ARTICLES
Archives of Veterinary Science
UFPR
https://www.ufpr.br/

Emerging Fungal Pathogens in Wildlife: a systematic review of Veterinary Implications and One Health Challenges

Submitted: *04/10/2025*
Accepted: *25/12/2025*

Tayná Padilha Basqueroto Antunes[1], *Débora Goulart Menegaz*[2]

[1]*Veterinary Diagnostic Laboratory, Michigan State University, 202, 4125 Beaumont Rd. Lansing, MI 48910, United States. ORCID: https://orcid.org/0009-0007-1292-0284.*
[2]*University of Southern Santa Catarina, Av. José Acácio Moreira, 787. Tubarão, SC, 88704-900. Brazil. ORCID https://orcid.org/0009-0007-6722-4411.*

Author for correspondence: Tayná Padilha Basqueroto Antunes – padilha1@msu.edu

Abstract: Emerging fungal pathogens represent an increasing threat to global biodiversity, animal health, and public health, particularly in wildlife populations, where outbreaks may result in ecological, veterinary, and zoonotic consequences. This systematic review aims to identify the main emerging fungal pathogens affecting wildlife and to evaluate the available evidence regarding their veterinary, environmental, and human health implications within a One Health framework. A comprehensive literature search was conducted across PubMed, Scopus, Web of Science, and CAB Abstracts for studies published between 2000 and 2025, using predefined keywords related to emerging fungal pathogens, wildlife mycoses, zoonotic fungi, and One Health. A total of 147 records were identified. After duplicate removal and relevance screening, 72 articles underwent full-text evaluation, and 48 studies met the eligibility criteria and were included in the qualitative synthesis. The most frequently reported pathogens included *Batrachochytrium dendrobatidis* and *Batrachochytrium salamandrivorans* in amphibians, *Pseudogymnoascus destructans* in bats, and *Paranannizziopsis* spp. in reptiles. Reports originated from North America, Europe, South America, Asia, and Oceania, affecting amphibians, bats, reptiles, birds, and small mammals. Diagnostic confirmation was commonly based on molecular assays and histopathology, given nonspecific clinical signs. From a One Health perspective, several wildlife-associated fungi show documented or potential relevance to human health, particularly among immunocompromised individuals and professionals with occupational exposure. Human cases, when reported, were diagnosed using culture, molecular methods, and histopathology. Environmental drivers such as climate change, habitat disturbance, and anthropogenic dissemination were consistently associated with pathogen emergence and spillover risk.
Keywords: emerging mycoses, wildlife health, One Health, veterinary diagnostics, fungal pathogens.

1. Introduction

Fungal pathogens have historically received less attention than bacterial or viral agents in both veterinary and public health contexts. However, in recent decades, the emergence and re-emergence of fungal diseases in wildlife populations have gained increasing recognition as significant threats to biodiversity, ecosystem stability, and animal health worldwide (FISHER *et al.*, 2020; FISHER *et al.*, 2022). These pathogens often cause high-mortality events, contribute to severe population declines, and, in some cases, drive species toward extinction. Unlike many bacterial or viral diseases, fungal pathogens frequently persist in the environment for extended periods, complicating eradication efforts and facilitating recurrent outbreaks (FISHER *et al.*, 2022).

Several high-impact fungal diseases illustrate the scale and complexity of this problem. The chytrid fungi *Batrachochytrium dendrobatidis* (Bd) and *B. salamandrivorans* have devastated amphibian populations globally, contributing to the decline of more than 500 species and the extinction of at least 90 since the 1970s (SCHEELE *et al.*, 2019; MARTEL *et al.*, 2013). Similarly, *Pseudogymnoascus destructans*, the causative agent of white-nose syndrome in bats, has killed millions of hibernating bats across North America, with cascading ecological consequences due to their role in insect population control (FRICK *et al.*, 2017). In reptiles, *Ophidiomyces ophiodiicola*, *Nannizziopsis spp.*, and *Paranannizziopsis spp.* have emerged as significant causes of mycotic dermatitis, threatening both free-ranging and captive populations and raising concerns about cross-species transmission (SIGLER; HAMBLETON; PARÉ, 2013; LORCH *et al.*, 2016).

