Review Article

NEOTROPICAL MICODIVERSITY OF MATO GROSSO, CENTRAL REGION OF BRAZIL: ETHNOMICOLOGICAL ASPECTS AND SYSTEMATIC RESEARCH OF THE LITERATURE

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Contribution of authors

All authors contributed equally. First author DPLJ conceived and designed the scope of the review. All authors read and approved the final manuscript, and gave their opinions to improve the manuscript. They read the final version and approved it for publication.

Conflict of Interest

The authors declare that they have no conflict of interest.

Abstract:

Introduction: The knowledge about fungal diversity in Mato Grosso, central Brazil records unknown and scattered information, some related to taxonomy, ecology and description of species listed for the geographic region, consisting of three main biomes: Cerrado, Amazon and Pantanal. **Aims:** To present fungi related to the Mato Grosso region, aspects and species cataloged for central region of Brazil, reported through an extensive review of integrative scientific literature in publications in databases from 1979-2021. **Results:** We identified 190 articles included in the review, of which 69 (36.3%) were highlighted, due to their fungal aspects for the Midwest region of Brazil, medical mycology shows a strong relationship in publications to pathogenic, mycelial and yeast fungi. The Cerrado of Mato Grosso is the main biome in the Brazilian Midwest, with the largest number of records, with 88.6% of the findings, followed by the Amazon biome with 8.6% and the Pantanal with 5.7%. The capital of Mato Grosso, Cuiabá (67.1%), contributes with most publications relevant to fungi for the Midwest region, showing a wealth and variety. The phylum Ascomycota (56%) had the highest number of records in research, the class of Eurotiomycetes (21.5%) had the highest number of records and the most expressive order was that of Onygenales (30%).

Researches with human clinical material (66.3%) were the most representative. **Conclusion**: Assessing the results presented in this study, we can observe that the medical and clinical mycology, including systemic fungi, mainly from the genera *Cryptococcus*, *Candida* and *Paracoccidioides*, were the most studied for the Mato Grosso region, as they present characteristics of pathogenic fungal entities that cause infections in immunocompetents and immunocompromised patients.

Keywords: Fungal Diversity, Brazilian Center-West, Fungal Pathogens, Mato Grosso Biomes, Savannah Mato Grosso.

1. INTRODUCTION

History of Mycology

Brazil is a country that has a great biological diversity, being able to house varieties of species in its great biomes. Mycology is a branch of the specialized science of Biology that is concerned with studying fungi; living beings of polyphyletic origin, due to their DNA limited by a double membrane, classified among eukaryotes, heterotrophs, cosmopolitan, ubiquitous, opportunistic entities, present in the soil, making saprophytism in decaying organic matter, in the air, in water, in the soil and also being part of the microbiota of living beings, they can reproduce asexually and/or sexually, achlorophylls, rarely cellulosic cell wall, normally chitinous, aerobic par excellence, reserve glycogen, present in different climatic conditions and abundant variety of places[1,2].

The history of mycology in Brazil begins around the 18th and 19th centuries, with the exploration of native mycota, where the first steps were taken with the identification of macroscopic species provided and described by Jean Pierre Camille Montagne (1784-1866), Paul Christoph Hennings (1841-1908), Giacomo Bresadola (1847-1929), Heinrich George Winter (1848-1887), Ernest Heinrich George Ule (1854-1915)[3,4] and was in Southern of Brazil that the study of the Brazilian mycobiota gained prominence mainly through the researches of Johannes Evangelista Rick (1869-1946), a Brazilian priest, of Austrian origin, botanist, mycologist and scientist, considered the father of Brazilian mycology[5].

The fungal specimens collected by these researchers came from several Brazilian states, such as Pará, Bahia, Rio de Janeiro, Goiás, São Paulo, Minas Gerais, Amazonas, Piauí, Santa Catarina, Pernambuco and Mato Grosso. These mycology scholars sent samples to international herbaria and later from 1900, the studied material was collected, analyzed and deposited in Brazilian herbaria[4].

More currently, mycology has been treated on a more careful level, extending to medical mycology, which for medicine, fungi raise problems of various importances and in the most varied human sectors, assuming significant importance in human medical pathology, veterinary and epidemiological.

In the primordial ages, studies of chromomycosis, hyalohifomycosis and paracoccidioidomycosis, described for the first time in Brazil by Adolpho Lutz (1855-1940)[3,5] There were important historical facts in Mato Grosso, which marked Brazilian history, such as the abolition of slavery (1888), the end of the Empire and the beginning of the Republican period (1889)[3].

Valuable contributions were made to the study of mycology by renowned scientists and mycologists such as Raymond Jacques Andrien Sabouraud (1864-1938), Rudolf Virchow (1821-1902), Maurice Langeron (1874-1950), David Gruby (1810-1898), Aldo Castelani (1877-1941), Raymond Vanbreuseghen (1909-1993), they are among many others who established the study of fungi in Brazil, and gave the initial start to the knowledge and importance of medical and scientific mycology.

Mato Grosso (MT) is a privileged state in terms of biodiversity, being the only Brazilian state to present three of the six major phytogeographic domains, called biomes in the country: Amazon, Cerrado (Brazilian Savannah) and Pantanal. In Mato Grosso, initial studies focused on the so-called environmental fungal “flora” and its representatives were characterized by botanists such as Frenchman Charles Gaudichand-Beaupré (1789-1854), who collected several fungi in several Brazilian states, including Mato Grosso, constituting a list where 65 species were described[4].

In 1845, the English Hugh Algernon Wenddell (1819-1877), visiting Brazil, passing through the central region of the country, reaching Mato Grosso, and visiting the region of Chapada dos Guimarães, Serra do Tombador and the city of Cáceres. He carried out small projects environmental excursions through the environmental areas of these locations recording fungal specimens[4]. As early as 1900, Paul Christoph Hennings (1841-1908) listed about 34 fungal species along the headwaters of the Cuiabá, Jatobá, and Paranatinga rivers in Mato Grosso[6].

From 1901 to 1903, the Swedish botanist Gustaf Oskar Andersson Malme (1864-1937) was the one who contributed the most to the collection of fungal specimens, making an excursion through Cuiabá, through the Paraguay and São Lourenço rivers, reaching the Chapada dos Guimarães where collected about 1,000 fungal specimens.

Results of this study contributed to Swedish mycologists to deepen their studies in fungal groups belonging to the phylum Basidiomycota identified by Hans Oscar Juel (1863-1931) who studied the group of Ustilaginomycetes/Ustiginales “smuts fungi” and Teliomycetes/ Puccinialles (formerly known as Uredinales), which cause rust in plants; Lars Gunnal Romell (1891-1981), was responsible for the study of Hymenomycetes and Karl Starback (1863-1931) was responsible for examining the fungi of the phylum Ascomycota[4,7,8].

2. MATERIALS AND METHODS

For the collection of information, bibliographic surveys were carried out in the Pubmed, Scielo, Lilacs, Science Direct and Google Scholar databases of scientific articles. Technical information involving the location and fungal identification carried out in Mato Grosso (MT), some encompassing Mato Grosso do Sul (MS) and Goiás (GO), which cover the central region of Brazil. For the collection of information, the available databases were used, in order to identify publications relevant to the area of mycology using mesh such as: "regional fungi", "central-west region of Brazil", "macrofungi", "microfungi", " medical mycology", "regional mycology", "Mato Grosso biomes" and mainly to information related to the State of Mato Grosso, its capital Cuiabá and its municipalities.

The historical method supported the investigations of bibliographic and documentary events that influenced the discoveries and current existences. An approach to the beginnings of mycology in the central west region was initially carried out, with emphasis on indigenous peoples and their contribution to the use of macrofungal species found in ethnomicological reports.

Next, we carry out a scientific medical approach on microfungi and the pathogenesis caused by these microorganisms in the MT region, as well as citation of studies on taxonomy, molecular biology and phylogeny of fungi groups. For the validity of species names, and the confirmation of scientific names, the respective names were verified by consulting the Taxonomy browser/NCBI (www.ncbi.nlm.nih.gov), Mycobank (www.mycobank.org) and Index Fungorum (www.indexfungorum.org) databases.

3. DESCRIPTION AREAS

Mato Grosso Biomes

The central region of Brazil is an environment of a huge variety of macro and microorganisms, which are still few known and exploited by science. Wealth and abundance of existing microorganisms in highlighted biomes in this region of the world are important not only to stimulate further research, but to demonstrate the biological potential present in the region, especially conservation and sustainable attitudes.

The great geographical extension and diversity of climate, soil and vegetation, indicate the existence of biological diversity incomparable to animals, but also in relation to vegetation, especially the registration of fungal species, and the degree of endemism, with uncertainties and few records.

The climate of MT, according to the Köppen-Geiger climate system, is characterized as Cwa: subtropical, dry winter and rainy in summer is characterized by the semi-arid region (semi-humid)[9], with an average annual precipitation of 1,500 mm and an average annual temperature of 25°C to 40°C. What defines two seasons is very characteristic a dry inverse and a rainy summer, presenting an average annual temperature of 26°C; the maximum can reach 38°C and the minimum 8°C[10].

The characteristic vegetation of MT is the Atlantic forest of transition to the cerrado, which is the main phytogeographic domain of the region, which consists of vegetation retained with the presence of various plant phytophysics, composing a very rich flora of the Brazilian Cerrado, with an exuberant biodiversity of animal species. Its river basins result in hundreds of springs, which descend the mountains and give rise to several streams that bathe the municipalities of the region[11].

Mato Grosso is a privileged state in terms of biodiversity. It is the only one in Brazil to have, alone, three of the main biomes in the country: Amazon, Cerrado and Pantanal.

The Amazon biome is a vast region that covers eight countries: Brazil, Bolivia, Peru, Ecuador, Colombia, Venezuela, Guyana, Suriname and French Guiana. It is one of the three large tropical forests in the world. The amazon rainforest climate is equatorial, hot and humid (continuous with the Atlantic forest), with temperature varying little during the year. The rains are plentiful, with average annual precipitation ranging from 1,500 mm to 1,700 mm. There are two types of forests in MT: the Amazon forest and the seasonal forest. Concentrated in the north of the State, the Amazon is the most complex in terms of biodiversity in the world[12].

The Brazilian Cerrado, the second largest biome, has very rich vegetation, being the main biome of the Brazilian center and also known as the Brazilian Savannah. Located mainly in the depressions of Alto Paraguay/Guaporé, South and Southeast of the Parecis Plateau for the limits of MS. It has a rich flora, with vegetation composed of grasses, shrubs and sparse trees. The trees have twisted and long root stems, which allow the water to be absorbed even during the dry winter season. The Cerrado concentrates the main rivers and some of the most important tributaries of the three largest river basins in South America (Amazonas, Paraguay and San Francisco)[12].

The pantanal biome is located in the depression of the Rio do Paraguay riverside 16-20s and 55-58ow, inserted in the Paraguay basin has the characteristic of periodic and annual floods, presenting a total area that covers about 195,000 km2. This flood area occupies 80% in the Brazilian territory, southern MT (20%) and northwest of MS (60%), totaling 151,000 km2; thus occupying 2% of the total area of Brazilian territory[13]. Another remaining part of this plain is located in Bolivia with 19% (about 31,898 km2), where it is called Bolivian Chaco, and in Paraguay with 1% (about 12,102 km2)[14].

The Pantanal climate is hot with a pronounced dry season from May to September and a rainy season from October to April. Annual precipitation decreases by 1,250 mm near Cuiabá, the monthly average temperature varies between 27.4°C and 21.4°C varying between months[15].

The vegetation of the Pantanal is a mosaic of five distinct regions: Amazon, Cerrado, Caatinga, Atlantic forest and Chaco (Paraguayan, Argentinean and Bolivian). During the drought, the fields are with yellowish vegetation aerial masses, and with cold temperatures with a drop of levels below 0°C, with a frost record, influenced by the winds coming from the southern continent[12]. Extreme periods of drought and rain lead to extreme events of floods and dried combined with large forest fires within the wetland with dramatic consequences for fauna and flora[15].

Due to this characterization, the Pantanal region is located in a climate instability zone called a circle-global belt, which promotes dramatic climatic changes that maintain the plain with floods in intermittent periods and other occasions in severe drought on a large scale (as observed in 2020), which entailed to disastrous fires, destroying vegetation, with episodes that are not yet fully understood.

4. RESULTS

According to the search terms, it was possible to access scientific articles and selected 190 articles that were used as a relevant basis for the discussion of the review results. Among these articles, 69 (36.3%) were selected because they contain information about fungi in the central region of Brazil and their description. These informations are contained in the presented retrospective table (Table 1).

About 88.1% of the articles found and selected were information relevant to the state of MT, followed by GO (7.5%) and MS (7.5%), respectively, for descriptions of the fungi reported for the region Central of Brazil. The city of Cuiabá, capital of MT, contributes with most of the results found, making up a total of 67.1% of the findings.

It was observed that 88.6% of the consulted articles referenced the Cerrado biome as predominant for studies involving fungal descriptions in the Midwest region, followed by 8.6% for the Amazon region and 5.7% referenced the Pantanal in studies in these phytogeographic domains (Table 1).

In the period from 1979 to 2021, the investigation, cataloging and description of fungal species were related, consisting of scientific articles, dissertations and theses related to the topic of fungi for the central region of Brazil. The year 2014 was the one with the most scientific papers, 14.9%, followed by the year 2016, with 11.9%, and then the year 2019 with 9% of the results found. The other years reached lower percentages in terms of publication.

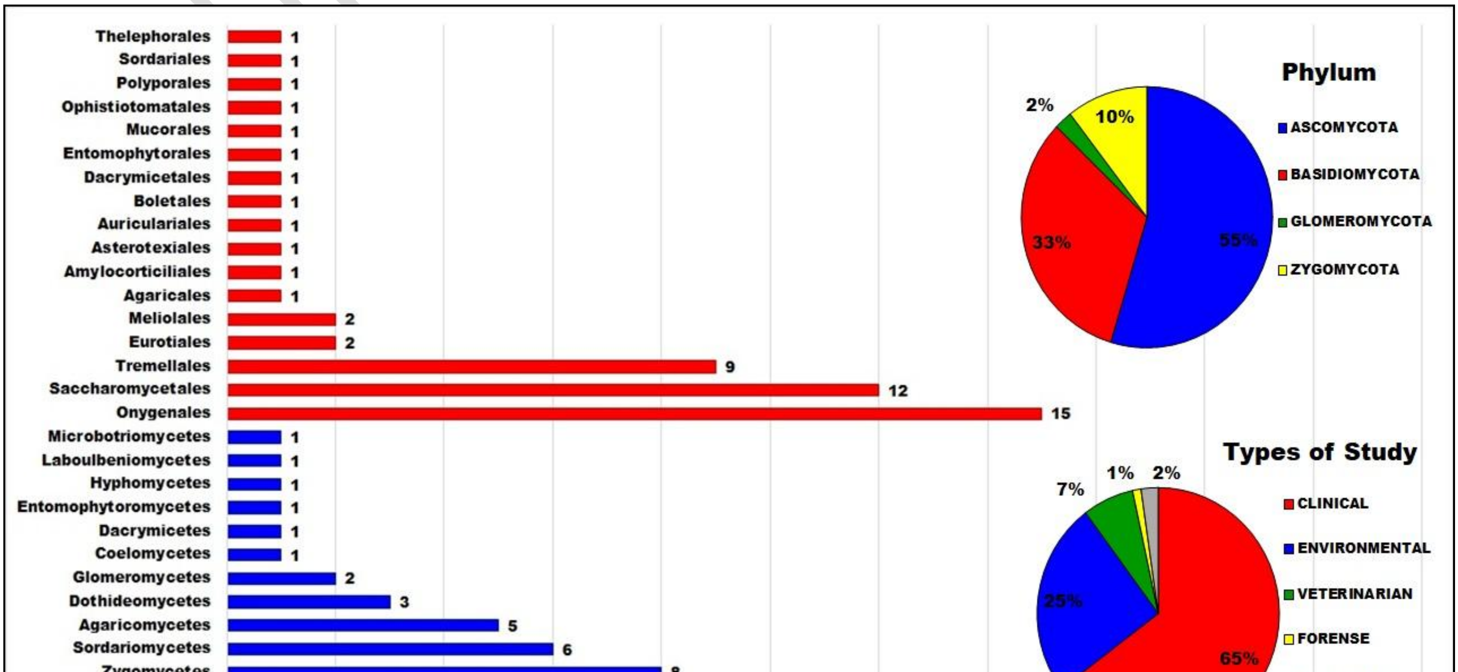
We observed that 56% of the researches were constituted by the phylum Ascomycota (33.3%) had the phylum Basidiomycota, followed by the phylum Zygomycota (10.7%) and the phylum Glomeromycota (2.4%), highlighting studies of macrofungi and microfungi (Figure 1).

