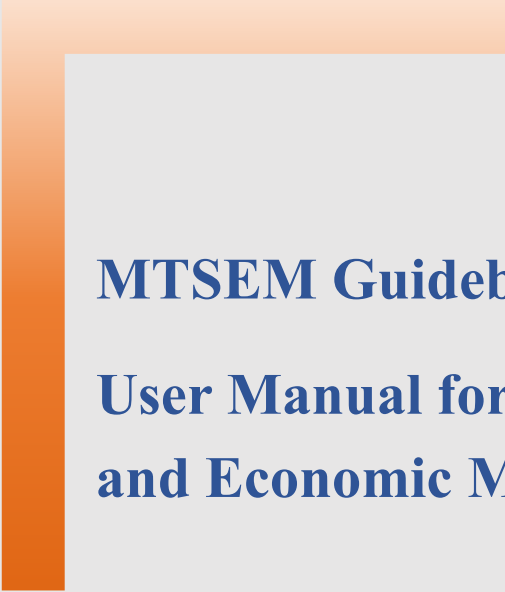




MTSEM Guidebook

User Manual for Macrofungal Taxonomic System and Economic Mushrooms (MTSEM)

National Microbiology Data Center



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What is MTSEM?

MTSEM (<https://nmcdc.cn/macrotungi/>) is a macrofungi-centered database that integrates taxonomic, genomic, and economic trait data across Dikarya. It currently contains information for 9,943 fungal genera, 142,349 species, 20,633 genomes, 101,489 specimens, and 213,138 strains, including 1,982 macrofungal genera and 51,899 macrofungal species. The inclusion of non-macrofungal taxa establishes a comprehensive taxonomic backbone that facilitates nomenclatural consistency and comparative analyses involving macrofungi. MTSEM provides an integrated platform for accessing taxonomic hierarchies, genome data, specimen and strain records, publications, and patents, while regular synchronization with external resources ensures nomenclatural consistency and continuous updates. Existing fungal resources serve complementary purposes. Fungal Names, Index Fungorum, and MycoBank primarily provide nomenclatural and taxonomic information; UNITE serves as the principal reference database for ITS-based molecular identification and species hypotheses; GBIF aggregates global biodiversity occurrence records and specimen information; and MycoCosm provides fungal genome assemblies, annotations, and comparative genomic resources. Rather than replacing these specialized resources, MTSEM integrates hierarchical taxonomy, species-level information, genome data, specimen and strain records, economic trait annotations (edible, medicinal, and poisonous), publications, patents, and scientometric analyses within a unified macrofungi-centered framework. This enables seamless exploration of diverse data types through a consistent taxonomic backbone while maintaining links to authoritative external resources.

Database Structure

MTSEM adopts a technical framework built with Spring Boot backend, Vue2 + Element-UI frontend, MySQL for metadata storage and Neo4j for bibliometric knowledge retrieval. The current version mainly aggregates publicly sourced multi-dimensional fungal resources. Large-scale unified de novo gene prediction and cross-species standardized genome reannotation pipelines are not implemented in the current release.

Data Sources

All integrated datasets are curated from authoritative public fungal resources. For taxonomic classification standards, Ascomycota follows the 2024 Outline of Fungi and fungus-like taxa, and Basidiomycota adopts the 2024 comprehensive fungal classification system. Lichenized fungi are excluded from the macrofungal classification system; any genera containing both macrofungal and microfungal species are categorized as macrofungal genera. All integrated data undergo taxonomic harmonization to map synonyms to accepted names via Fungal Names tools (<https://nmcdc.cn/fungalnames/standardization>), and entries with conflicting taxonomic status are manually verified against recent literature. A comprehensive inventory of herbaria and culture collections information housing the species in this study was compiled from the CCINFO

(<https://ccinfo.wdcm.org/>) and Fungal Names database (<https://nmdc.cn/fungalnames/>). Genomic metadata were sourced from NCBI (<https://www.ncbi.nlm.nih.gov/>) and JGI (<https://jgi.doe.gov/>), with duplicate entries eliminated in data processing. Certain JGI records only contain basic assembly metadata subject to release limitations. Economic trait labels covering edibility, medicinal value and toxicity of fungal taxa are manually verified based on peer-reviewed mycological publications. Bibliometric data integrated for visualization functions are retrieved and organized from the ABC database (<https://abc.wdcm.org/>) via structured graph queries.

Functional Modules Introductions

The top fixed navigation bar contains six unified entries: Home, Browse, Search, Visualization, Download, Help. All non-functional static auxiliary pages are consolidated under the Help entry to avoid redundant navigation items.

Home Module

The homepage serves as the unified entry point for all platform functions, aggregating resource overview statistics and quick access portals to all core sub-datasets, with direct jump links to six core navigation modules: Home, Browse, Search, Visualization, Download, and Help (1). Multiple auxiliary functional panels are embedded on the homepage to support one-stop data browsing and analysis. A top quick search bar equipped with real-time standardized keyword prompts streamlines precise multi-type data retrieval and avoids spelling or taxonomic revision errors (2). Visual statistical cards intuitively exhibit the overall scale of core resources, including valid species, living strains, type specimens, fungal genomes and specimen/germplasm preservation institutions (3). The Taxonomy Overview table delivers full hierarchical fungal classification spanning kingdom to species, with clickable taxon links and grouped statistical indicators for macrofungi, edible, medicinal and poisonous mushrooms (4). A rotating macrofungal image gallery enables visual browsing of representative fruiting-body species (5), and an embedded bibliometric knowledge graph maps collaboration relationships between well-studied macrofungal genera and research authors, supporting exploration of research hotspots and potential academic partners (6). External Resources provides curated hyperlinks to authoritative external microbial databases (7) and Citation module at the bottom of website supplies standardized citation templates for formal academic referencing of MTSEM (8).

This database system integrates core information on the taxonomy, genomic resources, specimens, strains, and research frontiers of macrofungi. It further provides specialized modules for edible, medicinal, and poisonous mushrooms, offering comprehensive and continuously updated data support for research, education, and industry.

Example: Agaricus | Ganoderma | Amanita



MTSE

Rank	Total	Macrofungi	Edible Fungi	Medicinal Fungi	Poisonous Fungi
Kingdom	1	1	1	1	1
Phylum	2	2	2	2	2
Class	44	15	10	9	5
Order	263	49	30	24	18
Family	1,013	247	117	99	71
Genus	9,943	1,982	345	203	168
Species	142,349	51,899	1,791	632	761

Category	Species	Strains
All Macrofungi	51,899	40,073
Edible Fungi	1,751	10,310
Medicinal Fungi	532	11,009
Poisonous Fungi	761	1,723

The image displays a grid of six database icons, each with a title and a brief description:

- Fungal Names**: Fungal Names, a global data repository of fungal taxonomy, is established by the Institute of Microbiology, Chinese Academy of Sciences.
- reStrain**: This catalogue was produced to enable broader and easier access to the reference strains listed by the ISO TC 34 SC 9...
- gctype**: Global Catalogue of Microorganisms (GCM) s' led type strain sequencing project is an international coordinated effort to...
- Outline Of Fungi**: Outlineof fungi.org is a website dedicated to the taxonomy and classification of the Fungi and is prepared and updated...
- CCINFO**: Culture Collections Information Worldwide is a database management system for culture collections in the world. It...
- ABC**: Analyzer of Bio-resource Citations(ABC) is a platform that could support the researchers on checking the citations...