A complex interplay of ecological, climatic, and anthropogenic factors drives the emergence of fungal pathogens in wildlife. Climate change alters temperature and humidity patterns, creating new niches conducive to fungal proliferation (Garcia-Solache and Casadevall, 2010). Human activities, including global trade in wildlife and exotic pets, habitat fragmentation, and translocation of animals, further facilitate the spread of pathogenic fungi beyond their original geographic ranges (Fisher et al., 2020). Moreover, shifts in host–pathogen dynamics caused by environmental stressors can compromise wildlife immune responses, increasing susceptibility to infections (Voyles et al., 2018).

From a veterinary perspective, emerging fungal pathogens pose unique diagnostic and management challenges. Clinical manifestations in wildlife are often nonspecific or subclinical, complicating early detection and surveillance (UGOCHUKWU *et al.*, 2022). Accurate diagnosis typically requires histopathology, culture, and molecular tools such as PCR and sequencing, which may not be readily available in field settings (LORCH *et al.*, 2016). Furthermore, therapeutic options for free-ranging wildlife are limited, and antifungal resistance in some emerging pathogens poses significant challenges for effective disease control (FISHER *et al.*, 2022; WIEDERHOLD, 2023).

The One Health framework emphasizes the interconnectedness of human, animal, and environmental health. Many wildlife-associated fungi have zoonotic potential or can indirectly affect human health through ecological disruption. For example, declines in insectivorous bats caused by *P. destructans* can increase agricultural pest burdens, thereby impacting food security (Frick et al., 2017). Similarly, disruptions in amphibian communities can alter aquatic ecosystems, with cascading consequences for biodiversity and ecosystem services (Scheele et al., 2019).

Therefore, the overall objective of this systematic review is to synthesize current evidence on emerging fungal pathogens affecting wildlife, with a particular focus on their veterinary implications, diagnostic challenges, environmental drivers, and relevance within a One Health framework, integrating impacts on animal, human, and ecosystem health.

2. Development

2.1. Type of study

This is a qualitative narrative review that compiles and critically analyzes scientific evidence on emerging fungal pathogens affecting wildlife from January 2000 to October 2025. The study aimed to describe the diversity, epidemiology, diagnostic approaches, host–pathogen interactions, antifungal resistance, and One Health implications associated with these pathogens. For the study design, the recommendations of the PRISMA 2020 guidelines were adopted and adapted, as described by Page et al. (2021) and complemented by the methodological principles outlined in Haddaway et al. (2022) and Peters et al. (2020), to ensure greater transparency, reproducibility, and methodological rigor in the review process and the results obtained.

2.2. Descriptors and Database

An active literature search was conducted in the Scientific Electronic Library Online (SciELO), PubMed (National Library of Medicine), Virtual Health Library (VHL), Scopus, and Web of Science. Articles published in English, Spanish, and Portuguese between January 2000 and October 2025 were considered. The search used descriptors and keywords in English, Spanish, and Portuguese, including Fungal Pathogens, Wildlife, Veterinary Medicine, and One Health, combined with specific pathogen names such as B. dendrobatidis, *P. destructans, O. ophiodiicola, Nannizziopsis spp.,* and *Paranannizziopsis spp*. Descriptors were combined using the Boolean operator "AND", which restricted the results to documents containing all specified.

The inclusion criteria considered peer-reviewed articles published between January 2000 and October 2025 in English, Spanish, or Portuguese that addressed emerging fungal pathogens in wildlife and their relevance to veterinary medicine and One Health. Eligible studies focused on topics such as epidemiology, ecology, diagnostic approaches (e.g., histopathology, fungal culture, PCR, sequencing, MALDI-TOF), host–pathogen interactions, antifungal resistance, and disease management strategies. Original research papers, case reports, surveillance studies, and review articles relevant to these themes were included. The exclusion criteria eliminated articles that focused exclusively on human or plant pathogens without relevance to wildlife, lacked sufficient methodological detail or data for interpretation, or were not peer-reviewed. Abstracts, theses, editorials, and opinion papers were also excluded from the final synthesis.