We can also inform that the taxonomic classes identified in the selected works showed that Eurotiomycetes (21.5%) were the most isolated and studied group of fungi, followed by Saccharomycetes (15.1%), Tremellomycetes (11.8%), Ascomycetes and Basidiomycetes (10.8%), respectively, and Zygomycetes (8.6%), from the fungi cataloged for the Brazilian Midwest region.

The order Onygenales was the most representative (30%), followed by *Saccharomycetales* (24%), Tremellales (18%), Eurotiales and Meliolales (4%). In addition to other orders: Entomophthrales, Asterotexiales, Auriculariales, Boletales, Polypolares, Amylocorticiliales, Thelephorales, Dacrymecetales, Mucorales, Sordariales, Ophistiotomatales and Agaricales were present and reached lower percentages (2%) respectively (Figure 1).

In the Central region of Brazil, the findings related to the medical/clinical area stood out, presenting studies involving the action of fungi in clinical research with humans, corroborating (66.3%) of the results found; environmental fungi (25.6%) of the researches, veterinary fungal infections (7%) and fungi in the agro-rural (2.3%) and finally, fungi involving the forensic area (1.2%) (Figure 1).

Among the most frequent fungal genera in the studies were the microfungi *Candida, Penicillium, Aspergillus, Cladosporium, Paracoccidioides* and *Cryptococcus,* which were shown to be representative in medical mycology, gaining prominence. During the period surveyed, with a rate of 54.4% of publications for the Midwest region, with emphasis on MT involved humans; focused on the Environment (29.4%); animals (14.7%) and with work involving associations with vegetables (4.4%) (Table 1).



The results presented show an analysis of the action of these eukaryotic organisms and their interaction with man and the environment. We started with the beginnings of mycology in MT, with knowledge of the use of fungi by indigenous peoples, followed by constant changes in the taxonomy of the kingdom and finally the pathogenic potential of microscopic fungi, issues related to the intrinsic resistance of some species to drugs, recognition of the action of pathogenic fungi studied in the State of MT, demonstrating the high plasticity with which these microorganisms are known.

Considering that information on research regarding the distribution of the occurrence of fungi in the various Brazilian biomes and ecosystems is still insufficient, many areas of Brazil remain unexplored and/or poorly studied and studies aimed at increasing knowledge of species richness for the South America, based on studies in temperate tropical climate regions.

Although we tried to briefly show the environmental characterization of the biomes found in the central portion of Brazil, it was not possible to determine with certainty which fungal species were endemic, which taxa predominate in the Central region of Brazil and which species are considered to be threatened with extinction; these aspects, which were not possible to determine, were therefore not addressed in depth in this study. The results discussed were grouped and tabulated by theme and presented below.

5. DISCUSSION

ETHNOMICOLOGY: THE HISTORY OF OCCUPATION AND THE BEGINNINGS OF MYCOLOGY IN MATO GROSSO

Mato Grosso is an indigenous state, due to the number of indigenous peoples who lived in the territory, contributing to the colonial and cultural formation of the region. The beginnings of mycology in the State of MT have a very strong contribution to its population from indigenous ancestors, the first historical reports date back to the first conquests of the São Paulo pioneers, followed by the encounter with São Paulo pioneers, the first inhabitants of the Bororo Indians, known as the Coxiponés Indians (1716-1718). With the conquests in the region, later, Pascoal Moreira Cabral (founder of Cuiabá city) discovered the gold that brought a population contingent attracted by the possibility of easy wealth, thus forming the name of the current city of Cuiabá, which presents in one of several versions for origin and mention that the (Tupi = Kuiaverá, bright otter river) or the expression of the Bororo word Ikuiapá (ikuia: arrow-harpoon, paddle: place) due to the existence of a tribe of Bororo Indians called Cuiabases[16].

Mato Grosso, after its first years of discovery, went through a long period of wars, the indigenous people existing between the Paraguay, São Lourenço and Cuiabá rivers, such as the Bororo, Paiaguá, Guató, Guaikuru and Kayapó indigenous populations, who inhabited the territorial regions, became to be persecuted, confronted and warred, as if they were intruders in their own territory, due to the advent of gold mines; therefore, the Indians, mainly the Paiaguás (canoeing Indians) and Guaikurus (riding Indians) were violently persecuted and the combination of the two skills resulted in constant attacks, which often attacked the pioneers and travelers in the new village that emerged called Villlage of Bom Jesus de Cuiabá[17,18].

In Brazil, studies in this area are limited and focused on indigenous peoples and, rarely, on rural and riverside populations[19]. The history of mycology in MT is based on the contributions of indigenous peoples to fungi species. There are few records and descriptions of forest peoples that present knowledge about fungi and that this information can be considered a relevant role in their cultures. Ethnomicology investigates the cultural, ceremonial and medicinal uses of fungi, in addition to their consumption as food.

One of the first reports on fungi in Brazil, are dated from the year 1560, made by the Spanish Jesuit priest José de Anchieta, who described the aspects of an organism with hardened characteristics known as "Indian Bread", indicating that this food consists of *Polyporus sclerotia sapurema* (Polyporaceae/Basidiomycota)[7]. Currently, for this fungal group, eleven species of the genus *Polyporus* recorded in the Brazilian Amazon region have been described, including the species *Polyporus indigenus* (Polyporaceae/ Basidiomycota)[20] in association with the delicacy consumed by the indigenous representatives.

However, around 1648, the Dutch zoologist Willem Pies described in his book seven species of fungi called "*Carapacu*" in the language of the Tupi-Guarani ethnic group, described for the Brazilian territory[8]. These fungi contained some poisonous species, mainly those that grew on decaying wood and, once ingested, caused sweating, chills, hiccups, and retention of urine; according to the records, these data constitute the first report in this area of knowledge[21].

The first records discussed according to Hidalgo (1968) in the ancient civilizations of the New World, macrofungi had a very special meaning for those who made use of their properties allowing them to even talk to the gods. Ethnomicology, a description defined by the researcher Robert Gordon Wasson (1898-1986) as the branch of Ethnobotany that studies the role of fungi in human societies, as these organisms are part of their past and present in the natural environment. However, nowadays, ethnomicological studies and assessments of indigenous knowledge seem to have been neglected for a long time and without due recognition.

For some dictionaries of different indigenous languages we find several terms corresponding to the existence and manipulation of fungi[4,22]. For Brazilian tribes, these behavioral patterns of use of hallucinogenic and medicinal fungi to encounter the divine are little used. The theme of shamanism was addressed by Jon Christopher Crocker in a research carried out with the Bororo Indians of Brazil in the 1970s[23]; being the greatest interest of these peoples in relation to fungi, in their sporadic use in medicine or for food.

Analyzing this evidence, we cannot say that the Brazilian forest peoples were totally unaware of the fungal properties. According to the ethnographic records carried out by Mense[24], the Mundurukús Indians (Tupi=red ants), people with a warrior tradition, culturally dominated the Tapajós Valley region and belonged to the Amazon basin, around twelve words refer to fungi and that we can also verify in the registers cited by Fidalgo[7].

In memorial times, among the Karajás Indians (=us) who inhabited the region of the Araguaia River, the Mortes River to its upper course, several names mentioned for higher fungi, designated by this indigenous tribe, were reported in a study, being the most used by the folk, the families Agaricaceae and Polyporaceae (both from the Basidiomycota division)[25].

Reports about the Bororó Indians (=village courtyard), who inhabited regions of the interior of MT, were reported by Albisetti & Venturelli[26] mentioning the use of wood ear fungi belonging to the phylum Basidiomycota representing the Agaricomycetes or Gasteromycetes classes " *stomatch fungi*".

The knowledge of the Nhambikwara tribes (tupi=perforated ear), in the municipality of Aripuanã, MT, we found reports that are highlighted, on the other tribes, regarding the use of fungi in food, other few records on the habit of mycophagy prominent among the Sateré-Mawé Indians (=fire caterpillar/intelligent parrot)[25,27,28]. These tribes fed mainly on xylophyll fungal groups (growing on wood) belonging to the sub-families Polyporioidea and Lentinoideae and the orders Aphyllophorales and Agaricales[29].

Ethnomycological records showed that there are twelve ethnic groups in the Amazon that sporadically consume mushrooms, as well a rural and riverside populations[19]. A total of 105 indigenous mycological names are listed and 21 species of fungi used in the indigenous diet were identified for that period[29].

In Mato Grosso, indigenous representatives, Amazonian caboclos make use of fungi in medicinal practice, a practice learned from the Rikbaktsá Indians (=human beings), immemorial inhabitants of the upper Juruena River basin, in the north of the State of MT, known o canoeists Indians or wooden ears[7,30].

Fidalgo & Hirata[22], portrayed the issue of the ethnomicology of the Indians belonging to the Caiabi, Txicão, Txucarramãe, Yanomâmis, Tupi-Guarani, Nhambikwara and Tucano tribes. These Brazilian indigenous tribes used fungi of the phylum Basidiomycota wood decomposers, *Pycnoporus sanguineus* (popularly known in Brazil as wood ear) family Poliporaceae and *Geastrum saccatum* of the family Geastraceae, found in more open areas of forests, being used for treatment against hemoptysis and for the healing of wounds, hemorrhages and uterine disorders[19,21,29].

Currently, chemical tests involving a group of fungi of the *Picnoporus cinnabarinus* species were carried out by Dias & Urban[31] showing efficacy against fungi (*Candida albicans*), viruses (Herpes simplex) and bacteria (*Escherichia coli*).

Abreu et al[32] also mentions that these mushrooms were used since ancient times for medicinal purposes to combat bleeding, cramps, wounds, asthma and other diseases. They also, indicating that the medicinal properties found in these eukaryotes have antiviral, antibacterial, anti- parasitic, anti-tumor, anti-hypertensive, anti-atherosclerotic, hepatoprotective, anti-diabetic, anti-inflammatory and even acted as modulators of the immune system.

Cardoso et al[33] reports that the criteria for classifying fungi among various indigenous peoples, as highlighted above, are similar to those of classical taxonomy. The Yanomami Indians (=human beings), for example, were recognized as an ethnic group that represent a wide knowledge of ethnoclassification of fungi, and that in some cases are similar to the recent phylogenetic classification proposed[29,33].

Other taxa were cited for fungi identified in MT, obtained in the contributions[7,8,34,35], being the microscopic fungi of the phylum Oomycota *Achlya radiasa* (water mold) and the fungus macroscopic view of the phylum Basidiomycota *Trametes cupreorosea*, receiving prominence.

In fact, this last fungus, *Trametes cupreorosea* (Polyporaceae), was used in MT by Rikbaktsa indigenous tribes for diseases related to the female sex[36], the caboclas of MT and the Amazon region use this fungal species to alleviate menstrual disorders, uterine cramps that occur as a result of menstrual flow[29].

Australian Aboriginal Indians used this same fungal genus, used in Brazilian indigenous folk medicine, to treat and cure oral wounds, small ulcerations in the oral cavity and also treat oral thrush in newborns[31].

In certain indigenous groups, skin diseases are defined almost exclusively as being of parasitic origin. Reports that the Nhambikwara Indians, who lived near the Guaporé tributary, on the Mato Grosso-Bolivia border, had an endemic dermatophytosis, known by them as “chimberê”[29] called tinea imbricata, provoked initially by the agent called “Endodermophyton” and currently known as the dermatophytic etiological agent *Trichophyton concentricum*[5] which was commonly called “tokeláu” because of its allusion, previously, among the indigenous peoples of the Tokelau Archipelago in the Pacific Ocean.

The disease was described in 1924, for the first time in Indians of the Purú-Borá tribe (Tupi=people of the jaguars) who lived in the MT backlands and at that time still quite isolated from contact with any other human group[4].

Cases of Jorge Lobo's blastomycosis (=Lacaziosis) found among Kaiabí Indians (Tupi=forest dweller) living in native villages on the banks of the Tatui river (Mato Grossense Amazonia) were recorded by Machado[27]. Among the Kaiabí Indians, Jorge Lobo's blastomycosis, caused by the implantation of the fungus Lacazia loboi, was found in very variable dermatological conditions and called by the indigenous people as “*miraip*”[22].

From the data mentioned and the conclusions, we can assume that there is a wide knowledge and application of fungi by the forest populations, which are actually expressed in the scientific literature, these records being cataloged very old and deserve greater attention in the history of the Brazilian people. The vast majority of these reports were obtained through information from indigenous tribes presented to botanists and none of them actually performed by a mycologist.

The ethnomicological contributions of the indigenous peoples of the MT and Amazon region can be found in the records compiled in the ethnic groups of the Brazilian, Peruvian, Venezuelan and Colombian Amazonian peoples[19].

SYSTEMATIC AND TAXONOMIC CLASSIFICATION

For decades estimates of the number of fungi on the planet were evaluated, first by Bisby and Ainsworth[37] who estimated around 100,000, then Martin[38] estimated this fungal biodiversity to be 250,000. In an accepted estimate that lasted for two decades, he estimated the fungal magnitude to be 1.5 million species on the planet[39].

Phylogenetic classifications occurred in the broad taxonomy of the kingdom Fungi, causing these eukaryotic organisms to undergo changes in their groups in recent decades, generating proposals, with reference to phylogenetic and molecular analyzes with input from several members of the taxonomic fungus community.

In 2011, a new hypothesis came into question, defended by Blackwell[40], saying that this estimate of the amount of fungi on the planet would reach 3.5 to 5.1 million worldwide. An updated estimate of fungal diversity showed that fungal species ranged from 2.2 to 3.8 million worldwide[41] with insertion of species that can infect humans and animals, especially in tropical countries, sub-tropical and temperate.

More recent data generated by Chinese researchers[42] from surveys of fungal species on Earth have been estimated at 12 to 13.2 million species, and it appears these estimates will change with new daily discoveries of the existence of these organisms on the planet.

Niskanena et al[43] reported in their records that 2,189 species were newly described in 2017, cataloging from mushrooms to sporulating fungi such as molds. In the records there is a predominance of the phylum Ascomycota (1,481 species) of new fungi, followed by Basidiomycota represented by (684 species) informed.

Recently, a collaborative effort of 200 scientists from 42 different countries published a report entitled “The State of the World for Plants and Fungi 2020”. In this manuscript in 2019 alone, 1,886 fungi were recently described by scientists, some closely related to known medicinal species and potentially new sources of medicines[44].

There is no accurate record of the total number of species of native fungi in Brazil that have been identified or collected across the country. The publication of the Catalog of Plants and Fungi in Brazil reports mycological groups constituting a milestone in the systematization and dissemination of data on the diversity recorded in Brazil, which indicate the records of 78 orders, 924 genera and 3608 species of Brazilian fungi comprising the phyla Ascomycota, Basidiomycota , Blastocladiomycota, Cryptomycota, Chytridiomycota, Entomophtoromycota, Glomeromycota, Hyphochytridiomycota, Labirinthulomycota, Myxomycota, Oomycota, Plasmodiophoromycota and Zygomycota[45].

