbrechts obtained her master's degree in Biotechnology at the University of Ghent (UGent, Belgium). In 2003 she joined the BCCM/LMBP Plasmid Collection, which was renamed BCCM/GeneCorner Plasmid Collection in 2018. BCCM/GeneCorner is embedded in the UGent Department of Biomedical Molecular Biology on the one hand and the VIB-UGent Center for Inflammation Research on the other hand. Anneleen has been the curator of the public plasmid collection since 2015 and is in charge of the acquisition, characterization (Sanger and next-generation sequence analysis, restriction enzyme analysis), and annotation of (mainly recombinant) plasmids and library clones from all over the world.

L. Rigouts obtained a PhD in Biological Science from the University of Ghent (Belgium), in 2000. She joined the Mycobacteriology Unit of the Institute of Tropical Medicine (Antwerp, Belgium) in 1989, where she currently has the position of senior scientific expert. Since 2008, she has been a professor in Tropical Infectious Diseases at the University of Antwerp. She has 30 years of research experience in the detection, isolation, identification, and drug susceptibility testing of mycobacteria using classical microbiological and (next-generation) molecular biological tools in biosafety level 3 (BSL3)-grade conditions and according to good practices (GxP). Her research focuses on diagnosis and underlying mechanisms of drug-resistant tuberculosis, as well as identification and phylogeny of (clinically relevant) nontuberculous mycobacteria. She has been the director and a curator of the BCCM/ITM public collection of mycobacteria since 2011, aiming to establish valid tools for research and product development with public health relevance.

A. Wilmotte has a PhD in Botanical Science from the University of Liège (ULiège, Belgium). She is research associate of the National Fund for Scientific Research of Belgium (FRS-FNRS) since 1996 and works at the InBios-Centre for Protein Engineering of ULiège. She has 36 years of research experience in the isolation, cultivation, and characterization of cyanobacteria. Her interests include cyanobacterial biodiversity, taxonomy, and evolution, with a focus on the Polar Regions, using traditional and molecular tools. She is also intrigued by the resistance of cyanobacteria to extreme conditions and the detection of signatures of cyanobacterial life in fossil rocks. She has been the director and a curator of the BCCM/ULC public collection of cyanobacteria since 2011 and aims to conserve a representative part of their (polar) biodiversity, that may be currently subject to changes.

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M. Hendrickx is a biologist and has a PhD in Science from the Vrije Universiteit Brussel (VUB). She is the head of the scientific service Mycology and Aerobiology at Sciensano, the Belgian public health institute. She has been the BRC manager of the BCCM/IHEM collection, dedicated to fungi that affect human and animal health, since 2010 and director of the collection since 2015. She has been a board member of the European Culture Collection Organization (ECCO) since 2013 and guest lecturer at the Katholieke Universiteit Leuven (KUL). She has a special interest in medical mycology and MALDI-TOF MS identification of fungi.

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