2.3. Search Strategy

The literature search strategy was designed to ensure a comprehensive and systematic identification of relevant studies on emerging fungal pathogens in wildlife. A total of 147 records were initially identified across the selected databases (SciELO, PubMed, Virtual Health Library, Scopus, and Web of Science) using predefined descriptors and Boolean combinations. Following the removal of duplicate records and the application of inclusion criteria based on topical relevance, 72 articles were retained for full-text review. These articles were then subjected to a detailed screening process to assess methodological quality, data completeness, and alignment with the scope of this review. After this critical evaluation, 48 studies met all eligibility criteria and were included in the final qualitative synthesis. The selection process followed PRISMA 2020 guidelines (PAGE et al., 2021).

3. Summary of Results

The search results from the selected databases were organized into a PRISMA flowchart. After independent evaluation by two reviewers, the studies that met the inclusion criteria were categorized according to the type of data reported, including pathogen species, host taxa, geographic distribution, diagnostic approaches, and disease outcomes. The following key aspects were systematically documented: year of publication, authors, host species, host country, and identified fungal pathogens.

Additionally, figures were created to illustrate the distribution of annual scientific production on emerging fungal pathogens at both global and regional levels, providing a more straightforward overview of research trends and growing scientific interest in this field over time. Comparative analyses were also conducted to highlight variations in the diversity of reported pathogens across different taxonomic groups (amphibians, bats, reptiles) and their geographic occurrence.

3.1. Active Search Flowchart

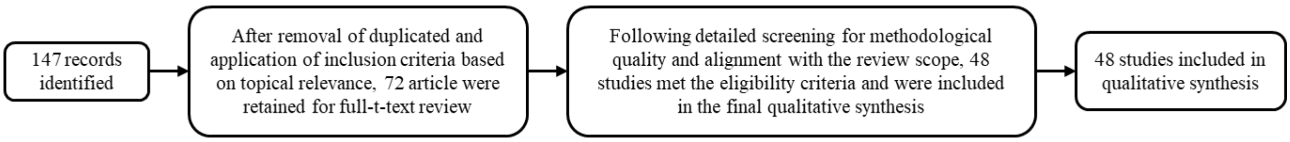

Figure 1 – Systematic Review Flowchart of Study Selection.

3.2. Geographic distribution of emerging fungal diseases in wildlife

The analysis of the 48 studies included in this qualitative narrative review demonstrates that research on emerging fungal diseases in wildlife is heavily concentrated in temperate regions of the Northern Hemisphere, particularly in Europe and North America, where the main surveillance networks and long-term monitoring programs are established (Fisher et al., 2012; Gibb et al., 2020).

Among these studies, 22 had a global scope; six were conducted in Europe, nine in North America, two involved collaborations between North America and Europe, and individual studies were conducted in Panama and Australia. Collectively, studies with a global scope discussed the emergence of these pathogens, including their ecological and health impacts, interactions with climate change, and implications within the One Health framework (Fisher et al., 2020; Fisher et al., 2024). In Europe, most studies reported infections by *Ophidiomyces ophiodiicola* in wild snakes (Franklinos et al., 2017; Müller et al., 2018) and chytridiomycosis outbreaks caused by *Batrachochytrium salamandrivorans* in amphibians (Martel et al., 2013; Martel et al., 2014), as well as transcontinental dissemination routes between Europe and Asia (Martel et al., 2020). A geographic heat map summarizing study locations and transcontinental collaborations is presented in Figure 2.