If you want to use MTESEM in your studies, please cite the following papers:

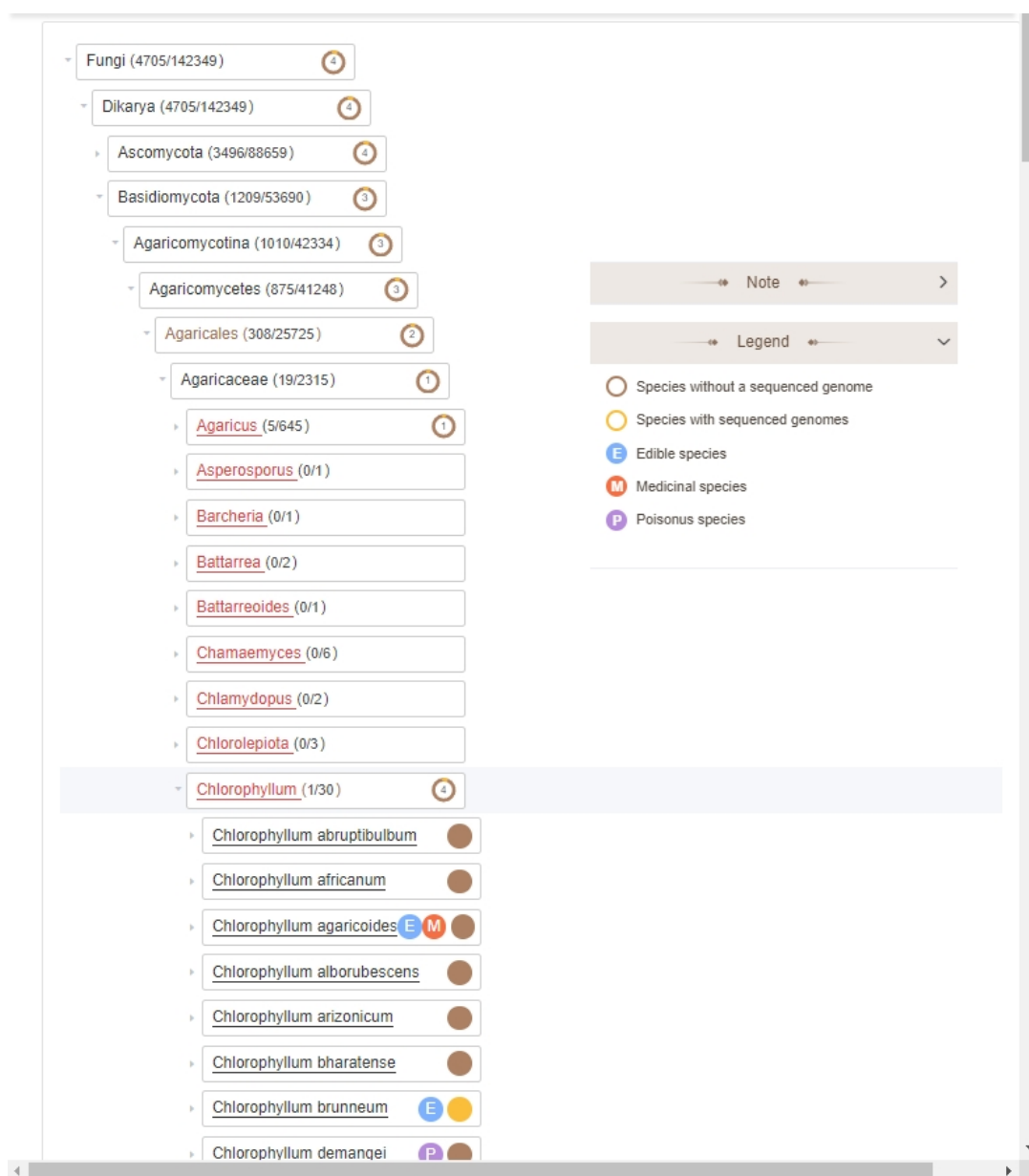
Zhao R, Li J et al (2017) A six-gene phylogenetic overview of Basidiomycota and allied phyla with estimated divergence times of higher taxa and a phylogenomics perspective. Fungal Diversity 84(1): 43–74 Download	Ho M-Q et al (2019) Notes, outline and divergence times of Basidiomycota. Fungal diversity 19(1): 105–367 Download
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Browse Module

The **Browse** module is the hierarchical taxonomic browsing portal built on the complete Ascomycota and Basidiomycota classification framework, supporting full-level browsing from kingdom down to species.

Taxonomic nodes carry multi-dimensional annotation tags. Each genus is marked whether it belongs to macrofungi by color; the page displays species richness and genomic sequencing proportion at each rank, paired with intuitive pie charts; each taxon retains nomenclatural status information referenced from Fungal Names. Economic trait labels are attached to every species record to mark edible, medicinal or toxic mushroom attributes.

Interactive operation: Users can expand subordinate taxa at each node, or click genus/species labels to jump to independent detail pages for in-depth data review. This module fits the demand for systematic taxonomic sorting and macrofungal group screening.



Search Module

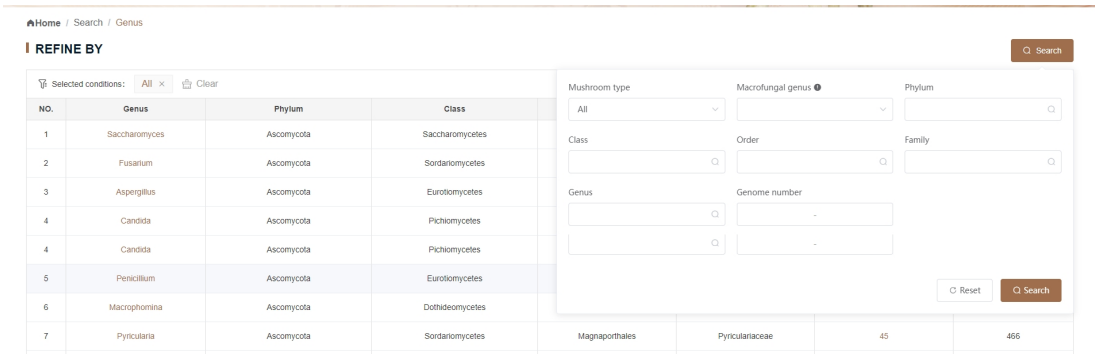
The **Search** module integrates six independent data subpages corresponding to MTSEM's core datasets: **Genus**, **Species**, **Specimen**, **Strain**, **Culture Collection**, and **Herbarium**. Each subpage provides tailored multi-condition filtering panels under the "REFINE BY" section, supporting flexible combined advanced retrieval customized to the characteristics of each data type. All six subpages share unified interactive logic: users input multiple filter terms simultaneously, click the Search button to output matched table records, and use the Reset button to clear all selected conditions. Every hyperlinked field including Genus, Species, Strain, Specimen, Culture Collection and Herbarium within the result tables is clickable; clicking any

entry will redirect users to its dedicated detail page to view complete supporting metadata.



Genus page

The filtering panel supports joint screening by mushroom type, macrofungal genus tag, full taxonomic ranks (Phylum, Class, Order, Family, Genus), and genome quantity. Users can filter genera with available genomic assemblies and quickly isolate macrofungal groups of economic value.



Species page

Retrieval dimensions cover mushroom type, macrofungal species tag, complete taxonomic hierarchy, species/genus keywords, and genome number thresholds, enabling targeted screening of species with sequenced genomes, edible, medicinal or toxic attributes.

Home / Search / Species

REFINE BY

Selected conditions: All x Clear

NO.	Species name	Genome number	Phylum
1	<i>Saccharomyces cerevisiae</i>	1673	Ascomycota
2	<i>Fusarium oxysporum</i>	821	Ascomycota
3	<i>Candida auris</i>	504	Ascomycota
4	<i>Macrophomina phaseolina</i>	466	Ascomycota
5	<i>Pyricularia oryzae</i>	445	Ascomycota
6	<i>Aspergillus neovulvatus</i>	364	Ascomycota
7	<i>Aspergillus flavus</i>	323	Ascomycota
8	<i>Fusarium asiaticum</i>	256	Ascomycota
9	<i>Beauveria bassiana</i>	216	Ascomycota
10	<i>Cryptococcus neoformans</i>	183	Basidiomycota

Mushroom type: All
 Macrofungal species:
 Phylum:
 Class:
 Order:
 Family:
 Species:
 Genus:
 Genome number:
 Reset Search

Total 142349 < 1 2 3 4 5 6 ... 14235 > Go to 1

Specimen page

This page focuses on fungal voucher germplasm metadata, with filters for herbarium code, herbarium full name, collection country, type specimen accession number and species name, facilitating quick lookup of type specimens from global preservation institutions.