In 2015, Maia[46]and his collaborators presented work on the diversity of Brazilian fungi, describing 13 phyla, 102 orders, 1,246 genera and 5,719 species of fungi, with a predominance of the phylum Basidiomycota (2,741 species) and Ascomycota (1,881 species).

Nowadays, the phyla destined for the classification of the kingdom Fungi have been continuously updated, with the frequent inclusion of DNA sequence data in recent studies[47]. Tedersoo et al[48] based on phylogenetic studies established the taxa in 18 phyla: Ascomycota, Aphelidiomycota, Basidiomycota Basidiobolomycota, Blastocladiomycota, Calcarisporiellomycota, Caulochytriomycota, Chytridiomycota, Entomophthoromycota, Glomeromycota, Kickxellomycota, Monoblepharomycota, Mortierellomycota, Mucoromycota, Neocallimastigomycota, Olpidiomycota, Rozellomycota and Zoopaggomycota.

However, more currently mycologists and scholars of the Fungi kingdom have proposed new changes, fixing 12 taxons for the controversial kingdom establishing: Ascomycota, Basidiomycota, Microsporidia, Chytridiomycota, Zoopagomycota, Mucoromycota, Cryptomycota, Neocallimastigomycota, Entorhizomycota, Aphelidiomycota, Monoblepharidomycota, Blastocladiomycota[2].

Wijayawardene and a group of collaborators[47] updated the classification in class, order, and families establishing 19 fungal taxons: Aphelidiomycota, Ascomycota, Basidiobolomycota, Basidiomycota, Blastocladiomycota, Calcarisporiellomycota, Caulochytriomycota, Chytridiomycota, Morophellomycota, Chytridiomycota, Morophellomycota, Chytridiomycota Mucoromycota, Neocallimastigomycota, Olpidiomycota, Rozellomycota and Zoopagomycota.

The hidden, silent, mysterious and microscopic nature of many fungi often ends up generating an underreported diversity with a much higher number of species that were, or are no longer formally described, as they claim[40,41]. These eukaryotic organisms still present a great classification that will become evident as the insistence on the studies of these groups become more and more productive.

ENVIRONMENTAL MYCOLOGY: THE "HOSTSPOTS" OF BIODIVERSITY

Brazil is known as having one of the highest biodiversity in the world. However, existing information on the biological diversity of some types of organisms, such as fungi, is restricted to research institutions, scientific collections, museums and much information taken abroad.

Brazil has six major biomes: the Amazon occupying (49.5%) of the Brazilian territory, followed by the Cerrado (23.3%), the Atlantic Forest (13%), the Caatinga (10.1%), the Pampa (2.3%) and finally the Pantanal (1.8%). In Mato Grosso, the three main representative biomes are: the Cerrado with 56.1% of the surface of the Center-West region[49], with very rich vegetation and immense biodiversity in fauna and flora; the Amazon, which covers 50% of the entire territory, and finally the Pantanal, which occupies 7.2% of the MT territory, being considered the largest eligible area on the planet, with an exuberant fauna and one of the most exalted biomes when it comes to MT[12] (Figure 2).

Initially, records of studies on fungi in the Mato Grosso region regarding fungal taxa and records of species identified in substrates and environments were reported in the publications of De Iamônica Freire[50], who studied 9 genera and 30 species of fungi in his dissertation Clavarioids (Basidiomycota) from the Amazon, Mato Grosso, Pará and Roraima; subsequently, in 1981, Bononi[51]described fungi of the phylum Basidiomycota, of the class Agaricomycetes identified for the regions of Serra do Roncador, Nova Xavantina and Aripuanã, and then Moraes[52], in his dissertation, recorded the occurrence of 50 taxa of the genus Meliola (Meliolaceae, Ascomycetes) for Mato Grosso.

For the central-west region of Brazil, some works were found on macrofungi in this region, highlighting the works carried out mostly with the Cerrado biome, a biogeographic region recognized by the scientific community along with other natural habitats as ecological hotspots, highlighting the research of Sampaio[34] carried out a fungal inventory of the Cerrado Domain. The results of Fidalgo[7] who cataloged a compilation with material collected from the Amazon and Cerrado phytogeographic domains and, subsequently, an inventory of species that occur in the Pantanal do Rio Negro in MS/Brazil, mentioned for the first time by the respective species *Collybia bakeri*, *Entoloma cerussatum*, *Epithelopsis fulva, Hypochniciellum subillaqueatum*, *Hypochnicium vellereum*, *Lentinus concavus, Mycena parabólica, Mycoaciella bispora, Nigroporus macroporus, Nothopanus hygrophanus, Pholiota polychroa, Pleurotous agaves, Trametes subectypus e Tricholomopsis tropica*[53].

More recently, studies of lignolithic Agaricomycetes in the Brazilian Cerrado were recorded[54] and the notes of Costa-Rezende et al[55] of polyporus fungi (Polyporiaceae) during collection expeditions in the Chapada dos Guimarães National Park, MT, Brazil recording for the first time the species of *Truncospora detrita, Pyrofomes lateritius, Hornodermoporus martius, Perenniporia aurantiaca, P. tephropora*.

In the municipality of Tangará da Serra-MT, Mato Grosso researchers carried out collections of the fungal diversity of the soil in that region, aiming to isolate and identify filamentous fungi through seasonal surveys in three areas of native cerrado vegetation. Thus, Hyphomycetes of the *genera Aspergillus, Acremonium Cladosporium, Fusarium, Glocladium, Humicola, Paecilomyces, Penicillium, Trichoderma, Verticillium, Coelomycetes* of the genus *Phoma* and Zygomycetes of the genera *Conidiobolus, Cunninghamella, Mucor* and Ascomycetes of the genera *Periconia, Pyrenochaeta* and *Mycelia sterilia*[56] were identify.

Another exploratory study carried out in the Cerrado, aiming to identify arbuscular mycorrhizal fungi of the Glomeromycota phylum, found 92 species by researchers from São Paulo, highlighting the first record for the savanna area, being *Ambispora brasilienses* and *Cetraspora auronigra,* reported exclusively in the phytophysiononic region of the Brazilian savannah[57].

Fungi associated with wild plants from the Brazilian Cerrado in the Serra Ricardo Franco State Park, located in Vila Bela da Santíssima Trindade, on the border with Bolivia, and also in Barra do Garças, both areas located in the State of MT, species of the genus Meliola (Meliolales/Ascomycota): *Meliola alibertiae*, *M. desmodii-laxiflori, M. stizolobii* var. *eriosematis, M. kernii, M. voocangae*[58].

Despite agribusiness being one of the driving forces of the Midwest region of Brazil, studies involving fungi for plantation and agricultural activities were not registered for MT. Two records were identified for MS for the Cerrado biome, with the work of Theodoro & Batista[59] with rubber trees and Cortina[60]et al with soybean seeds.

Also in 2017, Alvarenga & Xavier-Santos[61] reported the occurrence of gelatinous basidiomycetes belonging to the order Dacrymycetales, highlighting the species *Colocera cornea, Dacrymyces chrysospermus, Dacryopinax elegans, D. maxidorii, D. spathularia* identified as the first records for the Cerrado and Midwest region of Brazil.

More recently, Leite-Jr et al[10] recorded an extensive list of species identified for the Midwest region of Brazil, covering the Cerrado region in the central region of the State of MT. The extensive list encloses 26,194 fungus specimens from 342 samples of the dust substrate and their respective species such as: *Absidia, Acremonium, Alternaria, Aspergillus, Aureobasidium, Bipolaris, Bispora, Candida, Chaetomium, Chrysonilia, Chrysosporium, Circinella, Cladophialophora, Cladosporium, Cryptococcus, Cunninghamela, Curvularia, Cylindrocarpon, Epicocum, Exserohilum, Fonsecaea, Fusarium, Geotrichum, Graphium, Hanseniospora, Hansenula, Hormonema, Macrophomina, Mariannae, Monascus, Mycelia sterilia, Neocytalidium, Nigrospora, Paecilomyces, Penicillium, Pestalotiopsis, Phaeacremonium, Phialophora, Rhizopus, Rhodotorula, Rinocladiela, Saccharomyces*, *Scedosporium, Scopulariopsis, Syncephalastrum, Sporobolomyces, Stacybotrys, Stemphylium, Talaromyces, Trichoderma, Trichosporon, Tritirachium* and *Ulocladium.* This work stands out because it is one of the pioneering works, in the cataloging of microscopic species existing for the central region of Brazil, covering one of the biodiversity hotspots (Cerrado).

According to the records of the Virtual Herbarium of Flora and Fungi[62], which gathers information from herbaria from Brazilian institutions, researching the Midwest region of Brazil, we identified only seven described species and their species for the State of MT, respective collection dates: *Auricularia fuscosuccinea* (1986), *Auricularia polytrica* (2009); *Marasmius cladophyllus* (2009); *Morganella fuliginea* (1978), *Pycnoporus sanguineus* (2012), *Schizophyllum commune* (2012) e *Geastrum schewinitzii* (2012). For the State of MS and GO, only the registered species *A. polytrica* (2004) and *A. polytrica* (1995) was found respectively, and finally, in the Brazilian Federal District (Brasília, Federal Capital of the country), two registered species were found: *A. polytrica* (1980) and *G. schewinitzii* (2009).

One of the milestones in phytophysiognomy in the State of MT, the Pantanal's biodiversity is practically unknown, especially in relation to fungi, this biome is one of the "hotspots" of biodiversity and water resources on the planet due to its importance and degree of environmental threats that has been suffering in recent years. The only record of fungi in the Pantanal region were reports by Galvão et al[63] who verified the presence of arbuscular mycorrhizal endophytic fungi (AMF) in roots of plant species collected in the Pantanal de Poconé, MT, Brazil; classifying the findings as FMA and dark septate endophytic fungi (DSEF).

MT and MS despite having the same history of their emergence, colonization and creation, began to coexist independently after the division of states that occurred in 1977. In the Pantanal of MS, Brazil, neighboring state of MT, records carried out by Gomide et al[64] studying arbuscular mycorrhizal fungi (AMF) in soil phytophysiognomies of the Pantanal de Nhecolândia, finding spores of fungi of the phylum Glomeromycota belonging to the families (genus): Acaulosporaceae (*Acaulospora*), Paraglomeraceae (*Paraglomus*), Ambisporaceae (*Ambispora*), Claroideoglomeraceae (*Claroideoglomus*), Glomeraceae (*Rhizophagus, Glomus*), Gigasporaceae (*Gigaspora, Dentiscutata, Cetraspora, Racocetra*).

Bononi et al[65] in collections carried out in central Brazil, in the state of MS, identified 18 species of basidiomycete fungi for that region, referencing the species: *Athelopsis galzinii, Clitocybe infundibuliformis, Conocybe crispa, Coprinellus micaceus, Cymatoderma elegans, Fomitiporia robusta, Guepinia helvelloides, Gymnopus dryophilus, Hypholoma fasciculare, Marasmius androsaceus, Marasmius oreades, Mycena pura, Panaeolus rickenii, Pleurotus eryngii, Rhodocollybia butyraceae, Trametes ellipsospora, Tricholoma argyraceum, Tremella mesenterica.*

For the region of the State of GO and the Brazilian Federal District (DF) completing the federative regions of the Midwest region of Brazil, the records made by Alvarenga et al[66], reported the occurrence of 101 samples of basidiomycete fungi of the genus Auricularia, highlighting: *Auricularia nigricans, A. fuscosuccinea, A. mesentericae, A. delicata* for the State of GO and *A. delicata* for the Federal District.

In 2016, researchers from Goiás[67] recorded species of fungi of the phylum Ascomycota, coprophiles carried out in the State of GO in the morphoclimatic domain of the Cerrado, isolated from the excreta of domestic pig (*Sus scrofa domesticus*), cattle (*Bos taurus*), horse (*Equus caballus*) and peccary (*Tyassu pecari*), isolating species considered rare for the neotropical region *Cercophora coronata* and *Zopfiella latipes* of the Lasiosphaeriaceae family, *Hypocopra stercoraria* (Xylariaceae), the largest family of Ascomycota and *Pyxidiophora arvernensis* (Pyxidiophioraceae). In 2018, this same researcher and his collaborators[68] in the Cerrado of the region of GO, registered the fungus Basidiomycete *Phlebopus beniensis* (Boletinellaceae, Boletales).

General report of fungal strains with biotechnological potential of the genus Paecilomyces was carried out in geographic regions with high biodiversity, covering the Brazilian savannah, mainly the region of GO. The records of Lopes et al[69] isolated 20 species of this fungal genus highlighting *Paecilomyces formosus* and *P. parvisporus* for Brazil. This fungal genus has a broad relationship with the Cerrado region, located in the central portion of Brazil, studies carried out in Cuiabá, capital of MT, show that the Cerrado region is a probable ecological niche for the Fungal genus. Leite-Jr et al[10] in central Brazil, isolating seven species of the genus in library dust, with emphasis on *P. lilacinus* and *P. variottii* and further on, for the same region; Pereira et al[70] isolated *P. lilacinus* in large percentage from sand in children's recreational parks. This information denotes and reinforces the importance of cataloging the Brazilian biodiversity and especially those destined for the Central region of Brazil, as they raise hypotheses that these isolated species can contribute information that can be used and used for biotechnological purposes.

An illustrated guide made in the Cristalino State Park, one of the most remarkable points of biodiversity in the State of MT; Located on the border with Pará, between the Municipalities of Alta Floresta/MT and Novo Mundo, it was created by Lodge & Sourel[71] with photographic illustrations of fungi for the region, covering the forests of the Amazon biome. In the illustration we can see the genera of the Ascomycota Phylum: *Favolus, Flabellophora, Fomes, Ganoderma, Hexagonia, Lentinus, Microporellus, Panus, Perenniporia, Phellinus, Polyporus, Pynoporus, Rigidoporus, Trametes, Trichaptum;* and the representatives of the phylum Basidiomycota: Aphyllophorales, *Auriscalpium,Cotylidia, Cymatoderma, Flavodon, Hydnopolyporus, Inflatostereum, Mycobonia, Podoscypha, Stereum, Clavaria, Clavulina, Deflexula, Lentaria, Macotyphyla, Multiclavula, Pterula,Ramaria, Tremellodendron* and the representatives Myxomycetos *Arcyria, Ceratiomyxa, Lycogala, Physarum, Trichia*.

