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Frequency and distribution of fungal pathogens affecting teleost fish of commercial interest: a systematic review

Frecuencia y distribución de patógenos fúngicos que afectan a peces teleósteos de interés comercial: una revisión sistemática

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Abstract

Activities such as aquaculture and fishing provide employment and food for different populations around the world; however, teleost fish are susceptible to fungal infections that compromise their utilization. The objective of this work was to analyse the frequency of fungal infection in commercial teleost fish through a systematic review. A total of 26 articles were included in the data analysis; from these, 1 409 fish were identified as positive for fungi. This interaction involved 25 teleost species and 24 fungal species. The main host species were *Oreochromis niloticus* and *Salmo salar*, with 574 (40.73 %) and 539 (38.25 %) positive fish, respectively, while the most frequent fungus was *Saprolegnia* spp. (882 positive fish and 62.59 %) at the genus level and *Saprolegnia parasitica* (463 positive fish and 32.86 %) at the species level. In general, the positive fish were from aquaculture (1,265 positive fish, 89.77 %). The fungi were identified mainly by molecular techniques (837 positive fish, 59.40 %), where the class *Oomycota* was the most frequent (1,372 positive fish, 97.37 %). The profile of the fungal infection, as well as the analysis of the relationship between teleost fish and pathogenic fungi, are essential for establishing health monitoring strategies for these high-impact infections in fish populations.

Keywords: Fungi, Parasite, *Ascomycota*, *Oomycota, Saprolegnia* spp.

Resumen

Actividades como la acuicultura y la pesca brindan empleo y alimento a diferentes poblaciones alrededor del mundo; sin embargo, los peces teleósteos son susceptibles a infecciones fúngicas que comprometen su utilización. El objetivo de este trabajo fue analizar la frecuencia de infección fúngica en peces teleósteos comerciales, a través de una revisión sistemática. Se incluyeron un total de 26 artículos en el análisis de datos; de estos, 1 409 peces fueron identificados como positivos para hongos. Esta interacción incluyó 25 especies de peces teleósteos y 24 especies de hongos. Las principales especies hospedadoras fueron *Oreochromis niloticus* y *Salmo salar* con 574 (40,73 %) y 539 (38,25 %) peces positivos, mientras que el hongo más frecuente fue *Saprolegnia* spp. (882 peces positivos y 62,59 %) a nivel de género y *Saprolegnia parasitica* (463 peces positivos y 32,86 %) a nivel de especie. En general, los peces positivos fueron de acuicultura (1 265 peces positivos, 89,77 %). Los hongos se identificaron principalmente mediante técnicas moleculares (837 peces positivos, 59,40 %), donde la clase *Oomycota* fue la más frecuente (1 372 peces positivos, 97,37 %). El perfil de la infección fúngica, así como el análisis de la relación entre peces teleósteos y hongos patógenos, son esenciales para establecer estrategias de monitoreo sanitario para estas infecciones de alto impacto en las poblaciones de peces.

Keywords: Hongo, Parásito, *Ascomycota*, *Oomycota, Saprolegnia* spp

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Introduction

Fish are a large group of organisms distributed in almost all aquatic environments. Fish play an important ecological role in food webs because they provide highly digestible protein to the human diet; teleost fish are the most frequently consumed. Currently, 34 000 species of teleost fish have been described, representing 96 % of extant fish species (Bone y Moore 2007, Mayer y Pšenička 2024).

Worldwide, cyprinids (*Cyprinus carpio*, *Hypophthalmichthys nobilis* and *H. molitrix*), cichlids (*Oreochromis niloticus*, *O. aureus* and *O. mossambicus*), and salmonids (*Salmo salar* and *Oncorhynchus mykiss*) represent the main taxonomic groups of fish that are used for production and consumption (FAO 2021; Savaya *et al.*, 2020). The three previous groups, together with a great diversity of ray-finned fishes such as tuna (*Thunnus orientalis*), sardine (*Sardina pilchardus*), and cod (*Gadus morhua*), maintain a close relationship with humans through aquaculture, mariculture and fishing (Dávila-Camacho *et al.*, 2019, Mayer y Pšenička 2024), activities that play a fundamental role in nutrition and food security, in addition to contributing to the economic growth of various countries around the world.

