MIRRI IS21
IMPLEMENTATION AND SUSTAINABILITY FOR THE 21ST CENTURY
MICROBIAL RESOURCE RESEARCH INFRASTRUCTURE

D6.3

MIRRI-CWE Platform – Final version

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Abstract:	This document presents and describes the work and results obtained in the project IS_MIRRI21 regarding the MIRRI Collaborative Working Environment (CWE) platform. This description is synthetic as the deliverable was proposed and approved as of ORDP type. It means that the deliverable is constituted by a set of software modules and microorganisms related data, installed and fully functional in servers owned or made available to MIRRI universe of stakeholders, jointly forming the final version of the MIRRI collaborative working environment. Furthermore, in this document the consortium reports decisions taken in consortia for the CWE platform improvement from its preliminary version analysis and the tests performed with end-users.
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Dissemination level:	Public	X
	Confidential (for the Consortium and EU Commission Services only)	

Abstract

This document presents the modules and functionalities implemented for the Collaborative Working Environment (CWE) of the Microbial Resource Research Infrastructure (MIRRI) in its final version. The process of architecture definition and functionalities implementation was performed on the sequence of the work previously developed for requirements elicitation, which was reported in the ***Deliverable 6.1 - Report on the design and technical requirements of MIRRI-CWE***. Subsequently, the ***Deliverable 6.2 - MIRRI-CWE Platform – Preliminary version*** presented the first version of the CWE, including the general description of its features (gates) and modules along with a more detailed and illustrated presentation of the functionalities made available in each module.

All this sequence started from the definition of the CWE platform as described in the documents delivered by the MIRRI project in its preparatory phase, followed by its revision at the time of the IS_MIRRI21 project proposal preparation, then by the Deliverable 6.1 (for which many researchers, both computer scientists and biologists from the partner institutions, have contributed bringing their expertise and point of views), ending with the concrete utilization of the CWE preliminary version and the realization of a series of trials with a wide range of end-users representative of the most important MIRRI stakeholders. All these successive phases, supported by the regular and constant discussion among the IS_MIRRI21 partners, particularly those involved in WP6, resulted on technical decisions about, among many other aspects: the most suitable, sustainable and scalable technologies for software implementation; the CWE architecture; the use and integration of existing open (source) solutions; the re-utilization of existing software modules/platforms, particularly those developed in previous EU projects; the easiness of maintenance and information management in the CWE; the CWE platform security; the openness and open access of MIRRI data provided via the CWE. Everything together is embodied in the latest version of the CWE platform.

The team responsible for the implementation also considered with highest priority the aspects relative to the user interaction, user interface and user experience, considering the wide universe of MIRRI users and stakeholders. The experts on user studies and user experience brought their contribution for the development team, by orienting and technically supporting and validating the implementation, and more recently, validating the platform in production, by conceiving and realizing exhaustive and complete user studies aiming at finding improvements and valuable updates for the final version of the CWE.

The CWE platform in its final version is constituted by a set of software modules and data, available from https://www.mirri.org. It constitutes the ***Deliverable 6.3 - MIRRI-CWE Platform – Final version*** for which this document is a companion document aimed at supporting the platform interpretation and to serve as a reference for eventual future extensions and updates.

Contents

List of Figures

List of Acronyms

AAI - Authentication and Authorization Infrastructure

API - Application Programming Interface

CABRI - Common Access to Biological Resources and Information

CC - Culture Collection

CCU - Central Coordination Unit

CWE - Collaborative Working Environment

DOI - Digital Object Identifier

ERIC - European Research Infrastructure Consortium

FAIR - Findable, Accessible, Interoperable, Reusable

GDPR - General Data Protection Regulation

HTML - HyperText Markup Language

ICT - Information and Communication Technologies

JSON - JavaScript Object Notation

LMS - Learning Management System

mBRCs - microbial Biological Resource Centres

MIRRI - Microbial Resource Research Infrastructure

MIRRI-IS - MIRRI Information System

MoU - Memorandum of Understanding

ORCID - Open Researcher and Contributor ID

PDF - Portable Document Format

QMS - Quality Management System

RI - Research Infrastructure

TNA - Transnational Access

T&E - Training and Education

UI - User Interface

URL - Uniform Resource Locator

WDCM - World Data Centre for Microorganisms

WP - Work Package

1. Introduction

1 Introduction

This is a companion document for ***Deliverable 6.3 - MIRRI-CWE Platform - Final version*** and briefly reports on the improvements added to the design and technical implementation towards the final version of the common virtual interface for Microbial Resource Research Infrastructure (MIRRI), as well as the provision of its services in the form of a Collaborative Working Environment (CWE). Such increments are presented here in comparison to the CWE preliminary version (***Deliverable 6.2 – MIRRI-CWE Platform – Preliminary version***). The current version completes the CWE platform as the single-entry point for the related pan-European infrastructure, and contains dedicated customer service facilities and defined rules to guarantee responsiveness (i.e. automatic responses formulated when services are requested or inquiries sent, rules for follow-up with users on the ordered service, etc.).

The CWE platform was officially launched in its preliminary version before the expected deadline, back in March 2021, in order to promote MIRRI's visibility as early as possible and to start supporting some of its activities. The current CWE implementation includes all the features and requirements enumerated and presented in the initial phase of IS_MIRRI21 (***Deliverable 6.1 - Report with the design and technical requirements, characterization and knowledge acquisition of MIRRI-CWE),*** thus constituting the achievement of a fundamental platform for MIRRI as a research infrastructure. It supports the operation of remote services by taking advantage of the new technologies for communication and information storage, access and processing. These technologies include cloud computing, advanced databases, data analytics, secured data interoperability, among many other that were used and adopted.

Since the preliminary version, the CWE platform has been updated with new information, data and functionalities in order to meet the complete set of requirements to be achieved in the scope of the IS_MIRRI21 project. This evolution consisted in the addition of new modules and functionalities, the update of existing ones, bug correction, etc. It was validated through extensive user tests, performed under the **task 6.5** and reported in ***Deliverable 6.4 - Report with the usability tests' results and user feedback***.

The CWE in its final version includes both the front-end application (aimed at being used by any registered user) and one back-end application (accessible just to the MIRRI Central Coordination Unit members). The second one in particular is meant for the MIRRI IT officer, the content curators and the CWE administrators to manage the consortium's activities, administer tasks and update information in a dynamic way.

At the early stages of this project it was considered a priority to have a basic implementation of the gates and their corresponding modules. This was because preliminary analyses showed the urgency of MIRRI to have a presence on the web from which to promote its activities and provide tools to support them. The current version of the platform accomplishes the entire set of requirements and specifications by extending these priorities.

Although the current CWE platform meets the requirements and modules specified in the agreement, it can evolve further in the future by including new ones and by implementing suggestions made by users regarding usability and ease of interaction.

Chapter 2 of this document presents a summary on the initial structure of the CWE that was proposed. It was composed of four major pillars (henceforth called Gates), which reflect the thematic arrangement of the information, functionalities and features to be made available for the MIRRI stakeholders: (1) Gate to Research Infrastructure Information; (2) Gate to Resources, Data & Services; (3) Gate to Collaboration & Experts; (4) Gate to Training & Education and one 5th Gate (the Transversal Gate) containing those features and functionalities more transversal to the entire CWE platform (e.g. user registration and authentication).

Chapter 3 briefly presents the gates, focusing the modules that were developed since the preliminary version. It also presents their respective implementation, as well as the improvements made on their modules and features.

Chapter 4 consists of a summary of other developments over the MIRRI-IS module, regarding MIRRI data sharing, persistent data management and data FAIRness.

Chapter 5 closes this report with the conclusions and future prospect of improvements to be made on the CWE, as well as new features and functionalities that may be specified in detail and added in the future by MIRRI.

2. The MIRRI CWE Platform

2 The MIRRI CWE Platform

The MIRRI CWE is the main interface for MIRRI members and other stakeholders by which all can communicate and access information in a time-efficient way. It is accessible at www.mirri.org and, in addition, it delivers to the users a set of functionalities and tools to support their activities in the context of MIRRI. The CWE is therefore a valuable support for MIRRI in its mission of microorganisms' worldwide research and contribution for future generations of researchers.

The architecture of the CWE was described in detail in ***Deliverable 6.2 – MIRRI-CWE Platform – Preliminary version***. It is a modular platform, constituted by four main gates and the respective modules, with all the modules integrated and accessible as a single and unique virtual work environment. One fifth gate is also implemented, transversal to the entire CWE, containing modules and functionalities to be inherited by the other gates, like for example for user registration, user information management or user authentication and authorization.

Gate to Research Infrastructure Information: is the Public website that give access to the freely available repository of content, general information about events, news, text search over the entire platform, etc. It also contains the restricted Area, where registered IS_MIRRI21 project partners and other MIRRI Members and Partners have access to internal documents and reports. Additionally, this Gate serves as the support interface for all the other gates.

Gate to Resources, Data & Services: it is the central access point for the MIRRI users to access (1) information on the available microbial genetic resources; (2) their integrated, curated data and metadata (following FAIR criteria) and (3) highly specialized scientific services. To highlight the MIRRI Information System (MIRRI-IS) which is the module deploying an integrated, high-quality, automatically validated, manually annotated, non-redundant microbiological resources database, providing all relevant information and associated contextual data (metadata) about any particular microbial resource.

Gate to Collaboration & Experts: provides a unique environment for researchers in life sciences to exchange knowledge. The "MIRRI Expert Clusters" are organised around the typical key-activities of microbial Biological Resource Centres (mBRCs) to support research, development and innovation processes, driven by the needs and requests of the users.

Gate to Training & Education: provides extensive access and information to the MIRRI's training and education (T&E) offer, supporting mBRCs to improve their strategic training offer, whilst acting as effective models of open innovation.

The Transversal Gate: supports features and functionalities permanently present in the CWE portal, like disclaimers, links to social media, accessibility features, the storing of personal data according to the General Data Protection Regulation (GDPR), among many others. Contains the module for user registration, management, authentication, and authorization, as well as security features for the entire CWE

The entire management of all the gates, the respective modules the information contained, as well as other important tasks such as the management of users and modules access rights attribution, is performed using the CWE back-end application. The back-end application functionalities are accessible only for users with administrator profile.

3. The CWE Final Version

3 The CWE Final Version

The final version of the CWE reflects the result of the implementation of the different modules and functionalities according both to the WP6 team recommendations, established through multiple technical meetings regularly held, and to the results from the usability tests to validate decisions using their scientific experience as future CWE users. This chapter includes the improvements with respect to the preliminary version described in Deliverable 6.2 organized by Gates:

Gate 1 focuses on Research Infrastructure Information. Gate 2 focuses on the Resources, Data and Services. Gate 3 focuses on Collaboration and Experts. Gate 4 focuses on Training and Education. One fifth gate implements modules and features that are transversal to the entire CWE.

3.1 Transversal Gate and User Interface

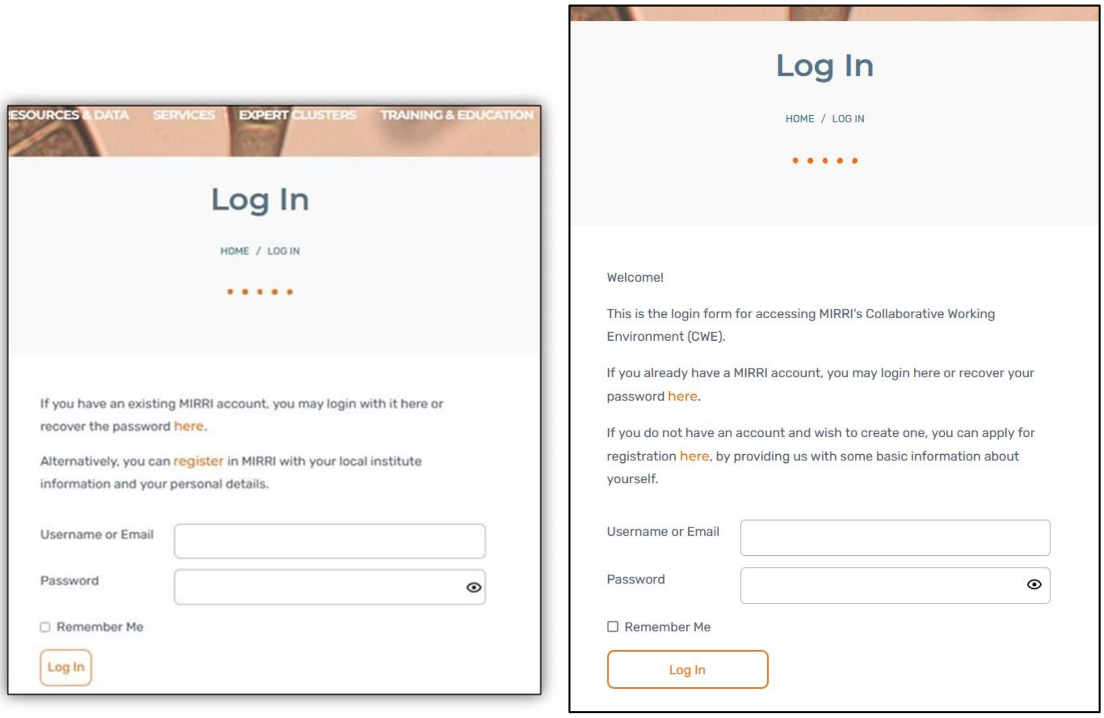
The Transversal Gate contains modules and features that are supportive or transversal to the entire CWE, the Management, Authentication and Authorization Module allowing the registration and maintenance of user information, but also the management of authentication and authorizations to access restricted functionalities in the CWE. Other features included are, for example, those related to security and functionalities of back-office to be used by CWE administrators. They are fully described in D6.2.

Regarding the Management, Authentication and Authorization Module, at present an authentication and user management system proprietary to MIRRI has been implemented to manage access to the MIRRI offer and activities. For the future, it can be updated to integrate user authentication by Single Sign-On systems, such as LS Login for The European Life Science Research Infrastructures (LS RIs), - derived from the EOSC-Life project -, Google Cloud Identity and Access Management (IAM), ORCID Identification system, etc., provided that they are compatible or implementing the OAuth2.0 protocols.

Based on the recommendations made by the WP3 collaborators, some improvements have been implemented to the process of user registration and authentication. Apart from minor text changes made to the login and registration forms, now the process follows the following structure:

1. The user submits information through the registration form.
2. The CCU is notified by email (through one of these addresses: *it.officer@mirri.org, access@mirri.org, info@mirri.org*), for the purposes of analysing the information. Simultaneously, the user is notified on the need for approval assessment and asked to confirm the email address that was submitted.
3. The CCU informs the CWE admin (the IT officer) on the approval and the attributed user profile/roles for update.

4. The user is then notified by email of the approval, and can, from that moment on, use the chosen authentication credentials.



Log In

HOME / LOG IN

If you have an existing MIRRI account, you may login with it here or recover the password here.

Alternatively, you can register in MIRRI with your local institute information and your personal details.

Username or Email

Password

☐ Remember Me

Log In

HOME / LOG IN

Welcome!

This is the login form for accessing MIRRI's Collaborative Working Environment (CWE).

If you already have a MIRRI account, you may login here or recover your password here.

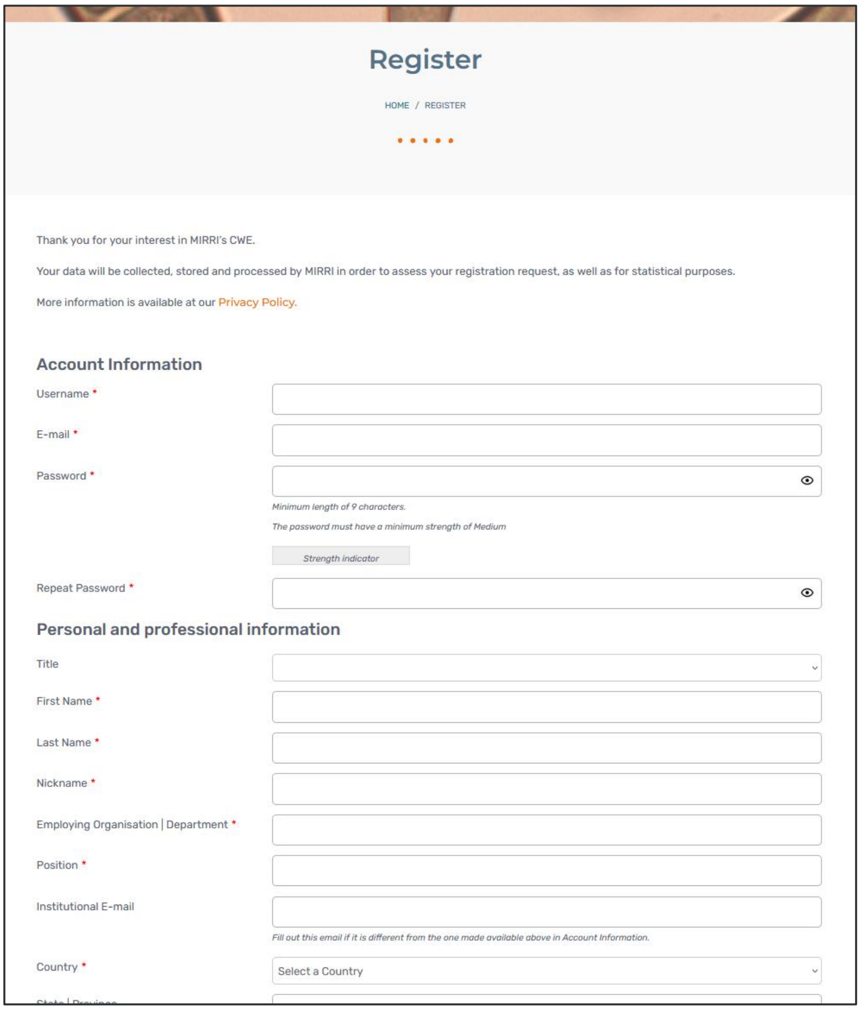
If you do not have an account and wish to create one, you can apply for registration here, by providing us with some basic information about yourself.

Username or Email

Password

☐ Remember Me

Figure 3-1 – The CWE user login form, from the preliminary and final versions of the CWE



Register

HOME / REGISTER

Thank you for your interest in MIRRI's CWE.

Your data will be collected, stored and processed by MIRRI in order to assess your registration request, as well as for statistical purposes.

More information is available at our Privacy Policy.

Account Information

Username *

E-mail *

Password *

Minimum length of 9 characters.

The password must have a minimum strength of Medium

Strength indicator

Repeat Password *

Personal and professional information

Title

First Name *

Last Name *

Nickname *

Employing Organisation | Department *

Position *

Institutional E-mail

Fill out this email if it is different from the one made available above in Account Information.

Country *

Select a Country

Figure 3-2 – Current user registration form

Additionally, this module implements the multiple user profiles defined and established by MIRRI to manage and control the access rights, according to the user affiliation, the role in MIRRI, etc. At the time of accessing the user registration, the MIRRI admin and/or the MIRRI CCU decide and manually attribute, using back-office functionalities, the appropriate user profile and the respective role in CWE.

Since their initial implementation, the user profiles have been updated, following the recommendations from WP3 team. There are currently four profiles for special user access and six profiles for regular users. The special profiles are the following:

- **Administrator:** users with full access and administration rights. They have permits to validate users, assign/modify profiles, eliminate user accounts, create clusters (forum) and subclusters (subforum), and all other features from lower level profiles. This profile is also required to perform other administration tasks in the CWE back-end, such as the backups, the software updates, the catalogues (services and education & training) updates, among many other.

- **Moderator:** users with access to the functionalities to moderate forum topics. They have permits to delete forum threads/replies, and all other features from lower level profiles.
- **MIRRI Access Officer:** cumulative profile for users who manage TNA applications and requests for MIRRI services.
- **MIRRI Support Agent:** cumulative profile for MIRRI supporting experts.

The user profiles have permits to create and answer posts, subscribe to forums and subforums and be notified upon any action on said (sub)forum(s). Furthermore, the implementation of a schema of multiple user profiles is also the basis for future automatic control of access to functionalities and sections or services provided in the CWE. They are the following:

- **Partner:** users affiliated to a partner organization, including users affiliated to a Member/Observer intergovernmental organization or to organizations signatories of a “Partnership MoU“ with MIRRI (depending on the specific terms and conditions), and users qualified as an individual partner (cf. Partner Charter)[1].
- **Academia, Member:** users affiliated to an Academic/Research organization or to a public, non-profit organization from a Member/Observer country (others than “Partners”).
- **Academia Non-Member:** users affiliated to an academic or research organization or to a public, non-profit organization from a non-member or non-observer country.
- **Industry Member:** users affiliated to a private, for-profit company from a member or observer country.
- **Industry Non-Member:** users affiliated to a private, for-profit company from a non-member or non-observer country.
- **Registered:** basic profile for the user, created after approval.

The implementation of this module allows to associate several profiles to a single user when required. For example, one user may be profiled as “Academia, Member” and “Moderator”. New profiles with other type of access permissions can be added in the future if needed.