REFINE BY

Selected conditions: All x Clear

NO.	Type number	Species name	Herbarium code
1	ACAD 11699	<i>Inocybe erythospila</i>	ACAD
2	ACAD 14897	<i>Sarcodon dissimulans</i>	ACAD
3	ACAD, Stuntz ST211492	<i>Inocybe heterochrominea</i>	ACAD
4	ACAD 10539	<i>Inocybe pernuoida</i>	ACAD
5	ACAD 11651	<i>Inocybe semifulva</i>	ACAD
6	AD-C 3544	<i>Melanoleuca cielandi</i>	AD
7	ADW 15885	<i>Mycoclelandia arenacea</i>	ADW

Herbarium code:
 Herbarium name:
 Country:
 Type number:
 Species:
 Reset Search

State Herbarium of South Australia State Herbarium of South Australia Australia
 Herbarium University of Adelaide Australia

Strain page

Filters include mushroom type, species/genus keywords and strain accession numbers, allowing users to retrieve viable living strain records of target macrofungal species with economic application value.

REFINE BY

Selected conditions: All x Clear

NO.	Strain number	Species name
1	BCRC MU30460	<i>Agaricus sinapiacomyces</i>
2	PNCM 3003	<i>Agaricus bisporus</i>
3	PNCM 3004	<i>Agaricus bisporus</i>
4	PNCM 3005	<i>Agaricus bisporus</i>
5	PNCM 3081	<i>Agaricus bisporus</i>

Mushroom type: All
 Species:
 Genus:
 Strain number:
 Reset Search

PNCM Philippines

Culture Collection page

Dedicated for live germplasm preservation institutions, it supports filtering by collection acronym and affiliated country to query global fungal strain resource banks.

REFINE BY

Acronym

Country

Reset

Search

NO.	Acronym	Country	Continent
1	LIPIMC	Indonesia	Asia
2	KCTC	Korea	Asia
3	MCC-MNH	Philippines	Asia
4	PNOM	Philippines	Asia
5	ITDI	Philippines	Asia

Herbarium page

For dry fungal specimen repositories, retrieval conditions contain herbarium standard code, full institute name and country, to browse and screen worldwide fungal specimen archives.

REFINE BY

Herbarium code

Herbarium name

Country

Reset

Search

NO.	Herbarium code	Herbarium full name	Herbarium name
1	LPS	Universidad Nacional de La Plata	Herbario
2	TUMH	Tottori University	Herbarium
3	IFP	Institute of Applied Ecology, Academia Sinica	Herbarium
4	AAU	Aarhus University	Herbarium
5	AAUF	Anhui Agricultural University	Dendrological Herbarium

Visualization Module

The Visualization module provides interactive bibliometric and genome-sequencing trends, and network graphs for each macrofungal genus and species with available data, serving unique research trend analysis tools exclusive to MTSEM. It provides two independent tab panels: Genus and Species, which separately display sorted lists of macrofungal genera and species with genomic or bibliometric records. A dedicated multi-condition filtering panel can be opened by clicking the Search button at the top right of the page, supporting customized screening of target taxa. All genus and species names in the table are hyperlinked, clicking any entry will jump to its corresponding genus or species detail visualization page. The page also includes two donut charts at the bottom to present quantitative statistics of genome-sequenced macrofungal genera and species, showing the proportion of macrofungal taxa with genomic assemblies against all macrofungal taxa recorded in MTSEM.

Visualization for Macrofungi

Q Search

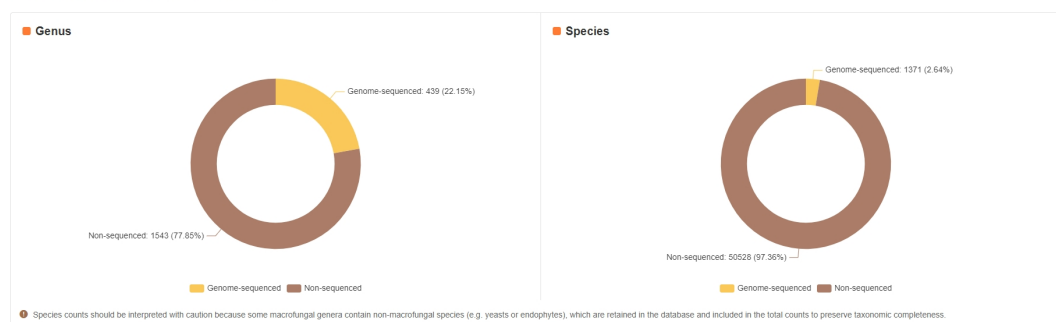
Selected conditions: All x Yes Clear

NO.	Genus	Phylum	Class	Order	Family	Number of species	Genome number
1	Beauveria	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	49	335
2	Trichoderma	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	491	313
3	Psilocybe	Basidiomycota	Agaricomycetes	Agaricales	Hymenogastraceae	300	145
4	Epichloe	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	50	99
5	Claviceps	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	82	89
6	Paecilomyces	Ascomycota	Eurotiomycetes	Eurotiales	Thermosaccaceae	69	80
7	Cordyceps	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	210	78
8	Morchella	Ascomycota	Pezizomycetes	Pezizales	Morchellaceae	101	77
9	Suillus	Basidiomycota	Agaricomycetes	Boletales	Suillaceae	113	70
10	Boletus	Basidiomycota	Agaricomycetes	Boletales	Boletaceae	257	65

Note: Macrofungal genera are defined as genera with at least one macrofungal species.

Total 1329 < 1 2 3 4 5 6 ... 133 > Go to 1

Statistic of Genome-sequenced Macrofungi



Genus-level visualization. When switching to the Genus tab, the data table displays genus name, phylum, class, order, family, total species count within the genus and total genome number. The corresponding filter panel contains screening dimensions including Mushroom type, Phylum, Class, Order, Family, Genus keyword and Genome number threshold. filtering panel supports joint screening by mushroom type, full taxonomic ranks, and genome quantity. Users can filter genera with available genomic assemblies and quickly isolate macrofungal groups of economic value.

Visualization for Macrofungi

Q Search

Selected conditions: All x Yes Clear

NO.	Genus	Phylum	Class	Order	Family	Number of species	Genome number
1	Beauveria	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	210	78
2	Trichoderma	Ascomycota	Sordariomycetes	Hypocreales	Hypocreaceae	491	313
3	Psilocybe	Basidiomycota	Agaricomycetes	Agaricales	Hymenogastraceae	300	145
4	Epichloe	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	50	99
5	Claviceps	Ascomycota	Sordariomycetes	Hypocreales	Clavicipitaceae	82	89
6	Paecilomyces	Ascomycota	Eurotiomycetes	Eurotiales	Thermosaccaceae	69	80
7	Cordyceps	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	210	78

Species-level visualization. When switching to the Species tab, the table lists species name, total genome number and taxonomic lineage information covering phylum, class, order and family. Its matching filter panel supports filtering by Phylum, Class, Order, Family, Species keyword, Genus keyword and Genome number range.

Home / Visualization

Genus Species

Visualization for Macrofungi

Selected conditions: All x Yes Clear

NO.	Species name	Genome number	Phylum	
1	<i>Beauveria bassiana</i>	216	Ascomycota	Sort
2	<i>Psilocybe subaeruginosa</i>	89	Basidiomycota	Agari
3	<i>Beauveria pseudobassiana</i>	88	Ascomycota	Sort
4	<i>Schizophyllum commune</i>	54	Basidiomycota	Agari
5	<i>Claviceps purpurea</i>	54	Ascomycota	Sort
6	<i>Rhizoctonia solani</i>	49	Basidiomycota	Agari
7	<i>Psilocybe cubensis</i>	41	Basidiomycota	Agaricomycetes

Mushroom type: All

Macrofungal species: Yes

Phylum:

Class:

Order:

Family:

Species:

Genus:

Genome number:

Reset Search

After configuring any combination of filter parameters, users can click the Search button to load matched table entries; the Reset button clears all selected filter conditions in one step, and the Clear button on the top of the table panel removes single selected screening tags.