It is estimated that nearly 100 million people worldwide depend economically on the aquaculture and fishing industry (González Razo *et al.*, 2017); in addition, teleost fish have also played an important role as ornamental organisms and as pets, including in the production of species that are used as models for scientific research, e.g., Danio rerio, known as the zebrafish (*Danio rerio*) (Astell & Sieger 2020; Saengsitthisak *et al.*, 2021; Silva Brito *et al.*, 2022). Given the dynamism of the sector, particular challenges arise; among them, monitoring the sanitary conditions in which teleost fish populations thrive (Oidtmann *et al.*, 2011), since various pathogens can affect both production systems and wild populations, causing low weight gain, developmental disorders, poor growth and mortality rates that can reach up to 100 % in cases that are not adequately treated (Zulbainarni y Megawati 2019).

Among infectious diseases, fungal diseases generate a significant ecological impact, affecting biodiversity and food security aspects (Liu *et al.*, 2015). Fungal infections in fish tend to recur when the host suffers immunosuppression, or failing that, when there are variations in the quality of the culture water, mainly due to temperature decreases, increases in corticosteroids, and the presence of cytotoxic factors, including those secreted by fungi (Singh *et al.*, 2018). In the case of infection, symptoms vary widely; for example, infection by Aphanomyces invadans (Oomycota) causes epizootic ulcerative syndrome, characterized by focal hemorrhages that progress to necrotizing dermatitis and ultimately death (Majeed *et al.*, 2017). This pathogen can infect various tropical fish, including *Trichopodus pectoralis*, *Cyprinus carpio,* and *Clarias macrocephalus* (Afzali *et al.*, 2015). Other fungi, belonging to the class *Oomycota*, which are recurrent in fish populations, are included in the genus Saprolegnia. These host-nonspecific fungi that can infect fish, amphibians, and crustaceans in various aquatic environments (Saraiva *et al.*, 2014), likewise, have been reported in populations of salmonids such as *Salmo marmoratus*, *S. trutta*, *S. salar,* and *Oncorhynchus mykiss* (Tedesco *et al.*, 2022), in cichlids (*Oreochromis niloticus*) and cyprinids (*Ctenopharyngodon Idella*) (Ali *et al.*, 2019; de Freitas Souza *et al.*, 2019). Other fungi that tend to cause problems in teleost fish include *Exophiala angulospora*, the causative agent of systemic mycoses, where the formation of black nodules on the skin and gills tends to be present during the disease, as well as *Veronaea botryosa*. This fungus causes systemic phaeohyphomycosis, known as "liquid belly" disease (Overy et al., 2015; Saraiva et al., 2019; Soto *et al*., 2022).

In view of the health risks, efforts have been made to treat mycoses, including the evaluation of plant extracts of garlic (*Allium sativum*), cinnamon (*Cinnamomum verum*), and buttonwood (*Eclipta alba*) as antifungals (Kumar *et al*., 2023); some molecules such as boric acid, copper nanoparticles, and miconazole nitrate have also been used (Ali *et al*., 2019; Kalatehjari *et al*., 2015; Singh *et al*., 2018). Even the use of β-defensins isolated from the mucus of *Cyprinus carpio* during infection has been explored (Shabir *et al*., 2022), and biological control of bacteria such as *Pseudomonas* spp. has been evaluated (Liu *et al*., 2015). The analysis of these strategies has shown promising results; however, the diversity and dynamics of infections represent a constant challenge for the aquaculture and fishing industries. This highlights the importance of understanding host-pathogen interactions. Therefore, the objective of this study was to conduct a systematic review of the specialized literature on fungal infections in commercially important teleost fish to contribute to understanding their ecological relationships and the characteristics associated with infection. This information can be key to developing sanitary management strategies against these pathogens.

Materials and methods

Search strategy.

The search for bibliographic resources was conducted in accordance with the PRISMA guidelines for systematic reviews (Hutton *et al*., 2015). The search for bibliographic resources was carried out during August 2025 based on the keywords "*Fish*", "*Teleostean*", "*Fungal infection*", "*Fungal disease*", "*Mycotic infection*", "*Mycotic disease*", "*Aquaculture*", and "*Fish farm*", which were used to form the general search entries (Table 1). Similarly, the words: "*Prevalence*", "*Saprolegnia*", "*Branchiomyces*", "*Aphanomyces*", "*Achlya*", "*Aspergillus*", "*Paecilomyces*", "*Sphaerothecum*", and "*Pythium*" were used to establish the specific search entries for fungal genera that can affect teleost fish (Table 1). The search engines selected to perform the resource search were PubMed® (https://pubmed.ncbi.nlm.nih.gov/), ScienceDirect® (https://www.sciencedirect.com/), and Wiley Online Library (https://onlinelibrary.wiley.com/).