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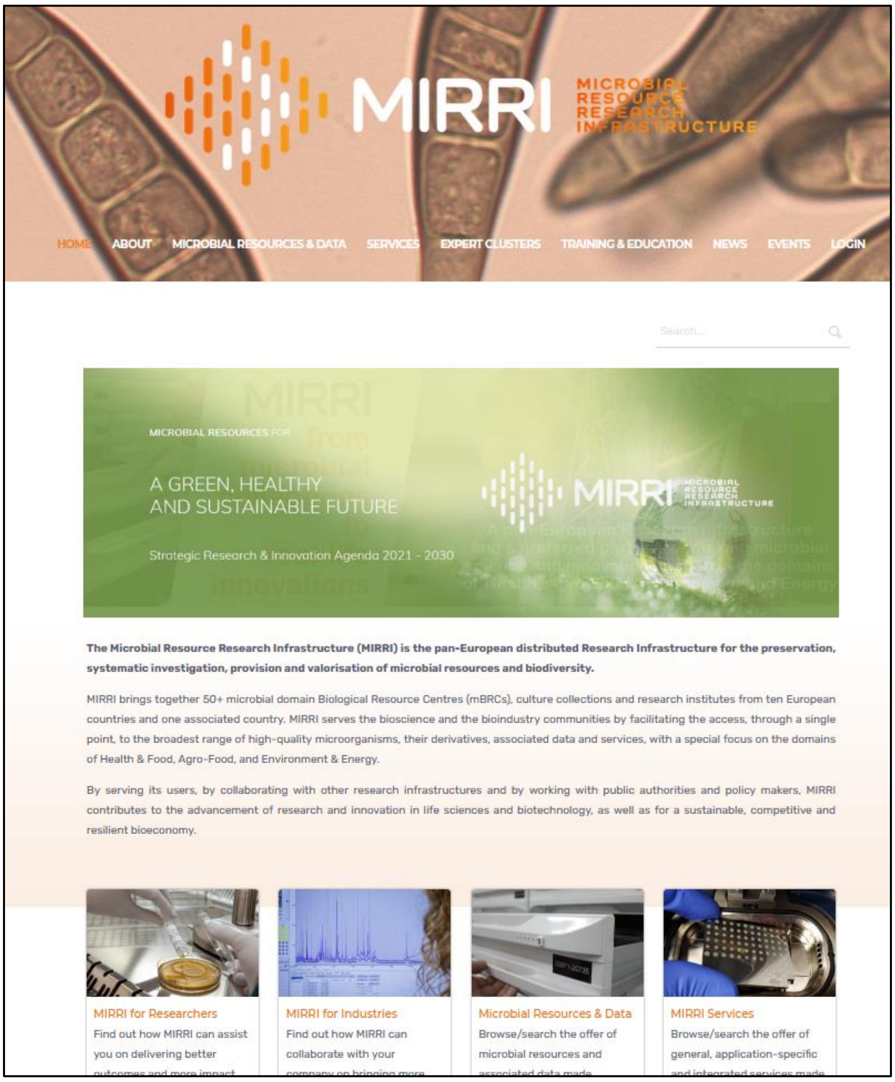
[1] https://mirri.org/wp-content/uploads/2021/03/MIRRI-Partner-Charter-V8-June-2020.pdf

3.2 Gate 1 - The Research Infrastructure Information

3.2.1 Module 1 - Public Website

MIRRI's public website, accessible via the URL https://www.mirri.org, which gives access to MIRRI's tools and services offered via the CWE. For all of them, an introduction is shown and the access to the respective supportive software application is provided seamlessly. The entire portal is fully responsive. It is, therefore, fully usable in different sized devices and compatible with all modern browsers.



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.

MIRRI brings together 50+ microbial domain Biological Resource Centres (mBRCs), culture collections and research institutes from ten European countries and one associated country. MIRRI serves the bioscience and the bioindustry communities by facilitating the access, through a single point, to the broadest range of high-quality microorganisms, their derivatives, associated data and services, with a special focus on the domains of Health & Food, Agro-Food, and Environment & Energy.

By serving its users, by collaborating with other research infrastructures and by working with public authorities and policy makers, MIRRI contributes to the advancement of research and innovation in life sciences and biotechnology, as well as for a sustainable, competitive and resilient bioeconomy.

MIRRI for Researchers
Find out how MIRRI can assist you on delivering better

MIRRI for Industries
Find out how MIRRI can collaborate with your

Microbial Resources & Data
Browse/search the offer of microbial resources and

MIRRI Services
Browse/search the offer of general, application-specific

Figure 3-3 – The CWE Gate 1 and MIRRI's portal home page

3.2.2 Module 2 - Partners Area

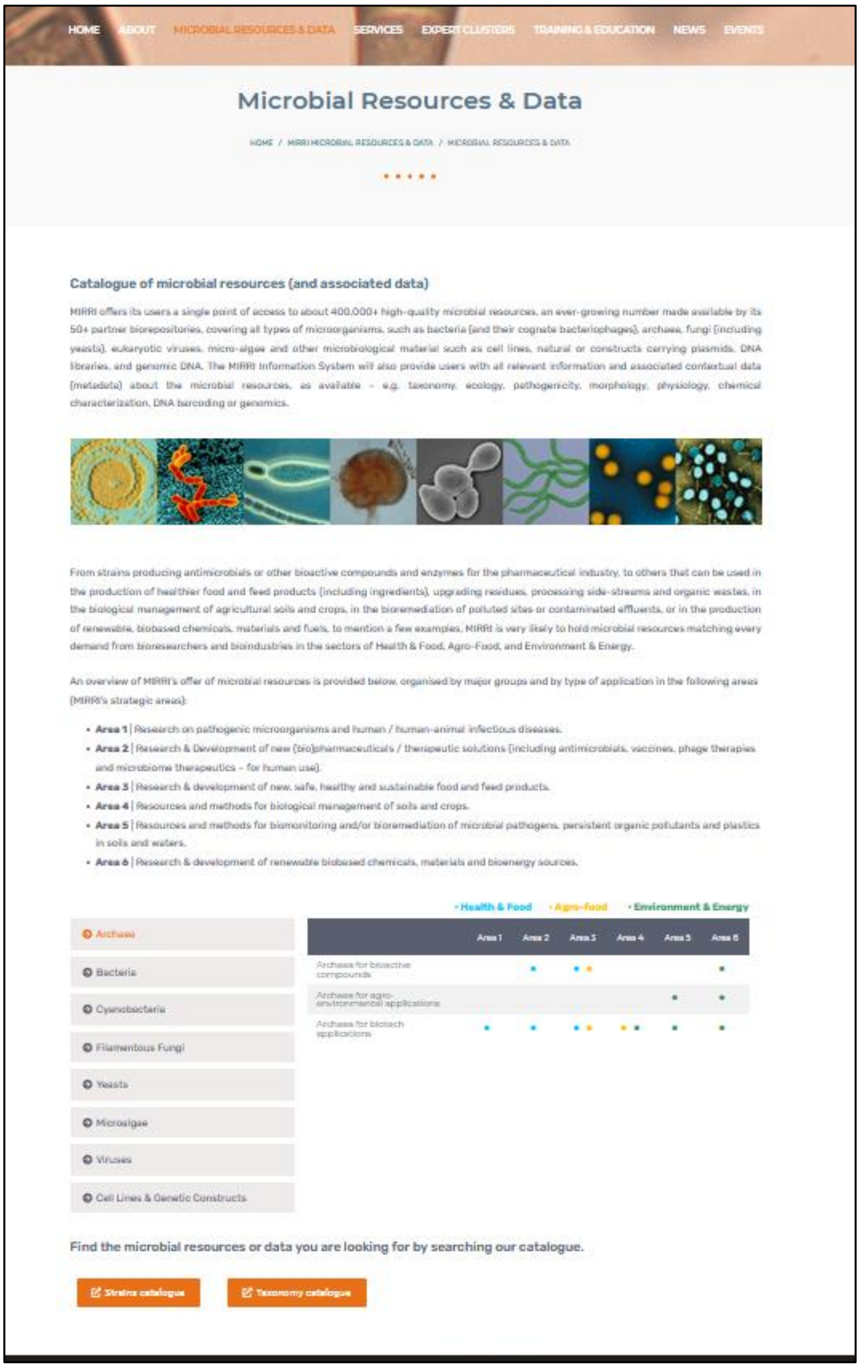
This partner working environment is based on Synology®, a software designed to share apps remotely, and is now available via the URL https://synology.mirri.org fully operative and in use. It includes the main functionalities and requirements enumerated in deliverable 6.1 and already presented in detail and illustrated in deliverable 6.2. The most recent improvements consisted in updating the software modules to the latest version and activities of management.

3.3 Gate 2 - The Microbial Resources, Data and Services

This gate holds three main modules Module 1 – Microbial Resources; Module 2 – Data; Module 3 – Services.

3.3.1 Module 1 - Microbial Resources

The module 1, *Microbial Resources*, exposes MIRRI´s Catalogue of microbial resources and respective areas of application and gives direct access to Module 2 (*Data*) by following a hyperlink at the bottom of the same page.



Microbial Resources & Data

HOME / MIRRI MICROBIAL RESOURCES & DATA / MICROBIAL RESOURCES & DATA

Catalogue of microbial resources (and associated data)

MIRRI offers its users a single point of access to about 400.000+ high-quality microbial resources, an ever-growing number made available by its 50+ partner biorepositories, covering all types of microorganisms, such as bacteria (and their cognate bacteriophages), archaea, fungi (including yeasts), eukaryotic viruses, micro-algae and other microbiological material such as cell lines, natural or constructs carrying plasmids, DNA libraries, and genomic DNA. The MIRRI Information System will also provide users with all relevant information and associated contextual data (metadata) about the microbial resources, as available – e.g. taxonomy, ecology, pathogenicity, morphology, physiology, chemical characterization, DNA barcoding or genomics.

From strains producing antimicrobials or other bioactive compounds and enzymes for the pharmaceutical industry, to others that can be used in the production of healthier food and feed products (including ingredients), upgrading residues, processing side-streams and organic wastes, in the biological management of agricultural soils and crops, in the bioremediation of polluted sites or contaminated effluents, or in the production of renewable, biobased chemicals, materials and fuels, to mention a few examples, MIRRI is very likely to hold microbial resources matching every demand from bioresearchers and bioindustries in the sectors of Health & Food, Agro-Food, and Environment & Energy.

An overview of MIRRI's offer of microbial resources is provided below, organised by major groups and by type of application in the following areas (MIRRI's strategic areas):

- **Area 1** | Research on pathogenic microorganisms and human / human-animal infectious diseases.
- **Area 2** | Research & Development of new (bio)pharmaceuticals / therapeutic solutions (including antimicrobials, vaccines, phage therapies and microbiome therapeutics – for human use).
- **Area 3** | Research & development of new, safe, healthy and sustainable food and feed products.
- **Area 4** | Resources and methods for biological management of soils and crops.
- **Area 5** | Resources and methods for biomonitoring and/or bioremediation of microbial pathogens, persistent organic pollutants and plastics in soils and waters.
- **Area 6** | Research & development of renewable biobased chemicals, materials and bioenergy sources.

🔵 Health & Food 🟡 Agro-food 🟢 Environment & Energy

Archaea
Bacteria
Cyanobacteria
Filamentous Fungi
Yeasts
Microalgae
Viruses
Cell Lines & Genetic Constructs

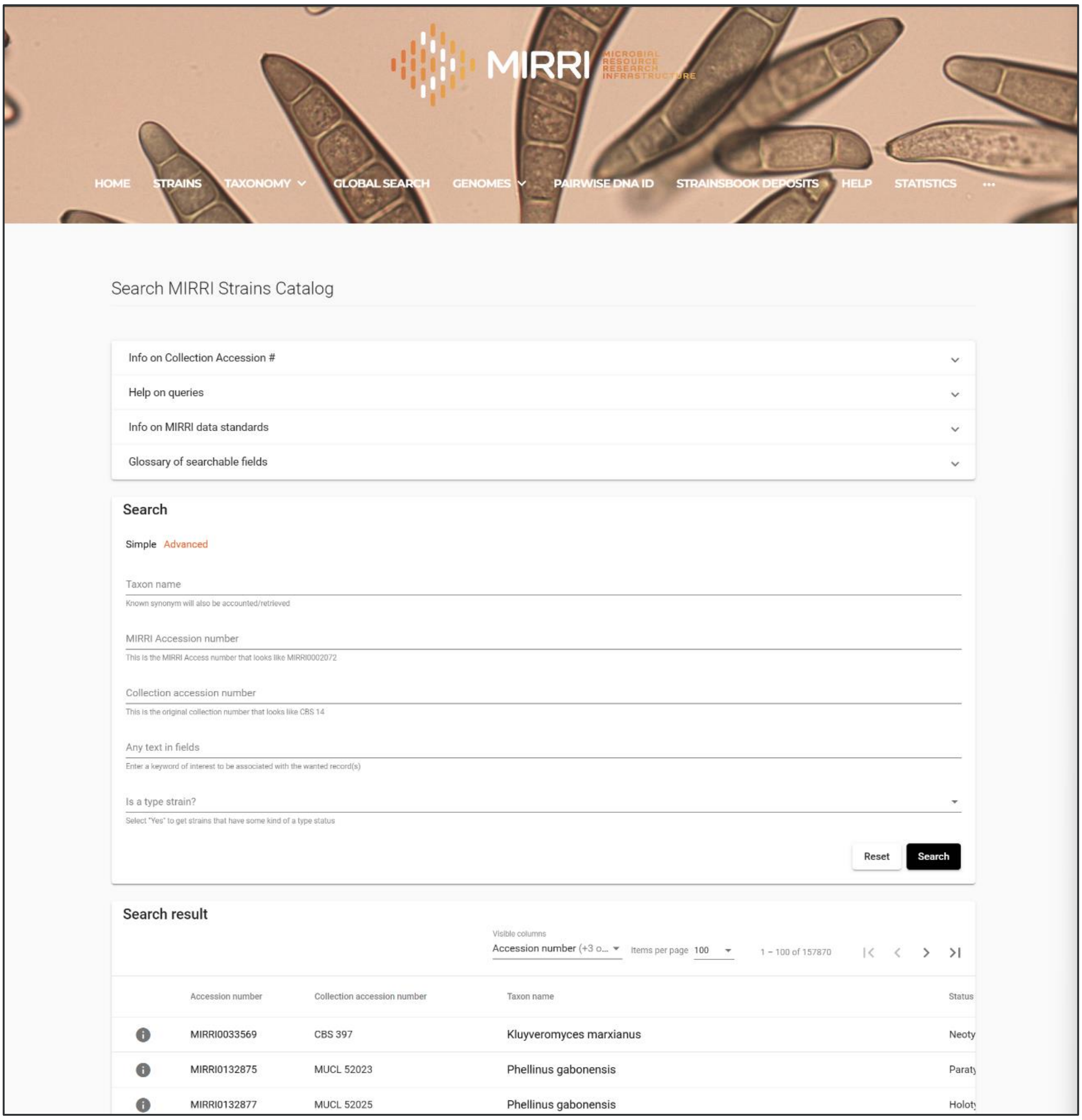
	Area 1	Area 2	Area 3	Area 4	Area 5	Area 6
Archaea for bioactive compounds		🔵	🔵 🟡			🟢
Archaea for agro-environmental applications					🟢	🟢
Archaea for biotech applications	🔵	🔵	🔵 🟡	🟡 🟢	🟢	🟢

Find the microbial resources or data you are looking for by searching our catalogue.

Figure 3-4 – Entry to the Catalogue of microbial resources and access to the associated Data

3.3.2 Module 2 - Data

This module integrates the CWE and constitutes the actual version of MIRRI Information System (MIRRI-IS). As referred before, it was implemented by customizing the BioloMICS framework (user interface, database structure, tables and management interface, addition of new functionalities like for example the “text search”, etc), and is actually running in virtual servers owned by BioAware SA and hosted at the Microsoft Azure West Europe Datacenter in Amsterdam. It is completely integrated in the CWE platform and the end-users do not have the feeling that two different systems are being used. The current version of the database contains data and metadata on 154,683 strains provided by culture collections that are members of MIRRI.



Search MIRRI Strains Catalog

Search

Taxon name
Known synonym will also be accounted/retrieved

MIRRI Accession number
This is the MIRRI Access number that looks like MIRRI0002072

Collection accession number
This is the original collection number that looks like CBS 14

Any text in fields
Enter a keyword of interest to be associated with the wanted record(s)

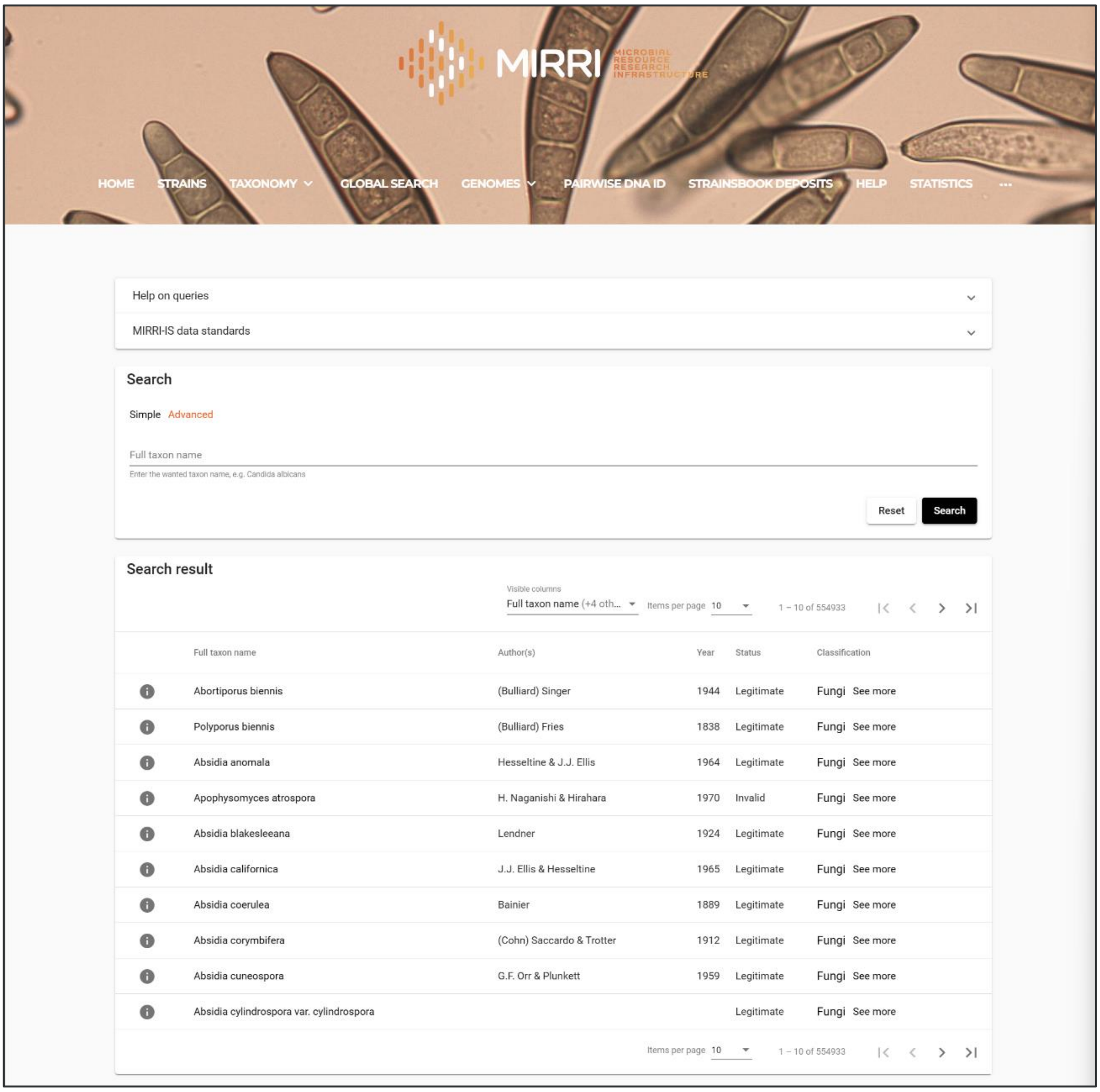
Is a type strain?
Select "Yes" to get strains that have some kind of a type status

Search result

	Accession number	Collection accession number	Taxon name	Status
ⓘ	MIRRI0033569	CBS 397	Kluyveromyces marxianus	Neoty
ⓘ	MIRRI0132875	MUCL 52023	Phellinus gabonensis	Paraty
ⓘ	MIRRI0132877	MUCL 52025	Phellinus gabonensis	Holoty

Figure 3-5 – Aspect of the interface for searching strains in the MIRRI's catalogue