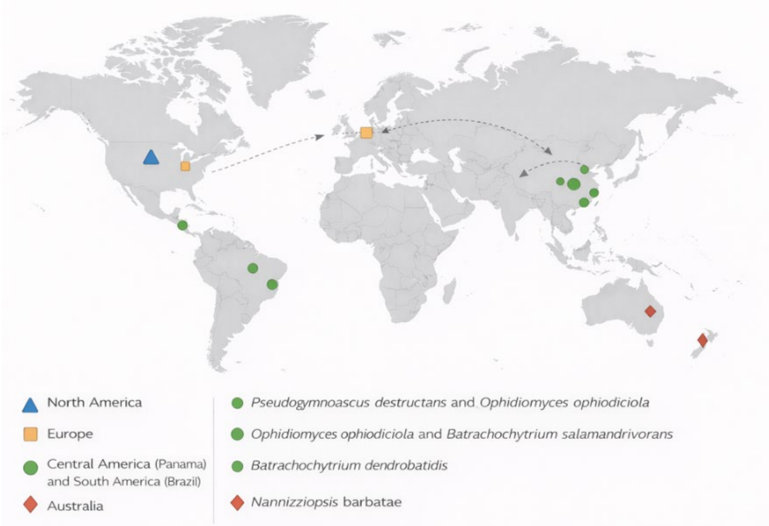

Figure 2 – Geographic distribution of studies on emerging fungal diseases in wildlife. The map summarizes the regional focus of published studies included in this review, highlighting Europe and North America as the main centers of research activity. Symbols indicate the primary fungal pathogens investigated in each region, including *Ophidiomyces ophiodiicola* and *Batrachochytrium salamandrivorans* in Europe, Pseudogymnoascus destructans and *O. ophiodiicola* in North America, *Batrachochytrium dendrobatidis* in Panama and Brazil, and *Nannizziopsis barbatae* in Australia. Dashed arrows indicate documented transcontinental dissemination routes between Europe and Asia. The map reflects study locations rather than pathogen prevalence.

In North America, most research focused on two ecologically significant fungal diseases: white-nose syndrome, caused by *Pseudogymnoascus destructans* in bat populations (Blehert et al., 2009; Frick et al., 2010), and ophidiomycosis in wild snakes associated with *O. ophiodiicola* (Allender et al., 2015; Lorch et al., 2016). These infections were shown to significantly affect host survival, reproductive success, and movement patterns. Across studies, molecular diagnostic approaches evolved, with earlier investigations relying primarily on histopathology and culture-based methods, and more recent studies incorporating DNA-based techniques such as conventional PCR, nested PCR, and quantitative real-time PCR targeting fungal ribosomal regions (e.g., ITS and 28S rRNA). These methods substantially improved pathogen detection and specificity. In addition, high-throughput approaches, including metagenomic sequencing, were applied in a subset of studies to characterize host-associated microbial communities and to explore environmental factors influencing pathogen persistence and transmission dynamics (Langwig et al., 2017; Davy et al., 2018).

In Central America, one study conducted in Panama documented shifts in disease dynamics within tropical amphibian assemblages affected by *B. dendrobatidis*, demonstrating changes in community composition and differential species susceptibility following pathogen emergence (Voyles et al., 2018). In Australia, one study reported the emergence of *N. barbatae* in free-living reptiles, affecting multiple lizard species across different regions and establishing this pathogen as an emerging threat at a continental scale rather than a localized or host-specific event (Boyle et al., 2020).

In the Southern Hemisphere, research remains limited and geographically uneven. In South America, Brazil is currently the only country with confirmed published records (n = 3 studies) documenting emerging fungal pathogens in free-living wildlife, specifically *Batrachochytrium dendrobatidis* (Bd) in amphibian populations. No eligible studies from other South American countries met the inclusion criteria of this review. Although fungal diseases affecting wildlife were reported before 2000, these early accounts were predominantly descriptive and lacked standardized surveillance frameworks or molecular diagnostic confirmation. Consequently, the increase in documented cases after 2000 is best interpreted as reflecting methodological advances, expanded surveillance efforts, and increased scientific awareness, rather than a true absence of emerging fungal pathogens in earlier periods. Overall, these results highlight a marked geographical bias in current research efforts and emphasize the need to strengthen surveillance and diagnostic programs in biodiversity-rich tropical regions that remain underrepresented in the global literature.

https://doi.org/10.5380/avs.v31i1.101497

3.3. Brazil in the Global Context of Wildlife Fungal Diseases

Brazil represents a key region for understanding the distribution, diversity, and ecological impact of emerging fungal pathogens in wildlife. As summarized in Table 1, multiple studies have documented the presence of *B. dendrobatidis* across several Brazilian biomes (the Atlantic Forest, Caatinga, and lowland Amazon Forest). This is the pathogen's broad ecological range and persistence in tropical and subtropical ecosystems (Jenkinson et al., 2016; Carvalho et al., 2017; Benício et al., 2020; Lambertini et al., 2022). These studies reveal that *Bd* has likely been present in Brazil for nearly a century, with the earliest evidence dating back to the 1930s in preserved amphibian specimens, suggesting that chytridiomycosis may have contributed to amphibian population declines long before it was recognized as a global threat (Rodriguez et al., 2014; Fisher et al., 2012).