A new illustrative series was conceived by Sourel et al[72] cataloging new species in the Cristalino RPPN (Private Reserve of Natural Heritage) in Alta Floresta/MT, Brazil. With records of the representatives of the Ascomycota phylum: *Akanthomyces, Ascocoryne, Ascopolyporus, Beauveria, Bionectria, Camillea, Colostilbe, Cookeina, Corallonectria, Cordyceps, Dicephalospora, Gibellula, Hypocrella, Hypocreopsis, Hypomyces, Hypoxylon, Metacordyceps, Moelleriella, Nigelia, Ophiocodrdyceps, Penicilliopsis, Scutellinia, Thamnomces, Thuemenella, Trichoderma, Xylaria. For the phylum Basidiomycota were registered: Agaricus, Amanita, Amparoina, Alboleptonia, Calliderma, Colocybe, Clitocybula, Coprinellua, Corpinopsis, Crepidotus, Crinipelli, Cyptotrama, Cystolepiota, Echinoderma, Favolaschia, Gerronema, Gloiocephala, Gymnopus, Hemymycena, Hohenbuchelia, Hygroaster, Hygrocybe, Inocephalus, Lactifluus, Lentinula, Lepiota, Lepista, Leptonia, Leucoagaricus, Leucoprinus, Macrobybe, Macrolepiota, Marasmiellus, Marasmius, Melanophyllum, Moniliophthora, Mycena, Nolanea, Oudemansiella,Pholiota, Phyllobolites, Physalactria, Ripartitella, Pluteus, Psylocybe, Russula, Tapinella, Xeromphalina, Phlebopus*. For the gelatinous Basidiomycetes/Jelly fungi (Heterobasidiomycetes) stand out: *Auricularia, Calocera, Pseudohydnum, Tremella.* For the fungi Basidiomycota gasteroides (Gasteromycetes informal) the respective genera were identified: *Calvatia, Geastrum, Lycoperdon, Mutinus, Myriostoma, Phallus, Sclroderma, Tulostoma*. For Basidiomycotas polyporales (Agaricomycetes) were recorded: *Abundisporus, Antrodiella, Amauroderma, Cerrena, Cyclomyces, Cymatoderma, Flabellophora, Fomes, Ganoderma, Leninus, Microporellus, Neofavolus, Panus, Phellinus, Podoscypha, Polyporus, Rigidoporus, Stiptopyllum, Trametes, Trichaptum.* The clavarioid fungi (Agaricomycetes): *Artomyces, Clavaria, Clavulinopsis, Lachnocladium, Lentaria, Macrotyphula, Phaeoclavulina, Pterula, Ramaria, Ramariopsis, Scytinopogon, Tremellodendropsis, Typhula.* Among the *Myxogastria* (Myxomycetes) were identified: *Arcyria, Ceratiomyxa, Hemitricia, Physarum, Tubifera*, and still others Basidiomycotas *Sarcodon* (Thelephorales), *Stereum* (Russulales) and *Trechispora* (Trechisporales).

And finally, a pioneering search for fungi in the Serra Ricardo Franco State Park region, located in the municipality of Vila Bela da Santíssima Trindade - MT, on the border with Bolivia, a region covered by a transitional forest connecting two important Brazilian biomes: the Cerrado and the Amazon Forest, these researchers, focusing on microfungi associated with native plants, recorded five species of Asterinaceae (Ascomycota/Dothideomycetes), four of which were documented for the first time: *Asterina indecora, A. cerradensis, A. malvacearum, A. Lembosia matogrossensis and L. miconiphylla*[73].

Graphic maps of the world's continents show the distribution of fungi around the world. According to the records, we can observe that the percentages in Asia and South America lead the world, followed by China and Brazil respectively[74]. This information diverges, when referring to Brazil, some studies present an abundant diversity, however information from the regions is scarce and disconnected. Europe ranks third with taxonomic descriptions and records of its species. Africa presents a low diversity, not due to the lack of described species, but due to the lack of investment in taxonomic research and the incentive to discover new fungal species that occur in the place (Figure 3).

These inconsistencies in fungal species descriptions are reflected in the IUCN (International Union for the Conservation of Nature) Red List of Endangered Species[75]. Although the list is quite comprehensive and presents sustainable records on the extinction of animal and plant species on the planet, the variations presented for fungi are much smaller; only 285 of 148,000[76] described fungal species (0.2%) are assessed on the Red List. The estimated percentages do not present reliable information, in contrast to the information described by several authors in their series, it is possible that, due to these unsatisfactory results, there are huge biases, gaps and deviations in the many records presented for Brazilian fungi species.

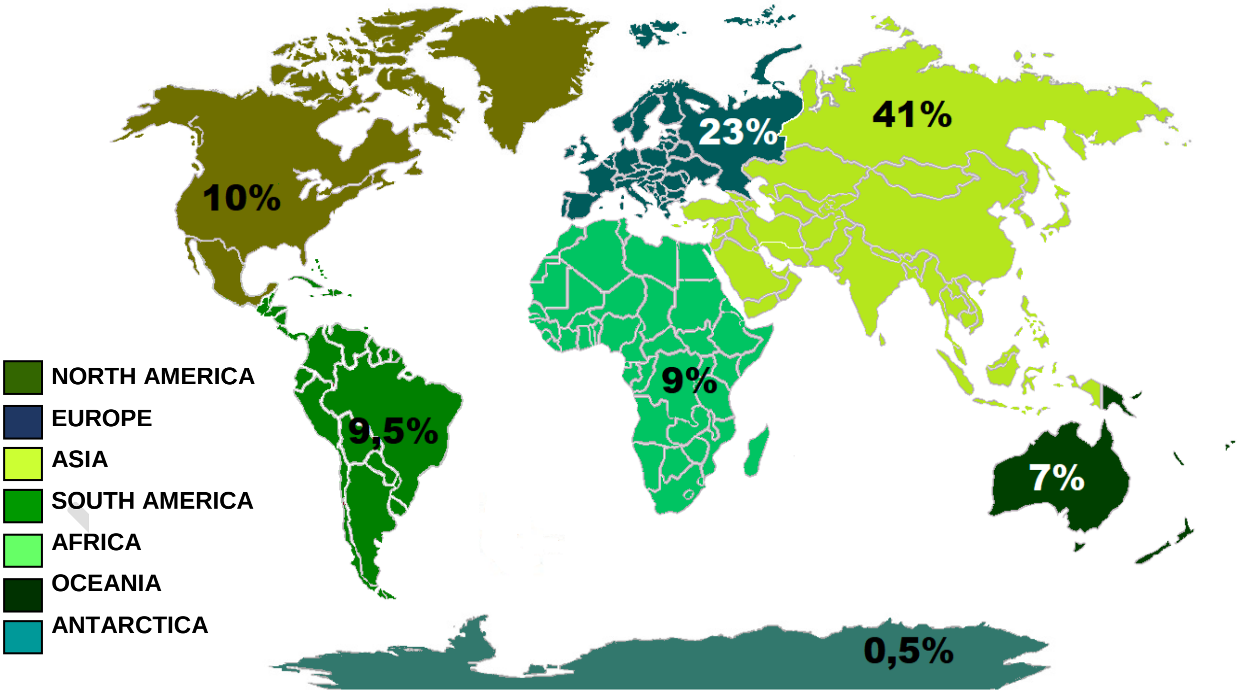


Figure 3. Geographic map of the continents showing the percentage distribution of recently described species of fungi [74]. Adapted Leite-Jr, D.P.

These questions are in line with the records by Mueller et al[77] who emphasize in the Species Survival Commission (SSC) report that of the 285 fungi assessed by the Red List of Endangered Species; 234 are species of Basidiomycota, one of the seven most representative phyla of the fungi kingdom, showing how far the Red List is from representing the true estimate of threats being blamed on the global diversity of fungal organisms on our planet.

FORENSIC MYCOLOGY: USE OF FUNGI IN CRIMINAL INVESTIGATIONS IN MATO GROSSO

Covering an overview and a field record of forensic mycology, with reference to the involvement of fungi in the degradation of decomposition processes, Leite-Jr et al[78] carried out a record of fungi involved in the degradation, indicating the forensic area for the State of MT and the applicability of a new science involved in criminal investigations for the region.

This researcher and his collaborators evaluating the thanatological processes and cadaveric phenomena in a region of the Brazilian Cerrado in the central portion of the country, Chapada dos Guimarães; isolated saprobic fungi that were involved in the decomposition process, where pig carcasses (*Sus scrofa domesticus*) were used as an experimental model and substrate for isolating the fungal specimens.

In the study, species representing the cadaveric mycobiota of the Ascomycota Phylum were isolated: *Aspergilus niger, A. ochraceus, A. terreus, Penicillium citrinum, P. expansum P. griseofulvum, Talaromyces rugulosus, Paecilomyces viride, Brothrytes cinerea, Fusarium graminearum, F. oxysporum, Trichoderma harzianum, T. viride, Alternaria alternata, Paecilomyces chartarum, Candida kefyr, C. krusei, C. tropicalis, Pichia anomala, Chrysonilia sitophila, Nigrospora nigri, Pestalotiopsis microspora;* Zygomycota Phylum: *Circinella muscae, Mucor hiemalis, M racemosus, Mycocladus ramosus, Rhizopus oryzae, R. stolonifer* e Basidiomycota Phylum: *Rhodotorula mucilaginosa* e *Trichosporon* spp.[78].

These isolated specimens can be found in closed environments, where they release spores, easily transported by air, considered anemophilous entities, in fact, dissemination by anemochoria is one of the main forms of propagation of many fungi, and extremely efficient as reported by Leite- Jr et al[10] and their collaborators in a study carried out in the city of Cuiabá/MT.

The isolation of these fungal specimens reinforces the guidelines of Lacaz et al[5], who emphasize that fungal agents can serve as opportunistic agents, causing colonization in preexisting cavities. Their conidia become easy to spread and can be easy agents of contamination.

In the same sense, in order to establish the real role of these entities, gaps in studies involving these microorganisms as a tool in technical-scientific and medico-legal investigations must be filled.

It is extremely important to observe the safety standards, their ecological and pathological characteristics, as these entities assume epidemiological relevance in front of professionals who perform the techniques and perform necropsy, making them exposed to these biological beings involved in human fungal infections such as mycoses, infections pulmonary diseases and even severe systemic manifestations with fatal conditions[10].

MEDICAL MYCOLOGY: FUNGI INFECTIONS AND ENVIRONMENTAL CONTAMINATIONS IN MATO GROSSO

Many records on the incidence of systemic mycoses and infectious diseases in Brazil are mostly unreliable. The records on cases, mortality, outbreaks in Brazil suffer from the incorrect filling of their records and consequently suffer from underreporting.

Since the discovery of penicillin by Alexander Fleming, a fact that marked the beginning of the antibiotic era, soldiers died during World War II from infection with *Staphylococcus aureus* and *Haemophilus influenzae* bacteria[79]. Before penicillin was synthesized, historical records report that soldiers placed moldy pieces of bread to heal wounds, due to the fungus' unknown antibiotic properties. Currently, from an economic point of view, the biotechnological applications of fungi present implicable actions in several areas: pharmaceutical, nutritional, human and veterinary medicine, phytopathology, among others; with amazing results.

Fungi are present in almost all environments on planet Earth, and the greatest diversity is found in the tropical regions of the world, whose hot and humid climate is favorable to their proliferation.

Over the last few decades, outbreaks of fungi caused by previously rare genotypes or even new species have emerged, where they are often observed as saprobes and/or invertebrate parasites, other fungi, oomycetes, algae, macrophytes, mammals, amphibians and even those that affect human beings[40].

As occurs in recent records of infections in groups of animals such as the extermination of amphibian populations caused by environmental fungi that have been standing out, such as those of the phylum Chytridiomycota: *Batrachochytrium dendrobatidis* and *B. salamandrivorans* and those that have been decimating populations of mammals of the Order Chiroptera called *Pseudogymnoascus destructans*, from the phylum Ascomycota[80].

This occurrence demonstrates the microscopic, hidden and silent nature of many fungi, indicating that their diversity is often underreported with a much higher number of species that have been formally described[40,41].

Studies related to publications with microscopic fungi seem to be the key motive for scientific investigations and analyzes in the MT region. Studies covering pathogenic species are relevant in the State of MT, covering a variety of fungal groups in hospitals, environmental analyzes and even those harbored in humans and animals.

Cataloging research, we can observe the studies related to environmental substrates and fomites, which were recorded by Simões et al[81] evaluating the microbiota of air conditioners in an intensive care unit in Cuiabá and its impact on hospital health in hospitalized patients, with emphasis on the fungi of the genera *Aspergillus, Penicillium* and *Cladosporium*.

In an approach to air-dispersed microbiota, isolating the genus *Cryptococcus*, a capsulated yeast, Leite-Jr et al[82] isolated this yeast complex housed in library dust recording the species of medical interest *Cryptococcus gattii* and *C. neoformans*, as well as *C. neoformans*. Other relevant species *C. terreus, C. luteolus, C. uniguttulatus, C. albidus* and *C. humiculus.*

We also have the isolation and identification of the group of capsulated yeasts, carried out by Takahara et al[83] who collected samples of this fungal agent from the metropolitan area of the capital of MT, isolating specimen samples from pigeon excreta (*Columba livia domestica*) recording *Cryptococcus neoformans* isolated in urban areas, predominantly in homes, constituting a risk of acquiring the disease by immunocompromised and immunocompetent individuals.

In the following year, Anzai et al[84] isolated *Cryptococcus gatti* from plant samples, highlighting the yeast form, from plant parts of *Phlathymenia reticulata* (Fabaceae), representing the flora of the Brazilian Cerrado of Mato Grosso.

Still evaluating the aerosol microbiota, Leite-Jr et al[85] contributed with a description of fungal species from the Trichocomaceae family, from the genera Aspergillus and Penicillium residing in the dust of library environments, contributing to the current knowledge of these characteristic genera. This family has currently redefined trichocomaceae into three distinct families, Aspegillaceae, Trichocomaceae and Thermoascaceae[86,87].

Still following this same line of environmental contamination by bioaerosols; more currently, Leite-Jr et al[10] recorded an extensive list of species identified for the Midwest region of Brazil, covering the cities of Cuiabá and Várzea Grande/MT. These results highlight the importance of the existence and identification of fungi, in order to minimize the risk of exposure to pathogenic and toxigenic fungal agents, identified in microenvironments in library collections. This extensive mycological list may have been the largest record of fungi species for the MT region, already cataloged so far.

A study by Simi et al[88] isolating fungal agents found in the excreta of psittacine birds and birds of prey in captivity, belonging to the Matogrossense fauna, evaluating the potential risk of these microorganisms on human health, the following species were isolated: *Aspergillus niger, Aspergillus flavus, Cryptococcus albidus, Rhodotorula mucilaginosa, Candida kefyr* and *Trichosporon inkin,* as eukaryotic organisms found in this type of substrate and prone to sources of contamination.

Lately, species found in hospital environments are drawing attention and gaining importance for the improvement of methods for identifying environmental fungi in hospitals. Coronavirus cases registered in Brazil and in the world have placed the planet on constant alert, taking advantage of this moment by other microbiological entities taking advantage of this to cause simultaneous infections in debilitated and hospitalized patients.

On this occasion, referring to Aspergillus latus, a fungus found in plants, which became opportunistic and was isolated for the first time in a hospital environment and which has shown more resistance to antifungal drugs than other fungi of its genus.

A group of international researchers composed of Brazilians, Americans, Portuguese and Belgians carried out the genetic sequencing on this species, indicating that the main fungi of this genus capable of causing an infection called Aspergillosis are caused by the species Aspergillus fumigatus, responsible for about 90 % of cases, followed by *A. flavus, A. terreus, A. niger* and *A. nidulans* can also affect the respiratory system, the latter being especially frequent in patients with chronic granulomatous disease that affects the body's defense cells[89].

Invasive fungal diseases can have high mortality rates and their association with COVID-19 has been recognized with greater frequency and criticality. Cases of coronavirus-associated pulmonary aspergillosis (CAPA) have been described in several studies. Interestingly, many of these patients do not have classic risk factors for invasive pulmonary aspergillosis, such as a history of malignancies such as cell transplants, neoplasms or neutropenias.

A study carried out in hospitals in Belgium, Germany, Italy, France, Mexico, Netherlands, Pakistan, Spain, Switzerland and the United Kingdom found that most ICU patients had been diagnosed with Acute Respiratory Distress Syndrome (ARDS) and other characteristics such as use of steroids, cardiovascular disease, diabetes mellitus, obesity and chronic lung disease. Most records occurred in male patients. *Aspergillus fumigatus* was the most commonly isolated species in clinical records, causing Aspergillosis cases followed by the species *A. niger, A. flavus, A. terreus, A. calidoustus, A. lentulus, A. nidulans, A penicillioides, A. versicolor, A. tubingensis* in their series[90,91].