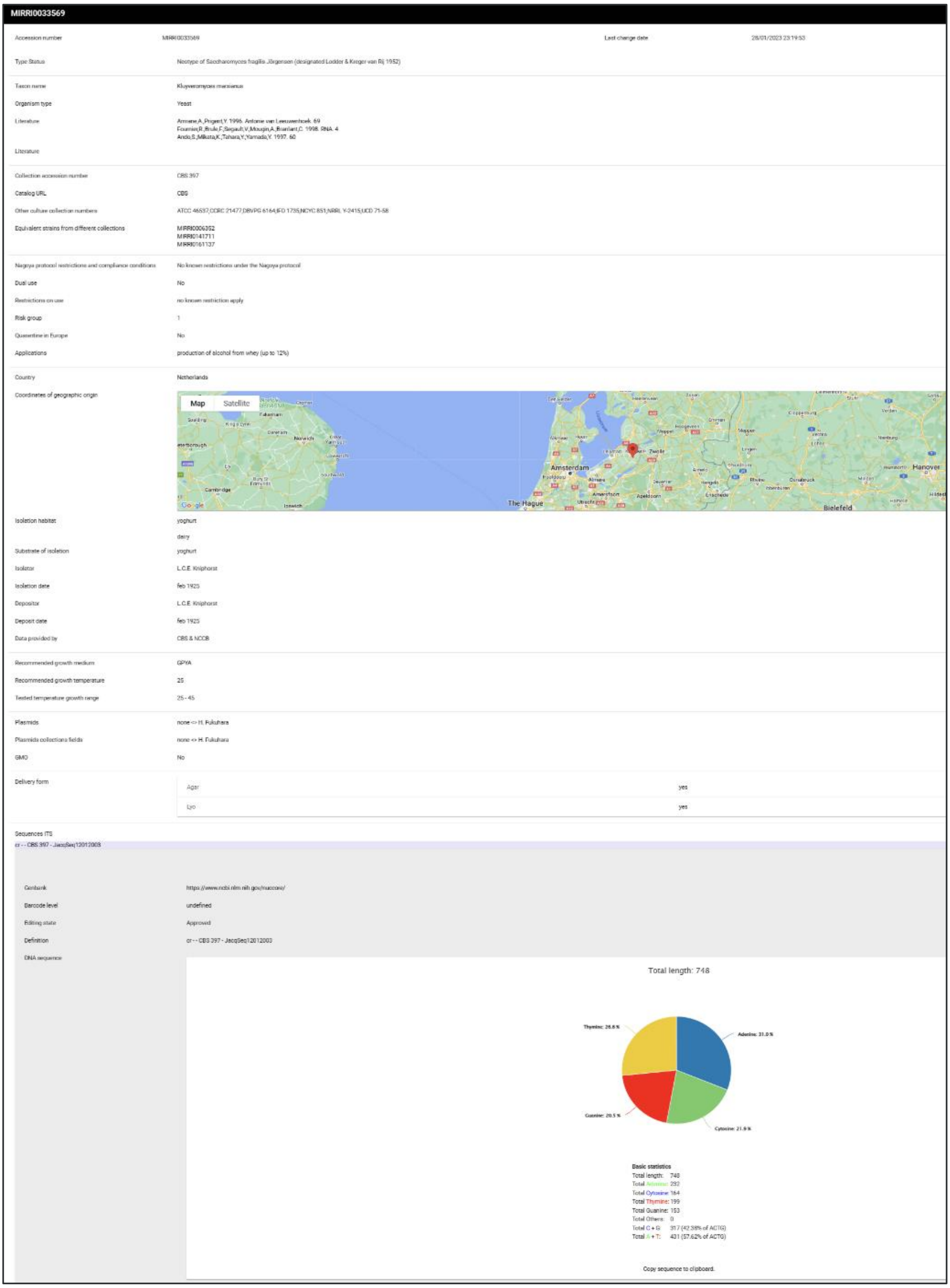
Furthermore, this module also contains functionalities to search for Virus and Non-Virus taxa. The taxonomic database contains more than 554933 data entries and information about synonyms and other taxonomic data points of interest for algae, archea, bacteria, filamentous fungi, and yeasts. Also, a specific virus taxonomy database has been implemented that contains 8480 names of viruses and associated data. The sources of these data, along with the relevant bibliographical references, are expanded upon on Annex I. Their entries are automatically updated, and their data transferred to MIRRI-IS thanks to a script.



Full taxon name	Author(s)	Year	Status	Classification
Abortiporus biennis	(Bulliard) Singer	1944	Legitimate	Fungi See more
Polyporus biennis	(Bulliard) Fries	1838	Legitimate	Fungi See more
Absidia anomala	Hesseltine & J.J. Ellis	1964	Legitimate	Fungi See more
Apophysomyces atrospora	H. Naganishi & Hirahara	1970	Invalid	Fungi See more
Absidia blakesleeana	Lendner	1924	Legitimate	Fungi See more
Absidia californica	J.J. Ellis & Hesseltine	1965	Legitimate	Fungi See more
Absidia coerulea	Bainier	1889	Legitimate	Fungi See more
Absidia corymbifera	(Cohn) Saccardo & Trotter	1912	Legitimate	Fungi See more
Absidia cuneospora	G.F. Orr & Plunkett	1959	Legitimate	Fungi See more
Absidia cylindrospora var. cylindrospora			Legitimate	Fungi See more

Figure 3-6 – Aspect of the interface for searching non-virus taxonomy in the MIRRI’s catalogue

This module innovates by presenting advanced functionalities, like for example the possibility of performing some statistics over the data records, permitting, among other, the presentation of graphical and easy to read presentation of Similarity matrices between the available strains of the database. It also provides hierarchical clustering of all the strains belonging to a given species or genus. This tool can also be used by the CCs to evaluate the identity of their strains and compare it to the ones of the other strains of the same species or genus.



MIRRI0033569

Accession number	MIRRI0033569	Last change date	28/01/2023 23:19:53

Type Status	Neotype of Saccharomyces fragilis Jörgensen (designated Lodder & Kreger-van Rij 1952)
Taxon name	Kluyveromyces marxianus
Organism type	Yeast
Literature	Arnene,A.,Prigent,Y. 1996. Antonie van Leeuwenhoek. 69 Fournier,R.,Brule,F.,Segault,V.,Mougin,A.,Branlant,C. 1998. RNA. 4 Ando,S.;Mikata,K.;Tahara,Y.;Yamada,Y. 1997. 60
Literature	
Collection accession number	CBS 397
Catalog URL	CBS
Other culture collection numbers	ATCC 46537,CCRC 21477,DBVPG 6164,IFO 1735,NCYC 851,NRRL Y-2415,UCD 71-58
Equivalent strains from different collections	MIRRI0006352 MIRRI0141711 MIRRI0161137
Nagoya protocol restrictions and compliance conditions	No known restrictions under the Nagoya protocol
Dual use	No
Restrictions on use	no known restriction apply
Risk group	1
Quarantine in Europe	No
Applications	production of alcohol from whey (up to 12%)
Country	Netherlands
Coordinates of geographic origin	
Isolation habitat	yoghurt dairy
Substrate of isolation	yoghurt
Isolator	L.C.E. Kniphorst
Isolation date	feb 1925
Depositor	L.C.E. Kniphorst
Deposit date	feb 1925
Data provided by	CBS & NCCB
Recommended growth medium	GPYA
Recommended growth temperature	25
Tested temperature growth range	25 - 45
Plasmids	none <> H. Fukuhara
Plasmids collections fields	none <> H. Fukuhara
GMO	No
Delivery form	Agar yes Lyo yes

Sequences ITS

cr - - CBS 397 - JacqSeq12012003

Genbank	https://www.ncbi.nlm.nih.gov/nuccore/
Barcode level	undefined
Editing state	Approved
Definition	cr - - CBS 397 - JacqSeq12012003
DNA sequence	

Basic statistics

Total length:	748
Total Adenine:	232
Total Cytosine:	164
Total Thymine:	199
Total Guanine:	153
Total Others:	0
Total C + G:	317 (42.38% of ACTG)
Total A + T:	431 (57.62% of ACTG)

Figure 3-7 – Partial view of a strain data visualisation

Similarity matrix between the available strains of the database

Minimum similarity: 0.000; Average similarity: 0.847; Maximum similarity: 1.000; Accepted similarity threshold: 0.900
◉ Most central strain; ▼ Strain below commonly accepted similarity threshold (0.900); ♦ The strain is a type (holotype, neotype, epitype, etc); ∝ Genome(s) available for the strain. Mouse hover to get more information.

	Status	MIRRI0095468 NCCB 100132 ▼	MIRRI0096122 NCCB 75010 ▼	MIRRI0096339 NCCB 85004 ▼	MIRRI0096917 NCCB 53042 ▼	MIRRI0136294 CECT 1 ▼	MIRRI0136296 CECT 10 ▼ ∝	MIRRI0136297 CECT 1
MIRRI0095468 NCCB 100132 ▼		1.000	1.000	0.857	0.811	0.800	0.861	0.839
MIRRI0096122 NCCB 75010 ▼		1.000	1.000	0.858	0.810	0.800	0.859	0.843
MIRRI0096339 NCCB 85004 ▼		0.857	0.858	1.000	0.864	0.813	0.808	0.815
MIRRI0096917 NCCB 53042 ▼		0.811	0.810	0.864	1.000	0.822	0.879	0.771
MIRRI0136294 CECT 1 ▼	type of Bacillus alcalophilus	0.800	0.800	0.813	0.822	1.000	0.887	0.866
MIRRI0136296 CECT 10 ▼ ∝	type of Bacillus circulans	0.861	0.859	0.808	0.879	0.887	1.000	0.904
MIRRI0136297 CECT 12 ▼ ∝	type of Bacillus coagulans	0.839	0.843	0.815	0.771	0.866	0.904	1.000
MIRRI0136298 CECT 14 ▼ ∝	type of Bacillus firmus	0.828	0.828	0.830	0.905	0.893	0.956	0.909
MIRRI0136300 CECT 17 ▼ ∝	type of Bacillus badius	0.824	0.828	0.817	0.823	0.843	0.904	0.906
MIRRI0136302 CECT 18 ▼ ∝	type of Bacillus lentus	0.869	0.871	0.850	0.896	0.876	0.935	0.908
MIRRI0136303 CECT 20 ▼ ∝	type of Bacillus licheniformis	0.851	0.854	0.946	0.661	0.446	0.853	0.817
MIRRI0136305 CECT 29 ▼ ∝	type of Bacillus pumilus	0.850	0.844	0.898	0.870	0.867	0.915	0.869
MIRRI0136312 CECT 39 ▼ ∝	type of Bacillus subtilis subsp. subtilis	0.878	0.879	0.979	0.841	0.883	0.910	0.887
MIRRI0136375 CECT 148 ▼ ∝	type of Bacillus cereus	0.998	1.000	0.429	0.404	0.437	0.455	0.445
MIRRI0136401 CECT 197 ▼ ∝	type of Bacillus thuringiensis	0.992	0.992	0.800	0.808	0.866	0.915	0.889

UPGMA Tree based on the above similarity matrix

Statistics on BioloMICS UPGMA tree:
Cophenetic Coef. Corr.: 0.515652; N obs.: 1081.00000; DF: 1080.00000; T value: 19.77834; ND P: 0.242174; D P: 0.484348; OTUs in tree: 47

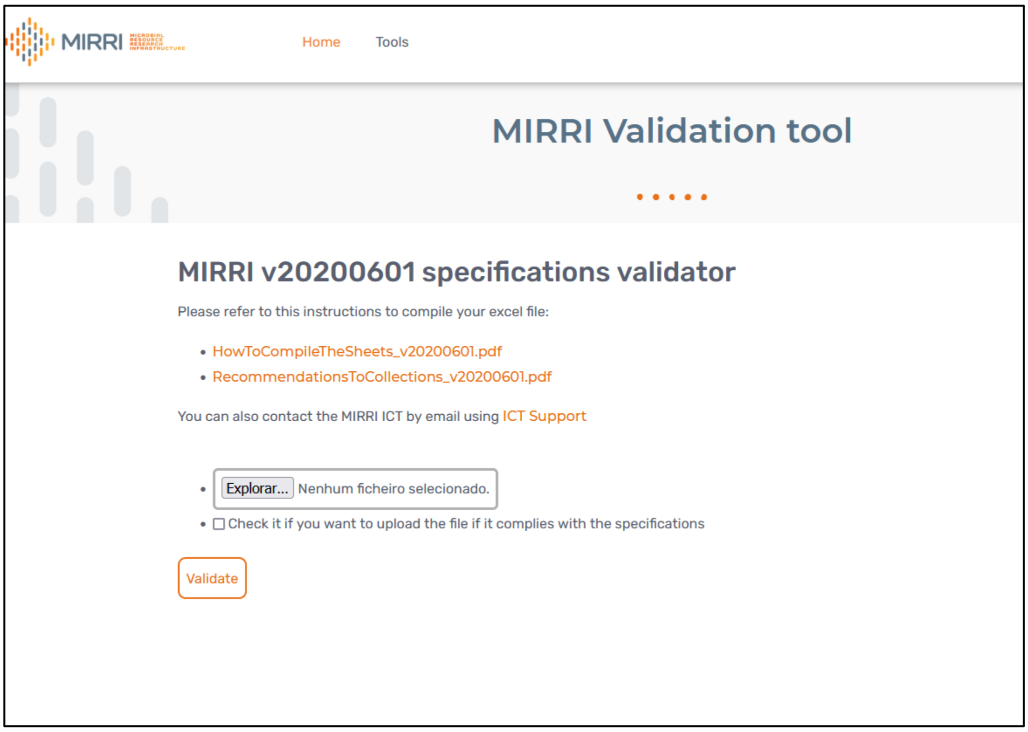
Column #1: Sequences 16s; ■ Data of the field included; ☐ Data of the field not available; ◉ Most central strain; ♦ The strain is a type (holotype, neotype, epitype, etc); ∝ Genome(s) available for the strain. Mouse hover to get more information.

Figure 3-8 – Partial view of a species level data visualisation including hierarchical clustering of strains belonging to a given species

To allow the Culture Collections (CC) to include their strains data in the MIRRI-IS, the data uniformization was identified as a mandatory task. For that, the ICT taskforce of the IS_MIRRI21 project decided to elaborate the specification of data records, as well as an Excel file template, composed of several thematic sheets, to be used by the CCs to prepare and provide the strains data. Both the files documenting the data specifications and the Excel file can be found under the 'MIRRI-IS data standard specifications' section of the 'Legal & Regulatory' information page (https://www.mirri.org/about/legal-regulatory/).

For all collections that use BioloMICS for the daily management of their data, scripts have been written to import strains, sequences, media, bibliography and other data in the MIRRI database, automatically.

Even though detailed specifications and the provision of templates have been given to the CCs, provided data may still present some errors/inconsistencies. To help the CCs to check the compliance of their data and validate it before importing to the MIRRI-IS, an auxiliary validation tool was implemented and made available online at https://tools.mirri.org/tools/validator/. The validation tool was updated to comply with the latest version of strains data specifications. Intensive curation has been done on all the datasets provided by the CCs and feedback given to them in order to improve future re-submissions of data.



MIRRI Validation tool

MIRRI v20200601 specifications validator

Please refer to this instructions to compile your excel file:

- HowToCompileTheSheets_v20200601.pdf
- RecommendationsToCollections_v20200601.pdf

You can also contact the MIRRI ICT by email using ICT Support

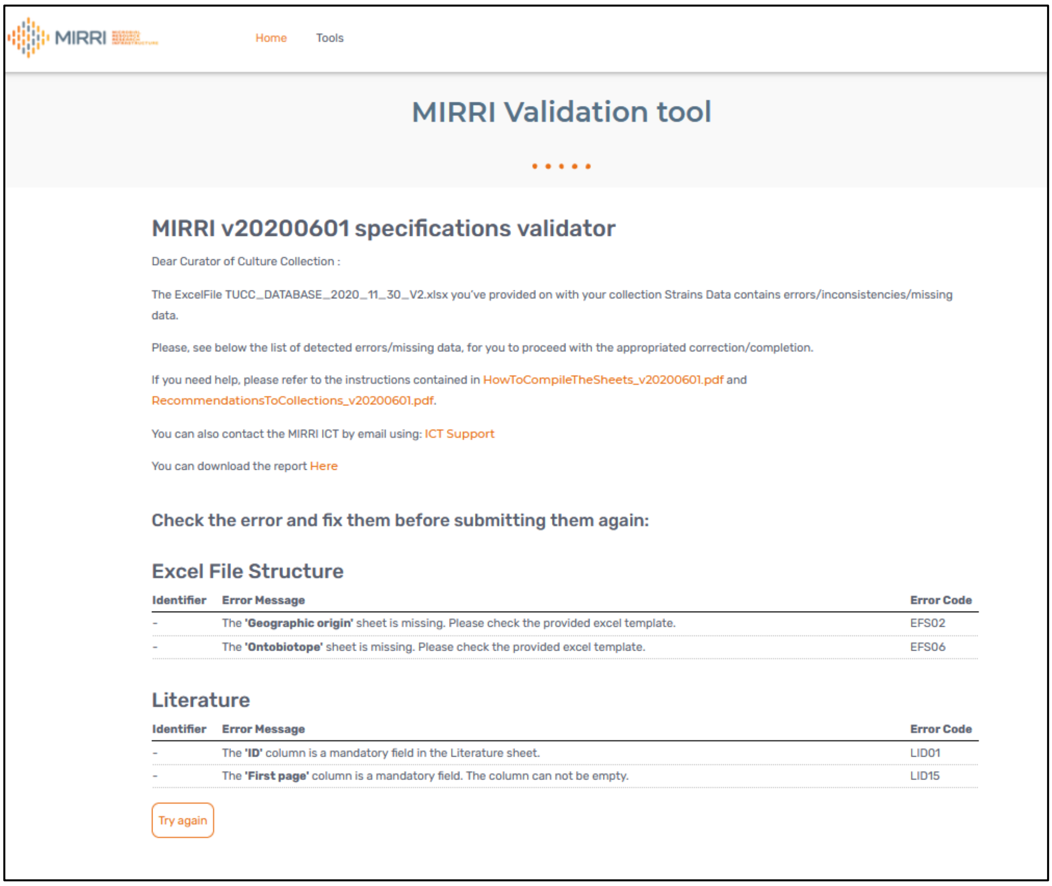
- Nenhum ficheiro selecionado.
- ☐ Check it if you want to upload the file if it complies with the specifications

Figure 3-9 – User interface for input of Data file for validation

Validation Tool

This tool applies a validation process to validate and standardize the data provided by the CCs before adding them to the MIRRI-IS catalogue. It consists of two components: a configurator and an interpreter. The configuration file defines the validation steps for each data item, while the interpreter applies such steps to the provided data, outputting a report with the detected errors. For each microbiological resource (strains and viruses), there is a configuration file establishing the rules to be validated.

There are two possible categories of errors detected: on the structure of the Excel file used to provide the data exported from the CCs and on the information contained. Regarding the Excel file structure, the main issues faced are related to missing columns. The second type of errors relates to the provided fields like, for example, a field where a number is expected and that contains alpha-numeric values. Each error has a code, a message, and an acronym associated with it. The validator uses the code to link the validation step to an error message and the acronym to group errors related to the same Excel sheet. Since structural errors would imply errors on the information, the validation process is interrupted if they are detected. The process of information validation only continues once the CC fixes all structural errors. The error logger outputs a PDF report with a list of errors grouped by acronym. This list is limited to a certain number of errors to avoid displaying too much information at once. As the CC fixes the reported errors, the logger will output the remaining errors.



MIRRI Validation tool

MIRRI v20200601 specifications validator

Dear Curator of Culture Collection :

The ExcelFile TUCC_DATABASE_2020_11_30_V2.xlsx you've provided on with your collection Strains Data contains errors/inconsistencies/missing data.

Please, see below the list of detected errors/missing data, for you to proceed with the appropriated correction/completion.

If you need help, please refer to the instructions contained in HowToCompileTheSheets_v20200601.pdf and RecommendationsToCollections_v20200601.pdf.