Moreover, molecular analyses based on PCR amplification and sequencing of fungal DNA, including multilocus genotyping approaches, have demonstrated the coexistence of a unique endemic lineage (Bd-Brazil) and a globally distributed lineage (Bd-GPL), indicating both long-term historical persistence and potential introductions from external sources. Despite this growing body of evidence, significant knowledge gaps remain, as no confirmed detections of *Batrachochytrium salamandrivorans*, *Ophidiomyces ophiodiicola*, or fungi of the genera *Nannizziopsis* and *Paranannizziopsis* have been reported in Brazilian wildlife to date (Waddle et al., 2020; Basanta et al., 2022).

This absence underscores the urgent need for expanded surveillance programs, improved diagnostic capacity, and targeted ecological studies. Given Brazil's exceptional biodiversity and complex ecosystems, addressing these gaps is crucial to advancing global understanding of fungal disease dynamics and strengthening wildlife conservation efforts.

Reference	Biome / Region	Location	Key Findings/Species
Jenkinson et al., 2016 (*Mol. Ecol.*)	Atlantic Forest (Southeast)	São Paulo, Paraná, Santa Catarina	Coexistence of endemic (*Bd-Brazil*) and globally distributed (*Bd-GPL*) lineages; evidence of local diversification and historical persistence.
Carvalho et al., 2017 (*Proc Royal Soc. B*)	Atlantic Forest (Southeast)	Various states in SE Brazil	Historical amphibian declines in Brazil linked to chytridiomycosis since mid-20th century.
Benício et al., 2020 (*Trop. Conserv. Sci.*)	Caatinga (Northeast)	Pernambuco, Paraíba	First evidence of high Bd prevalence in semi-arid species (*Rhinella granulosa*, *R. jimi*).
Lambertini et al., 2022 (*Sci. Rep.*)	Amazon (Lowland)	Pará, Amazonas	Detection of Bd in 57 amphibian species by qPCR and experimental infection.
Carvalho et al., 2017 (*Proc. Royal Soc. B*)	Atlantic Forest (Southeast)	Museum collections	Historical records of Bd dating back to the 1930s in preserved amphibian specimens.

Table 1 – Documented studies of *Batrachochytrium dendrobatidis* (Bd) in wild animals in Brazil.

3.4. Temporal Trends in Research on Emerging Fungal Pathogens in Wildlife (2012–2024)

The temporal distribution of the 48 studies analyzed in this review (Table 2) demonstrates a clear expansion of research on emerging fungal pathogens in wildlife over the past decade, reflecting shifting scientific priorities, improved diagnostic capacity, and increasing awareness of fungal threats. Although the literature search covered the period from 2000 to 2025, all eligible studies were published between 2012 and 2024. This pattern highlights that substantial scientific attention to fungal diseases in wildlife emerged primarily in the last decade, coinciding with their recognition as major drivers of biodiversity loss and significant challenges within the One Health framework (Fisher et al., 2012; Fisher et al., 2020).

Period	Number of Studies	Key Focus and Milestones	Representative References
2012–2015 – Foundational discoveries and early frameworks	12	Identification of key pathogens (*Batrachochytrium dendrobatidis*, *B. salamandrivorans*, *Ophidiomyces ophiodiicola*, *Pseudogymnoascus destructans*); development of conceptual models; recognition of wildlife trade as a driver of pathogen spread.	Fisher et al., 2012; Martel et al., 2013; Lorch et al., 2015; Frick et al., 2015; Fisher et al., 2015
2016–2019 – Expansion of taxonomic scope and geographic range	14	Inclusion of reptiles and bats; documentation of transcontinental spread; refinement of diagnostic and histopathology standards; focus on environmental and thermal ecology influences on disease dynamics.	Martel et al., 2016; Franklinos et al., 2017; Langwig et al., 2017; Voyles et al., 2018; Lorch et al., 2016
2020–2024 – Methodological	22	Adoption of environmental DNA (eDNA) detection; development of point-of-care assays; study of host	Walker et al., 2022; Woodhams et al., 2020;

Period	Number of Studies	Key Focus and Milestones	Representative References
innovation and One Health integration		microbiome interactions; research on antifungal resistance; establishment of surveillance networks; integration of One Health approaches.	Basanta et al., 2023; Thomas et al., 2024; Fisher et al., 2024

Table 2 – Temporal distribution of studies on emerging fungal pathogens in wildlife from 2012 to 2024.