DERMATOPHYTOSIS AND DERMATOMYCOSIS

Dermatophytosis comprises a wide variety of distinct clinical conditions. The most common were included in the cutaneous mycoses under the generic name of “tinhas” (from the Latin tinea = worm), and classified according to location: *Tinea capitis, Tinea corporis, Tinea barbae, Tinea unguium, Tinea pedis, Tinea manuum* and *Tinea cruris*[92], entities capable of extracting nutrients from the keratin protein, an abundant substance present in the epithelial cells of higher vertebrates (mammals, birds and reptiles) is the basic component of human and animal skin, present in hair, fur, hooves, nails, scales, horns, feathers, an item richly addressed in the classic work of mycology – Les Teignes, by Raymond Jacques Andrien Sabouraud[5].

Currently, based on advanced molecular studies (ITS, rDNA and partial sequencing of LSU, 60S ribosomal subunit, β-tubulin fragments and translation elongation factor 3), american researchers phylogenetically analyzed trees from the dermatophyte groups and showed degree of correspondence between the phylogen groups reaching an acceptable level of stability[93].

In Mato Grosso, dermatophytes and the group of keratin-loving fungi that affect the skin and its appendages (hair and nails) were researched and found in the records of Araújo et al.[94] These authors isolated dermatophytic agents from the city's public health services from cities Cuiabá and Várzea Grande. We also found records by Leite-Jr et al[85] with research in the occupational area in analyzes involving material collected (skin, hair and nails) from military professionals in the city of Cuiabá, isolating *Trichophyton rubrum, Trichophyton mentagrophytes, Trichophyton verrucosum, Trychophyton tonsurans, Trichophyton interdigitalis, Epidermophyton floccosum, Microsporum canis, Microsporum gypseum*. This last species is currently reclassified in the genus Nannizzia[93].

The reports found in the study by Leite-Jr et al[85] showed that some dermatophytic strains showed a cellular adaptation or transition of species to different anatomical sites. As reported in cases of *Trichophyton tonsurans* and *T. verrucosum* diagnosed in glabrous skin (*tinea corporis*) and nail (*tinea unguim*) infections, other than the original site of infection, ectotrix invasion of the scalp (*tinea capitis*), as reported by several authors[5,95-97].

A clinical veterinary study in the city of Cuiabá, capital of MT, carried out by the veterinary department of the Federal University of Mato Grosso, indicated a high rate of infection by dermatophytes in cats without clinical signs, with a predominance of the dermatophytic agent Microsporum spp., in addition of the isolation of the genera *Trichophyton, Candida, Malassezia, Aspergillus* and *Penicillium.* The researchers warned that animals can harbor these fungi, acting as asymptomatic carriers, contaminating the environment and increasing the rate of infection[98].

In the taxonomy recently proposed by De Hoog[93]and his collaborators; 56 species were classified and considered dermatophytic. The genus Arthroderma had the highest number with 21 species, followed by *Trichophyton* with 16 representative species, followed by *Nannizzia* with nine described species, followed by *Microsporum* and *Paraphyton* with three species, respectively, and finally *Ctenomyces, Epidermophyton, Lophophyton* and *Guarromyces* one species each, respectively[93].

More recently, involving possible infections by these fungal groups in the MT region, Pereira et al[70] reported the importance and danger of pathogenic fungi in children's recreation areas, highlighting the genus *Trichophyton* with (86.2%) of the isolates, in addition to isolating other agents such as *Aspergillus, Penicillium, Paecilomyces* and *Fusarium* as possible agents of non-dermatophytic fungal infections.

SYSTEMIC FUNGI: LETHAL FUNGI INFECTIONS

Endemic systemic mycoses in Brazil are: Paracoccidioidomycosis, Histoplasmosis, Coccidioidomycosis and Cryptococcosis. In the area of medical mycology and hospital practice, the records found involving fungal species in MT were human clinical isolates involving systemic fungi, diseases and biological injuries caused by these eukaryotic agents.

Zygomycosis (mucormycosis) a rare but highly invasive infection caused by fungi of the order Mucorales (*Absidia, Apophysomyces, Cunninghamella, Cokeromyces, Rhizopus, Rhizomucor, Mucor, Rhizomucor, Apophysomyces, Saksenaea,* and *Syncephalastrum*) are the representative types of genera infection.

One of the first records of fungal infection caused by fungi in this group was the case record of Zygomycosis (order Mucorales and Entomophthorales), a subcutaneous mycosis caused by fungi found in the soil. The scientific report describes a manifestation of chronic granulomatous infiltration of the rhinofacial region caused by the fungus *Conidiobolus coronatus,* a saprophytic fungus capable of infecting men and animals[99].

Subsequently, Ribeiro et al[100] described systemic mycoses associated with patients carrying the HIV virus, isolating the fungal species *Cryptococcus neoformans, Cryptococcus gatti, Cryptococcus* spp., *Histoplasma capsulatum* and *Paracoccidioides brasiliensis* in their findings.

Subsequently, Ribeiro et al[100] described systemic mycoses associated with patients carrying the HIV virus, isolating the fungal species *Cryptococcus neoformans, Cryptococcus gatti, Cryptococcus* spp., *Histoplasma capsulatum* and *Paracoccidioides brasiliensis* in their findings. In mucormycosis, the most frequent fungal genus is *Rhizopus*; however, other organisms associated with human infection may be present. The report found by researchers from MT[101] described cases of mucormycosis caused by fungi of the genus *Rhizopus* in hospitalized patients, recording *Rhizopus microsporus* var. *oligosporus* and *Rhizopus microsporus* var. *rhizopodiformis* causing lethal infection in patients with diabetes mellitus.

In Brazil, cases of Histoplasmosis (Onygenales), an endemic systemic mycosis caused by the dimorphic fungus *Histoplasma capsulatum* var. *capsulatum*, were reported more frequently in the Southeast and South regions, with few reports and studies in the Center-West region. Records of classical human histoplasmosis, which occurs in its mycelial form during its saprophytic life cycle, have been recorded in MS, Brazil, reporting 30 cases of the disease[102].

More currently, Antinori et al[103] in a systematic review listed from 2005 to 2020 in Europe and Israel, recorded 728 cases in 17 countries, showing that histoplasmosis infection could be imported by immigrants and travelers from other countries and that the infection affected more men (60.4%) of the analyzed cases and the spread was quite high in patients with the HIV syndrome with 89.5% of the registered cases.

As with a range of fungal species in their phylogenetic unfolding, molecular analyzes have evaluated the isolates, and researchers have been proposing a taxonomic rearrangement for this eukaryotic fungal organism, which comprises eight clades geographically distributed across Australia, Netherlands, Eurasia, America, Latin America and Africa[104].

The original name Histoplasma capsulatum sensu stricto (*S. Str*.) (Classical Histoplasmosis) kept the new proposals, however the new taxonomic proposals were suggested as *Histoplasma mississipiense* (NAm1), *Histoplasma ohiense* (NAm2), *Histoplasma suramenicanum* (LAm A) and the African strain *H. capsulatum* var. *duboisii* (African Histoplasmosis) which awaits confirmation to become the fifth species for human pathogens. *H. capsulatum* var. *farciminosum* pathogen of perissodactyl mammals (horses), responsible for epizootic lymphagititis, was considered polyphyletic, which indicates that the traditional methods of delimitation of Histoplasma varieties have significant and arbitrary deficiencies[105,106].

Although most infections are associated with outbreaks involving humans, the disease can be associated with common sources and often involve activities that reach the ground, promoting environmental contamination, especially in samples that contain bird or bat excreta, especially those enriched with nitrogen.

One of the first records of Histoplasmosis in MT was described by Moraes and Almeida[107] isolating from the common soil of houses that kept chicken coops in backyards, in the locality of Aripuanã, in the State of MT, revealing a high rate of positivity among the inhabitants in the village at that time according to scientific records.

Other findings; were revealed by Veloso et al[108] who found records of association of this fungal entity in Mato Grosso in co-infection with Pneumocystis spp. in animals of the order Chiroptera. The high occurrence of *Histoplasma capsulatum* was observed in 24 species of bats in the region, with emphasis on the species *Desmodus rotundus, Tadarida brasiliensis, Histiotus velatus* and *Molossus molossus.* Ludiwig et al[109] also evaluated the isolation of fungi from bats of the Phyllostomidae family in the city of Sinop/MT.

Research involving phylogeographic isolates identified two new divergent clades among the Latin American isolates (LAm A1 and LAm A2) constituting Histoplasma suramenicanum, harboring a cryptic cluster in association with bats, suggesting a rapid adaptation to the environmental host, according to the records of Brazilian and American researchers[110].

Sporotrichosis, a subcutaneous mycosis caused by the *Sporothrix schenckii* complex, is cosmopolitan and the most frequent in Latin America, caused by fungi of the *Sporothrix* genus. This type of infection appears to be an uncommon type of infection common in the central west region of Brazil. Reports of the manifestation of this subcutaneous disease, caused by implantation, which affects humans and several animal species, such as dogs, cats, among others, with a characteristic manifestation is the appearance of wounds and ulcers on the skin and mucous membranes.

Sporotrichosis is historically associated with the thermally dimorphic fungus *Sporothrix schencki*, however nowadays[111], they have suggested that *S. schenckii* should not be considered the only species causing sporotrichosis since through the combination of characteristics based on in phenotypic and genotypic analyses, he proposed four new species: *S. globosa, S. brasiliensis, S. mexicana* and *S. luriei*. However, other identified species were inserted in an "environmental clade", with lower pathogenic potential for the mammals *S. chilensis, S. humicola, S. pallida* and *S. stenoceras,* inserted in complexes[105].

Currently, this fungal infection finds more substantial evidence, in reports of outbreaks caused by the zoonotic transmission of Sporotrix brasiliensis, from contact with infected felines to humans. Northeastern researchers reported an epidemic in the Brazilian Northeast region, reporting 121 cases of the disease in that region[112]. The largest reports of this fungal entity are more present in the Northeast, Southeast (especially the State of Rio de Janeiro) and Southern Brazil. In the Center-West region of Brazil, records in lower magnitude, found in the Brazilian Federal District.

During the researched period, only one report on this type of fungal infection, in Mato Grosso, was described by Fernandes et al[113] of a case of feline sporotrichosis in Cuiabá in two cats that presented pustular-crusted alopecic dermatopathy, mainly in the face, confirmed by histopathological studies.

In relation to *S. schenckii*, it is important to consider, according to the descriptions of the phenotypic and genotypic patterns of the strains from this endemic disease, that in Brazil, it is suggested that the species most commonly isolated in the country is caused by the species *Sporothrix brasiliensis*[111]. Second, Rodrigues et al[105] the Midwest region of Brazil is restricted to three species: *Sporothrix brasiliensis, S. schenckii* and *S. globosa.* Due to alarming records that show that sporotrichosis, although recorded in several countries and transmitted by animals, can reach critical levels in Brazil, requiring further studies of this fungal group for the Central region of Brazil.

CRYPTOCOCCUS NEOFORMANS **COMPLEX &** ***CRYPTOCOCCUS GATTII*** **COMPLEX**

Cryptococcosis is a systemic disease caused by a fungal lineage of encapsulated basidiomycete fungi. Having two species that are highlighted with impact on human health and risk of life, *Cryptococcus neoformans* and *Cryptococcus gattii*, which today, are classified as complex. The importance of cryptococcosis in medical mycology has increased significantly as a result of the AIDS epidemic and organ transplants, being the most observable disease in causes of infections in immunocompromised and immunocompetent individuals, with T cell deficiency, causing infection with lung lesions, often asymptomatic, disseminated with course to dimension for neurological problems and meningoencephalitis.

The genus *Cryptococcus*, is the agent of cryptococcosis is a fungal infection caused by encapsulated yeasts of the phylum Basidiomycota (Tremellales). Although more than 70 different species of *Cryptococcus* have been identified so far, isolated from human and environmental samples and considered saprophytes, considered emerging pathogens, in immunosuppressed patients the following species stand out: *C. laurentii, C. adeliensis, C. macerans, C. albidus, C. uniguttulatus, C. humicola, C. luteolus, C. terreus* and *C. curvatus*[114].

Only two closely related anamorphic (asexual) species: *Cryptococcus neoformans* (sensu stricto) and *Cryptococcus gattii* (sensu stricto) cause most fungal infections in humans, with teleomorphic (sexual) varieties, *Filobasidiella neoformans* and *F. bacillispora*, respectively[114].

Cryptococcosis is the infection caused by the naturally encapsulated basidiomycete of the genus *Cryptococcus*, which has recently become the most important opportunistic fungal pathogen. *C. neoformans* is found associated with pigeon droppings and in tree hollows throughout the world. *C. gattii* was found in tropical and subtropical regions primarily associated with eucalyptus, which was considered its environmental niche. However, the ecology of *C. gattii* is changing with its ability to associate with a wide variety of trees. With the AIDS epidemic, the species *C. neoformans* became the most critically important opportunistic infection. Furthermore, *C. gattii* caused a localized epidemic of cryptococcosis in humans and apparently immunocompetent animals on Vancouver Island, Canada, where it originated[115].

The incidence of fungal infections in humans finds answers because these agents are related to the similarity between the cellular structures observed in fungi and humans, since these infections maintain a close relationship with human cells by fungi, as they are also eukaryotes; which ends up leading to antifungal therapy often associated with significant side effects and low efficiency[116].

In MT, central region of Brazil, scientific records refer to this fungal entity in a high degree of complexity for the region observed in studies by Favalessa et al[117] described the association of yeasts of the genus *Cryptococcus* causing infections in immunosuppressed patients. In 2014, this same researcher and her collaborators[118] described the molecular identification and antifungal susceptibility of *Cryptococcus* spp. causing infections in hospitalized patients and that same year, this researcher and her collaborators[119] isolated the fatal agent *Cryptococcus gatti.*

In 2019, Maruyama et al[120] described the genetic diversity of species of the *Cryptococcus gatti* complex found in the region of the State of MT in animals, humans and the environment.

Despite the records in MT, this yeast group shows extensive genetic variability, which can be observed between the isolates in the State of MT and the previously described *C. gattii* and *C. neoformans* in these complexes, indicating a global expansion and adaptation of isolates and strains in several other countries and regions of the globe.

A recent study carried out by Siqueira et al[121] evaluated samples of extracts of passerines and psittaciformes in captivity, identifying *C. neoformans* (AFLP1/VNI genotype) and *C. deuterorogattii* (AFLP6/VGII genotype), reaching the conclusion that the isolates of *C. deuterogattii*, showed genetic variability indistinguishable from other clinical isolates.

Although, as a characteristic, *Cryptococcus neoformans* mainly infects immunocompromised patients, *C. gattii* can cause disease in immunocompetent patients, recent estimates show that *C. neoformans* meningitis is the second leading cause of morbidity and mortality in individuals with AIDS. Worldwide, the number of reported cases of meningitis caused by *C. neoformans* and *C. gattii* has increased from a few hundred to about 1 million cases per year, mainly in people with HIV/AIDS. In Africa, it is currently estimated that more people die from cerebral cryptococcosis than from tuberculosis[122].

Recent studies, carried out using a vast arsenal of antifungal drugs with action against cryptococcal meningitis, with the purpose of breaking and blocking the action and dissemination of the fungus through the blood-brain barrier were recommended by Californian researchers[123].

Based on specific polysaccharide capsule antigen analysis, subtyping data, and genomic sequence comparisons, pathogenic cryptococcosis was divided into five serotypes according to the capsular components mucopolysaccharides (MPS), galactoxylomannan (GalXM) and glucuronoxylomannan (GXM)[114].

Currently, *Cryptococcus* spp. is classified into five capsular serotypes and eight molecular genotypes, based on this information, the following serotypes determined for *Cryptococcus gatti* in five species/serotypes were suggested: serotypes A (*C. deuterogattii*) (AFLP6/VGII), serotypes B (*C. decagattii*) (AFLP10), serotypes C (*C. bacillisporus*) (AFLP5/VGII), serotypes D (*C. gattii*) (AFL4/VGI), serotypes E (*C. tetragattii*) (AFLP7/VGIV); and for *Cryptococcus neoformans* in two species/serotypes: serotypes F,G,H (*C. neoformans*) (AFLP1/VNI, AFLP1A;VNB/VNII, AFLP1B/VNII) and serotypes I (*C.*

deneoformans) (AFLP2/VNIV) and also the hybrid serotypes (AD (AFLP3/VNIII), AB (AFLP9), BD (AFLP8)) in miscellaneous with *C. neoformans* and *C. gattii* species[124,125].