You can also contact the MIRRI ICT by email using: ICT Support

You can download the report Here

Check the error and fix them before submitting them again:

Excel File Structure

Identifier	Error Message	Error Code
-	The **'Geographic origin'** sheet is missing. Please check the provided excel template.	EFS02
-	The **'Ontobiotope'** sheet is missing. Please check the provided excel template.	EFS06

Literature

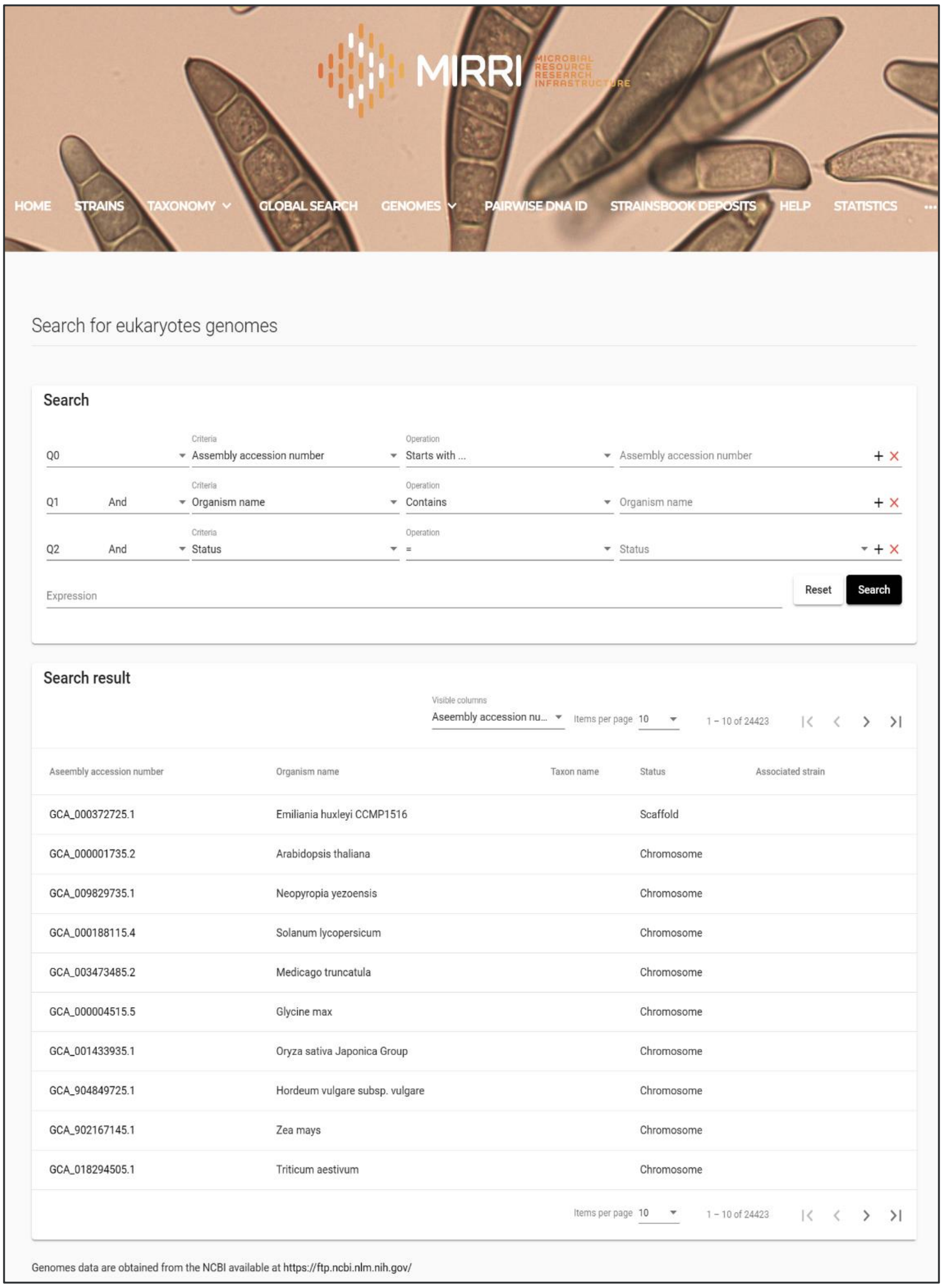
Identifier	Error Message	Error Code
-	The **'ID'** column is a mandatory field in the Literature sheet.	LID01
-	The **'First page'** column is a mandatory field. The column can not be empty.	LID15

Figure 3-10 – Example of visualization of the results of Data validation

Until the end of the IS-MIRRI21 project, the consortium aims at providing un update to be used by the CCs for the Virus data validation, which will constitute, together with some functionality improvements and additions, an evolution of the Module *Data,* towards the final version of CWE.

Genomes Tool

It is a new tool allowing to know which strains in the MIRRI catalogue already have a complete or partial genome associated with them as well as which species and genera already have some associated genomes. Some scripts are available that automatically mine NCBI genome databases for Prokaryotes and Eukaryotes genomes, link them to MIRRI strains and to the species and genera in a cascade way. With this new module, one can know if one or more genomes are associated with strains, species or genera. Genomes are searchable as shown in the Figure 3-11. They are also displayed in the descriptions and in then phylogenetic trees when available (see Figure 3-8). At this stage the Eukaryotes genome database contains 24.423 records while the Prokaryotes one contains 429.013 genomes.



Search for eukaryotes genomes

Search

Q0 — Criteria: Assembly accession number — Operation: Starts with ... — Assembly accession number
Q1 And — Criteria: Organism name — Operation: Contains — Organism name
Q2 And — Criteria: Status — Operation: = — Status
Expression

Search result

Visible columns: Aseembly accession nu...
Items per page: 10
1 – 10 of 24423

Aseembly accession number	Organism name	Taxon name	Status	Associated strain
GCA_000372725.1	Emiliania huxleyi CCMP1516		Scaffold	
GCA_000001735.2	Arabidopsis thaliana		Chromosome	
GCA_009829735.1	Neopyropia yezoensis		Chromosome	
GCA_000188115.4	Solanum lycopersicum		Chromosome	
GCA_003473485.2	Medicago truncatula		Chromosome	
GCA_000004515.5	Glycine max		Chromosome	
GCA_001433935.1	Oryza sativa Japonica Group		Chromosome	
GCA_904849725.1	Hordeum vulgare subsp. vulgare		Chromosome	
GCA_902167145.1	Zea mays		Chromosome	
GCA_018294505.1	Triticum aestivum		Chromosome	

Items per page: 10
1 – 10 of 24423

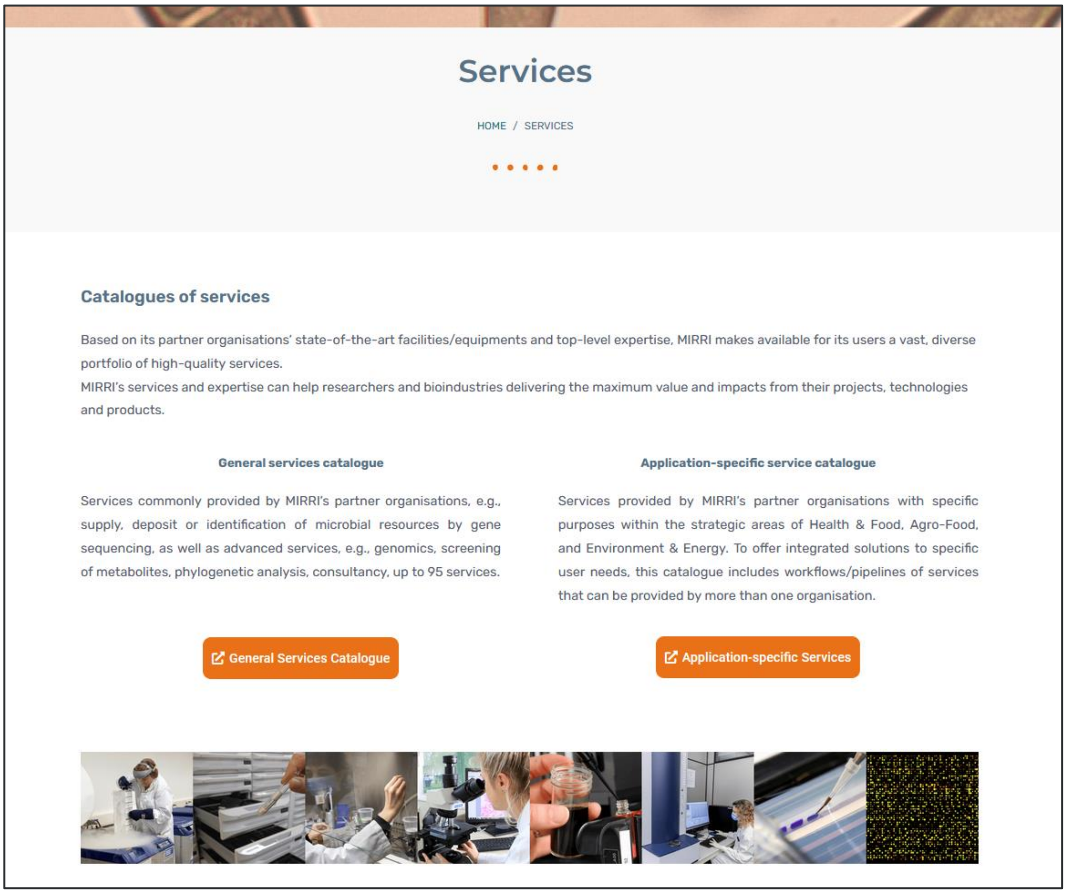
Genomes data are obtained from the NCBI available at https://ftp.ncbi.nlm.nih.gov/

Figure 3-11 – Search page on eukaryotegenomes associated with MIRRI strains

3.3.3 Module 3 - Services

Module 3, *Services*, is aimed at enabling access to services offered both by mBRCs and by the RI, including transnational access (TNA) to laboratories (that is also an objective of the IS_MIRRI21 project), state-of-the-art experimental facilities, services and a wide variety of microbiological resources.

Since the implementation of the services catalogue in the preliminary version of the CWE, it has experienced a number of changes. One of the main ones is the division of the catalogue in two separate pages (one for the general services and another for the application-specific services), which was done following the feedback from usability tests (detailed in Deliverable 6.4), in order to clarify the difference between the two types of services.



Catalogues of services

Based on its partner organisations' state-of-the-art facilities/equipments and top-level expertise, MIRRI makes available for its users a vast, diverse portfolio of high-quality services.
MIRRI's services and expertise can help researchers and bioindustries delivering the maximum value and impacts from their projects, technologies and products.

General services catalogue

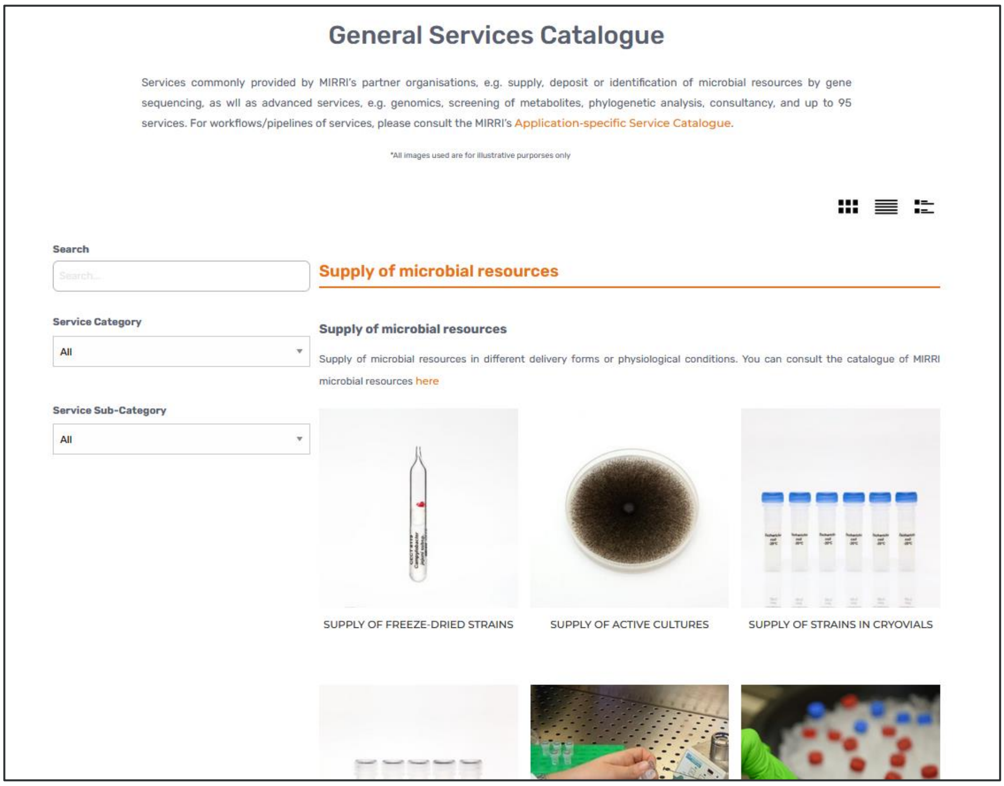
Services commonly provided by MIRRI's partner organisations, e.g., supply, deposit or identification of microbial resources by gene sequencing, as well as advanced services, e.g., genomics, screening of metabolites, phylogenetic analysis, consultancy, up to 95 services.

Application-specific service catalogue

Services provided by MIRRI's partner organisations with specific purposes within the strategic areas of Health & Food, Agro-Food, and Environment & Energy. To offer integrated solutions to specific user needs, this catalogue includes workflows/pipelines of services that can be provided by more than one organisation.

Figure 3-12 – Entry to the MIRRI services catalogues

The catalogues themselves have been improved by styling them after online shopping websites: they now include images, categories, a search box and individual pages with a description of each service and a contact form. It is also possible to filter the services by category and sub-category and by freely entering a search query.



General Services Catalogue

Services commonly provided by MIRRI's partner organisations, e.g. supply, deposit or identification of microbial resources by gene sequencing, as wll as advanced services, e.g. genomics, screening of metabolites, phylogenetic analysis, consultancy, and up to 95 services. For workflows/pipelines of services, please consult the MIRRI's Application-specific Service Catalogue.

*All images used are for illustrative purposes only

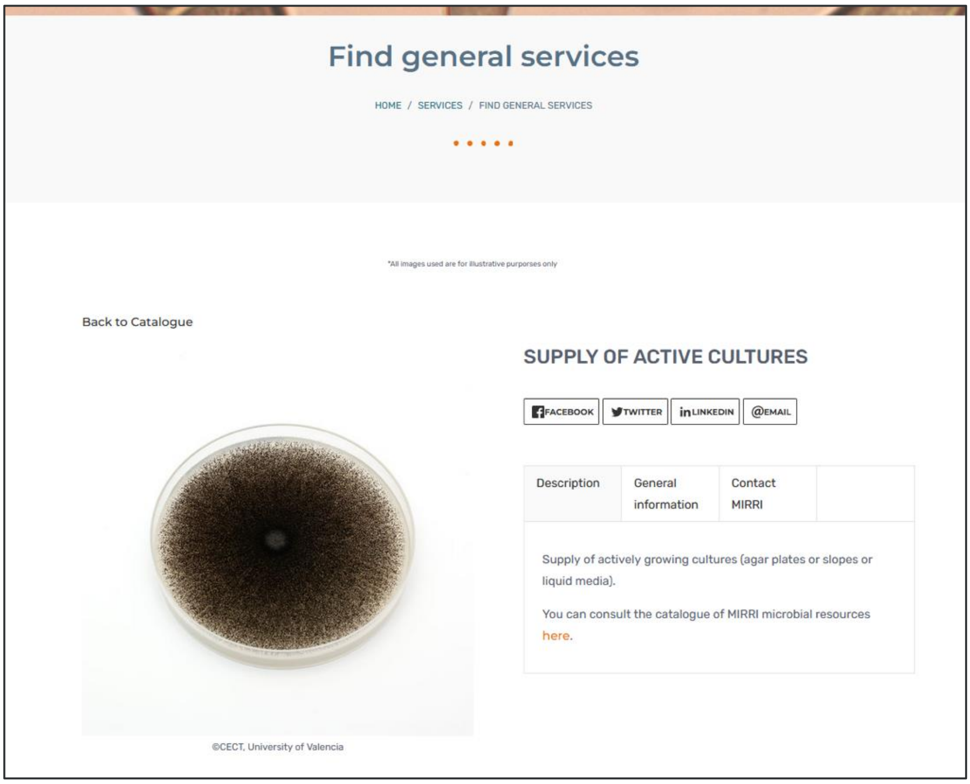
Supply of microbial resources

Supply of microbial resources

Supply of microbial resources in different delivery forms or physiological conditions. You can consult the catalogue of MIRRI microbial resources here

Search: Search...
Service Category: All
Service Sub-Category: All

Figure 3-13 – MIRRI General Services catalogue



Find general services

HOME / SERVICES / FIND GENERAL SERVICES

*All images used are for illustrative purposes only

Back to Catalogue

SUPPLY OF ACTIVE CULTURES

Supply of actively growing cultures (agar plates or slopes or liquid media).

You can consult the catalogue of MIRRI microbial resources here.

©CECT, University of Valencia

Figure 3-14 – Example of service page

The Transnational Access Programme

The TNA platform gathers the information concerning the Transnational Access program, which provides free-of-charge access to MIRRI microbial resources, services and facilities. All the information about the calls and procedures to apply (including the link to the platform for the submission of applications) is organised into different tabs. Additionally, it contains key documents in pdf format to be downloaded. The TNA programme is one of the services that will be provided by MIRRI and it has been tested with two calls supported by the IS_MIRRI21 project as a pilot. The detailed configuration of the platform is described in Deliverable 6.2. Following the feedback from usability tests (detailed in Deliverable 6.4), some recommendations arose regarding the general design of the webpage (e.g. information embedded in the webpage instead of PDFs, a search tool, position of images, etc.) that will be considered when offering the new calls. At present this section contains the general information about the program, the TNA results from the two calls, and Success stories.

The TNA programme aims at financially and logistically supporting the access (physical, remote and virtual) of external users to the IS_MIRRI21 partners' research facilities across Europe to carry out their research projects.

The Transnational access includes:

- ✓ Technical and scientific support
- ✓ Administrative and logistic support
- ✓ Access to the products, services and facilities offered in the IS_MIRRI21 TNA catalogue
- ✓ Hands-on training needed to access the facilities

TNA funding does not include:

- ⊗ Non-standard consumables
- ⊗ Expenses required before or after the TNA visit

The TNA programme sponsors researchers'

- ✓ Access to the IS_MIRRI21 partners' installations (microbial resources, facilities, laboratories, standard consumables, chemicals and disposables)
- ✓ Travel expenses (one round trip/person)
- ✓ Subsistence (meals and accommodation for up to 30 days, weekends included).
- ✓ Shipping costs of project materials from the IS_MIRRI21 partner's facility to the home institutions.

Modality of access

The TNA programme provides three means of access: physical, remote, and virtual access.

Physical access can be defined as the hands-on access of any user, i.e., the users physically visit the Access Provider and use its laboratories and equipment.

Virtual access can be defined as any access through communication networks in which resources can be simultaneously accessed by an unlimited number of users. This is the typical case of the access to data and on-line applications.

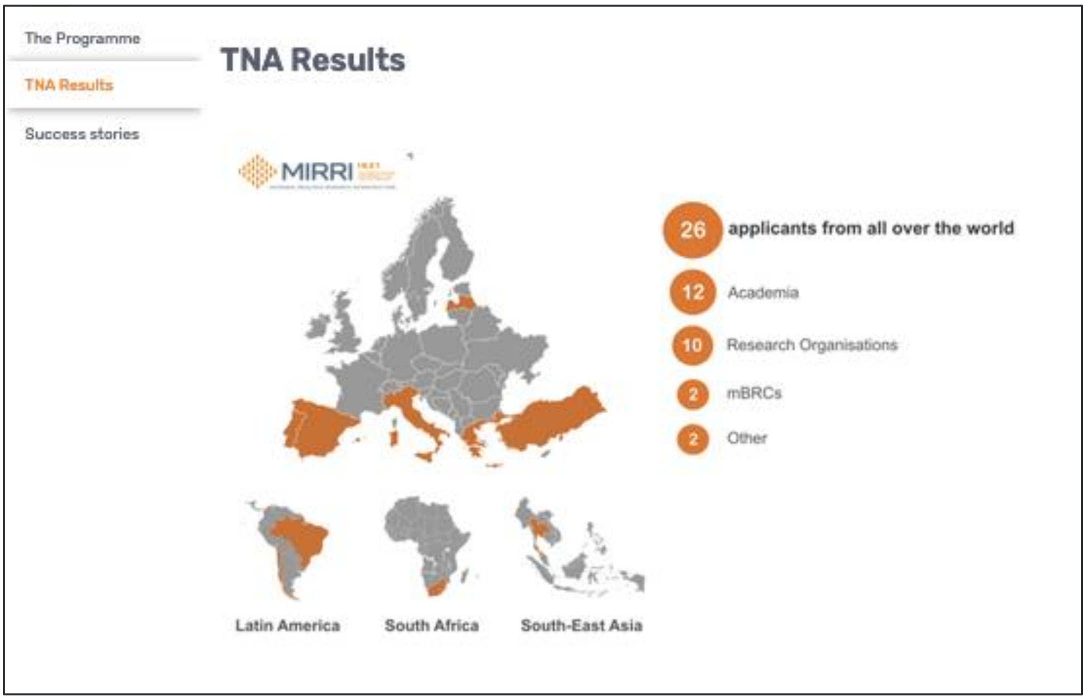
Remote access can be defined as the non-physical access to the services of the Access Provider. There are two types of remote access:

- Set of experiments carried out at the Access Provider's location, but the user is not physically present at the installations (e.g., sample analysis and processing).
- Shipping of microbial strains/biological materials, based on the users' requests.

The **Access Officer** is the main contact person to discuss the details about the TNA application.