Download Module

An independent Download module is accessible directly from the main navigation bar, delivering standardized open datasets derived from the full curated taxonomic and genomic metadata of MTSEM for offline analysis and secondary data mining. The Download module provides outline of macrofungi and comprehensive metadata files for all publicly available and restricted-access genomes housed in the database. Users can download standardized metadata tables to facilitate custom batch screening of target species and their sequencing status. The downloadable metadata includes essential genome attributes, taxonomic classifications, and data availability statuses, supporting downstream comparative analyses, large-scale data mining, and integration with external bioinformatics workflows. The standardized downloadable datasets are available on the page:

Outline of macrofungi: Complete hierarchical taxonomic records of macrofungi built upon the unified Ascomycota and Basidiomycota classification system in this study.

Taxonomy of Genome-Sequenced Dikarya Fungi: Unified kingdom-to-species classification for all sequenced fungal taxa.

Dikarya fungal genomes metadata: Full curated assembly metadata for all fungal genomes, including sequencing parameters and NCBI accession information.

Home / Download

Download

Resources	Download	Records	Size	Last Modified Date
Outline of macrofungi	MTSEM_Outline_of_macrofungi.csv	1,982	44.4 KB	2026-06-24
Dikarya fungal genomes metadata	MTSEM_Fungal_genome_metadata.csv	20,633	3.5 MB	2026-06-24
Taxonomy of Genome-Sequenced Dikarya Fungi	MTSEM_Fungal_taxonomy.csv	4,075	546.0 KB	2026-06-24

Citation

If you want to use MTSEM in your studies, please cite the following papers:

Zhao R-L et al (2017) A six-gene phylogenetic overview of Basidiomycota and allied phyla with estimated divergence times of higher taxa and a phyloproteomics perspective.

Fungal Divers 84(1):43-74.

[Download](#)

He M-Q et al (2019) Notes, outline and divergence times of Basidiomycota.

Fungal diversity, 99(1), 105-367.

[Download](#)

Help Module

All static auxiliary pages are integrated into the single Help entry, including six sub-pages:

About: Full introduction of platform development background, positioning and core construction goals.

Release History: Version update logs recording revision time and updated content of each release.

Guidance: Step-by-step operation tutorials for Home, Browse, Search, Visualization, Download, and Help modules.

Expert Team: Introduction of international advisory expert panel covering multiple countries.

Copyright Statement: Platform data usage specifications and intellectual property declaration rules.

Contact Us: Official communication channels for data use, technical consultation and platform feedback.

MTSEM Macrofungal Taxonomic System and Economic Mushrooms

Home Browse Search Visualization Download Help

Macrofungal Taxonomic System and Economic Mushrooms

This database system integrates core information on the taxonomy, genomic resources, strains, and research frontiers of macrofungi. It further provides specialized modules for medicinal, and poisonous mushrooms, offering comprehensive and continuously updated data support for research, education, and industry.

- About
- Release History
- Guidance
- Expert Team
- Copyright Statement
- Contact Us

Detail Page

All core data entries (Genus, Species, Strain, Specimen, Culture Collection, Herbarium, Visualization) are equipped with independent dedicated detail pages, aggregating full standardized metadata and linked multi-dimensional resources for quick cross-checking. All taxon, germplasm and institutional labels on every detail page are hyperlinked to jump to their corresponding detail pages, and embedded external hyperlinks lead to raw resources on NCBI, JGI, gcFungi and preservation institution official websites for data verification.

Genus Detail Page

Accessed by clicking any hyperlinked genus name across the platform, this page serves as a comprehensive overview hub that consolidates all taxonomic, germplasm, genomic and bibliometric resources associated with a single fungal genus.

Basic information: Shows genus name, standardized nomenclatural status from Fungal Names, macrofungal identifier tag and complete taxonomic lineage spanning kingdom to genus.

Basic Information

Genus Name	<i>Agaricus</i> 
Name Status	Current Name
Macrofungal genus	Yes
Rank	p__Basidiomycota sb__Agaricomycotina c__Agaricomycetes o__Agaricales f__Agaricaceae g__Agaricus

Switchable germplasm tabs: Tabulated lists of all affiliated species, strains and specimens under this genus, with every entry clickable to open its detail page.

Species | Strains | Specimens

Species						
Strains						
Specimen						
Q Search						
NO.	Species name	Phylum	Class	Order	Family	Genus
1	<i>Agaricus bisporus</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
2	<i>Agaricus sinodeliciosus</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
3	<i>Agaricus subrufescens</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
4	<i>Agaricus blazei</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
5	<i>Agaricus bitorquus</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
6	<i>Agaricus bobosii</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
7	<i>Agaricus xuchliensis</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
8	<i>Agaricus iodolens</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
9	<i>Agaricus earlei</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus
10	<i>Agaricus murinoccephalus</i>	Basidiomycota	Agaricomycetes	Agaricales	Agaricaceae	Agaricus

Total 645 < 1 2 3 4 5 6 ... 65 > Go to 1

Curated genome metadata table: Displays full assembly information for all sequenced genomes of the genus, covering assembly accession, total sequence length, GC

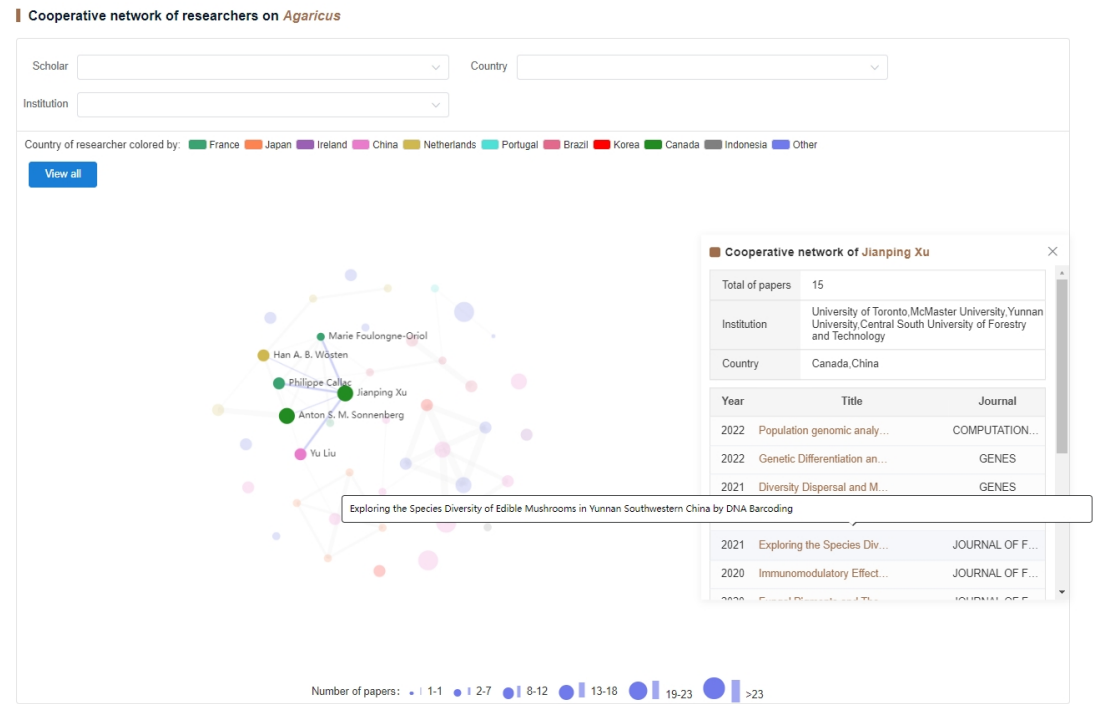
content, sequencing technology and release information.