Despite the contribution of genetic diversity presented by these researchers, this taxonomy proposed by Hagen et al[124] has recently become controversial and quite controversial, as other researchers believe that this proposed classification may be broader and more revealing than just defining the seven species for the species complex.

Kwon-Chung et al[126] refute the classification, indicating that this naming process can lead to nomenclatural instability in the species, which can lead to confusion in naming, there are still non-obvious biological differences between the proposed clades, and indicated that for species evaluation, an insufficient number of sequence samples were used, without a consensus on the sequencing of the samples.

More recently Shi et al[127], used diagnostic tests on all seven pathogenic species of *Cryptococcus* detected and analyzed the unique characteristics of each of the seven serotypes presented and their dogmatic characteristics were confirmed.

Despite efforts in the studies by Hagen et al[125] for the characterization of yeast strains of the genus *Cryptococcus*; an extensive review of the taxonomy of this genus of capsular yeasts was carried out by Liu[128] and his group of researchers in 2015, after thorough molecular phylogenetic analysis of this complex fungal grouping. Several splices were made in the Tremellomycetes lineage (Cystofilobasidiales, Filobasidiales, Tremellales, Trichosporonales and Holtermannia)[128].

The researchers observed that the criteria for inclusion of species in the genus *Cryptococcus* were highly artificial and presented species with multiple evolutionary histories and distributed among the existing lineages, where the species mixed with the genera due to their characteristics of anamorphism and teleomorphism characteristic of this fungal lineage.

Other studies, however, emphasize infections by *Cryptococcus* species, which do not grow at 37ºC and do not present capsules, characteristic of the species and are considered rare in the literature and these; associated with nervous system infections and fungemia, with high resistance and high MIC values. Some are difficult to identify by available commercial methods, making sequencing the internal transcriber spacer (ITS) and D1/D2 regions mandatory[129].

There are several species incriminated, involving rare cases of Cryptococcosis in human infections caused: *Cryptococcus* (Naganishia) *adeliensis*, *C.* (Cutaneotrichosporon) *arboriformis, C.* (Filobasidium) *chernovii, C.* (Cutaneotrichosporon) *cyanovorans, C.* (Cutaneotrichosporon) *curvatus, C.* (Cutaneotrichosporon) *curvatus, C.* (Cutaneotrichosporon) *curvatus, C. diffluens, C.* (Papiliotrema) *flavescens, C.* (Naganishia) *friedmannii, C.* (Vanrija) *humicola, C.* (Naganishia) *liquefaciens, C.* (Hannaella) *luteolus, C.*

(Cystofilobasidium) *macerans, C.* (Filobasilico) *magnus, C. Cryptococcus* (Filobasidium) *uniguttulatum,* and *C.* (Naganishia) *uzbekistanensis*[129].

However, we know that the possibility of neglecting certain genetic diversity of a specific group, or even making arguments that generate types of instability in fungal biodiversity, can make the diagnosis of infections by *Cryptococcus* species or any other fungal genera difficult.

PARACOCCIDIOIDOMYCOSIS AND ITS COMPLEXES

Adolpho Lutz's research represented a fundamental milestone in the history of basic medical mycology and the introduction of the genus *Paracoccidioides* (division Ascomycota, order Onygenales, Family Ajellomycetaceae) which currently includes related species of thermally dimorphic or thermodimorphic fungi, with mycelial life cycle found in the soil and that cause fungal infection, in the yeast phase, called paracoccidioidomycosis, which affects tissues of host mammals, being considered a human systemic mycosis that can be lethal, being endemic in Latin America.

This chronic lung disease that affects immunocompetent and immunosuppressed individuals, reported mainly in individuals involved in rural activities in Latin America, and observed from Mexico to southern Argentina[130]. The fungus inhabits agricultural places where there are soil conditions for its development and thus the infection of the host is facilitated by the large amount of particles that are suspended in the air when the environment is disturbed.

In the scientific literature, historical reports of this systemic disease were evidenced in the studies by Forjaz et al[131], where these researchers reported the occurrence of this mycosis among Brazilian Indians of the Suruí ethnic group in Rondônia. Extensive environmental disturbances may be involved in the transmission of fungi, coffee cultivation after the deforestation of the Amazon forest with the opening of new agricultural frontiers, resulted in infections by paracoccidioidomycosis; these reports involving indigenous populations affected by this systemic fungus were reported by Santos & Coimbra Jr.[132] and by Valle et al[133] attributed to the Amazon region, in case studies of the Tupi-Mondé, associated with the cultivation of coffee in the early 1980s.

After tinea inbricata, caused by the dermatophytic agent Trichophyton concentricum, which is perhaps the only mycosis recognized by the Indians since time immemorial, of which there are reports of its existence; *Paracoccidioides* is a fungal infection well evidenced by indigenous peoples today. This etiological agent is very present in the Center-West region of Brazil and has been highlighted by its epidemiological importance.

One of the first historical reports recorded in MT of this etiological agent was a case report of infection by *Paracoccidioides brasiliensis,* diagnosed in 1996, in a male patient, a gold prospector, from Peixoto de Azevedo/MT, treated in the Capital, who had a severe multifocal chronic form of paracoccidioidomycosis, where the clinical diagnosis was performed in a bone marrow aspirate[134].

Records involving infections by the systemic fungus of the genus *Paracoccidioides* were described by researchers from MT, Batista Júnior et al[135] emphasizing the geographic origin of the fungus and then Grossklaus et al[136] identified the first record of this entity in children, where clinical cases of paracoccidioidomycosis in children, diagnosed in the State of MT, central-west region of Brazil, are rare, although the state is classified as having moderate to high incidence.

However, analyzes involving the fungal genus verified that characteristics of different conidia of the only species of the genus *Paracoccidioides brasiliensis* until then existing, led to studies comparing P. brasiliensis isolates from central-west and northern regions of Brazil, these studies led to the arrival of *Paracoccidioides lutzii*, which was housed for centuries hidden in disguise within the species *P. brasiliensis.*

Comparative studies and genetic analyzes concluded and revealed that there were differentiated isolates, and these characteristics led to the baptism of a new species of the genus called *Paracoccidioides* lutzii, indicating that the findings may have significant clinical consequences for the diagnosis and treatment of paracoccidioidomycosis (PCM) in Mato Grosso and Brazil. Most of the clinical isolates from MT, in view of the phylogenetic and morphological analyzes contributed and led the researchers to declare the new species in 2006[137].

Paracoccidioidomycosis is traditionally considered to be caused only by *Paracoccidioides brasiliensis*, but a new species, *Paracoccidioides lutzii*, was discovered in the Midwest region of Brazil, this new fungal agent of paracoccidioidomycosis (PCM) has its epicenter located in this Central region of Brazil[138-140].

The first case of fungemia, caused by the etiological agent, *P. lutzii*, was registered in a 51-year-old rural worker from the central-west region of Brazil. The fungal agent described was isolated in blood cultures, confirming the identification after phylogenetic analysis[141]. Subsequently, and in the development of research involving the dimorphic fungus, researchers from Mato Grosso and São Paulo analyzed the antigenic variability, existing in the phylogenetic gap between *Paracoccidioides* spp. isolated between different regions of Central America, and evaluated the different antigenic profiles of Exoantigens that the isolated species produce, both for *P. brasiliensis* and for *P. Lutzii*[139].

Previously, this researcher and his collaborators in 2010[142], will evaluate pulmonary macrophages CD11b/CD18(+) and CD23(+), which may be involved in the production of inflammatory events caused by *Paracoccidioides brasiliensis* in lungs, concluding that the low production of Nitric Oxide by lung macrophages is associated with a change in CD11b/CD23 expression and a high proliferative response to lymphocytes.

From the identification methods, the detection of the 130 kDa protein, of high molecular weight, explanations in relation to the reactions obtained with the use of the antigen of the reference strain of *P. brasiliensis* in the comparison with *P. lutzii*, profile tests were performed immunochemistry of exoantigens determined this relationship in clinical samples of *P. lutzii* from the State of MT, Brazil in a study by Grossklaus et al[143].

Next, Hahn et al[138] and his collaborators described the clinical manifestations of 34 patients suffering from PCM caused by *P. lutzii*, undergoing treatment over 5 years at a referral service for systemic mycoses in MT, Brazil.

The epidemiological profile of this systemic fungus was presented in the survey of PCM records found in health reference services in MT, considering it is endemic in the state, being more frequent in the North and Center-South mesoregions of the state of MT, affecting mostly adult individuals male from the State of MT, with work activity related to rural areas, being more exposed to dust inhalation[144].

In 2016, a group of dentists diagnosed 125 cases of PCM with oral manifestations in 141 municipalities in MT. The municipalities with the highest number of cases were Alta Floresta (n=10; 8.0%), Colíder and Cuiabá (n=7; 5.6%) respectively. A high concentration of cases was observed in the North and South regions of the state (marked in red) (Figure 3). However, these researchers did not register cases of PCM in indigenous and ecological reserves[145].

In the same year, another group of dentists evaluated the prevalence of PCM in a Public Laboratory of the Unified Health System in Mato Grosso. A total of 3,670 reports of cytological and histopathological examinations of exfoliative oral lesions issued by the MT Laboratory over a period of 4 years (2004-2008) were analyzed[146].

In 2021, Nery and his collaborators[147,148], carried out an epidemiological study in the Midwest of the high cases of *Paracoccidioides lutzii* and the use of biomarkers to support early diagnosis.

Currently, *Paracoccidioides brasiliensis* is considered a monophyletic fungus composed of distinct lineages classified as S1a, S1b, PS2, PS3, PS4 and *P. lutzii*. The *P. lutzii* strains are a single monophyletic and recombinant population found to date in the central west, southwest and north of Brazil and Ecuador. The S1 lineage is widely distributed in PCM cases in South America. PS2 has so far been identified only in Brazil and Venezuela, while PS3 and PS4 are found geographically in regions of endemicity in Colombia and Venezuela, respectively[104].

However, Cocio et al[149] report the isolation of PS3 in Brazil in the southeastern region of Brazil, in the State of São Paulo, where *P. brasiliensis* sensu stricto is characterized as the prevalent genotype. Finally, *P. lutzii*, a divergent relative of the *P. brasiliensis* complex, occurs in Brazil with its epicenter in the Midwest region[140] (Figure 4).

Lineage analyzes support the main subdivisions in the population of *P. brasiliensis*, suggesting that some lineages have similar phylogenetic relationships with various formations suggesting the existence of other lineages[150] (Figure 4).

Studies evaluating the molecular family that were incorporated into the current *P. brasiliensis* complex involving the SI, PS2, PS3, PS4 strains were classified as *P. brasiliensis* sensu stricto, receiving taxonomic classification called *P. brasiliensis* sensu stricto (S1a and S1b), for the cryptic species *P. americana* (PS2), *P. restrepiensis* (PS3) and *P. venezuelensis* (PS4), and the lutzii clade containing *P. lutzii* species[151].

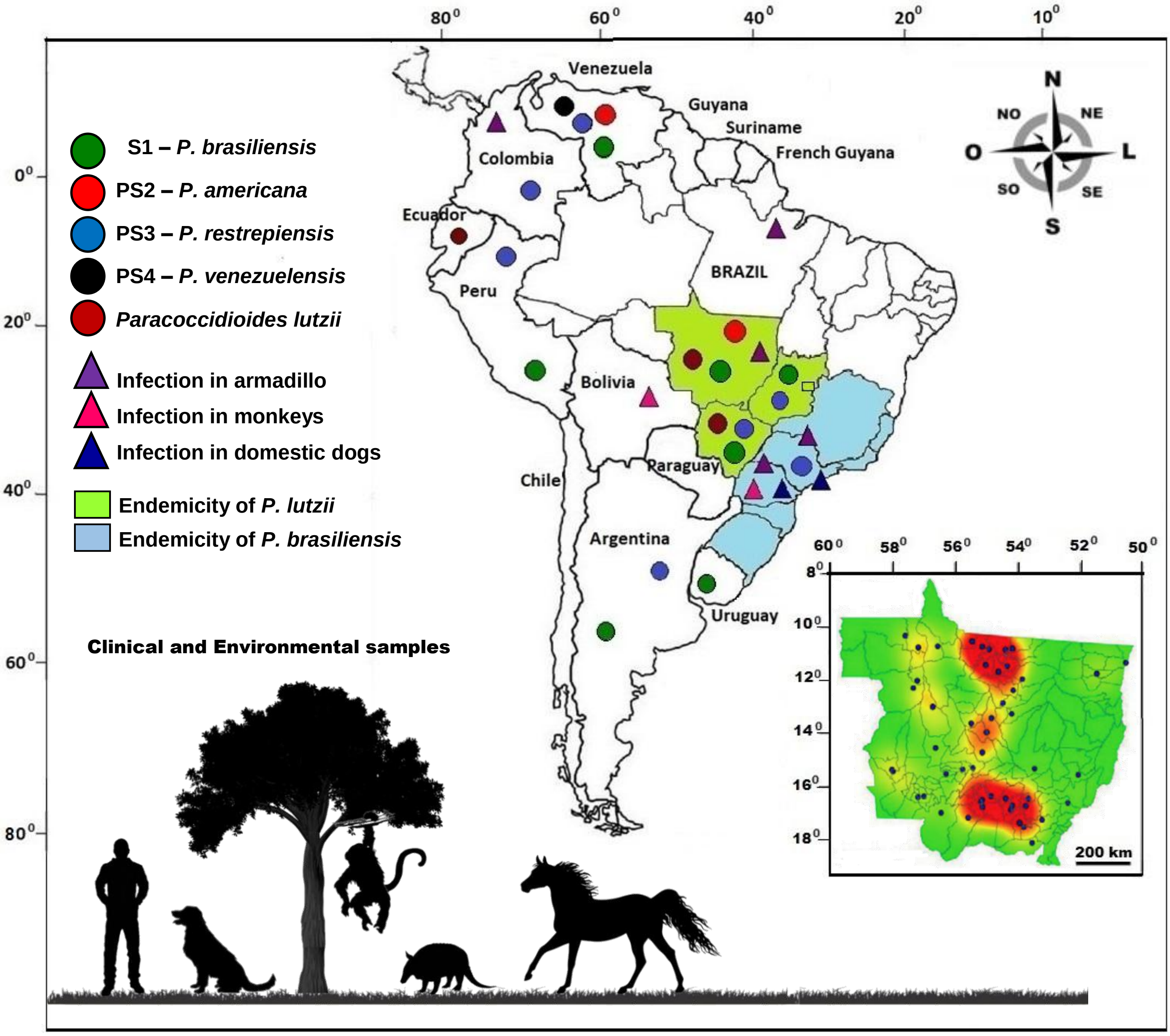


Figure 4 - Geographical distribution of *Paracoccidioides* lineages across Latin America (larger image), highlighting the Midwest region (light green) where P. lutzii predominates and the South and Southeast regions (light blue) where the cryptic species of *P. brasiliensis* in Brazil. In the lower right part (small map), spatial distribution of cases of paracoccidioidomycosis in oral manifestations in Mato Grosso, central region of Brazil. [140,145,149,150,156,157,160,190]. Adapted Leite-Jr, D.P.

Recent reports indicate a speciation for species included in the *P. brasiliensis* complex (especially PS3 and PS4), while *P. brasiliensis* sensu lato (S1) and *P. lutzii* strains maintain their reproductive relationship isolated from nature[137,152], other studies concluded the interspecies genetic variations of the fungal genus related to morphology and geographic distribution, sequencing the GP43 and ARF genes of isolates compatible with S1, PS2, PS3, PS4 and *P. lutzii*[153].