Inclusion and exclusion criteria

The bibliographic resources used in this study were managed according to the PRISMA guidelines, following the stages of identification, review, eligibility and inclusion (Figure 1) (Moher *et al*., 2009), once the four stages of bibliographic management were completed, 26 bibliographic resources were included, selected from the following inclusion criteria: 1) scientific articles, 2) English language, 3) temporality within the last 10 years, 4) data content on prevalence, sample number and number of positive fish in the pathogenic fungus-teleost fish relationship, and 5) the reported fish must be of commercial importance in fishing or aquaculture. In addition, the management of bibliographic resources allowed the exclusion of bibliographic resources with the following characteristics: 1) reviews, systemic reviews, bibliometric analyses and meta-analyses, 2) reports in languages other than English, 3) articles published before 2015, 4) resources that do not report the prevalence or data to calculate the prevalence (sample size and number of positive fish for the pathogenic fungus), and 5) the reported fish represents a fortuitous find and does not represent a commercial interest for fishing or aquaculture.

Data extraction

For each bibliographic source, compliance with the inclusion and exclusion criteria established for the analysis was verified. From the 26 articles selected in this systematic review (Appendix 1), data were collected and labeled with the following categories: author, year, country, continent, activity, animal husbandry, analysis method, fish species, fungus species and class, sample size, number of positive fish, and prevalence. All authors validated data extraction before analysis.

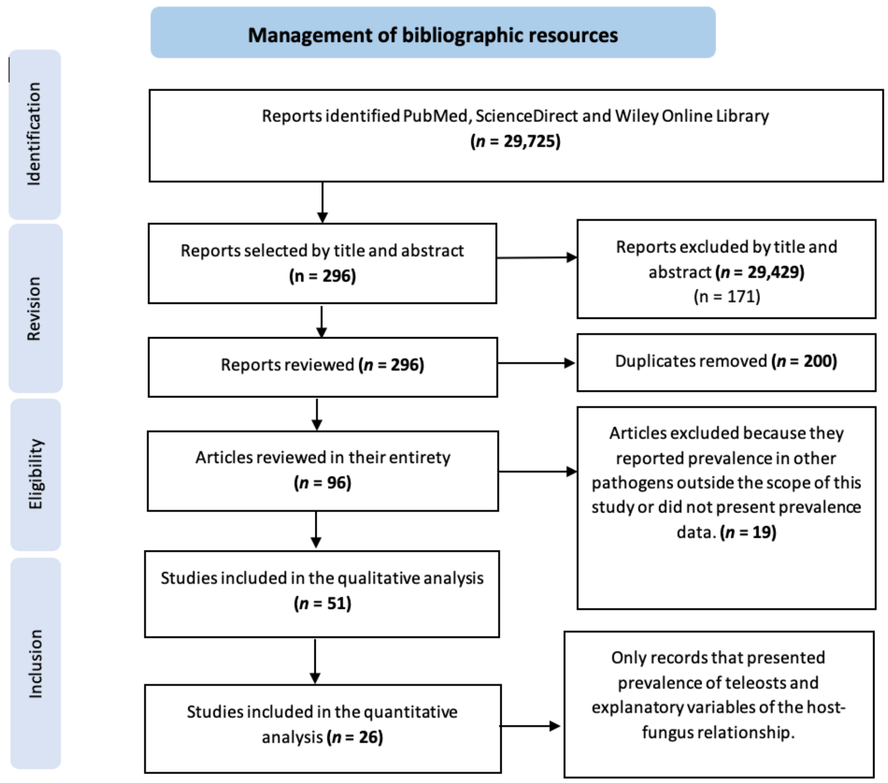

Figure 1. Flowchart of bibliographic resources according to the PRISMA guidelines for preparing systemic reviews.

Table 1. Search entries used to identify bibliographic resources related to fungal diseases affecting teleost fish.