Genomes

Q Search

Assembly Accession	Links	Organism Name	Current Name	Total Sequence Length	Assembly Level	Release Date	Number of Scaffolds	GC %	Sequencing Technology	Submitter	BioProject Accession	BioSample Accession
GCA_000300555.1	NCBI gcFungi	Agaricus bisporus var. burnettii J8137-S8	Agaricus bisporus	32614392	Scaffold	2012/10/16	2016	47	454, Illumina	JGI	PRJNA61007	SAMN00188834
GCA_000300575.1	NCBI gcFungi	Agaricus bisporus var. bisporus H97	Agaricus bisporus	30233745	Scaffold	2012/11/30	29	47	Sanger	JGI	PRJNA61005	SAMN02744070
GCA_000300575.2	NCBI gcFungi	Agaricus bisporus var. bisporus H97	Agaricus bisporus	30417944	Chromosome	2016/7/15	13	47	Sanger dideoxy sequencing; Reconstructed using linkage maps	JGI-PSF	PRJNA61005	SAMN02744070
GCA_001682475.1	NCBI gcFungi	Agaricus bisporus var. bisporus	Agaricus bisporus	30784214	Chromosome	2016/7/8	13	47	PacBio	JGI-PSF	PRJNA61005	SAMN04800541
GCA_006228365.1	NCBI gcFungi	Agaricus bisporus	Agaricus bisporus	33045762	Chromosome	2019/6/11	13	47	Oxford Nanopore GridION	Chungbuk National University	PRJNA534383	SAMN11489404
GCA_006491665.1	NCBI gcFungi	Agaricus bisporus var. bisporus	Agaricus bisporus	33350360	Contig	2019/7/3	168	47	Illumina HiSeq; PacBio RSII	Maynooth University	PRJNA544931	SAMN11866897
GCA_008271545.1	NCBI gcFungi	Agaricus bisporus	Agaricus bisporus	30068126	Contig	2019/9/4	18	47	PacBio Sequel	Jilin Agricultural University	PRJNA529780	SAMN11284169
GCA_014872705.1	NCBI gcFungi	Agaricus bisporus var. burnettii	Agaricus bisporus	30702502	Chromosome	2020/10/21	16	47	PacBio RSII	Utrecht University	PRJNA635555	SAMN15043479

Genus-level co-authorship network: Constructed based on the top productive authors of the target genus, where node size correlates with total publication volume, node color corresponds to author's affiliated country, and edge thickness represents co-authorship frequency. Users can filter researchers by name, country or institution, drag and zoom the graph canvas, and click author nodes to view matched publications, identifying core experts and research collaboration communities.



centralizes all taxonomic, germplasm, genomic, literature and patent data for a single fungal species alongside dedicated trend visualizations for research dynamics.

Basic taxonomic overview: It stores standardized species name, official nomenclatural status referenced from Fungal Names, macrofungi marker tag, and complete hierarchical taxonomic lineage from kingdom down to species.

[Home](#) / [Visualization](#) / [Species](#) / *Agaricus bisporus*

Basic Information

Species name	<i>Agaricus bisporus</i>
Name Status	Current name
Rank	p__Basidiomycota sb__Agaricomycotina c__Agaricomycetes o__Agaricales f__Agaricaceae g__Agaricus s__Agaricus bisporus
Mushroom Type	Edible Macrofungi, Medicinal Macrofungi
Database Link	JGI NCBI GCM
Genome Number	18

Germplasm resource tabs: Switchable tables of all affiliated strains and type specimens of this species; every strain and specimen entry carries hyperlinks to access their independent detail pages.

Strain and Specimen List

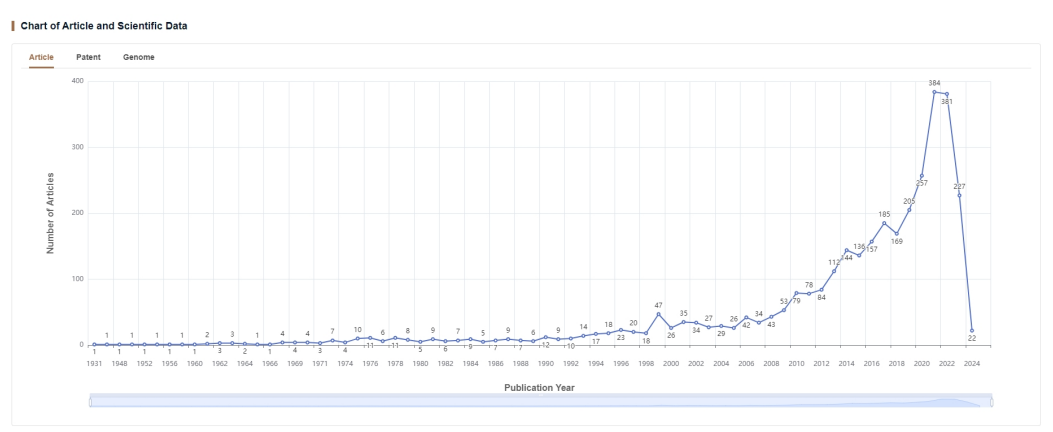
Strains					
NO.	Strain number	Species name	Other collection number	Acronym	Country
1	ACCC 50032	<i>Agaricus bisporus</i>		ACCC	China
2	ACCC 50033	<i>Agaricus bisporus</i>		ACCC	China
3	ACCC 50037	<i>Agaricus bisporus</i>		ACCC	China
4	ACCC 50041	<i>Agaricus bisporus</i>		ACCC	China
5	ACCC 50213	<i>Agaricus bisporus</i>		ACCC	China
6	ACCC 50215	<i>Agaricus bisporus</i>		ACCC	China
7	ACCC 50216	<i>Agaricus bisporus</i>		ACCC	China
8	ACCC 50217	<i>Agaricus bisporus</i>		ACCC	China
9	ACCC 50255	<i>Agaricus bisporus</i>		ACCC	China
10	ACCC 50257	<i>Agaricus bisporus</i>		ACCC	China
Total 300 < 1 2 3 4 5 6 ... 30 > Go to 1					

Genome assembly inventory: Complete curated metadata table of all public genome assemblies belonging to this species, including assembly accession IDs, total sequence length, GC content, sequencing platforms, assembly grades, and direct external links to NCBI/JGI/gcFungi for raw sequence download.