Access Officer
Adriana Chiarelli

Figure 3-15 – TNA program presentation



The Programme

TNA Results

Success stories

TNA Results

26 applicants from all over the world

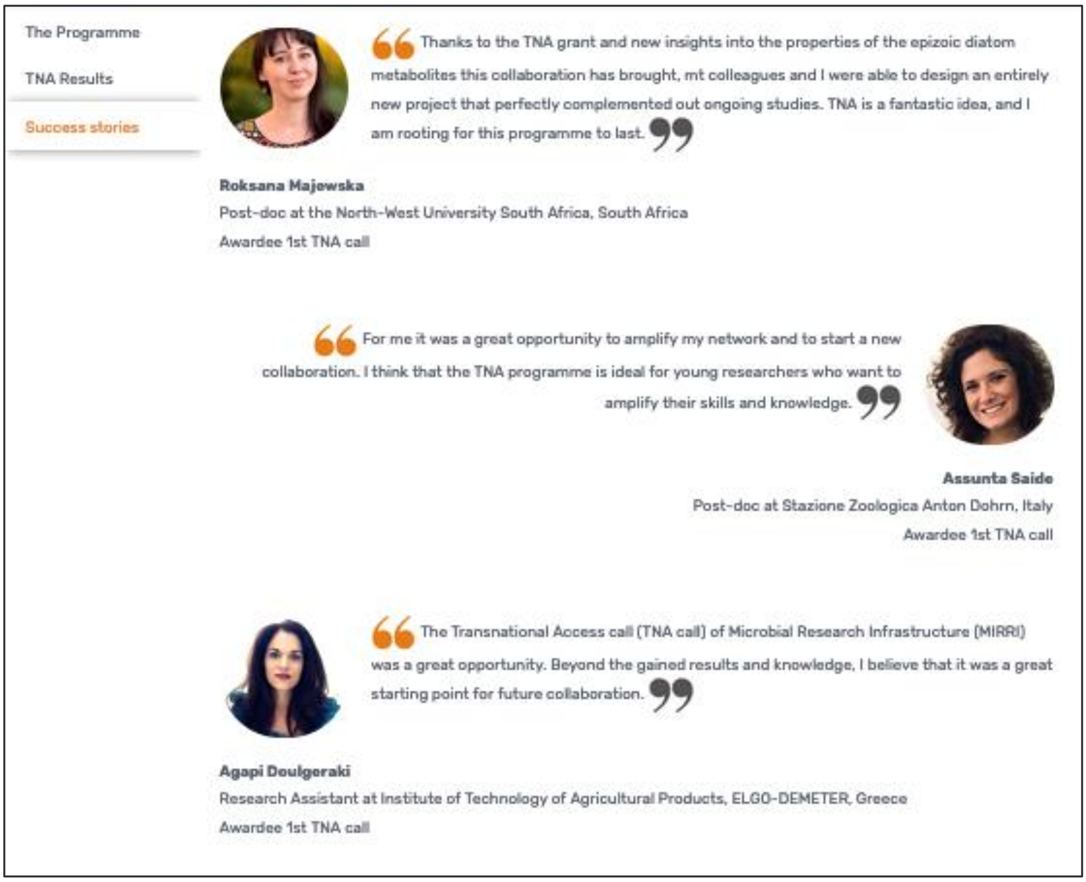
12 Academia

10 Research Organisations

2 mBRCs

2 Other

Figure 3-16 – TNA results presentation



The Programme

TNA Results

Success stories

“Thanks to the TNA grant and new insights into the properties of the epizoic diatom metabolites this collaboration has brought, mt colleagues and I were able to design an entirely new project that perfectly complemented out ongoing studies. TNA is a fantastic idea, and I am rooting for this programme to last.”

Roksana Majewska
Post-doc at the North-West University South Africa, South Africa
Awardee 1st TNA call

“For me it was a great opportunity to amplify my network and to start a new collaboration. I think that the TNA programme is ideal for young researchers who want to amplify their skills and knowledge.”

Assunta Saide
Post-doc at Stazione Zoologica Anton Dohrn, Italy
Awardee 1st TNA call

“The Transnational Access call (TNA call) of Microbial Research Infrastructure (MIRRI) was a great opportunity. Beyond the gained results and knowledge, I believe that it was a great starting point for future collaboration.”

Agapi Doulgeraki
Research Assistant at Institute of Technology of Agricultural Products, ELGO-DEMETER, Greece
Awardee 1st TNA call

Figure 3-17 – TNA program success stories

3.4 Gate 3 - Gate to Collaboration and Experts

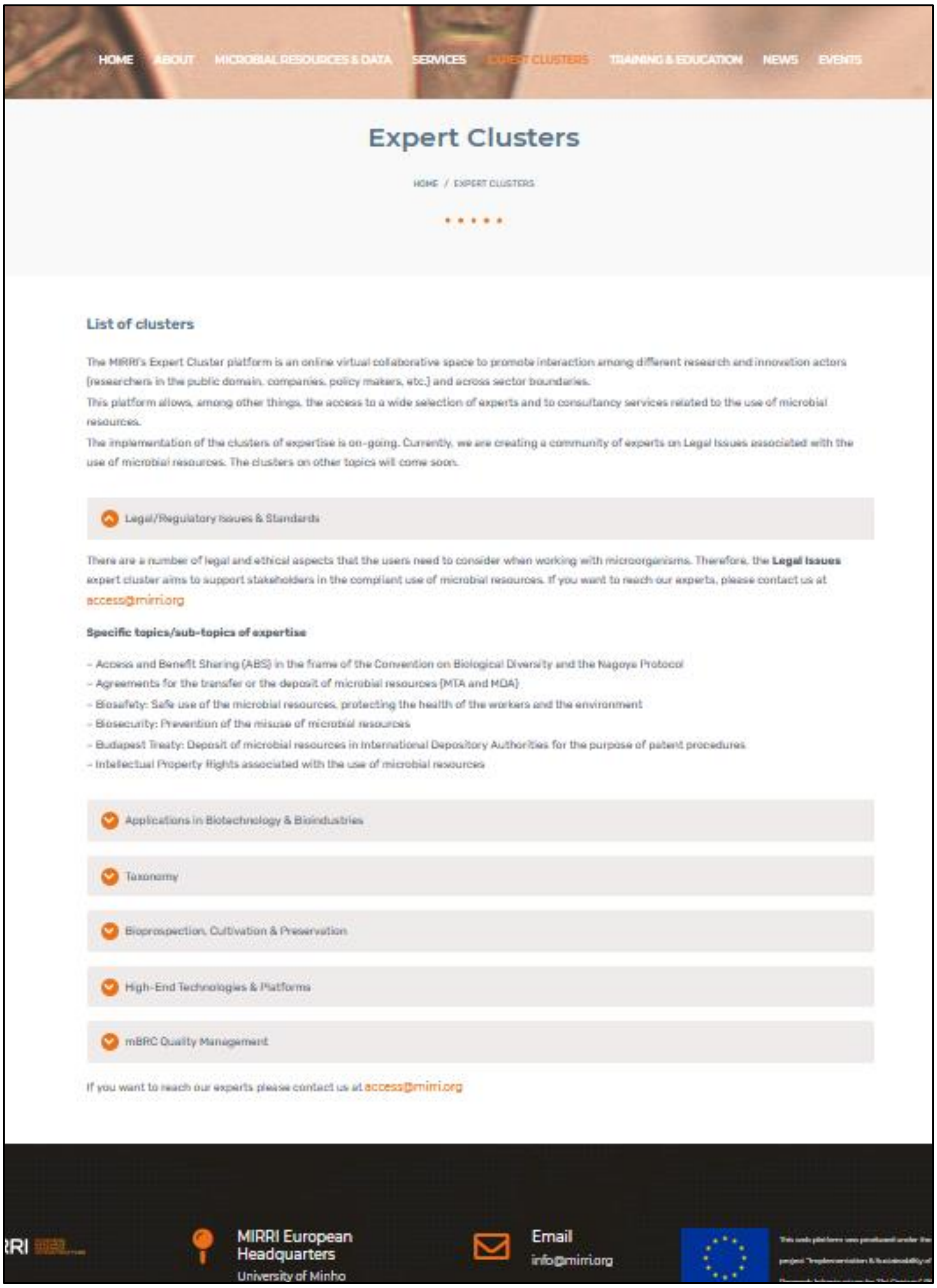
The focus of the Gate to Collaboration and Experts is to provide the MIRRI Expert Cluster platform. Such platform is part of the CWE and its constituent modules provide a unique environment for researchers in life sciences to exchange knowledge, further permitting other stakeholders to access the researcher's expertise and knowledge. The MIRRI Expert Clusters will be organised around the key-topics of mBRCs' activities to support research, development, and innovation processes at the demand of the users.

For this, the platform provides:

- Cluster sections aligned with the stakeholder demands (e.g., Applications & Technologies, Legal issues, Taxonomy, IT & Data management, etc.);
- Pool of experts selected to provide an extensive range of responses and knowledge;
- Cluster tools selected for optimal and efficient intercommunication and exchange of knowledge and experience;
- Highly automated request matching, enabling a multilayer reply to incoming requests.

3.4.1 Module 1 - Expert Clusters

This module is implemented in CWE. It presents MIRRI's clusters of expertise and it gives access to two software applications: the first is a forum and the second is a system for management of on demand expertise provision. Despite the second application being implemented and available in the CWE, it was decided to prioritize the use of the first for stakeholders' interaction with MIRRI experts. The access and use of the second will be made available for all the registered users in a future stage.



Expert Clusters

List of clusters

The MIRRI's Expert Cluster platform is an online virtual collaborative space to promote interaction among different research and innovation actors (researchers in the public domain, companies, policy makers, etc.) and across sector boundaries.
This platform allows, among other things, the access to a wide selection of experts and to consultancy services related to the use of microbial resources.
The implementation of the clusters of expertise is on-going. Currently, we are creating a community of experts on Legal Issues associated with the use of microbial resources. The clusters on other topics will come soon.

Legal/Regulatory Issues & Standards

There are a number of legal and ethical aspects that the users need to consider when working with microorganisms. Therefore, the **Legal Issues** expert cluster aims to support stakeholders in the compliant use of microbial resources. If you want to reach our experts, please contact us at access@mirri.org

Specific topics/sub-topics of expertise

- Access and Benefit Sharing (ABS) in the frame of the Convention on Biological Diversity and the Nagoya Protocol
- Agreements for the transfer or the deposit of microbial resources (MTA and MDA)
- Biosafety: Safe use of the microbial resources, protecting the health of the workers and the environment
- Biosecurity: Prevention of the misuse of microbial resources
- Budapest Treaty: Deposit of microbial resources in International Depository Authorities for the purpose of patent procedures
- Intellectual Property Rights associated with the use of microbial resources

Applications in Biotechnology & Bioindustries

Taxonomy

Bioprospection, Cultivation & Preservation

High-End Technologies & Platforms

mBRC Quality Management

If you want to reach our experts please contact us at access@mirri.org

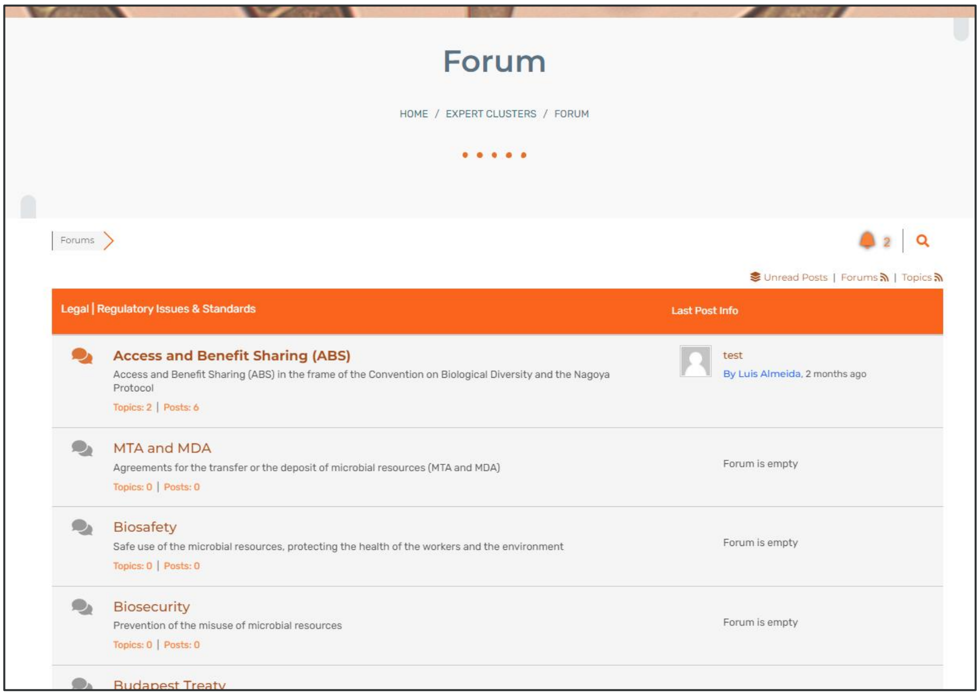
Figure 3-18 –MIRRI’s Expert Clusters module in CWE

The forum

The forum is a software module completely integrated in CWE and implementing the features and functionalities necessary for public discussions and sharing of information related to the clusters of expertise defined in MIRRI and moderated by experts.

It permits the setup of both public and private forums, and the respective management of accessibility rights, depending on the registered user profile. Several profiles were defined by the

MIRRI partners and implemented in the Back-end management application for attribution to each new registered user. The actual profiles for the forum are: **Administrator** (all rights, including validating users, modifying/assigning profiles, eliminating accounts and creating clusters and subclusters), **Moderator** (quality control of answers, answer and delete posts, make sure all posts are responded), **Partner** (MIRRI partners are committed to participate in clusters by signing the Partner Charter), and **User** (external party that registers and post comments/requests and answers). Users have been further classified into whether they belong to a member/observer country and whether they are members of the Industry or Academia.



Legal | Regulatory Issues & Standards — Last Post Info

Access and Benefit Sharing (ABS)
Access and Benefit Sharing (ABS) in the frame of the Convention on Biological Diversity and the Nagoya Protocol
Topics: 2 | Posts: 6
test
By Luis Almeida, 2 months ago

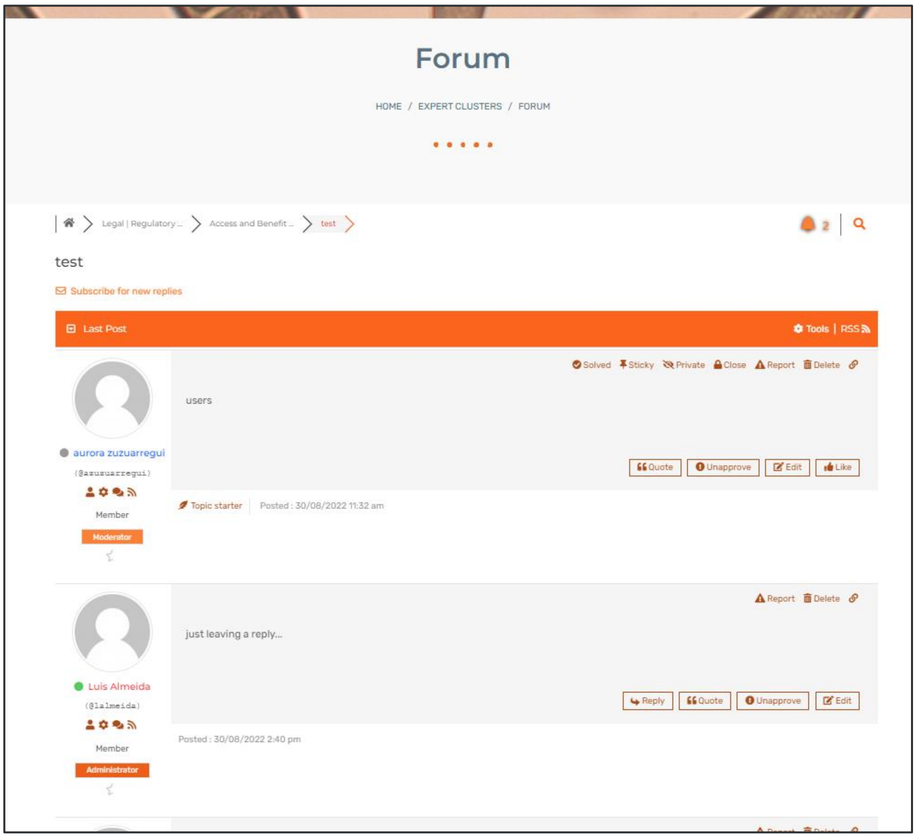
MTA and MDA
Agreements for the transfer or the deposit of microbial resources (MTA and MDA)
Topics: 0 | Posts: 0
Forum is empty

Biosafety
Safe use of the microbial resources, protecting the health of the workers and the environment
Topics: 0 | Posts: 0
Forum is empty

Biosecurity
Prevention of the misuse of microbial resources
Topics: 0 | Posts: 0
Forum is empty

Budapest Treaty

Figure 3-19 – The Expert Clusters forum interface



test

aurora zuzuarregui (@azuzuarregui)

users

Topic starter | Posted : 30/08/2022 11:32 am

Luis Almeida (@lalmeida)

just leaving a reply...

Posted : 30/08/2022 2:40 pm

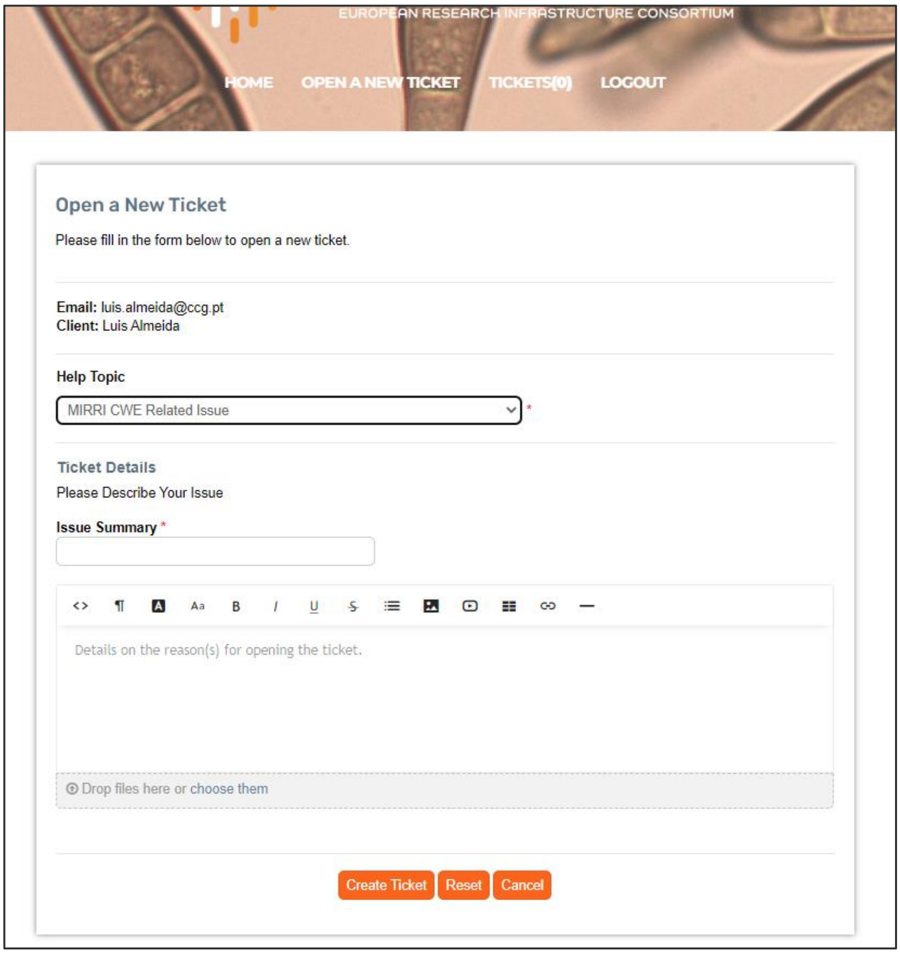
Figure 3-20 – Example of an Expert Clusters forum thread

Additional features allow, for example, the subscription to forums to receive automatic email notifications related to new posts or the sharing of posts in some of the most important professional social networks.

The system for management of expertise provision on demand

Another software to integrate the package of tools to be used for MIRRI’s expertise provision is a system able to manage requests on a “one-to-one” basis, that for simplicity may be called a “ticketing system”. This tool allows MIRRI expert clusters to provide specific advice, support and information to MIRRI’s stakeholders.

Since deliverable 6.2, this system has been implemented in the CWE. It now features an interface where the users can open a ticket in order to consult with a specific cluster of experts, and the members of said cluster can respond to the user’s queries. Both for the user and the Expert, the system sends email notifications containing direct access link to visualize and reply to messages using the platform interface (see images below).



Open a New Ticket

Please fill in the form below to open a new ticket.

Email: luis.almeida@ccg.pt
Client: Luis Almeida

Help Topic
MIRRI CWE Related Issue *

Ticket Details

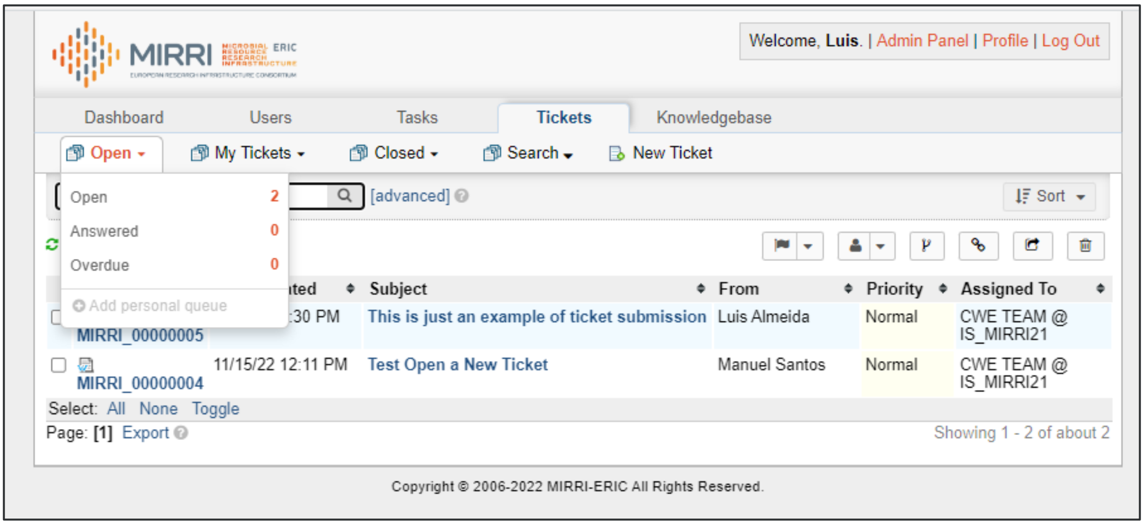
Please Describe Your Issue

Issue Summary *

Details on the reason(s) for opening the ticket.