Paracoccidioides brasiliensis presents natural infection in mammals of the order Cingulata, family Dasypodidae, found in armadillos of the species *Dasypus novemcinctus* identified in several endemic areas in Brazil and Colombia, where the pathogen was isolated in the species *Cabassous* centralis[154,155]. In MT, a new endemic area in the Central region of Brazil, strains of *P. brasiliensis* (S1b) were isolated from nine-banded armadillos (*Dasypus novemcinctus*) in the cities of Alta Floresta and Paranaíta/MT, regions of predominance of the Amazon biome[156].

Corte et al[157] studied the seroprevalence of infection by *Paracoccidioides brasiliensis* in 93 New World wild apes of the genus *Cebus* sp. and species *Alouatta caraya* (capuchin monkeys and golden howler monkeys), captured in the Paraná River basin, Paraná State, Brazil (Figure 4), suggesting that the positivity found by immunodiffusion tests suggest that the natural disease may be occurring in monkeys wild animals living in endemic areas for paracoccidioidomycosis.

This same researcher[158] evaluating other mammals, the results obtained suggested that horses (Equus caballus) can be indicators of the presence of the fungus in the environment and still in 2012[159]; carried out an epidemiological study in dogs from the Brazilian Western Amazon, suggesting that the high positivities found for the infection in this group of mammals, suggest that we should be alert to detect the natural disease in dogs in endemic areas for paracoccidioidomycosis.

The reports presented assume that paracoccidioidomycosis; although there are several studies on the diagnosis and pathology of this mycosis, its habitat probably lives saprophytically in the soil. There are few reports of the participation of other animal species in eco-epidemiology, they were probably not reproducible and these factors on the fungus are not yet clarified. To date, what is known is that the fungus has been isolated more frequently in armadillos (*Dasypus novencinctus*) and in rural areas in domestic dogs.

Molecular methods are currently supported in the identification of species isolated from the *P. brasiliensis* and *P. lutzii* complex, previously characterized by molecular techniques and advances in their target genes and species discrimination power. Polymerase chain reaction, PCR; RFLP (restriction fragment length polymorphism); qPCR (real-time quantitative polymerase chain reaction); FISH (fluorescent in situ hybridization); MALDI-TOF MS (Matrix Assisted Laser Desorption Ionization – Time of flight); LAMP (loop-mediated isothermal amplification), SSR/Microsatellite (single sequence repeats), MLSA (multilocus sequence analysis), in addition to taxonomic methods[151,160,161].

More recently, a study carried out in MS, Brazil, a neighboring state to MT; sixteen clinical isolates and their genomic DNAs were submitted to genotyping by tub1-PCR-RFLP and showed *Paracoccidioides brasiliensis* sensu stricto (S1) (11; 68.8%), *P. restrepiensis* (PS3) (4; 25.0%) and *P. lutzii* (1; 6.2%) as *Paracoccidiodes* species for that region, showing *P. brasiliensis* sensu stricto (S1) as the predominant species in Brazil and for the first time, the occurrence of *P. restrepiensis* (PS3) in the state of MS[160].

The studies carried out in the areas comprised in the central-west region of Brazil, considered to be of probable occurrence of *P. lutzii*, a species found with predominance in this region, present points whose ecology and geographic distribution, despite the statements in scientific reports, are still not well defined and understood and many of the mycological findings available in the literature raise questions about the existence of biological, morphological and ecological differences between the species of *P. lutzii* and *P. brasiliensis.*

YEAST OF THE GENUS *CANDIDA*

Candida yeasts are the most studied and evidenced fungi in the literature. Candidiasis or candidosis is a form of mycosis caused by opportunistic, saprobic yeasts of the *Candida* genus; which are ubiquitous in the environment, and from exogenous sources, found in different substrates: soil, marine environments, inanimate objects, plants and animals[5].

Invasive candidiasis is the most frequent fungal infection associated with healthcare. It is also associated with high morbidity, mortality and cost. The most frequent etiologic agent is *Candida albicans*, but non-albicans species are increasing and associated with reduced antifungal susceptibility and outbreaks. *Candida auris* is a recently described emerging multidrug-resistant species with a high mortality rate; Nosocomial infections have been reported worldwide, causing a major challenge for medical staff, microbiological laboratories[162] and mycologists.

Yeasts of genus *Candida* is the fungal pathogen most implicated in the clinical setting. This fungal genus belongs to the Clavispora clade of the Metschnikowiaceae family of the Saccharomycetales order, belonging to the ascomycete group of yeasts. The order Saccharomycetales has about 1000 species already described, including domesticated species used in industry such as Saccharomyces cerevisiae and the commensal human species and free-living saprobes pathogens, most studied *C. tropicalis, C. glabrata* and *C.*

parapsilosis, in addition to the more common and recognized of all of them, *Candida albicans*[163].

Several factors play important roles in *Candida* spp. pathogenesis, involved in multiple transcriptional circuits, morphology and phenotyping, biofilm, hydrolytic enzymes, metabolic flexibility, genome plasticity, environmental pH adaptation, adherence and invasions, phagocytosis escape, immune system evasion of the host, resistance to antifungal agents are some of the main pathogenic determinants of *Candida* species[164].

Although *Candida albicans* is the most detected species in genital and urinary infections and other clinical lesions; The species that currently keeps the world on alert is *Candida auris*, a species isolated for the first time from the ear canal of a Japanese patient at a hospital in Tokyo/Japan[165].

The phylogenetic relationship of this species with other known species of the group, due to the rarity of some of its closest relatives, has not yet been elucidated, relatives of which are more distantly related and which have their genome sequenced, include *C. haemulonii, C. pseudohaemulonii* and *C. duobushaemulonii*, which was reported by Boatto et al[166] as causes of recurrent vulvovaginal candidiasis (CVVR) in Brazil.

The ITS and rDNA sequencing, however, suggests that *C. auris* clusters more phylogenetically with *C. heveicola*, isolated from tropical tree sap in China, and still maintains proximity to *C. ruelliae*, isolated from floral species of the *Ruellia* genus (Acanthaceae) of the which is closely related to *C. haemulonii*, isolated for the first time from the intestine of bluestriped grunt fish (*Haemulon sciurus/Haemulidae*)[165].

For the understanding that involves the sphere of this pathogen, although the ecological niche of *C. auris* and its emergence as a pathogen remain enigmatic; this yeast, its genomic diversity and its close relatives still need to be well known and evidenced. We can observe that hypotheses have been suggested for its emergence and they present several chromosomal rearrangements confirming their genetic divergence.

Currently in Mexico Villanueva-Lozano et al[167]described an outbreak of this yeast and its clinical and microbiological characteristics, which affected 12 patients with severe co-infection by COVID-19 and *Candida auris*, even with the use of adequate antifungal therapy, the mortality was of 83.3%. All isolates studied were resistant to amphotericin B.

The study by Aljindan et al[168] in Saudi Arabia sheds light on this emerging public health threat. The objective was to describe new cases of *C. auris* and to detect mutations associated with drug resistance through gene sequencing. After confirmation via MALDI-TOF MS and antifungal sensitivity tests using VITEK 2. The results showed that all isolates were resistant to Fluconazole and the presence of two mutations in the genomes associated with drug resistance (F132Y and K143R) associated with ERG11.

In New Delhi (India) researchers using whole genome sequencing and multilocus microsatellite genotyping observed colonized patients in hospital in that region and found that up to 75% of colonized patients remained with the presence of yeast after receiving discharge and results of whole genome analysis and microsatellite typing revealed that several strains contaminated the fomites and colonized different sites in the patients' bodies[169].

Candida auris presents itself as an emerging fungus that poses a serious threat to public health where it is being detected. This species isolated for the first time in a patient's ear canal draws attention to the need to improve fungal identification methods for emerging and reemerging species. And finally, we note that there is a critical need to monitor antifungal resistance in different geographic areas and implement effective guidelines for the treatment of this pathogen.

As currently Aspergillus lattus has shown great concern for its high resistance to antibiotics; one of the biggest concerns in relation to this category of fungi, is directed to global warming as one of the factors that helped the fungus *Candida auris* to proliferate, other situations related to climate change, arguments found by Casadevall et al[170].

Hypotheses guide and emphasize that this fungus is the first example of a new fungal disease emerging from climate change, and points out that other factors may have contributed to the direction of this fact, such as the use of antifungal drugs and fungicides in plantations, without proper control, may have helped the fungus to create this resistance, since the fungus emerged simultaneously on three continents with genetically distinct clades[170].

Studies carried out by a group of researchers from several countries[171-173] globally disseminated the identified Clades of this pathogenic yeast, isolating clade I, considered the most widespread found in the countries (Canada , France, Germany, India, Kenya, Pakistan, Saudi Arabia, United Kingdom, United Arab Emirates and United States), then the Clade II located (Canada, Japan, South Korea and the United States), then the Clade III found (Australia, Canada, Kenya, South Africa, Spain and United States) and finally isolated clade IV (Colombia, Israel, Panama, United States and Venezuela) and isolated clade V restricted to Iran. Multiple clades were observed found in the United States (clades I, II, III and IV), Canada (clades I, II and III) and Kenya (clades I and III), which appeared interspersed in the phylogeny, suggesting multiple introductions of *C. auris* in these countries (Figure 5).

In Brazil, there was no report of any case of infection by *C. auris*. These researchers probably did not collect information about this yeast in the country. The first case of *C. auris* in Brazil was notified to the Brazilian health surveillance agency (ANVISA) on 12/07/2020, a record of *C. auris* infection, detected in Brazil in the northeast region of the country. Catheter tip samples and urine of patients admitted to the ICU at a hospital in the State of

Bahia/Brazil[174] (Figure 5). Probably, according to the first described report of this yeast in Brazil[174], this genotype would belong to clade IV, like those already isolated in countries bordering Brazil (Colombia and Venezuela).

In December 2021, ANVISA received notification of another outbreak by pathogenic yeast in a Public Hospital in Salvador, Bahia/Brazil. More recently, ANVISA confirmed new records in 2022 of infections in urine samples from patients admitted to a Hospital of the Public Network of Recife in Pernambuco/Brazil (Figure 5). The results confirmed by the Maldi-Tof (Matrrix-Assisted Desorption Ionization Time-of-Light) method confirmed the identifications of infections to be by *Candida auris*[175].

Some strains of this yeast-like specimen are resistant to existing antifungal drug classes and their identification requires specific laboratory methods, since *C. auris* can be easily confused with other yeast species, such as *Candida haemulonii* and *Saccharomyces cerevisiae.*

Reports of *Candida* spp. yeast, and records in the State of MT, were recorded and proved to be quite evident and promising in this region. One of the first records of this fungal entity in MT was diagnosed in a case of fungal endocarditis in a newborn, hospitalized for treatment of Kernictures[176]. Further on, studies of *Candida* yeasts described by Hahn et al[177], involving candidiasis infections and susceptibility to antifungal agents; as well as records in pregnant women, causing vulvovaginal candidiasis[178].

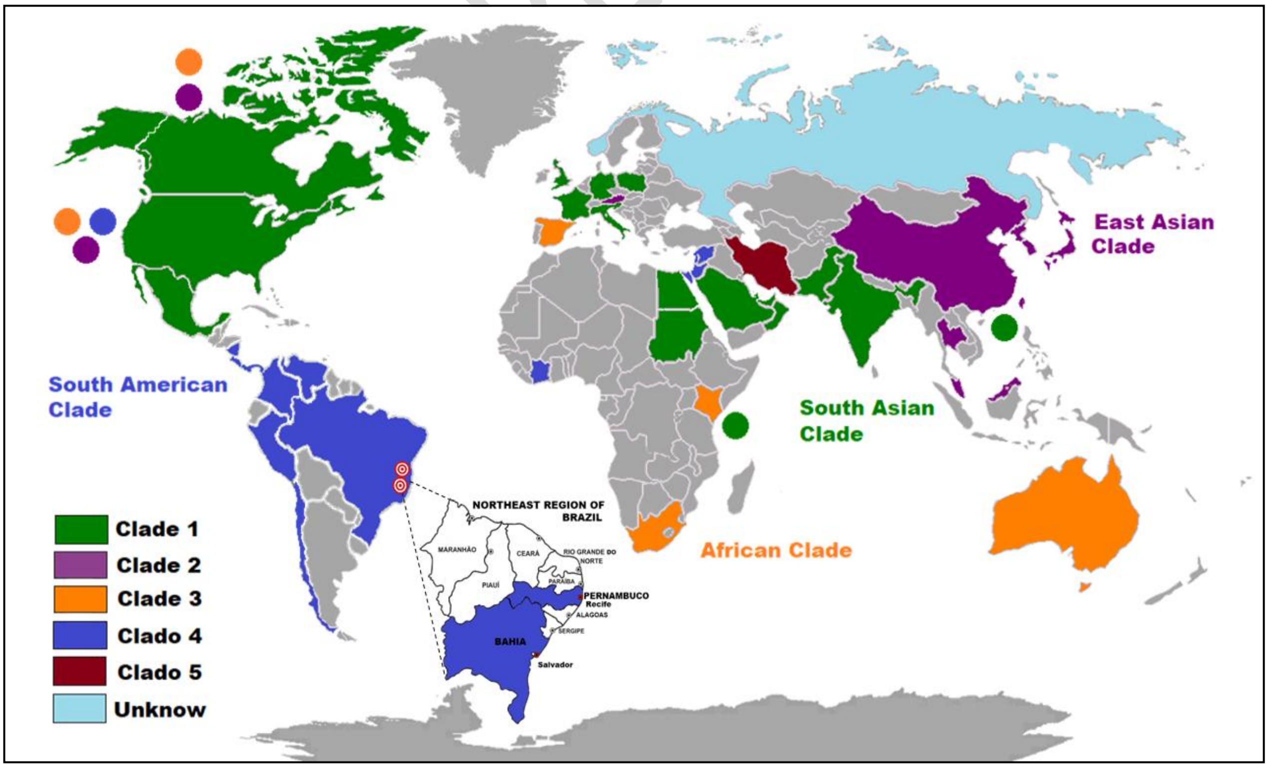


Figure 5. Global map of the distribution of *Candida auris* clades with reported and confirmed cases. Map of Brazil, in South America (in blue), with target showing the location of *Candida* auris records in Brazil (Bahia and Pernambuco) [122,171-175]. Adapted Leite-Jr. D.P.

The records by Leite-Jr et al[179] emphasizing yeasts of *Candida* spp. in a male group involving the military population of the city of Cuiabá report skin, hair and nail infections and infections in the male genital sphere; the records of Amadio & Hahn[180] in reference to oral candidiasis in neonates and their nursing mothers; as well as oral candidiasis reports, we found the work by Carvalho-Bianchi et al[181] describing infections in removable dental prostheses caused by yeasts of the genus *Candida* and subsequent work, Bianchi et al[182] evaluating the enzymatic activity of these fungal entities, in the sphere oral and the results using laser therapy in applications of onychomycosis cases caused by yeasts of the genus *Candida*[183].

When we then moved on to recording these infections for hospital environments, we observed the reports described by Akeme Yamamoto et al[184] presenting the nosocomial characteristics of candidiasis in hospitals in Cuiabá, capital of MT, and in the sequence Hoffmann-Santos et al[185] emphasizing the same theme in Cohort performed in two intensive care units in the same city. In 2017; this researcher reported the factors associated with candidemia caused by non-albicans species[186].

In 2019, in MT, Santana et al[187] evaluated the epidemiology of 93 hospitalized patients with candiduria, finding *Candida tropicalis* (37.6%) as the most commonly isolated agent, followed by *C. albicans* (36, 6%), *C. glabrata* (19.3%), *C. parapsilosis* (4.3%) and finally *C. lusitaniae* and *C. kusei*, both with (1.1%) contributing with the isolates.