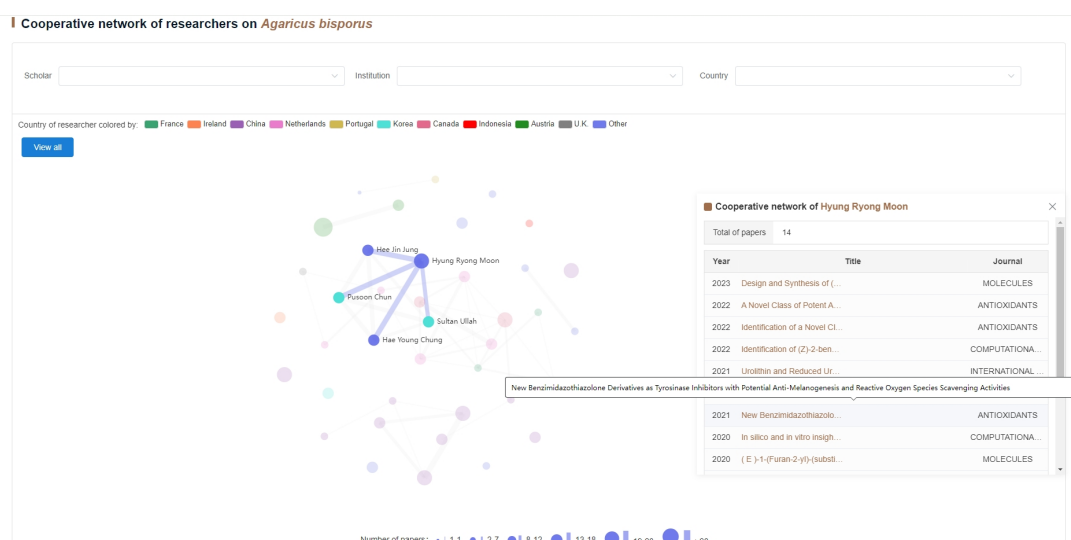
Genomes

Assembly Accession	Links	Organism Name	Current Name	Total Sequence Length	Assembly Level	Release Date	Number of Scaffolds	GC %	Sequencing Technology	Submitter	BioProject Accession	BioSample Accession
GCA_000300555.1	NCBI gcFungi	<i>Agaricus bisporus</i> var. <i>burnettii</i> JB137-S8	<i>Agaricus bisporus</i>	32514392	Scaffold	2012/10/16	2016	47	454; Illumina	JGI	PRJNA61007	SAMN00188834
GCA_000300575.1	NCBI gcFungi	<i>Agaricus bisporus</i> var. <i>bisporus</i> H97	<i>Agaricus bisporus</i>	30233745	Scaffold	2012/11/30	29	47	Sanger	JGI	PRJNA61005	SAMN02744070
GCA_000300575.2	NCBI gcFungi	<i>Agaricus bisporus</i> var. <i>bisporus</i> H97	<i>Agaricus bisporus</i>	30417844	Chromosome	2016/7/15	13	47	Sanger dideoxy sequencing. Reconstructed using linkage maps	JGI-PSF	PRJNA61005	SAMN02744070
GCA_001682475.1	NCBI gcFungi	<i>Agaricus bisporus</i> var. <i>bisporus</i>	<i>Agaricus bisporus</i>	30784214	Chromosome	2016/7/8	13	47	PacBio	JGI-PSF	PRJNA61005	SAMN04880541
GCA_006228365.1	NCBI gcFungi	<i>Agaricus bisporus</i>	<i>Agaricus bisporus</i>	33045762	Chromosome	2019/5/11	13	47	Oxford Nanopore GridION	Chungbuk National University	PRJNA534383	SAMN11489404
GCA_005491665.1	NCBI gcFungi	<i>Agaricus bisporus</i> var. <i>bisporus</i>	<i>Agaricus bisporus</i>	33350360	Contig	2019/7/3	168	47	Illumina HiSeq; PacBio RSII	Maynooth University	PRJNA544531	SAMN11865897
GCA_006271545.1	NCBI gcFungi	<i>Agaricus bisporus</i>	<i>Agaricus bisporus</i>	30069126	Contig	2019/9/4	18	47	PacBio Sequel	Jilin Agricultural University	PRJNA529780	SAMN11284169
GCA_014672705.1	NCBI gcFungi	<i>Agaricus bisporus</i> var. <i>burnettii</i>	<i>Agaricus bisporus</i>	30702502	Chromosome	2020/10/21	16	47	PacBio RSII	Utrecht University	PRJNA635555	SAMN15043479

Annual trend visualization: For species with sufficient published data, the page provides three independent yearly trend charts to reflect research dynamics: annual publication output trend, annual patent application trend, and annual genome release accumulation trend, which intuitively show the changing research attention toward this species over time.



Species-specific co-authorship network: Constructed based on the top productive authors of the target species, where node size correlates with total publication volume, node color corresponds to author's affiliated country, and edge thickness represents co-authorship frequency. Users can filter researchers by name, country or institution, drag and zoom the graph canvas, and click author nodes to view matched publications, identifying core experts and research collaboration communities.



Strain Detail Page

Accessed by clicking any hyperlinked strain number across the platform, this page

fully displays the preservation metadata of an individual viable fungal strain, together with supporting literature, patent records and genomic release trend statistics.

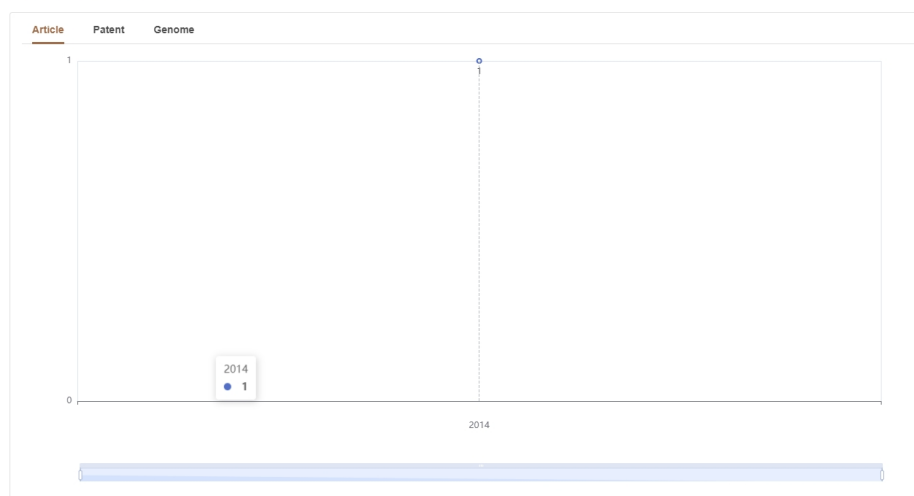
Basic germplasm metadata: Strain accession number, affiliated species name, alternative collection numbers, culture collection acronym, full repository name, collection country and continent.

Basic Information

Strain number	CECT 2008
Species name	<i>Agaricus bisporus</i>
Other collection number	CBS 57266
Acronym of collection	CECT CCINFO GCM
Full name	Coleccion Espanola de Cultivos Tipo
Country	Spain
Continent	Europe

Auxiliary analytical panels: Complete lists of publications and patents related to the strain, plus an annual genome release trend chart.

Chart of Article and Scientific Data



Specimen Detail Page

Accessed by clicking any hyperlinked specimen number across the platform, this page archives complete voucher specimen metadata for each dried fungal specimen stored in global herbaria, recording all core identification and preservation information for taxonomic reference.

Displays full voucher specimen metadata, including specimen number, associated species name, standard herbarium code, full herbarium institute name, collection

country and official herbarium website link.

Basic Infomation

Specimen number	HMAS 75888A
Species name	<i>Tuber taiyuanense</i>
Herbarium code	HMAS 
Herbarium full name	Fungarium (HMAS), Institute of Microbiology, Chinese Academy of Sciences
Country	China
Website	https://nmdc.cn/fungarium/

Culture Collection Detail Page

Accessed by clicking any hyperlinked acronyms of culture collections across the platform, this page introduces full background information of a live fungal strain repository and lists all species and strains preserved within the institution.

Basic institutional information: Repository acronym, full official name, located country and continent.

[Home](#) / [Culture Collection](#) / [ACCC](#)

Basic Infomation

Acronym	ACCC CCINFO GCM
Full name	Agricultural Culture Collection of China
Country	China
Continent	Asia

Attached resource catalogs: Complete lists of all preserved species and strains within this collection, with each entry linked to its dedicated detail page.

Species and Strains

Species						
Strains						
Q Search						
NO.	Species name	Phylum	Class	Order	Family	Genus
1	<i>Saccharomyces cerevisiae</i>	Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	Saccharomyces
2	<i>Fusarium oxysporum</i>	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium
3	<i>Macrophoma phaseolina</i>	Ascomycota	Dothideomycetes	Botryosphaerales	Botryosphaeriaceae	Macrophoma
4	<i>Pyricularia oryzae</i>	Ascomycota	Sordariomycetes	Magnaporthales	Pyriculariaceae	Pyricularia
5	<i>Aspergillus fumigatus</i>	Ascomycota	Eurotiomycetes	Eurotales	Aspergillaceae	Aspergillus
6	<i>Aspergillus flavus</i>	Ascomycota	Eurotiomycetes	Eurotales	Aspergillaceae	Aspergillus
7	<i>Fusarium asiaticum</i>	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium
8	<i>Beauveria bassiana</i>	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae	Beauveria
9	<i>Botryosphaeria dothidea</i>	Ascomycota	Dothideomycetes	Botryosphaerales	Botryosphaeriaceae	Botryosphaeria
10	<i>Fusarium graminearum</i>	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Fusarium

Total 525 < 1 2 3 4 5 ... 53 > Go to 1

Herbarium Detail Page

Accessed by clicking any hyperlinked herbarium code or name across the platform, this page records comprehensive institutional background and collection coverage information of a fungal specimen archive, paired with a full inventory of all archived type specimens and covered fungal taxa.

Comprehensive herbarium archive information: Herbarium standard code, short name, full institute name, institution type, country, physical address, collection notes, global specimen distribution, key historical collectors and taxonomic coverage range.