Drop files here or choose them

Figure 3-21 – MIRRI expert ticketing system: ticket creation interface



Welcome, **Luis**. | Admin Panel | Profile | Log Out

Open	2
Answered	0
Overdue	0

	ted	Subject	From	Priority	Assigned To
☐ MIRRI_00000005	:30 PM	This is just an example of ticket submission	Luis Almeida	Normal	CWE TEAM @ IS_MIRRI21
☐ MIRRI_00000004	11/15/22 12:11 PM	Test Open a New Ticket	Manuel Santos	Normal	CWE TEAM @ IS_MIRRI21

Select: All None Toggle

Page: **[1]** Export

Showing 1 - 2 of about 2

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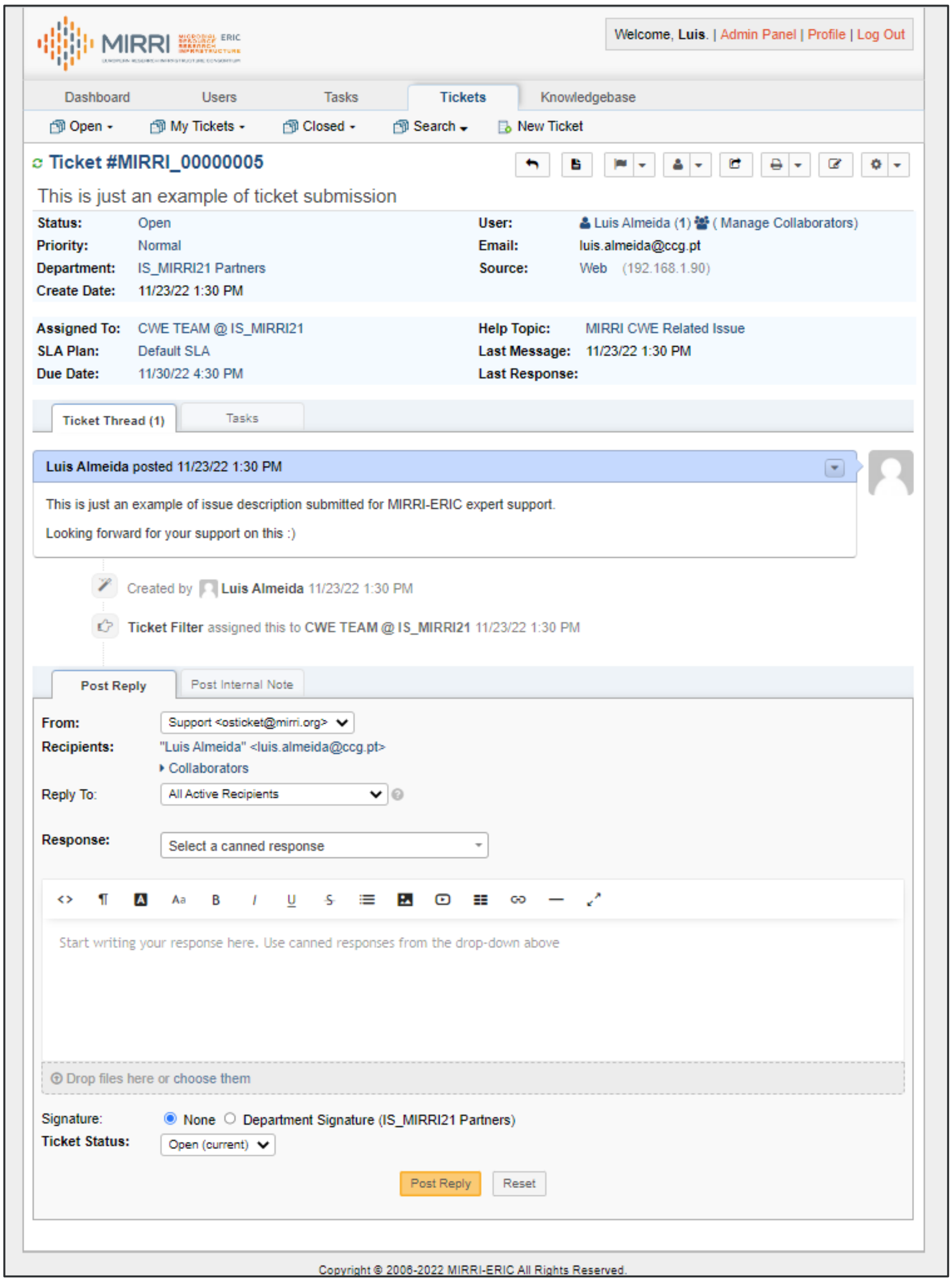
Figure 3-22 – MIRRI expert ticketing system: expert/agent interface



Ticket #MIRRI_00000005

This is just an example of ticket submission

Status: Open
Priority: Normal
Department: IS_MIRRI21 Partners
Create Date: 11/23/22 1:30 PM
User: Luis Almeida (1) (Manage Collaborators)
Email: luis.almeida@ccg.pt
Source: Web (192.168.1.90)
Assigned To: CWE TEAM @ IS_MIRRI21
SLA Plan: Default SLA
Due Date: 11/30/22 4:30 PM
Help Topic: MIRRI CWE Related Issue
Last Message: 11/23/22 1:30 PM
Last Response:

Luis Almeida posted 11/23/22 1:30 PM

This is just an example of issue description submitted for MIRRI-ERIC expert support.

Looking forward for your support on this :)

Created by **Luis Almeida** 11/23/22 1:30 PM

Ticket Filter assigned this to **CWE TEAM @ IS_MIRRI21** 11/23/22 1:30 PM

From: Support <osticket@mirri.org>
Recipients: "Luis Almeida" <luis.almeida@ccg.pt>
Collaborators
Reply To: All Active Recipients
Response: Select a canned response

Start writing your response here. Use canned responses from the drop-down above

Drop files here or choose them

Signature: ● None ○ Department Signature (IS_MIRRI21 Partners)
Ticket Status: Open (current)

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Figure 3-23 – MIRRI expert ticketing system: example of message

3.4.2 Module 2 - Events

The CWE, in its actual version, already contains a module to manage and present events, which was already presented in deliverable 6.2. This module was already fully implemented in the preliminary version of CWE, therefore the changes in it were just for adding new events and making them available in the MIRRI portal.

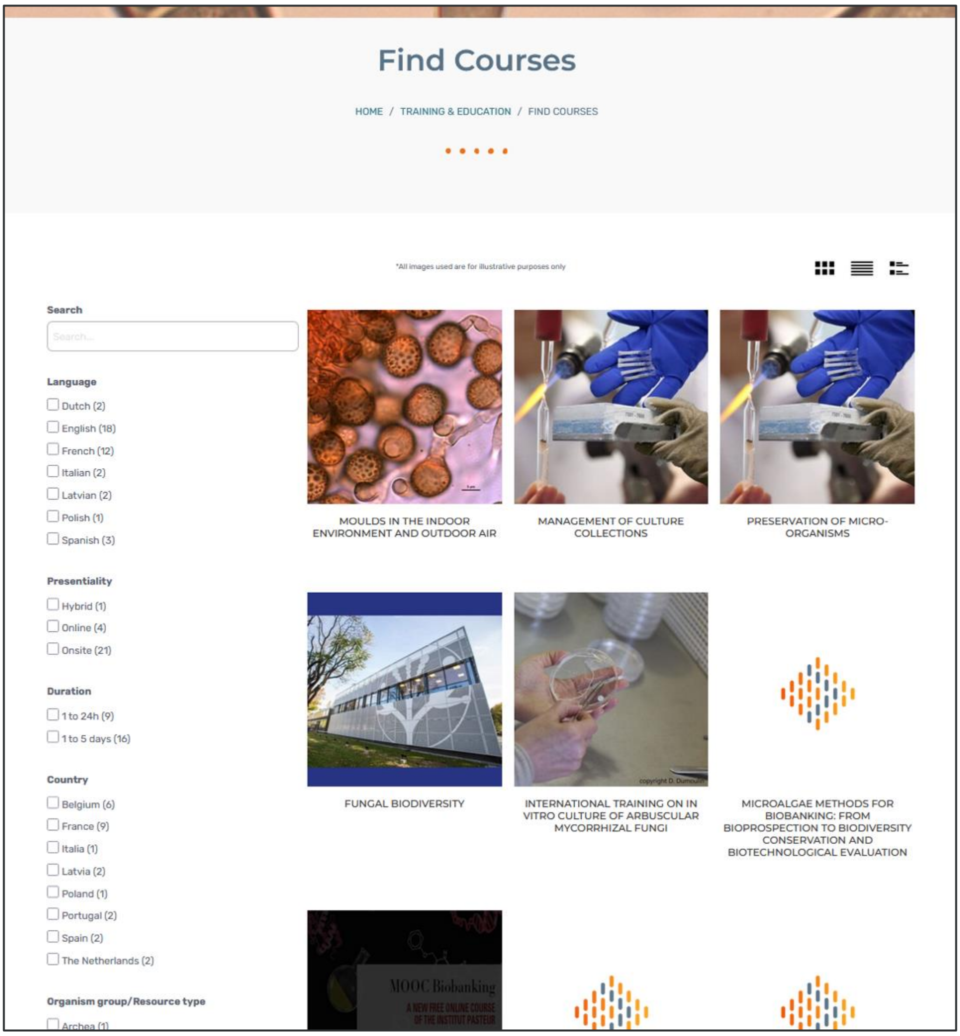
3.5 Gate 4 – Training and Education

The Training and Education (T&E) gate of CWE aims to allow access to MIRRI training programs for different categories of users (for example, scientists, industry professionals, young professionals, partners, etc…), contributing to the development of capacities in the scientific community and of industrial users.

In the context of MIRRI, this gate aims at providing access, to online, onsite and hybrid training courses and seminars. The content covers different aspects of the use of microbiological resources, and the access to official academic schemes, different learning materials and workshops, among others, improving the training for mBRC and Culture Collection professionals, among other potential trainees.

The actual version of the CWE implements features and functionalities to manage and present, as a catalogue, MIRRI's offer of training and education. The back-end management functionalities allow the edition and publication of the most important information for each T&E action, while the front-end shows the catalogue and provides direct access to the portal and/or platform where additional information and/or content and e-learning functionalities are available. Furthermore, the entire catalogue is searchable and filtering features are now available to give the user the possibility of easier selection of the training actions more aligned to her/his interest, among the total offer.

The current catalogue of course is styled after online shopping websites: it includes images, categories, a search box and individual pages with a description and details of each course and a contact form.



Find Courses

HOME / TRAINING & EDUCATION / FIND COURSES

*All images used are for illustrative purposes only

Search

Search...

Language

- ☐ Dutch (2)
- ☐ English (18)
- ☐ French (12)
- ☐ Italian (2)
- ☐ Latvian (2)
- ☐ Polish (1)
- ☐ Spanish (3)

Presentiality

- ☐ Hybrid (1)
- ☐ Online (4)
- ☐ Onsite (21)

Duration

- ☐ 1 to 24h (9)
- ☐ 1 to 5 days (16)

Country

- ☐ Belgium (6)
- ☐ France (9)
- ☐ Italia (1)
- ☐ Latvia (2)
- ☐ Poland (1)
- ☐ Portugal (2)
- ☐ Spain (2)
- ☐ The Netherlands (2)

Organism group/Resource type

- ☐ Archea (1)

MOULDS IN THE INDOOR ENVIRONMENT AND OUTDOOR AIR

MANAGEMENT OF CULTURE COLLECTIONS

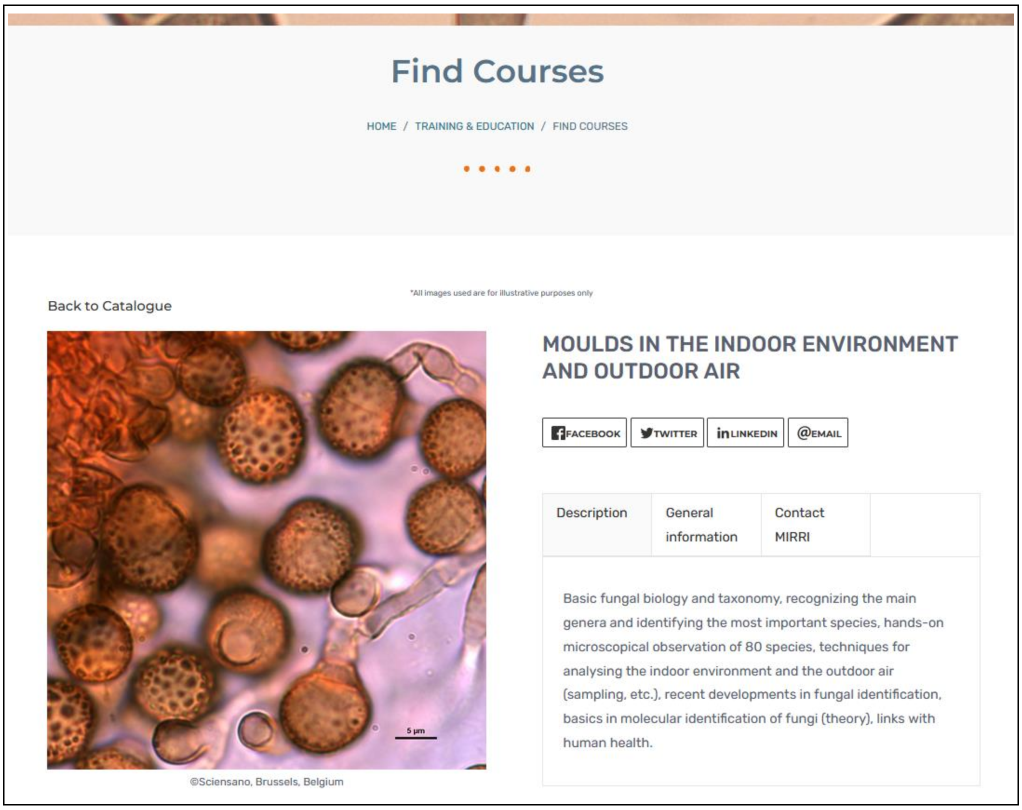
PRESERVATION OF MICRO-ORGANISMS

FUNGAL BIODIVERSITY

INTERNATIONAL TRAINING ON IN VITRO CULTURE OF ARBUSCULAR MYCORRHIZAL FUNGI

MICROALGAE METHODS FOR BIOBANKING: FROM BIOPROSPECTION TO BIODIVERSITY CONSERVATION AND BIOTECHNOLOGICAL EVALUATION

Figure 3-24 – Course catalogue



MOULDS IN THE INDOOR ENVIRONMENT AND OUTDOOR AIR

Basic fungal biology and taxonomy, recognizing the main genera and identifying the most important species, hands-on microscopical observation of 80 species, techniques for analysing the indoor environment and the outdoor air (sampling, etc.), recent developments in fungal identification, basics in molecular identification of fungi (theory), links with human health.

Figure 3-25 – Course description and details presentation in the catalogue

A special section, under Training and Education, has been designated to host information regarding the European Advanced Studies Course on Microbial Resource Centres (EuroMIRC) as well as the link to the applications platform at University of Minho, the entity delivering the course. The first edition of this course, that was organized within the IS_MIRRI21 project, was publicised in this way. Unfortunately, since only 5 applications were received the course will not be delivered this year.

EuroMiRC first edition (March – July 2023)

European Advanced Studies Course on Microbial Resource Centres (EuroMiRC)

March 1st - July 14th 2023, University of Minho (Braga, Portugal)

Valorisation of microbial resources and biodiversity through training of a new generation of professionals that will serve the bioscience and the bioindustry communities.

EuroMiRC aims to develop a new generation of highly qualified professionals that recognize the necessity of undergoing advanced training to acquire state-of-the-art technical and managerial skills tailored to provide and perform better services to the microbial Culture Collections or Microbial Resource Centres user communities.

The **European Advanced Studies Course on Microbial Resource Centres (EuroMiRC)** aims to create a new generation of highly qualified professionals that will work in microbial Culture Collections (CC) or the more advanced concept of Microbial Resource Centres (mBRCs). The prepared 30 ECTS curricular program is designed to give science professionals the skills and knowledge they need to take on greater responsibilities in the management of microbial resources. Students who successfully complete the 30 ECTS program are awarded a *Diploma in Advanced Studies on*

Figure 3-26 – EuroMIRC catalogue

4. The Open Data specifications and FAIR access

4 The Open Data Specifications and FAIR access

This chapter reports on the work done for the data specifications of biological resources and their FAIR access. The latest version of the MIRRI Information System (MIRRI-IS) data standard specifications (which, at the time of writing, is version 5.1) may be found under the 'Legal & Regulatory' section of the CWE (https://www.mirri.org/about/legal-regulatory/). The specifications developed are a contribute for the uniformization of data among the MIRRI CCs, but mainly guidelines to culture collection curators for the provision of their catalogues to MIRRI for inclusion in the MIRRI-IS. Furthermore, they may serve as a key guide for the CCs to revise/modernise their internal information systems. They may also serve as reference for implementations of information systems by the actual and future CCs.

For these reasons, and by also considering that the level of IT expertise at the CCs is very variable, the specifications have been defined as a starting, common point among CCs, able to consider and include a widely acceptable format for the most relevant and useful information on microbial strains. With the progression of CCs information systems, an improved standardization of a larger dataset will be defined. The developed specifications are not absolute and will likely be revised by the MIRRI scientific experts, based, among other, on scientific criteria.

This activity was carried out in the context of the WP6 by a task force of experts affiliated to the IS_MIRRI21 project partners (MIRRI ICT Task Force), starting from some of the existing, or under development, standards and comparing them with the information effectively available in most of the CC catalogues. The specifications have also been defined by considering the most recent and relevant international regulations and European rules.

The main documents were:

- Annex A "From CABRI data fields to MIRRI data objects: the evolution of a standard" of the Deliverable D8.3 of MIRRI preparatory phase. This document also includes a simple table that examines CABRI data sets for bacteria (which were developed in the context of the successful EU project CABRI - Common Access to Biological Resources and Information, http://www.cabri.org/) and, for each of the related data field, specifies how it could be better implemented for MIRRI, along with the possible data validation processes.
- Mapping between data fields of about 20 catalogues submitted by CCs to MIRRI for this activity and the CABRI full data sets (CABRI included mandatory data fields in its Minimum Data Set, recommended data fields in the Recommended Data Set, and all data fields available in the partner collections in the Full Data Set).
- The ISO/AWI 21710:2020 document on "Specification on data management and publication in microbial resource centres" (TC 276, WG 5).

Starting from the above documents, the task force analysed each data field with the aim of defining:

- whether it had to be included in the MIRRI-IS dataset or not,
- whether the CABRI and ISO/AWI 21710 definitions were in correspondence or not and, in the latter case how to reconcile them,
- the format that it should have in the MIRRI-IS dataset, its related possible values and mandatoriness.

A special attention was devoted to data fields related to regulations since these were deeply changed during last years, also because of the effects of the introduction of the Nagoya Protocol on Access and Benefit-sharing. To this aim, a few additional data fields were included in the MIRRI-IS dataset, although not explicitly mentioned in CABRI and ISO standard definitions. Examples of these are information related to the compliance with the Nagoya protocol, to the dual use of strains and to their quarantine. For some of these fields, advice was obtained from experts outside the task force. A special effort was put on the definition of codes and enumerations to be associated to data fields, instead of free text, whenever possible, although the latter format remained for the majority of data fields due both to the absence of terminologies and ontologies and to the poor structure of the information systems of partner collections.

4.1 Microbial Data Specification

As anticipated, distinct documents related to microorganisms (bacteria, archaea, filamentous fungi, yeasts, algae and cyanobacteria), plasmids and viruses, were produced since the related data are substantially different.

In the specifications, all data fields are “strongly recommended” and should be provided in the requested format. Presently there are only a few mandatory fields that are highlighted in the description of the datasets. Submitted data will be checked: records missing mandatory data may be discarded.

The taxonomic identity of resources must be compiled according to the exact and complete taxonomy from authoritative sources. These include:

- Fungi and yeasts: MycoBank (see https://www.mycobank.org/),
- Bacteria and archaea: List of Prokaryotic names with Standing in Nomenclature (LPSN) (see https://lpsn.dsmz.de/),
- Algae and cyanobacteria: AlgaeBase (see http://www.algaebase.org/).

Genomic reference data is of extreme importance in view of the development of MIRRI-IS and of the tools that will exploit its data.

For each data field, the following information is reported in the specifications:

Each data field included in any of the MIRRI-IS specifications is described as follows:

- Name: the name assigned to the field
- Short name: a simplified version of the name for the field, usually a single term following the camel format, where spaces are removed and word initials are made uppercase, such as *shortName* or *camelFormat*
- Description: the description of the intended meaning and contents of the field
- Syntax: the syntax of the field, including its type (text, number, date, enumeration, etc…) and possible syntactic components. Not all fields have an associated syntax.
- Values: the values allowed for the information or a link to a reference list or nomenclature or ontology. Not all fields have a restricted list of allowed values, e.g. free text information.
- Validation: the list of actions carried out by MIRRI in order to validate the information.
- Examples: some examples of valid data for the field.

Both the specifications for plasmids and for viruses include one additional descriptor that specifies if the data field corresponds to one of the fields of the specifications for microorganisms.

Specifications are associated with two documents supporting the preparation of data by the CCs for the submission and inclusion in the MIRRI-IS: an MS Excel file created as a template for the compilation and submission of data in this format and a guide to the format of the template supporting its compilation, either manual or automatic, by CC curators.