Entry type	Search entry
General	*(Fish OR Teleosts) AND ("Fungal infection" OR "Fungal disease") AND (Aquaculture OR "Fish farm")* *(Fish OR Teleosts) AND ("Mycotic infection" OR "Mycotic disease") AND (Aquaculture OR "Fish farm")*
Specific	*(Prevalence OR Determination) AND (Saprolegnia) AND (Fish OR Teleosts)* *(Prevalence OR Determination) AND (Branchiomyces) AND (Fish OR Teleosts)* *(Prevalence OR Determination) AND (Aphanomyces) AND (Fish OR Teleosts)* *(Prevalence OR Determination) AND (Achlya) AND (Fish OR Teleosts)* *(Prevalence OR Determination) AND (Aspergillus) AND (Fish OR Teleosts)* *(Prevalence OR Determination) AND (Paecilomyces) AND (Fish OR Teleosts)* *(Prevalence OR Determination) AND (Sphaerothecum) AND (Fish OR Teleosts)* *(Prevalence OR Determination) AND (Pythium) AND (Fish OR Teleosts)*

Data analysis

The data was tabulated in a Microsoft® Excel® spreadsheet for analysis of the relationship between teleost fish and pathogenic fungi. The total number of sampled fish ("sample *n*") and the total number of positive fish ("*n*" positive fish) reported in the 26 articles included in the analysis were obtained. Using the "*n*" of positive fish for each fungus, the frequencies and percentages related to each explanatory variable were calculated. Subsequently, the graphic expression was presented as a Sankey plot created in VisualParadigm® software, in which the categorical variables were linked by the frequency of positive fish. Finally, the frequency distribution map of fungal classes was created using the TomTom® Map Chart tool in Microsoft® Excel®.

Results

Relationship between pathogenic fungi and teleost fish

The quantitative analysis was performed on 26 articles selected for this study; the extracted data included 29 332 fish, of which 1 409 cases of fungal infection were reported, representing an overall prevalence of 4.80%. The authors reported 25 fish species and one population at the genus level (Pseudanthias sp.) affected by 18 fungal genera, indicating multiple interactions between taxonomic groups (Figure 2). Among the reported genera, eight were identified to the species level, bringing the total to 24 fungal species. The fish *Oreochromis niloticus* and *Salmo salar* presented the highest number of positive samples for fungal infection, with 574 (40.73 %) and 539 (38.25 %), respectively, and presented infection by three and four fungal genera, followed with less frequency by the species *Oncorhynchus mykiss*, with 108 (7.66 %) positive fish, and infection by five fungal genera. Among the pathogenic fungi reported at the genus level, *Branchiomyces* sp. stood out with a high frequency of positive fish in relation to the fish species *Oreochromis niloticus*. At the same time, *Saprolegnia* sp. (391 [27.75 %]) and *Pythium* sp. (134 [9.51 %]) were more related to *Salmo salar*; however, other genera showed lower occurrence, with a maximum of 19 positive fish for *Aphanomyces* sp. (1.34 %). In contrast, genera such as *Alternaria* sp., *Cephalotheca* sp., *Didymella* sp., *Emmia* sp., *Mucor* sp. and *Phoma* sp. reported one positive fish for per fungus, representing only 0.07 %. On the other hand, the fungi that were reported at the species level corresponded to eight fungal genera, among which four species for the genus *Exophiala* spp., five for the genus *Pythium* spp. and up to 10 species for the genus *Saprolegnia* spp., being this the one that presented the highest frequency with 822 (62.59 %) positive fish, in particular the species of *Saprolegnia parasitica*, *S. diclina*, *S. ferax* and *S. australis*, were the most prevalent with 463 (32.86 %), 58 (4.11 %), 40 (2.83 %) and 30 (2.12 %) positive fish respectively.

Variables related to fungal infection

Reported fungal infections are associated with study variables that enable characterization of trends in the host-fungal relationship (Figure 3). Among the 1 409 fish positive for fungal infection, the majority were classified as fish used in meat production, with 1,255 positive fish (89.07%), complemented by just 10 positive fish (0.70%) sampled from ornamental fish populations. On the other hand, 144 positive fish (10.22%) for fungal pathogens were sampled from fishing activities, all of them from fish caught for meat production.