Basic Information

Herbarium code	HMAS
Herbarium name	Fungarium (HMAS), IMCAS
Herbarium full name	Fungarium (HMAS), Institute of Microbiology, Chinese Academy of Sciences
Agency type	Herbarium
Country	China
Address	1 Beichenxilu, Chaoyang District, Beijing 100101
Notes	HMAS is the abbreviation of the previous name of Herbarium Mycologium Academic Sciences. Updated May 2022 (Full name). Updated Mar 2015 (updated address, new staff).
Distribution	Mainly China
Important Collectors	J. C. Arthur, J. B. Chen, S. L. Chen, C. C. Cheo, W. F. Chiu, C. E. Cummins, S. Q. Deng, J. B. Ellis, B. M. Everhart, W. G. Farlow, Y. Hashioka, H. Hertel, N. Hiratsuka, Y. M. Jiang, H. Kashiwadani, S. Kurokawa, E. Licent, L. Ling, T.-n. Liou, X. J. Liu.
Taxonomic Coverage	Fungi and lichens, especially Uredinales, Erysiphales, Ustilaginales, Agaricales, Aphyllophorales, and allies, and discomycetes; other higher basidiomycetes and ascomycetes, Cladoniales, Umbilicariales

Attached resource catalogs: Full inventory of archived type specimens and covered fungal species, with clickable links to each specimen and species detail page.

Specimen and Species List

Specimen	Species
NO.	Type number
2201	HMAS, Wang WZR2012-821
2202	HMAS, Wang WZR2012-8212
2203	HMAS, Wei & Chen, 1057
2204	HMAS, Wei 1727
2205	HMAS, Wu 0205
2206	HMAS, Wu 12519
2207	HMAS, Wu 1315a
2208	HMAS, Wu 2252
2209	HMAS, Wu 5006
2210	HMAS, You et al. 120

Species name

Agaricus sinodeliciosus

Agaricus dejudinii

Cetraria ladigera

Hypogymnia prunioidea

Ganoderma oehringense

Xylaria palmicola

Linkosia acutispora

Hoehnella triopata

Linkosia subramaninii

Hypoderma berberidis

Total 2315 < 1 ... 219 220 221 222 223 ... 232 > Go to 221

Visualization Detail Page

The independent Visualization navigation module is built exclusively for macrofungal taxa with bibliometric metadata (publication trends, author collaboration networks). Two hierarchical detail pages are provided: genus-level visualization page and species-level visualization page. Users can access these pages via search results of Visualization module. All visualization charts support interactive zoom and hover tooltip data display. The time-series trend data are obtained by standardized statistical calculation of annual publication, patent and publicly released genome records. Genus collaboration networks are generated from the top 10 high-output species and top 50 authors of the genus, while species collaboration networks are constructed based on the top 50 authors publishing on the target species. Only core productive researchers are displayed in the network graph, rather than all authors of related literature.

Genus-level

This genus-level visualization page displays basic taxonomic information of the target genus, pie chart statistics of genome-sequenced species, and a collaboration network of top productive researchers, which jointly reveal the genus-wide sequencing status and core academic partnership patterns of its leading investigators.

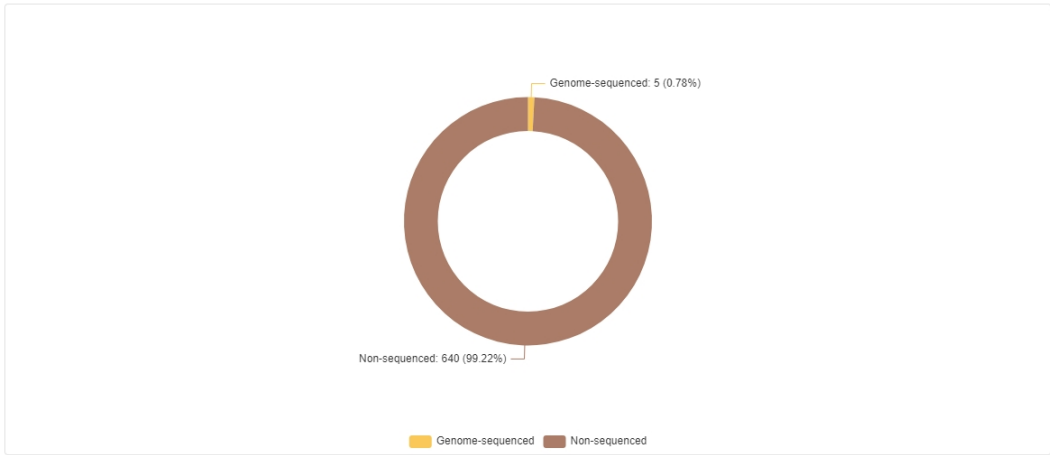
Basic information: Shows genus name, standardized nomenclatural status from Fungal Names, macrofungal identifier tag and complete taxonomic lineage spanning kingdom to genus.

Basic Information

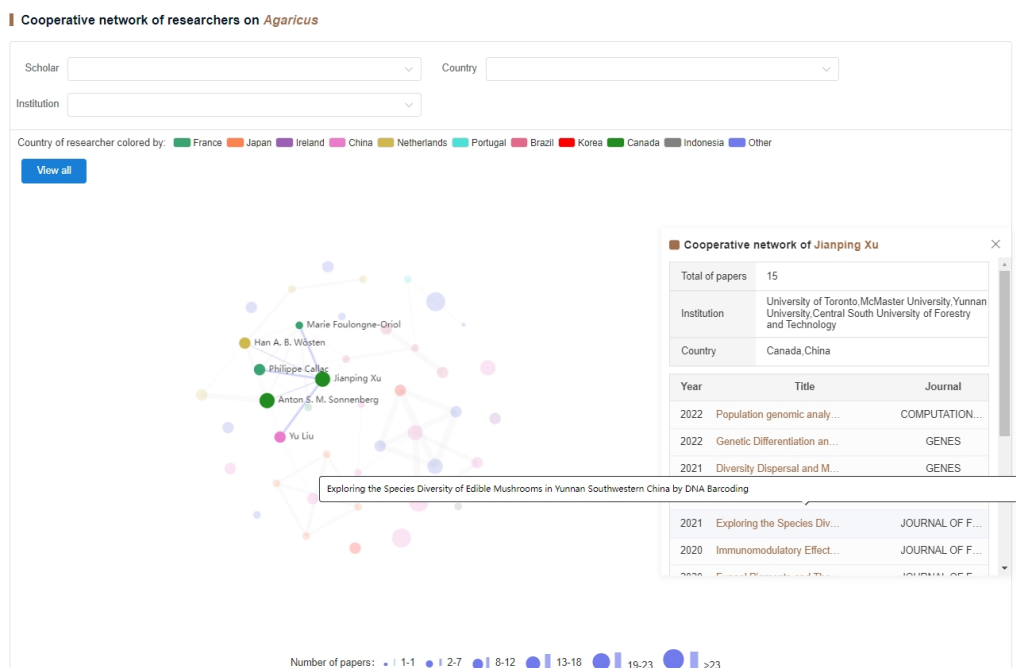
Genus Name	<i>Agaricus</i> 
Name Status	Current Name
Macrofungal genus	Yes
Rank	p__Basidiomycota sb__Agaricomycotina c__Agaricomycetes o__Agaricales f__Agaricaceae g__Agaricus

Genome-sequencing species statistic: This panel quantitatively presents genome resources of the target genus, with unified display format: record count (percentage proportion). Two core metrics are calculated automatically: Number of genome-sequenced species in this genus / total species count of the genus.

Genome-sequencing species statistic



Cooperative network of researchers: Constructed based on the top productive authors of the target genus, where node size correlates with total publication volume, node color corresponds to author's affiliated country, and edge thickness represents co-authorship frequency. Users can filter researchers by name, country or institution, drag and zoom the graph canvas, and click author nodes to view matched publications, identifying core experts and research collaboration communities.



Species-level

This species-level visualization page displays taxonomic metadata, total recorded genome counts (including inaccessible entries with sequencing metadata only), annual trends of publications, patents and publicly available genomes, and a top researcher collaboration network, reflecting both the full genomic record inventory and long-term core research profile of the target species.