Subsequent research expanded to include wildlife as a major driver of pathogen spread, documenting the emergence of additional fungal diseases across diverse taxa and ecosystems (Fisher et al., 2015). But how severe were these impacts? In several affected species, population declines exceeded 70–90%, with some local extinctions reported within a few years of pathogen introduction. For example, snake fungal disease caused by *O. ophiodiicola* has been associated with significant reductions in survival, body condition, and recruitment in wild snake populations. In contrast, white-nose syndrome caused by *Pseudogymnoascus destructans* has resulted in the loss of millions of bats across North America, with mortality rates surpassing 90% in some hibernacula. These dramatic declines illustrate not only how widely these pathogens have spread, but also the profound ecological consequences of fungal epizootics in wildlife populations.

Between 2016 and 2019, research diversified geographically and taxonomically, expanding beyond amphibians to include reptiles and bats. Studies during this period advanced understanding of *Ophidiomyces ophiodiicola* infections by describing lesion progression, host inflammatory responses, and impacts on survival in wild snakes (Lorch et al., 2016; Franklinos et al., 2017). The transcontinental spread of *B. salamandrivorans* was also documented, highlighting the role of wildlife trade in pathogen dissemination (Martel et al., 2016). Research further clarified how climate and thermal ecology influence disease dynamics by showing that temperature-dependent fungal growth, host thermoregulatory behavior, and seasonal conditions affect infection intensity, pathogen persistence, and transmission risk (Lorch et al., 2016; Franklinos et al., 2017). Advances in histopathology have improved the identification of diagnostic skin lesions, while molecular diagnostic approaches such as species-specific PCR and quantitative PCR have enhanced pathogen detection and surveillance capacity (Lorch et al., 2016; Franklinos et al., 2017).

The most recent phase (2020–2024) was marked by rapid methodological innovation and a shift toward predictive and applied research. Environmental DNA (eDNA) methods (Walker et al., 2022), point-of-care diagnostics (Thomas et al., 2024), and studies on host microbiomes (Woodhams et al., 2020) advanced the field, while antifungal resistance, cross-species transmission, and surveillance design became central topics.

3.5. Molecular and Genomic Insights into Emerging Fungal Pathogens

Molecular and genomic approaches have provided critical insights into the evolution, pathogenicity, and spread of emerging fungal pathogens in wildlife. Genomic studies on *Batrachochytrium dendrobatidis* revealed the coexistence of endemic and globally distributed lineages in Brazil, highlighting both historical persistence and multiple introductions (Jenkinson et al., 2016). Comparative genomics and population-level analyses have also elucidated the evolutionary origins and virulence determinants of *P. destructans* in bats and *O. ophiodiicola* in snakes (Lorch et al., 2016; Franklinos et al., 2017). eDNA and metagenomic tools further enhance surveillance by enabling direct detection of fungal DNA in soil and water samples, facilitating early outbreak detection without laboratory culture (Walker et al., 2022). These molecular advancements are transforming wildlife disease research, improving diagnostic precision, and providing valuable data on transmission dynamics and adaptive evolution. These molecular advancements are transforming wildlife disease research by improving diagnostic accuracy and generating high-resolution data on transmission dynamics and pathogen evolution. For example, whole-genome sequencing has been used to trace the geographic spread and evolutionary diversification of *B. salamandrivorans*, thereby enabling researchers to identify introduction pathways, detect multiple lineages, and assess adaptive changes associated with host susceptibility and environmental conditions (Martel et al., 2014; Farrer et al., 2017).