For diagnosis, molecular techniques were identified as the most frequently used; the authors used molecular techniques to identify the fungus in 837 (59.40 %) positive cases. Histopathological studies were performed on 572 (40.59 %) samples. However, the frequency of diagnosis is roughly similar; molecular techniques identified a total of 13 genera and 24 species of fungi, while histopathological techniques identified only two pathogenic fungi at the genus level (*Branchiomyces sp.* and *Saprolegnia sp.*); it is noteworthy that, in both cases, the initial isolation was performed using fungal culture techniques.

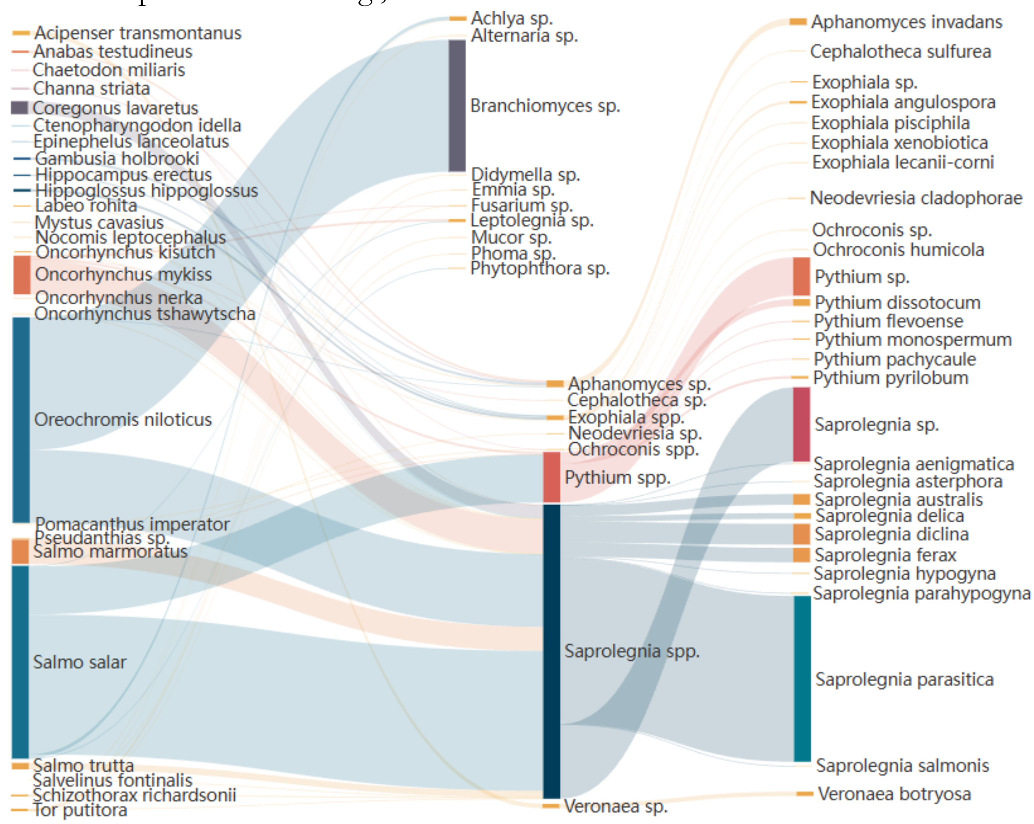

Figure 2. The Sankey diagram indicates the relationship between teleost fish species and the pathogenic fungi that infect each species. The thickness of the lines indicates the reporting frequency (number of fish positive for each pathogenic fungus). In the nomenclature of the biological groups analyzed, "sp." refers to the singular and "spp." to the plural of related species.

In addition, up to 13 families of fish were reported with at least one individual positive for infection by pathogenic fungi; however, only salmonids and cichlids presented 1,348 cases of positive fish (99.67%), far below were cyprinids, with 17 (1.20%) positive fish. In contrast, the ten remaining families of fish had a maximum of 12 (0.11 %) positive fish (*Acipenseridae*) and a minimum of one positive fish for the families Bagridae, Chaetodontidae, and Pomacanthidae, representing only 0.07 % of the fish positive for mycosis in the reports analyzed. Likewise, pathogenic fungi corresponding to four classes of fungi were reported, among them the studies focused on the determination of *Oomycota* fungi with 1 372 positive fish (97.37 %). In isolation, the occurrence of a fish positive for the *Mucormycota* fungus class (0.07 %) stood out, which corresponded to *Mucor sp.* infection in the cyprinid *Schizothorax richardsonii* and what was reported for the *Basidiomycota* (0.07 %) *Emmia sp.* in a cyprinid of the *Tor putitora* species (Figure 3).