In the following tables some examples of data fields are reported. For the current version of the complete specifications, refer to the MIRRI-IS data standard specifications, included under the Legal & Regulatory section of the CWE platform.

This is an example of a field of type enumeration, with multiple values allowed.

Table 4-1 –Specification for the ‘supplyForm’ data field

Name	Form of supply (**MANDATORY FIELD**)
Short name	supplyForm
Description	The forms of supply of the strain to users.
Syntax	One or several of the allowed values, separated by a “;”.
Values	Allowed values: Agar, Cryo, Dry Ice, Liquid Culture Medium, Lyo Oil, Water.
Validation	Check for the validity of the format. Report errors to the CC.
Examples	Cryo Agar; Lyo

This is an example of a field of numeric type. The units, meters in this case, are omitted.

Table 4-2 – Specification for the ‘altitude’ data field

Name	Altitude of geographic origin
Short name	altitude
Description	The altitude of the location where the sample was collected.
Syntax	None
Values	Decimal number.
Validation	Check for the validity of the format and values. Report errors to the CC.
Examples	1286 -20

This is an example of a field of type enumeration, referring to an external list of values (the appropriate taxonomy, according to the type of organism).

Table 4-3 – Specification for the ‘speciesName’ data field

Name	Taxon name (**MANDATORY FIELD**)
Short name	speciesName
Description	Taxon name including genus, species and variant names, as taken from an authoritative nomenclature reference, including Mycobank for fungi and yeasts, the Prokaryotic Nomenclature Up-to-date for bacteria and archaea, AlgaeBase for algae and cyanobacteria, and ICVT for viruses.
Syntax	According to the appropriate nomenclature. For Archaea, Bacteria, Filamentous Fungi and Yeasts, genus name followed by species name and by the subspecies and variant names, when appropriate. The subspecies name must be preceded by “subsp.”. The variant name must be preceded by “var.”. When the species name is not available, do not include “sp.”. When the genus name is not available, specify the family name instead. In order to cope with delays in nomenclature updates, the most updated taxon name can be used, even when it is missing from the current version of the reference. In this case, a remark must be included in the ‘Comment on taxonomy’ data field. For hybrid strains, more than one taxon name can be specified. The semicolon “;” must be used as a separation character.
Values	All taxon names included in the authoritative nomenclature references, reported according to the given syntax.
Validation	Check for the correct syntax and the existence of the taxon name(s) in the reference nomenclatures. Report errors to the CC.
Examples	Candidaceae Candida Candida albicans Candida albicans var. claussenii Actinomyces globisporus subsp. Flaveolus

4.1.1 Specification for microorganisms’ data

The specifications for Microorganisms were first created in 2021. Various versions have been created during the following years and, especially, as an outcome of the efforts carried out in this project. The current one is version 5.1 that was delivered as a draft on February 24th, 2023. This version includes 56 data fields, 12 of which are mandatory. In this version, two new data fields were added, namely those related to QPS (Qualified Presumption of Safety) and to axenic cultures.

4.1.2 Specification for plasmids data

The specifications for Plasmids were first drafted in March 2022. the most recent version was completed in December 2022 as version 2022.12.1 and it has been defined as release candidate 1. They include 50 data fields, 13 of which are mandatory. 24 data fields are exclusive for plasmids and four more have some differences in respect to the corresponding field of the microorganisms' specifications, thus making more than half of the specifications unique. Fields have been grouped in six categories, which are respectively related to: Identity, General information, Properties, Sequence information, Literature, and Growth conditions.

4.1.3 Specification of viruses' data

The specifications for Viruses were first drafted in March 2021 and are now available, since November 2022, as Release candidate 3, version 2022.11.18. They include 45 data fields, 15 of which are mandatory. 15 data fields are exclusive for viruses and 12 more have some differences in respect to the corresponding field of the microorganisms' specifications, thus making more than half of the specifications unique also in this case. Fields have been grouped in six categories, which are respectively related to: Identity, Distribution, Taxonomy, Origin, History of deposit, Properties.

4.2 From MIRRI-IS datasets to their schema

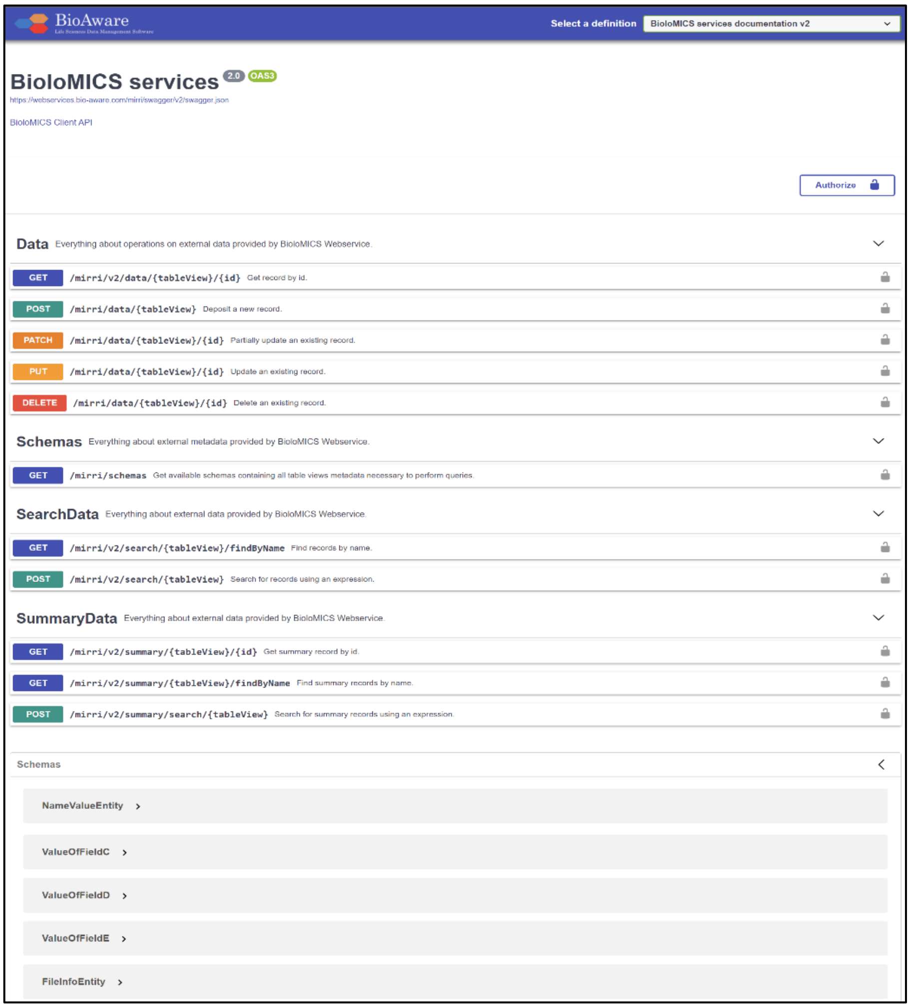
In order to improve FAIRness of MIRRI-IS, its interoperability (the ability of a system to be automatically queried by external software, without direct human intervention and by using standard definitions of data, and return semantically annotated data) is a key issue.

A draft version of a data exchange schema for MIRRI-IS datasets based on JSON-LD is being developed to support this aim with the following assumptions:

- It is based on the agreed MIRRI-IS specifications
- It provides basic syntactic metadata for each data field
- It is based on a standard format (JSON-LD)
- Can be used for data exchange (submission and query) with MIRRI-IS and Dataverse
- Can be extended to incorporate all specifications (microorganisms, plasmids, viruses)

4.3 Dynamic webservices for data sharing

In order to share data with third parties and to allow the seamless integration of data passing the conformity check of the automated validation tool, a webservice system has been implemented within the BioloMICS software. It uses the “OpenAPI Specifications”, formerly known as the Swagger Specification and is available at https://webservices.bio-aware.com/mirri/index.html. This tool enables MIRRI-IS data Programmatic accessibility, along the lines of the FAIR principles. Code samples have been written and made available via GitHub to interested end-users. The webservices are called dynamic because they can be changed and adapted without (or with minor) extra programming to the needs of the administrators and end-users of MIRRI.



BioloMICS services

https://webservices.bio-aware.com/mirri/swagger/v2/swagger.json

BioloMICS Client API

Data Everything about operations on external data provided by BioloMICS Webservice.

GET `/mirri/v2/data/{tableView}/{id}` Get record by id.
POST `/mirri/data/{tableView}` Deposit a new record.
PATCH `/mirri/data/{tableView}/{id}` Partially update an existing record.
PUT `/mirri/data/{tableView}/{id}` Update an existing record.
DELETE `/mirri/data/{tableView}/{id}` Delete an existing record.

Schemas Everything about external metadata provided by BioloMICS Webservice.

GET `/mirri/schemas` Get available schemas containing all table views metadata necessary to perform queries.

SearchData Everything about external data provided by BioloMICS Webservice.

GET `/mirri/v2/search/{tableView}/findByName` Find records by name.
POST `/mirri/v2/search/{tableView}` Search for records using an expression.

SummaryData Everything about external data provided by BioloMICS Webservice.

GET `/mirri/v2/summary/{tableView}/{id}` Get summary record by id.
GET `/mirri/v2/summary/{tableView}/findByName` Find summary records by name.
POST `/mirri/v2/summary/search/{tableView}` Search for summary records using an expression.

Schemas

NameValueEntity
ValueOfFieldC
ValueOfFieldD
ValueOfFieldE
FileInfoEntity

Figure 4-1 – Dynamic webservices based on OpenAPI Specifications formerly known as the Swagger Specification allowing FAIR sharing of data

4.4 Dataverse Implementation: DataMIRRI

4.4.1 Main Features

The DataMIRRI repository is implemented with the Dataverse Harvard solution[2], which is an opensource web application for preserving, sharing, quoting, searching and analyzing research

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[2] https://dataverse.harvard.edu/

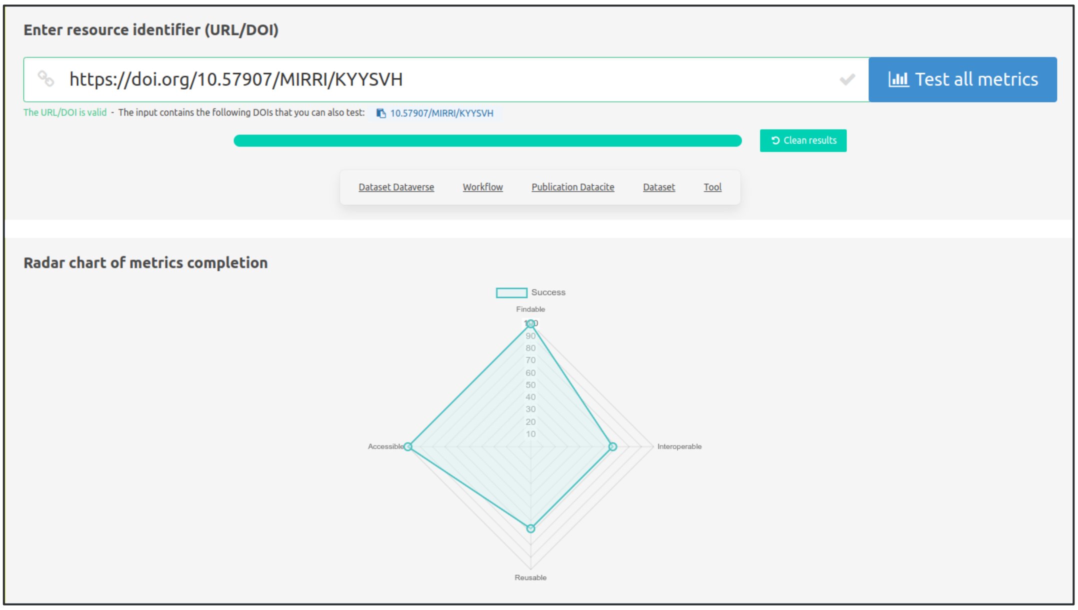
data. It is used by many public institutes internationally, such as the French government's Recherche Data Gouv repository[3].

The MIRRI database and its DataMIRRI dataverse are interconnected. After registration in the MIRRI database, the resources are then declared in the dataverse through the API. The data related to the strain is gathered in a standardized JSON file. The resource is described (mandatory fields of the system) by metadata which are also standardized (BioPortal, INRAE Thesaurus, DataCite Metadata Schema V4). The Dataverse Harvard solution systematically assigns a persistent identifier of the DOI type (INIST/CNRS provider). An internal mechanism allows DOIs and associated metadata to be registered in the DataCite repository which is an international consortium of libraries and services specialized in information sciences aiming at making DOIs available for scientific data.

DataMIRRI has been in production since September 2022. The data can be accessed via web service and directly by computer (machine actionable and readable). DataMIRRI also has a web interface available[4] .

4.4.2 FAIR checker

The Datacite Harvard application, included with DataCite, provides a way to measure how far DataMIRRI meet the FAIR recommendations. Tools are available to check compatibility with the FAIR principles and to assess the level of FAIRness. Here's an example using two of these tools for the strain MIRRI0159440 (DOI: https://doi.org/10.57907/MIRRI/KYYSVH):



Enter resource identifier (URL/DOI)

https://doi.org/10.57907/MIRRI/KYYSVH

The URL/DOI is valid - The input contains the following DOIs that you can also test: 10.57907/MIRRI/KYYSVH

Radar chart of metrics completion

Figure 4-2 – Evaluation by the FAIR-Checker tool (ELIXIR France)

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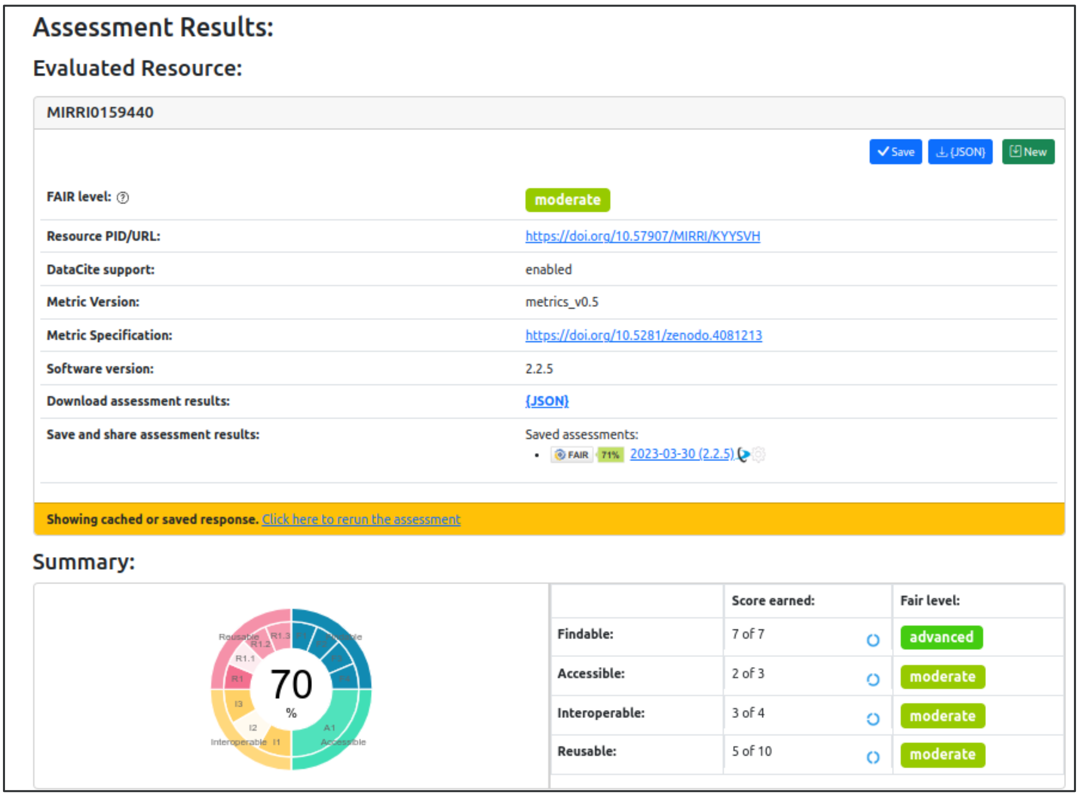
[3] https://recherche.data.gouv.fr/en
[4] http://dataverse.mirri.org:8080/dataverse/datamirri



Assessment Results:

Evaluated Resource:

MIRRI0159440

FAIR level: ⓘ	moderate
Resource PID/URL:	https://doi.org/10.57907/MIRRI/KYYSVH
DataCite support:	enabled
Metric Version:	metrics_v0.5
Metric Specification:	https://doi.org/10.5281/zenodo.4081213
Software version:	2.2.5
Download assessment results:	{JSON}
Save and share assessment results:	Saved assessments: • FAIR 71% 2023-03-30 (2.2.5)

Showing cached or saved response. Click here to rerun the assessment

Summary:

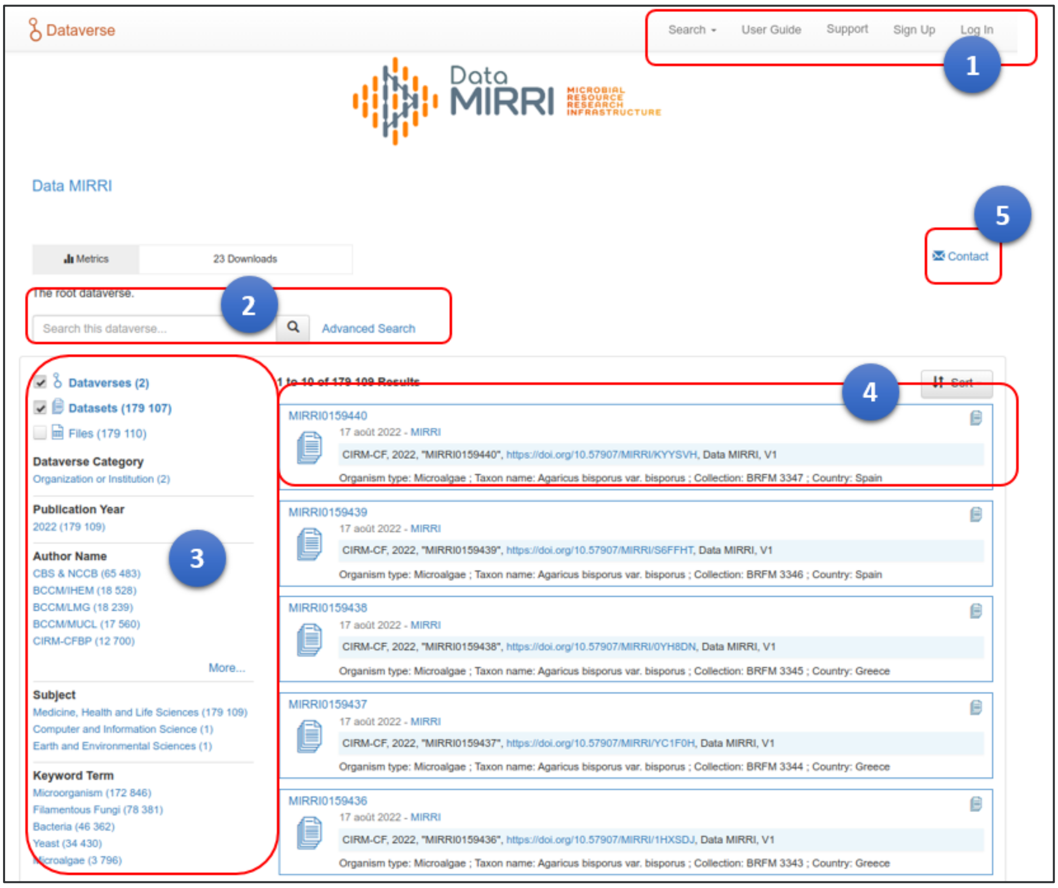
	Score earned:	Fair level:
Findable:	7 of 7	advanced
Accessible:	2 of 3	moderate
Interoperable:	3 of 4	moderate
Reusable:	5 of 10	moderate

Figure 4-3 – Evaluation by the F-UJI tool based on the FAIRsFAIR Data Object Assessment Metrics

In both tools, DataMIRRI's FAIR scores are satisfactory. They are excellent for both the "Findable" and "Accessible" requirements (100%). However, the "Interoperable" (60%-70%) and "Reusable" (50%-60%) aspects are correct but with room for improvement. MIRRI-IS data specifications are registered in FAIRsharing.org, which is largely adopted by LS RIs, but the construction of a thesaurus-type vocabulary or an ontology of the microbial domain declared in a FAIR repository (such as Thesaurus INRAE or BioPortal) would improve these aspects. The data (MIRRI database) will be described with interoperable, long-lasting and community-recognized concepts. Then, the strains deposited in DataMIRRI with their associated metadata can be updated (DataMIRRI allows versioning while keeping the same DOI).