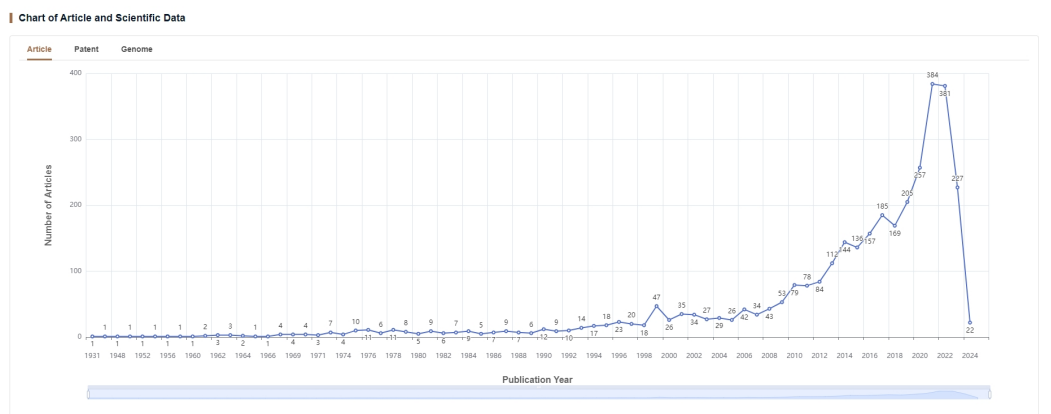
The Basic Information section lists standard taxonomic information of the target species, with an exclusive Genome Number field that tallies all genome records stored in MTSEM, containing both fully downloadable public genomes and entries that only retain sequencing metadata without open sequence files.

[Home](#) / [Visualization](#) / [Species](#) / *Agaricus bisporus*

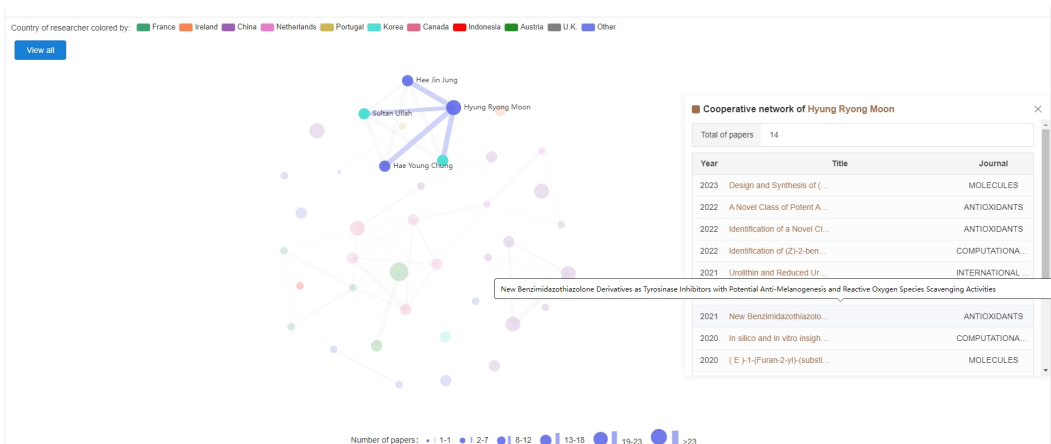
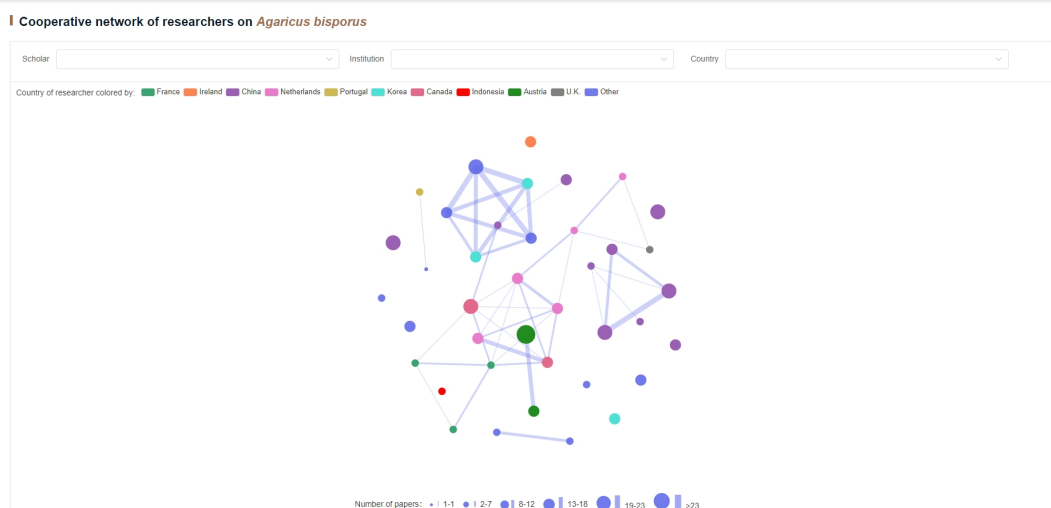
Basic Information

Species name	<i>Agaricus bisporus</i>
Name Status	Current name
Rank	p__Basidiomycota sb__Agaricomycotina c__Agaricomycetes o__Agaricales f__Agaricaceae g__Agaricus s__Agaricus bisporus
Mushroom Type	Edible Macrofungi, Medicinal Macrofungi
Database Link	NCBI GCM
Genome Number	18

The Chart of Article and Scientific Data is an interactive timeline tracking annual outputs of publications, patents and genomes. The genome curve only counts assemblies with publicly downloadable sequences, differing from the full genome total shown in Basic Information. You may hover over chart points to view exact annual values, and drag or zoom the chart to observe local data details.



The Cooperative Network of Researchers visualizes partnerships between high-output scholars focusing on this species; node size corresponds to total publication counts, and node colors mark researchers' affiliated countries. Built-in filters allow quick screening by scholar name, country or institution, and hovering over nodes reveals individual paper counts, institutions and co-author links. This network only displays core productive researchers instead of every author from related literature.



Field Descriptions

This section uniformly defines all core metadata fields displayed on search tables and detail pages of MTSEM, categorized into taxonomic fields, genomic fields, germplasm fields, bibliometric and economic trait fields.

Taxonomic Fields

Outline of macrofungi: Standard hierarchical classification (Phylum / Class / Order / Family / Genus) following 2024 taxonomic references for Ascomycota and Basidiomycota.

Macrofungal genus: Binary marker to distinguish macrofungal taxa from other fungi (yes or no).

Name status: Nomenclatural status information sourced from Fungal Names (current name or synonym).

Genomic Fields

Genome Number (Basic Info panel): Total count of all JGI & NCBI genome records of the taxon, including metadata-only entries without downloadable raw sequences.

Public genome count (trend charts): Only assemblies with publicly accessible sequence files from NCBI or released JGI projects.

Assembly accession: Unique ID assigned by NCBI or JGI to each fungal genome assembly.

Sequencing platform: The sequencing technology used to generate the genome.

GC content: GC proportion of the assembled genome sequence.

Assembly level: Genome assembly completeness grade or sequencing status provided by original repositories.

Germplasm Fields

Strain number: Unique identifier for living culture strains from culture collections.

Specimen number: Voucher ID of dried fungal specimens preserved in herbaria.

Culture collection acronym: Standard short codes of culture collections registered in CCINFO.

Herbarium code: Standard short codes of herbaria released by Index Herbariorum.

Collection country: Geographic location where specimens or strains were collected.

Bibliometric Fields

Number of Articles: Total peer-reviewed papers linked to a species.

Number of Patents: Number of authorized patents associated with the target taxon.

Scholar: Author node displayed in the researcher collaboration network; the size of each node is proportional to the total publications this author contributed to the corresponding genus or species.

Institute: Affiliated research institution of the scholar, supporting network filtering operations.

Country: The country of the scholar's affiliated institute; nodes on the graph are rendered with distinct colors to represent different countries.

Author publication volume: Total papers published by a single researcher, used to scale node size in collaboration networks.

Economic Trait Fields

Mushroom type: Economic trait tag (edible / medicinal / poisonous) manually curated from published mycological literature.