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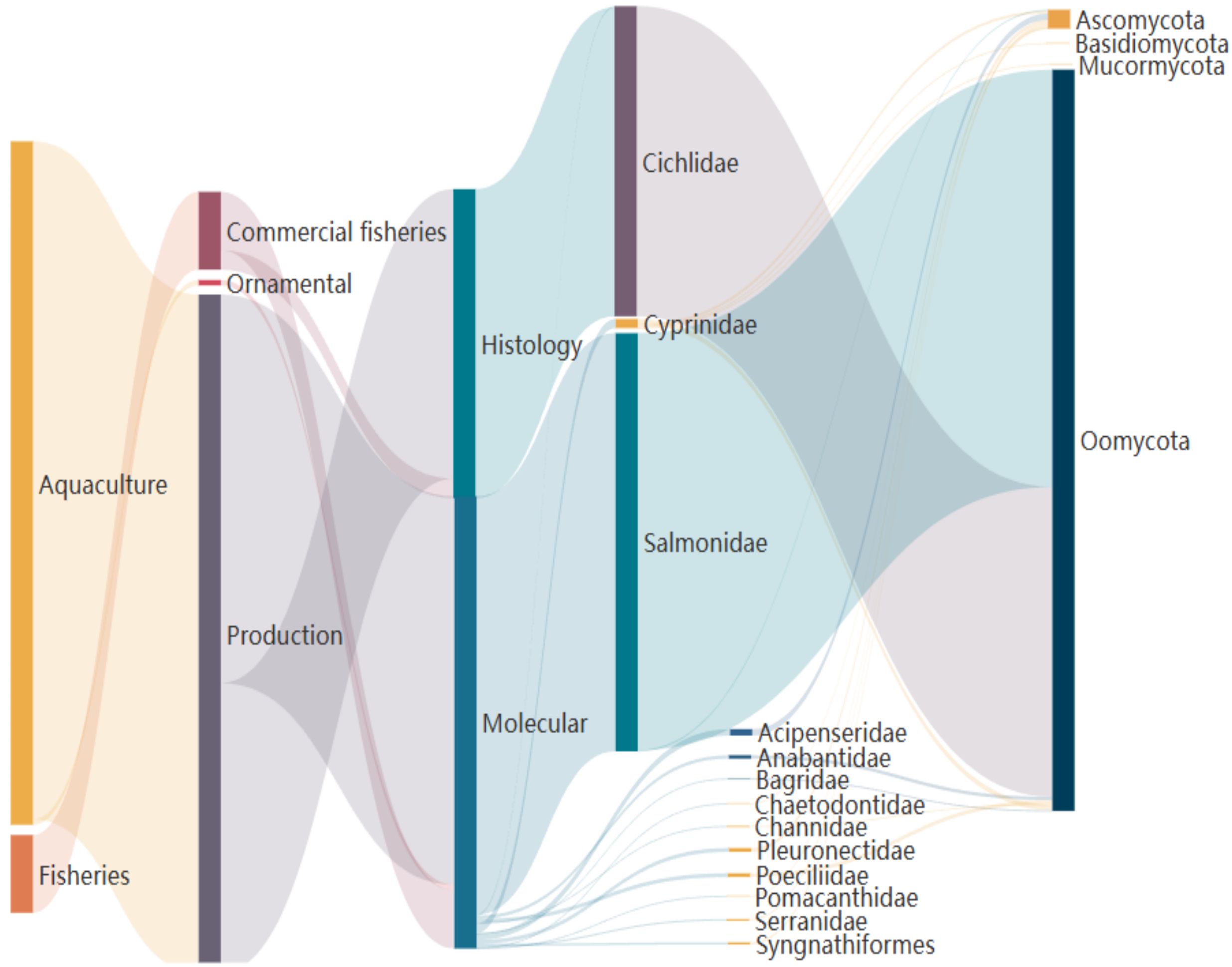

Figure 3. Sankey diagram, showing the explanatory variables related to the samples analyzed for the detection of pathogenic fungi; the thickness of the lines indicates the reporting frequency (number of positive fish for each variable analyzed).