3.6. Environmental Reservoirs and Transmission Pathways

Environmental reservoirs play a crucial role in the persistence and dissemination of emerging fungal pathogens. Species such as *B. dendrobatidis* and *P. destructans* can survive for extended periods in water, soil, and organic matter. Remaining infectious even in the absence of hosts through persistence within environmental biofilms that enhance survival and resistance to environmental stressors (Garcia-Solache and Casadevall, 2010). Studies have demonstrated that *Ophidiomyces ophiodiicola* persists in moist soil and organic substrates, contributing to the recurrence of ophidiomycosis outbreaks in snake populations (Lorch et al., 2016; Franklinos et al., 2017). Global wildlife trade and the movement of animals have been implicated in the transcontinental introduction of *B. salamandrivorans*, as documented in Europe and Asia (Martel et al., 2013; Martel et al., 2020). These findings underscore how abiotic reservoirs, environmental conditions, and anthropogenic activities collectively shape the distribution and transmission of fungal pathogens, with environmental biofilms acting as protective niches that enhance pathogen persistence and facilitate repeated exposure of wildlife hosts. For example, *B. dendrobatidis* has been shown to persist within aquatic biofilms, where biofilm-associated cells exhibit increased survival under fluctuating environmental conditions, reinforcing the importance of targeted biosecurity and habitat management strategies (Garcia-Solache and Casadevall, 2010; Johnson and Speare, 2005).

3.7. Host–Pathogen Interactions and Immune Responses

Host–pathogen dynamics in emerging mycoses are governed by intricate molecular interactions and immune mechanisms. Pathogens such as *B. dendrobatidis* employ a range of virulence factors to invade host tissues and evade immune defenses. In contrast, hosts mount innate responses, including the production of antimicrobial peptides and inflammatory activation (Fisher et al., 2020). Research in Panama revealed that amphibian population recovery from chytridiomycosis is often linked to shifts in host immune response rather than pathogen attenuation (Voyles et al., 2018). Additionally, the skin microbiota of amphibians has been shown to provide natural protection by producing antifungal metabolites, influencing susceptibility to *Bd* infection (Woodhams et al., 2020). Environmental stressors, co-infections, and genetic diversity further modulate disease outcomes, emphasizing the complexity of host–pathogen interactions and the need for integrative approaches to enhance host resilience and disease management.

3.8. Antifungal Resistance and Therapeutic Challenges

Antifungal resistance is an emerging obstacle in controlling fungal diseases in wildlife, reducing the efficacy of available treatments and complicating management efforts. Mechanisms such as mutations in target genes, efflux pump overexpression, biofilm formation, and changes in cell membrane composition have been described in several pathogenic fungi (Fisher et al., 2022; Hui et al., 2024). The widespread use of azoles in agriculture has contributed to the development of cross-resistance in environmental isolates, posing additional challenges for veterinary applications (Fisher et al., 2024). Treating free-ranging wildlife is often unfeasible due to logistical constraints, ecological concerns, and the absence of approved antifungal protocols. As a result, alternative strategies such as the use of beneficial microbial communities, environmental interventions, and novel antifungal compounds are under investigation (Wiederhold, 2023). Addressing resistance will require integrated surveillance, stewardship, and One Health–oriented strategies that combine environmental, veterinary, and public health efforts. Evidence of antifungal treatment failure has been reported in wildlife, including cases of chytridiomycosis in amphibians treated with itraconazole, in which therapeutic responses were transient or ineffective, and reinfection occurred following treatment cessation (Garner et al., 2009; Berger et al., 2010).

3.9. Predictive Modeling and Climate Change Scenarios

Predictive modeling offers valuable tools for anticipating the dynamics of emerging fungal pathogens under changing environmental conditions. Species distribution models have been applied to forecast the spread of *B. salamandrivorans* under future climate scenarios, informing targeted surveillance and conservation strategies (Grisnik et al., 2023). Similar approaches in bat populations have used microclimate data from hibernacula to predict the expansion and impact of *P. destructans* (McClure et al., 2022). Changes in temperature, humidity, and precipitation patterns driven by climate change are expected to expand the ecological niches of many fungal pathogens, increasing disease risk in new regions (Garcia-Solache and Casadevall, 2010). Integrating climatic data with host distribution and land-use information strengthens predictive accuracy, providing essential insights for early intervention, risk assessment, and adaptive management in wildlife disease control.

3.10. Policy, Surveillance, and One Health Implementation

Coordinated regional and international policy frameworks and robust surveillance systems are vital to mitigating the impacts of emerging fungal pathogens. European risk assessments for *B. salamandrivorans* have led to recommendations for stricter trade regulations, quarantine measures, and improved biosecurity protocols (EFSA, 2018). Integrated surveillance programs that combine environmental sampling, wildlife diagnostics, and genomic monitoring enhance early detection and rapid response capabilities (Woods et al., 2023). The One Health approach promotes collaboration among veterinary, public health, environmental, and agricultural sectors, facilitating data sharing and coordinated action (Fisher et al., 2024). Expanding diagnostic capacity and surveillance infrastructure in biodiversity-rich regions remains a global priority. Strengthening these measures is crucial not only for protecting wildlife populations but also for preventing ecological disruption and safeguarding public health.