More recently, Anh and colleagues[188], in a hospital in Vietnam, showed the prevalence of vaginal yeast colonization in non-pregnant women, found 51.3% of participants. Nine different yeast species were identified *Candida albicans* (51.37%), followed by *C. parapsilosis* (25.88%), *C. glabrata* (11.37%), *C. tropicalis* (4.31%), *C. krusei* (3.92%), *C. africana* (1.57%), *C. nivariensis* and *C. lusitaniae* (0.39%), respectively. Among *C. albicans*, it was the most prevalent species and all 46 isolates were 100% susceptible to micafungin, caspofungin and miconazole.

Cândido et al[189] isolated in MT from veterinary samples of species of domestic animals and wild animals from 13 collection sites, among them: hair, feces, milk, urine, cavity fluid, liver, lymph nodes, nasal swab, ocular swab, oral swab, otologic swab, ingluvial and lung swab; isolating *Candida* yeasts from the harvested material. Twelve different *Candida* species were identified, where *C. rugosa* was the most isolated species, followed by *C. parapsilosis, C. albicans, C. glabrata, C. tropicalis, C. orthopsilosis, C. metapsilosis, C. heivecola, C. haemulonii, C. pararugosa, C. quercitrusa, C. michaelii.*

These reports show the diversity of species that can be isolated from both the human and animal microbiota, without distinction between species.

6. CONCLUSION

Even observing results with relevant identifications and discoveries of fungi for the State of Mato Grosso, the results found can still be considered incipient. Considering that the information, already described, on the distribution of occurrence and research in the different Brazilian biomes and ecosystems may still be insufficient, to determine with certainty which species and taxa are endemic and the information of this complex information network of the fungi kingdom, still need to be analyzed more information.

The results verified in the checklist databases, it was possible to verify that few records of species identification in the biogeographic regions of Mato Grosso, its main biomes highlighted the Pantanal and Cerrado, still demonstrate the low research and scientific exploration of the study of fungi in these respective areas, despite assuming the existence of a large number of species, specimens and groups that need to be studied and cataloged.

However, we emphasize that the rich diversity of previously identified fungi offers enormous socioeconomic potential and variability of studies on these organisms. However, they need to be properly documented for optimal application. The recent discoveries listed demonstrate the importance of the Cerrado as a highly biodiverse biome, as they harbor an important biological material to be explored, especially with regard to the mycobiota, and corroborate the need for urgent actions aimed not only at its conservation, but at the amplification and use of their findings.

The systematic and organized study of the biodiversity of native fungi in Brazil, especially the region of Mato Grosso, must include in its records the collection and identification of species, but also biotechnology and bioprospecting, agriculture, pharmaceuticals, food and everything available at the service of man.

We can still mention that the direct and indirect effects of climate change on living organisms on the planet, induced by the lack of control and exponential growth of the human population and the indiscriminate use of reserves and areas of the planet, have contributed to an exponential growth of the problems generated by the human consumption. This also contributed to the explosion and emergence of new fungi and evolution of existing ones, as demonstrated in scientific research in the last 20 years.

The increase and geographical enlargement of these eukaryant organisms, their technological potentials, exacerbance and characterization of thermotolant pathogenic species or not, show that the traces of virulence to man, is one of the preponderant characteristics of these living beings representing expansion and importance for the studied region. Mato Grosso, is a promising state in agribusiness, monitoring and continuous surveillance in science and research, are of fundamental importance for investments in the region. Studies involving fungal species that may affect productions, need higher investments in research and knowledge, and serve as driving keys to the discoveries of possible diseases that can achieve human beings, fauna and flora of the region, and consequently the world.

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Table 1 - Retrospective study on fungi isolated in clinical, environmental, veterinary, forensic and agro-rural samples, with emphasis on the State of Mato Grosso (MT) and other states in the Midwest region of Brazil, Mato Grosso do Sul (MS) and Goiás (GO) in their respective biomes, published in the period between 1979 and 2021.

Author publication	Year	Search area	Research region Abbreviation	Local biome	Target/ Collect	Taxonomic Phylum	Taxonomic class	Order/Family/ Specie/Group
De Lamônica-Freire[50]	1979	Environmental	Amazônia, Mato Grosso, Pará, Roraima	Amazon Cerrado	Environment	Basidiomycota	Agaricomycetes	Agaricales
Bononi[65]	1981	Environmental	Serra do Roncador, Aripuanã, Nova Xavantina, MT	Amazon	Environment	Basidiomycota	Basidiomycetes	Thelephorales Amylocorticiliales Polyporales
Moraes[52]	1983	Environmental	Cuiabá, MT	Cerrado	Environmet	Ascomycota	Sordariomycetes	Meliolales: Meliolaceae
Ozaki et al,[134]	1996	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides brasiliensis*
Farah & Fontes[176]	1997	Clinical	Cuiabá, MT	Cerrado	Humans Neonatal	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Fernandes et al,[113]	2004	Veterinarian	Cuiabá, MT	Cerrado	Animals	Ascomycota	Sordariomycetes	Ophiostomatales: Ophiostomataceae – Sporotrix
Tadano et al,[99]	2005	Clinical	Cuiabá, MT	Cerrado	Humans	Zygomycota	Entomophthoromycetes	Entomophthorales: Ancylistaceae – *Conidiobulus coronatus*
Bononi et al,[53]	2008	Environmental	Rio Negro, MS	Pantanal	Environment	Basidiomycota Ascomycota	Basidiomycetes Ascomycetes	Diverse species
Hahn et al,[177]	2008	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Saccharomycetes	*Saccharomycetales: Saccharomycetaceae – Candida* spp.
Ribeiro et al,[100]	2009	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota Basidiomycota	Eurotiomycetes Tremellomycetes	Tremellales Onygenales
Favalessa et al,[117]	2009	Clinical	Cuiabá, MT	Cerrado	Humans	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae – Crypotoccus spp.
Batista-Jr et al,[135]	2009	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides brasiliensis*
Grossklaus et al,[136]	2009	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides brasiliensis*
Gilbertoni & Dreschler-Santos[54]	2010	Environmental	MT	Cerrado	Enviroment	Basidiomycota	Agaricomycetes	Diverse species

Author publication	Year	Search area	Research region Abbreviation	Local biome	Target/ Collect	Taxonomic Phylum	Taxonomic class	Order/Family/ Specie/Group
Queiroz-Jr et al,[142]	2010	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Simões et al,[81]	2011	Clinical	Cuiabá, MT	Cerrado	Humans/ICU	Ascomycota Basidiomycota	Ascomycetes Basidiomycetes	Diverse species
Dias et al,[178]	2011	Clinical	Cuiabá, MT	Cerrado	Humans/ Pregnant	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Leite-Jr et al,[179]	2011	Clinical	Cuiabá, MT	Cerrado	Humans/ Military	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Leite-Jr et al,[82]	2012	Clinical	Cuiabá, MT	Cerrado	Humans/dust/ Librarians	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae - *Cryptococcus* spp.
Ribeiro et al,[101]	2012	Clinical	Cuiabá, MT	Cerrado	Human	Zygomycota	Zygomycetes	Mucorales: Mucoraceae – Rhizopus spp.
Amadio & Hahn[180]	2012	Clinical	Cuiabá, MT	Cerrado	Humans/ mothers and babies	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Akeme Yamamoto et al,[184]	2012	Clinical	Cuiabá, MT	Cerrado	Humans/ Nosocomial	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Takahara et al,[83]	2013	Clinical	Cuiabá, MT	Cerrado	Animal Excreta	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae – *Cryptococcus* spp.
Leite-Jr et al,[85]	2013	Clinical	Cuiabá, MT	Cerrado	Humans/dust/ Librarians	Ascomycota	Eurotiomycetes	Eurotiales: Aspergilaceae – *Aspergillus* and *Penicillium* spp.
Teixeira et al,[137]	2013	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Hoffman-Santos et al,[185]	2013	Clinical	Cuiabá, MT	Cerrado	Humans/ Nosocomial	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Cortina et al,[60]	2013	Agro-rural	Chapadão do Sul, MS	Cerrado	Plant	Ascomycota Basidiomycota Zygomycota	Sordariomycetes Dothideomycetes Agoricomycetes Zygomycetes Eurotiomycetes	Diverse species

Author publication	Year	Search area	Research region Abbreviation	Local biome	Target/ Collect	Taxonomic Phylum	Taxonomic class	Order/Family/ Specie/Group
Galvão et al,[63]	2014	Environmental	Poconé, MT	Pantanal	Plant	Not quoted	Not quoted	AMF - Arbascular Micorrhizal Fungi
Gomide et al,[64]	2014	Environmental	MS	Pantanal	Environment	Glomeromycota	Glomeromycetes	AMF - Arbascular Micorrhizal Fungi
Anzai et al,[84]	2014	Clinical	Cuiabá, MT	Cerrado	Environment/ Three holow	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae – *Cryptococcus* spp.
Veloso et al,[108]	2014	Veterinarian	Cuiabá, MT	Cerrado	Animals/ Bats	Ascomycota	Eurotiomycetes	Onygenales: Ajelomycetaceae – *Histoplasma* spp.
Favalessa et al,[118]	2014a	Clinical	Cuiabá, MT	Cerrado	Humans	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae – *Cryptococcus* spp.
Favalessa et al,[119]	2014b	Clinical	Cuiabá, MT	Cerrado	Humans	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae – *Cryptocccus* spp.
Queiroz-Jr et al,[139]	2014	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides brasiliensis*
Hahn et al,[141]	2014	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Almeida et al,[144]	2014	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Theodoro & Batista[59]	2014	Agro-rural	Chapadão do Sul, MS	Cerrado	Plant	Ascomycota Basidiomycota Zygomycota	Eurotiomycetes Zygomycetes Dothideomycetes Sordariomycetes	Diverse species
Costa-rezende et al,[55]	2015	Environmental	Chapada Guimarães, MT	Cerrado	Environment	Basidiomycota	Agaricomycetes	Diverse species
Garcia et al,[56]	2015	Environmental	Tangará Serra, MT	Cerrado	Environment	Ascomycota	Hyphomycetes Coelomycetes Ascomycetes	Imperfect fungi Diverse species
Alvarenga et al,[66]	2015	Environmental	Goiás, GO	Cerrado	Environment	Basidiomycota	Agaricomycetes	Auriculariales: Auriculariaceae
Lodge & Sourel[71]	2015	Environmental	Alta Floresta, MT	Amazon	Environment	Ascomycota Basidiomycota Zygomycota	Ascomycetes Basidiomycetes Zygomycetes	Diverse species
Jobim et al,[57]	2016	Environmental	*Sensu lato*	Cerrado	Environment	Glomeromycota	Glomeromycetes	AMF - Arbascular Micorrhizal Fungi
Calaça & Santos[67]	2016	Environmental	Goías, GO	Cerrado	Animals/ Excreta	Ascomycota	Sordariomycetes Laboulbeniomycetes	Sordariales: Lasiosphaeriacae, Xilariaceae Pyxidiophioraceae

Author publication	Year	Search area	Research region Abbreviation	Local biome	Target/ Collect	Taxonomic Phylum	Taxonomic class	Order/Family/ Specie/Group
Lopes et al,[69]	2016	Environmental	Goiás, GO	Cerrado	Environment	Ascomycota	Eurotiomycetes	Eurotiales: Trichocomaceae - *Paecilomyces* spp.
Lima et al,[98]	2016	Veterinarian	Cuiabá, MT	Cerrado	Animals	Ascomycota	Eurotiomycetes Saccharomycetes	Diverse species
Grossklaus et al,	2016	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Volpato et al,[145]	2016	Clinical	Alta Floresta, Colíder, Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Carvalhosa et al,[146]	2016	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Carvalho-Bianchi et al,[181]	2016	Clinical	Cuiabá, MT	Cerrado	Humans/ oral mucosa	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Zambrano & Dianese[58]	2017	Environmental	Vila Bela S. Trindade, MT	Cerrado	Environment	Ascomycota	Sordariomycetes	Meliolales
Alvarenga & Xavier-Santos[61]	2017	Environmental	Goiás, GO	Cerrado	Environment	Basidiomycota	Dacrymicetes	Dacrymicetales Gelatinous fungi
Bononi et al,[65]	2017	Environmental	Aquidauana, MS	Pantanal	Environment	Basidiomycota	Basidiomycetes	Diverse species
Bianchi et al,[182]	2017	Clinical	Cuiabá, MT	Cerrado	Humans/ oral mucosa	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Hoffman-Santos et al,[186]	2017	Clinical	Cuiabá, MT	Cerrado	Humans/ Nosocomial	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Leite-Jr et al,[10]	2018	Clinical	Cuiabá, MT	Cerrado	Humans/dust/ Librarians	Basidiomycota Ascomycota Zygomicota	Basidiomycetes Ascomycetes Zygomycetes	Diverse species
Calaça et al,[68]	2018	Environmental	Goiás, GO	Cerrado	Environment	Basidiomycota	Basidiomycetes	Boletales: Boletinellaceae
Sourel[72]	2018	Environmental	Alta Floresta, MT	Amazon	Environment	Ascomycota Basidiomycota Zygomycota	Ascomycetes Basidiomycetes Zygomycetes	Diverse species
Firmino et al,[73]	2019	Environmental	Vila Bela S. Trindade, MT	Cerrado Amazon	Environment	Ascomycota	Dothideomycetes	Asterotexiales: Asterinaceae
Leite-Jr et al,[78]	2019	Forensic	Chapada Guimarães, MT	Cerrado	Environment/ Decaying Material	Ascomycota Basidiomycota Zigomycota	Ascomycetes Basidiomycetes Zigomycetes	Diverse species

Author publication	Year	Search area	Research region Abbreviation	Local biome	Target/ Collect	Taxonomic Phylum	Taxonomic class	Order/Family/ Specie/Group
Simi et al,[88]	2019	Clinical	Cuiabá, MT	Cerrado	Animals/ Captive birds	Ascomycota Basidiomycota	Tremellomycetes Microbotriomycetes Saccharomycetes	Diverse species
Maruyama et al,[120]	2019	Clinical, Environmental, Veterinarian	Cuiabá, MT	Cerrado	Humans and animals	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae – *Cryptococcus* gattii
Hahn et al,[138]	2019	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Eurotiomycetes	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Santana et al,[187]	2019	Clinical	Cuiabá, MT	Cerrado	Humans/ Urinary Infection	Ascomycota	Saccharomycetes	Saccharomycetales: Saccharomycetaceae – *Candida* spp.
Pereira et al,[70]	2020	Clinical	Cuiabá, MT	Cerrado	Humans/ Recreational Parks	Ascomycota Basidiomycota Zygomycota	Ascomycetes Basidomycetes Zygomycetes	Diverse species
Nery et al,[147]	2021a	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Ascomycete	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Nery et al,[148]	2021b	Clinical	Cuiabá, MT	Cerrado	Humans	Ascomycota	Ascomycete	Onygenales: Ajellomycetaceae – *Paracoccidioides* spp.
Ludwig et al,[109]	2021	Environmental	Sinop, MT	Amazon	Animals/ Bats	Ascomycota Basidiomycota	Eurotiomycetes Sardariomycetes Tremellomycetes	Diverse species
Siqueira et al,[121]	2021	Veterinarian	Cuiabá, Várzea Grande, Campo Verde MT	Cerrado	Animals/birds	Basidiomycota	Tremellomycetes	Tremellales: Tremellaceae *Cryptococcus neoformans* *Cryptoccus deuterogattii*
Cândido et al,[189]	2021	Veterinarian	Cuiabá, MT	Cerrado	Domestic and wild animals	Ascomycota	Saccharomycetes	Saccharomycetales: Sccharomycetaceae – *Candida* spp.