Geographic distribution of pathogenic fungi reported in teleost fish

Teleost fish positive for fungal infection were distributed across 16 countries, with presence on four of the five continents (Figure 4). Fungi in the classes *Ascomycota* and *Oomycota* have been reported in North America, Canada, and the United States. Meanwhile, five European countries reported *Oomycota* fungi, and only the Czech Republic and Georgia reported *Ascomycota* fungi. In Asia, India was particularly notable, with up to four distinct classes of fungi identified: *Ascomycota*, *Basidiomycota*, *Mucorales*, and *Oomycota*. In contrast, only Egypt was reported to have *Oomycota* fungi. Notably, Europe and Africa had the highest numbers of reported positive fish, with 745 (52.87 %) and 572 (40.59 %) records, respectively. On the other hand, although Egypt was the only country with reports in Africa, it had the highest number of infected fish per country (572 positive fish, 40.59 %), while only one positive fish was documented in China, the Czech Republic, and South Korea (0.07 %).

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Figure 4. Geographic distribution of the classes of fungi detected in teleost fish, in parentheses, the number of positive fish reported by country is shown.

Discussion

Teleost fishes make up a group of organisms with a high richness of described species, a situation that represents difficulties for their ecological and health monitoring given the different environments they colonize (Mayer y Pšenička 2024), correspondingly, the biological diversity of pathogens related to fish is high, different pathogens have been associated with infections in teleost fish, including a wide diversity of fungi (Austin 2011, Bricknell 2017, Choudhury *et al*., 2014, Crane y Hyatt 2011). In this context, the present study analyzed 1,409 fish positives for fungal infection, present in 25 species of teleost fish that are susceptible to fungal infection and used commercially for food production, fishing, and ornamental production.
Aquaculture and fishing alone account for the production and consumption of 182 million tons of food (FAO 2023), while the aquarium industry markets nearly 30 billion dollars in ornamental specimens (Peh y Azra 2025). However, high production is threatened by outbreaks of fungal infections. These pathogens are commonly aquatic saprophytes associated with the decomposition of organic matter. However, they establish themselves as secondary infections due to immune suppression or mechanical damage to fish (Choudhury *et al*., 2014, Singh *et al*., 2018).

In this study, the fish most frequently infected with fungal infection were *O. niloticus* and *S. salar*, two species with a long history of farming. *O. niloticus* tilapia has been introduced in up to 90 countries around the world and are frequently farmed due to the species' biological attributes, which include high disease resistance and a good production profile (Gjedrem *et al*., 2012, Gu *et al*., 2019), however, this study identified that *O. niloticus* populations are primarily affected by fungi of the genus *Branchiomyces*, an infection characterized by gill disease. Infected fish exhibited respiratory disorders, lethargy, and surface swimming accompanied by rapid movements of the mouth and gill cover in search of improved oxygenation. Infected fish populations usually have high prevalence rates (26.67-100.00 %) and postmortem examination usually shows necrotic lesions at the gill level (El-Bouhy *et al*., 2014, Khalil *et al*., 2015); similarly, the species *O. niloticus* is affected by *Saprolegnia* spp., an *Oomycota* fungus that presents outbreaks associated with low temperatures. Its infection results in focal lesions at the cutaneous level, associated with the development of cottony patches of filamentous hyphae (Mahboub y Shaheen 2021).

Saprolegnia spp. was highly prevalent in its relationship with *S. salar* (391 positive fish and 27.75 %); in particular, the species *Saprolegnia parasitica* was the most frequent, a highly relevant relationship, given that this pathogen has been reported to cause economic losses in salmonid production of nearly 10 % annually (Sandoval-Sierra *et al*., 2014). The virulence of this species of fungal is related to factors such as kinases, the lectin ricin B, disintegrins and proteases (Srivastava *et al*., 2018). Furthermore, this study analyzed 10 fungi within the genus *Saprolegnia* spp. at the species level, indicating high diversity and infection potential across teleost species. It is worth noting that the profile of the reports primarily covered aquaculture fish, which underscores the importance and growth of this industry. Between 2020 and 2022, the FAO reported a 6.6 % growth in aquaculture production, which allowed for 130.9 million tons of products to be reported worldwide (FAO 2024). However, farmed fish, unlike wild fish, are under stressors that can trigger disease outbreaks, due to an increase in culture densities, stress caused by management and the high dynamics of mobility of organisms in the development of aquaculture practices, which can be related to the high frequency of aquaculture fish that tested positive for fungi (Sharmin *et al*., 2020, Wanja *et al*., 2020).