4.4.3 DataMIRRI Web interface

4.4.3.1 HomePage



MIRRI0159440
17 août 2022 - MIRRI
CIRM-CF, 2022, "MIRRI0159440", https://doi.org/10.57907/MIRRI/KYYSVH, Data MIRRI, V1
Organism type: Microalgae ; Taxon name: Agaricus bisporus var. bisporus ; Collection: BRFM 3347 ; Country: Spain

MIRRI0159439
17 août 2022 - MIRRI
CIRM-CF, 2022, "MIRRI0159439", https://doi.org/10.57907/MIRRI/S6FFHT, Data MIRRI, V1
Organism type: Microalgae ; Taxon name: Agaricus bisporus var. bisporus ; Collection: BRFM 3346 ; Country: Spain

MIRRI0159438
17 août 2022 - MIRRI
CIRM-CF, 2022, "MIRRI0159438", https://doi.org/10.57907/MIRRI/0YH8DN, Data MIRRI, V1
Organism type: Microalgae ; Taxon name: Agaricus bisporus var. bisporus ; Collection: BRFM 3345 ; Country: Greece

MIRRI0159437
17 août 2022 - MIRRI
CIRM-CF, 2022, "MIRRI0159437", https://doi.org/10.57907/MIRRI/YC1F0H, Data MIRRI, V1
Organism type: Microalgae ; Taxon name: Agaricus bisporus var. bisporus ; Collection: BRFM 3344 ; Country: Greece

MIRRI0159436
17 août 2022 - MIRRI
CIRM-CF, 2022, "MIRRI0159436", https://doi.org/10.57907/MIRRI/1HXSDJ, Data MIRRI, V1
Organism type: Microalgae ; Taxon name: Agaricus bisporus var. bisporus ; Collection: BRFM 3343 ; Country: Greece

Figure 4-4 – DataMIRRI Web Interface home page

The main areas/elements in the interface home page are:

1. Identification (advanced user and administrator), help and support

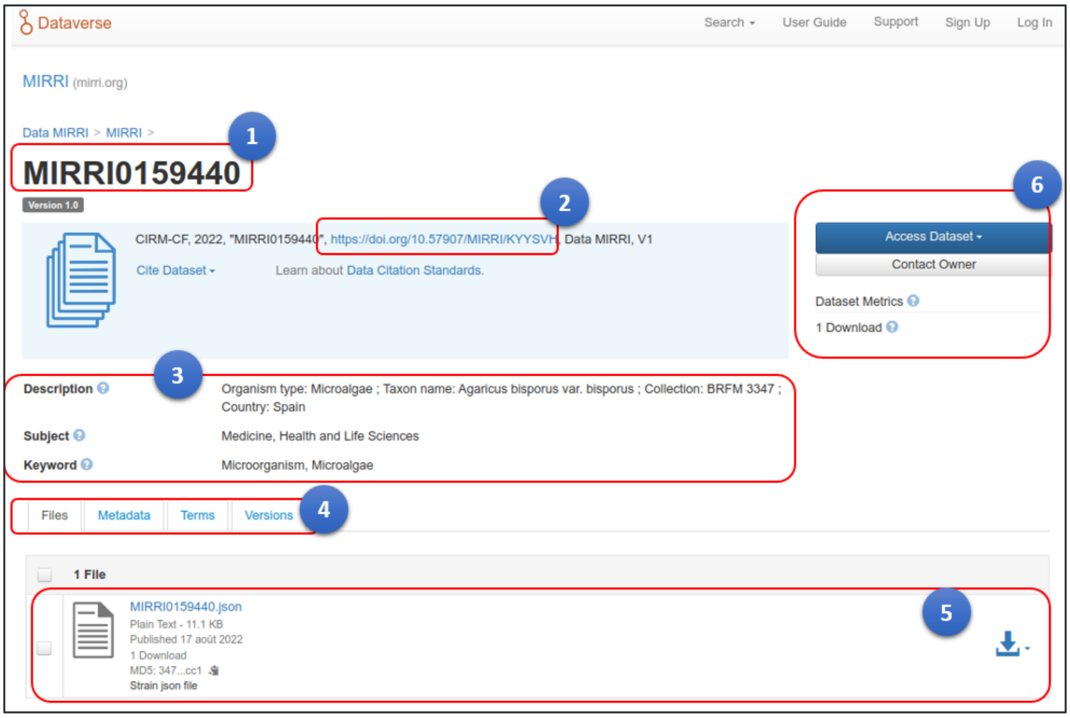
2. Keyword search area

3. Display filters

4. Strain

5. Contact form (administrator)

4.4.3.1 Strain Sheet



MIRRI0159440

CIRM-CF, 2022, "MIRRI0159440", https://doi.org/10.57907/MIRRI/KYYSVH, Data MIRRI, V1

Learn about Data Citation Standards.

Dataset Metrics

1 Download

Description	Organism type: Microalgae ; Taxon name: Agaricus bisporus var. bisporus ; Collection: BRFM 3347 ; Country: Spain
Subject	Medicine, Health and Life Sciences
Keyword	Microorganism, Microalgae

1 File

MIRRI0159440.json
Plain Text - 11.1 KB
Published 17 août 2022
1 Download
MD5: 347...cc1
Strain json file

Figure 4-5 – DataMIRRI Web Interface strain sheet

The main areas/elements in the interface for a strain sheet are:

1. MIRRI identifier of the strain

2. DOI identifier of the strain

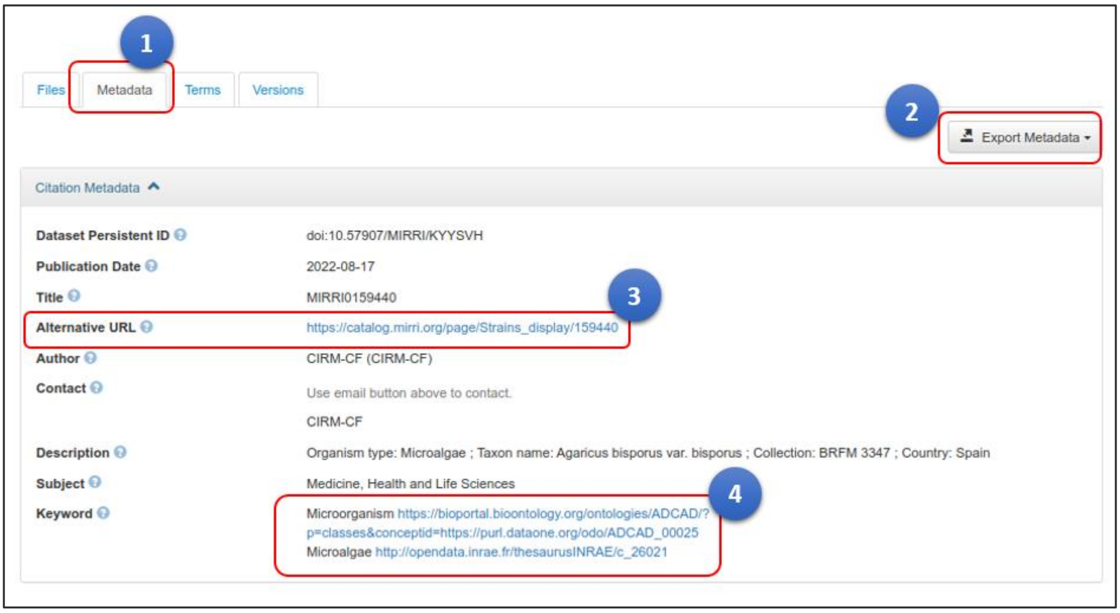
3. Description and general information

4. Tabs for dataset or file repository, metadata description, licence (CC-BY by default) and versions.

5. Tool for downloading the metadata of the strain with display option

6. Tool for downloading the metadata as a file in ZIP format and information on viewing and downloading

4.4.3.1 Strain Sheet Metadata Tab



Dataset Persistent ID	doi:10.57907/MIRRI/KYYSVH
Publication Date	2022-08-17
Title	MIRRI0159440
Alternative URL	https://catalog.mirri.org/page/Strains_display/159440
Author	CIRM-CF (CIRM-CF)
Contact	Use email button above to contact. CIRM-CF
Description	Organism type: Microalgae ; Taxon name: Agaricus bisporus var. bisporus ; Collection: BRFM 3347 ; Country: Spain
Subject	Medicine, Health and Life Sciences
Keyword	Microorganism https://bioportal.bioontology.org/ontologies/ADCAD/?p=classes&conceptid=https://purl.dataone.org/odo/ADCAD_00025 Microalgae http://opendata.inrae.fr/thesaurusINRAE/c_26021

Figure 4-6 – DataMIRRI Web Interface (metadata tab)

The main areas/elements in the interface for a strain Metadata are:

1. Tab selector.

2. Tool for downloading metadata in standardised formats

3. URL link to the MIRRI catalogue’s strain page

4. Description of the strain through keywords from ontologies such as BioPortal or INRAE thesaurus

4.5 Workflow for data interchange between CCs and MIRRI-IS

The main interaction between CCs and MIRRI-IS consists in the new strains data insertion and current strains data update. BioAware updates the data from customer CCs using internal tools.To allow strains data insertion and update from CCs that do not use the BioloMICS, two different methods are available:

- BioloMICS desktop version data import/update. In this case, data must be provided to the system according to the file format required by the software.

- BioloMICS APIs + MIRRI Tools. The strains data are provided by the CC according to the MIRRI specifications in the defined excel file. The MIRRI Tools are used to get data from the excel file and insert strains data into the MIRRI-IS.

Before the CCs excel files are accepted for data import into the MIRRI-IS, these files must pass the MIRRI validation tool, that checks if the excel file includes the required sheets and if data fields are formatted according to the MIRRI-IS data standard specifications. When the excel file does not pass the validation, the system provides a detailed document containing the errors found. This report must be used by the CC to correct the data before sending the excel file again for validation.

For data update, in the case of the strains that already exist in the MIRRI-IS, CCs can send only data from strains that changed since last data export or send all strains data again. In the second case, changes must be checked to decide if the strain data must be updated in the MIRRI-IS. Each strain data must first be retrieved from the MIRRI-IS through the APIs, then compared with the data provided by the CC and finally re-submitted to the MIRRI-IS if different. This is a time-consuming process that requires getting all strains data for the CC from the MIRRI-IS.

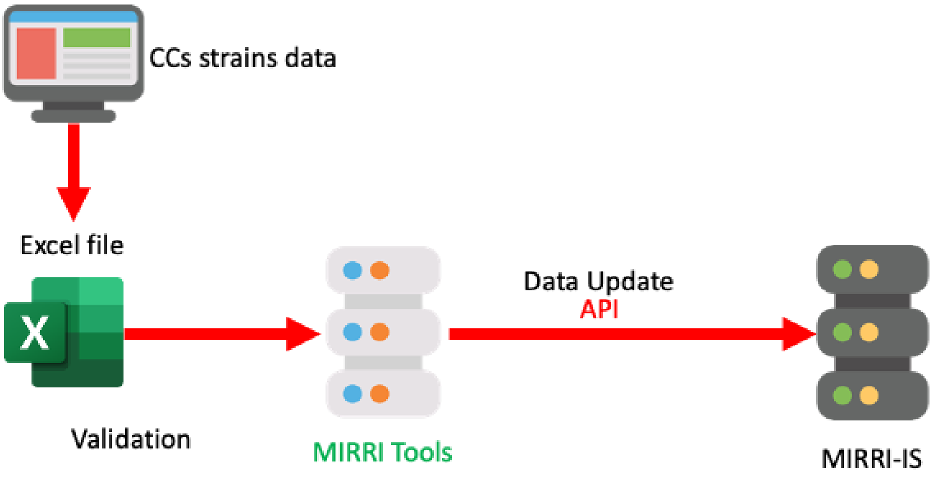


Figure 4-7 – Schema of the MIRRI-IS update

5. Conclusions and Future Work

5 Conclusions and Future Work

This report is a summary of Deliverable 6.3 included in the European Commission management platform. Deliverable 6.3 is a set of software modules and associated data, with the respective back-end applications, altogether constituting the CWE platform proposed for implementation under the project IS_MIRRI21.

The current version of the CWE is according to the specifications, exposing the complete set of features and functionalities specified by the MIRRI partners and stakeholders, both in the scope of IS_MIRRI21 project and during the MIRRI preparatory phase.

The different modules in the five gates are fully operative and prepared for future improvements. Despite the achievement of the actual results in terms of CWE implementation, as any other online platform, updates and next developments can/must be addressed in the future. Further to the updates regarding the evolution of the technologies in use, for example, for the Gate for Microbial resources, Data and Services, the MIRRI-IS must be improved with more data and new features, providing the appropriate interfaces for accessibility and interoperability with other platforms and reuse of MIRRI data. Part of these updates resulted from feedback received from the CCs. Also, for this gate, the additional tools for data validation by the CCs (for virus, plasmids, etc) must be published and made available to all. The work of the ICT team for data Fairification (exploring synergies with the EOSC-Life project) will also be continued. In this regard, the aspects of “interoperability” and “reusability” of MIRRI Data must be addressed in order to improve and raise the respective scores (as analysed by reputed tools), for example, but not exclusively, by investing in the creation of a thesaurus-type vocabulary or an ontology of the microbial domain declared in a FAIR repository.

The information on MIRRI services can also be complemented and updated in the future, for example delivering the catalogue based on a database, that implies deeper work in terms of specification and uniformization among the MIRRI partners.

The tools available for the collaboration and Experts may be extended by adding new modules and functionalities, as necessary for specific direct support access and provision by MIRRI experts, complying with the MIRRI Business model in practice.

With respect to the Gate for Microbial resources, Data and Services, the MIRRI-IS provides access to all the strains data in a database and, therefore, allowing to develop several tools that will improve the utility of the MIRRI-IS data. Prospects for the MIRRI-IS include:

i) Development of a system to connect directly the CCs databases with the MIRRI-IS using the so called “MIRRI Tools”. This system will not require the export of the CCs strains data in excel format and will allow a more efficient way of keeping track on data changes.

ii) Improving the strains data quality in CCs. This could be achieved by running intensive comparison in certain strain fields like “other collections” to be able to get the equivalences of a certain strain in the maximum number of culture collections possible. This will also permit to define an “abstract strain entity” including all the equivalent strains in the different CCs. This abstract strain entity could facilitate to establish relationships between “equivalent” strains in MIRRI-IS similarly to the WDCM references for strains appearing in the ISO norms.

iii) Harmonizing the information about the strains culture media using publicly available databases.

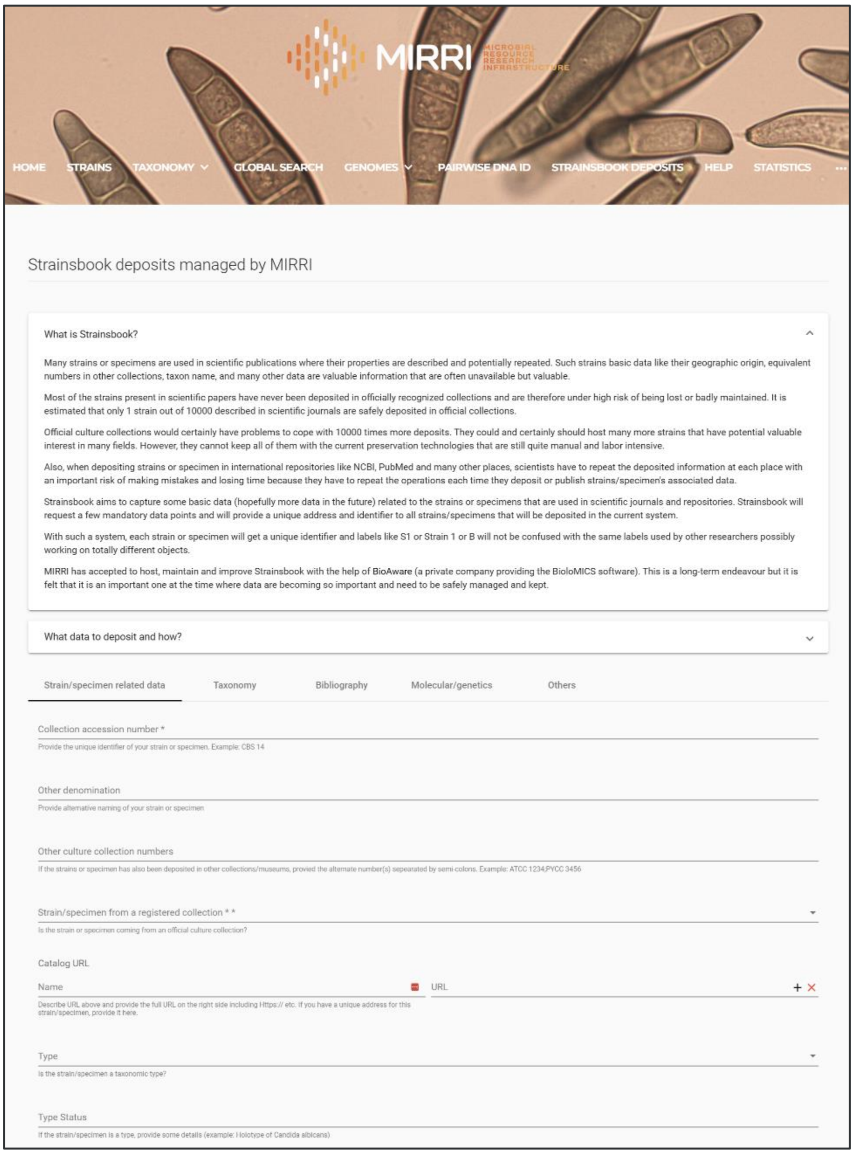
The Training and education gate may have in the future a proper Learning Management System (LMS) for future training courses organized and ministered by MIRRI-ERIC. This implies working to find an uniformization agreement among the MIRRI partners to use this common platform on behalf of their actual multiple and difficult to interoperate LMS platforms.

External strains deposit tool (StrainsBook)

The development of a tool meant for the deposit of strain data from strains that are not present in culture collections is something that has been discussed within MIRRI as a possibility for expanding the utility of the CWE. This tool, dubbed ‘StrainsBook’, would facilitate the integration of basic data related to strains or specimens that are used in scientific journals and repositories, data which can be re-used for a future deposit of the corresponding strain in an international repository. It may also contribute for the conservation of data from strains which are difficult or impossible to preserve with the CCs’ current technological capabilities.

With StrainsBook, each strain or specimen will be tagged with a unique identifier, therefore eliminating any possibility of confusion when different researchers use similar labels to refer to the objects of their study. The data requested by StrainsBook before such a tag can be provided would include basic information such as taxon name, geographic origin or existing identifiers in other collections. In the future, more data could be requested and added.

This tool can be implemented in the MIRRI CWE or deployed in a specific portal of access to the MIRRI tools, for now available under https://tools.mirri.org.



Strainsbook deposits managed by MIRRI

What is Strainsbook?

Many strains or specimens are used in scientific publications where their properties are described and potentially repeated. Such strains basic data like their geographic origin, equivalent numbers in other collections, taxon name, and many other data are valuable information that are often unavailable but valuable.

Most of the strains present in scientific papers have never been deposited in officially recognized collections and are therefore under high risk of being lost or badly maintained. It is estimated that only 1 strain out of 10000 described in scientific journals are safely deposited in official collections.

Official culture collections would certainly have problems to cope with 10000 times more deposits. They could and certainly should host many more strains that have potential valuable interest in many fields. However, they cannot keep all of them with the current preservation technologies that are still quite manual and labor intensive.

Also, when depositing strains or specimen in international repositories like NCBI, PubMed and many other places, scientists have to repeat the deposited information at each place with an important risk of making mistakes and losing time because they have to repeat the operations each time they deposit or publish strains/specimen's associated data.

Strainsbook aims to capture some basic data (hopefully more data in the future) related to the strains or specimens that are used in scientific journals and repositories. Strainsbook will request a few mandatory data points and will provide a unique address and identifier to all strains/specimens that will be deposited in the current system.

With such a system, each strain or specimen will get a unique identifier and labels like S1 or Strain 1 or B will not be confused with the same labels used by other researchers possibly working on totally different objects.

MIRRI has accepted to host, maintain and improve Strainsbook with the help of BioAware (a private company providing the BioloMICS software). This is a long-term endeavour but it is felt that it is an important one at the time where data are becoming so important and need to be safely managed and kept.

What data to deposit and how?

Strain/specimen related data | Taxonomy | Bibliography | Molecular/genetics | Others

Collection accession number *
Provide the unique identifier of your strain or specimen. Example: CBS 14

Other denomination
Provide alternative naming of your strain or specimen

Other culture collection numbers
If the strains or specimen has also been deposited in other collections/museums, provied the alternate number(s) sepearated by semi-colons. Example: ATCC 1234;PYCC 3456

Strain/specimen from a registered collection * *
Is the strain or specimen coming from an official culture collection?

Catalog URL
Name
URL
Describe URL above and provide the full URL on the right side including Https:// etc. If you have a unique address for this strain/specimen, provide it here.

Type
Is the strain/specimen a taxonomic type?

Type Status
If the strain/specimen is a type, provide some details (example: Holotype of Candida albicans)

Figure 5-1 – Preliminary interface for Strains/specimens deposit system for data not associated with culture collections linked to MIRRI strains (StrainsBook)

For all of these developments and implementations, deliverable *D6.1- Report with the design and technical requirements, characterization and knowledge acquisition of MIRRI* must be a reference, in combination with the users and partners feedback and in particular those reported in deliverable *D6.4 - Report with the usability tests' results and user feedback,* regarding the tests performed for assessing the CWE conformance to the requirements and needs of MIRRI stakeholders. For sure, now that the MIRRI-ERIC is formally established, the works and discussions among the members will lead to hints and clues for many other needs and future CWE developments and extensions, to happen beyond the IS_MIRRI21 project time-frame.

Annex I- Source of database entries and references

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