In this review, the organisms analyzed most frequently corresponded to fish focused on obtaining food, given that up to 89 % of all products generated by the industry are destined for human consumption (FAO 2024). Furthermore, the reports showed that mycological diagnosis was carried out almost equally by molecular and histological methods; however, molecular methods allowed the determination of up to 24 fungi at the species level. In this study it was identified that the genera *Exophiala* spp., *Pythium* spp. and *Saprolegnia* spp. presented a greater number of fungi identified at the species level, with four, five and ten respectively; for the first case, internal transcribed spacer (ITS) sequencing, D1/D2 gene of the large ribosomal subunit (60S) and the *RPB2* gene were used (Armwood *et al*., 2021), likewise, for the determination of *Pythium* spp. and *Saprolegnia* spp., the sequencing of the internal transcribed spacer rDNA ITS was used (Elameen *et al*., 2021, Tedesco *et al*., 2021).

Regarding fungal distribution, it was observed that the most significant proportion of pathogenic fungi associated with teleost fish belonged to the *Oomycota* group, which were found in 14 of the 16 countries that submitted reports. Southeast Asia was particularly prominent, with up to five countries reporting the presence of *Oomycota* fungi. This is likely related to the region's long tradition of fish farming and consumption (Jia, *et al*., 2017). India, in particular, showed the highest number of positive fish and the greatest diversity of fungal agents in the region. As the world's second-largest aquaculture producer, second only to China, its high demand and the mobility of organisms may be contributing factors to the occurrence and distribution of pathogens, including fungi (Koteshwar Rao, 2023). Furthermore, the frequency of *Oomycota* fungi is closely related to the frequency of reports of infection by *Saprolegnia* spp., while the high frequency of reports of *Saprolegnia* spp. may be due to the low host specificity it presents and the presence of flagellated zoospores in its life cycle, a developmental stage that allows it to disperse in the aquatic environment (Derome *et al*., 2016). In contrast, only the Czech Republic and Georgia did not report infections by *Oomycota* fungi, in both cases their reports concerned *Ascomycota* fungi affecting the analyzed fish. These fungi are classified as thick-walled and rigid fungi that lack motile spores, although they are normally opportunistic parasites with low host specificity (Gozlan *et al*., 2014). On the other hand, northern European countries showed a high frequency of pathogenic fungi; the United Kingdom, with 336 positive fish, ranks first in our study. However, the high frequency may be associated with greater and more exhaustive sampling efforts related to the prevention and control of pathogens (Minor et al., 2014). The generalist nature of fungi leads to the need for specific study of the different etiological agents that affect crops and wild fish populations that are relevant to their use by humans (Pavić *et al*., 2022, Sandoval-Sierra *et al*., 2014). Furthermore, the removal or elimination of fungi in production and environmental water is an unviable task, so the development of prophylactic and treatment strategies appear to be the way forward for the control of fungal infections, such as the development of vaccines (Minor *et al*., 2014) as well as the characterization of biosynthesis pathways for the generation of specialized antifungal drugs (Rzeszutek *et al*., 2019, Saraiva *et al*., 2014). This is aimed at better health management of outbreaks of pathogenic fungi in teleost fish populations.

Conclusion

Quantitative analysis of the relationship between teleost fish and pathogenic fungi identified 25 species and one fish genus affected by 24 genera of fungi with a dynamic interaction. The presence of fungi from the *Oomycota* group was more frequent and had a heterogeneous distribution, mainly including countries in Southeast Asia and Northern Europe. Particularly the genus *Saprolegnia*, which infects fish species such as *O. niloticus* and *S. salar*, stands out. Furthermore, the reports showed that the diagnosis of fungal infections is primarily performed in fish of value in aquaculture and socioeconomic relevance in food production. This diagnosis is carried out using molecular and histological techniques to identify pathogenic fungi. However, due to their parasitic, opportunistic behavior and their role as decomposers in aquatic ecosystems, fungi exhibit low host specificity. Therefore, monitoring the health of this interaction is essential for developing effective management and control strategies for mycoses affecting teleost fish in diverse environments. These findings can contribute to a better understanding of fungal infections in the aquaculture industry and assist in sanitary management.

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