3.11. Limitations of the Present Review

As with most narrative reviews, this work has certain inherent limitations that should be acknowledged while interpreting its findings. The synthesis presented here is based on studies published in English, Portuguese, and Spanish, which may limit the inclusion of relevant literature available in other languages. Additionally, the existing body of research on emerging fungal pathogens remains geographically biased, with a predominance of studies from Europe and North America, reflecting current surveillance efforts rather than gaps in this review's design (Fisher et al., 2020; Gibb et al., 2020). Moreover, variation in methodologies and diagnostic approaches among published studies can influence the comparability of reported data. These aspects highlight broader challenges in the field and underscore the importance of expanding research efforts, particularly in biodiversity-rich tropical regions. Despite these constraints, this review provides a comprehensive synthesis of current knowledge. It identifies critical directions for future research and contributes valuable insights into the One Health implications of emerging fungal pathogens in wildlife.

4. Conclusion

Emerging fungal pathogens represent a significant and growing threat to wildlife, biodiversity, and ecosystem stability, with far-reaching implications for veterinary medicine and One Health. This review highlights the complex interplay of ecological, climatic, and anthropogenic drivers that facilitate the emergence, persistence, and spread of these pathogens, as well as the diagnostic and therapeutic challenges they pose. Advances in molecular tools, genomic analyses, and predictive modeling have deepened our understanding of pathogen diversity, transmission dynamics, and host–pathogen interactions, while emphasizing the importance of environmental reservoirs and changing climatic conditions in shaping disease outcomes. Despite geographical and methodological gaps in current research, the synthesis presented here underscores the crucial roles of surveillance, interdisciplinary collaboration, and integrative approaches in addressing the emergence of fungal diseases. By consolidating current scientific evidence, this work contributes to a broader understanding of fungal threats in wildlife. It provides a foundation for future efforts to safeguard animal health, preserve biodiversity, and protect ecosystem function.

5. Reference

Allender, M. C.; Raudabaugh, D. B.; Gleason, F. H.; Miller, A. N. The natural history, ecology, and epidemiology of *Ophidiomyces ophiodiicola* and its potential impact on free-ranging snake populations. Fungal Ecol., v. 17, p. 187–196, 2015.

Basanta, M. D.; Martel, A.; Pasmans, F. Emerging fungal pathogens in wildlife: current knowledge and future challenges. Front. Vet. Sci., v. 9, 891324, 2022.

Benício, R. A.; Toledo, L. F.; Becker, C. G.; Haddad, C. F. B. First evidence of high prevalence of *Batrachochytrium dendrobatidis* in semi-arid species. Trop. Conserv. Sci., v. 13, p. 1–9, 2020.

Blehert, D. S.; Hicks, A. C.; Behr, M. et al. Bat white-nose syndrome: an emerging fungal pathogen? Science, v. 323, n. 5911, p. 227, 2009.

Boyle, D. G. et al. Emergence of *Nannizziopsis barbatae* in free-living Australian reptiles. PLoS Pathog., v. 16, n. 11, e1008893, 2020.

Carvalho, T.; Becker, C. G.; Toledo, L. F. Historical amphibian declines in Brazil linked to chytridiomycosis. Proc. Biol. Sci., v. 284, n. 1853, 20162254, 2017.

Davy, C. M.; Donaldson, M. E.; Willis, C. K. R. White-nose syndrome is associated with increased replication of a naturally persisting coronavirus in bats. Biol. Lett., v. 14, n. 9, 20180490, 2018.

EFSA Panel on Animal Health and Welfare (AHAW). Risk of survival, establishment and spread of *Batrachochytrium salamandrivorans* (Bsal) in the EU. EFSA J., v. 16, n. 4, 5259, 2018.

Farrer, R. A. et al. Genomic innovations linked to infection strategies across emerging pathogenic chytrid fungi. Nat. Commun., v. 8, 14742, 2017.

Fisher, M. C.; Alastruey-Izquierdo, A.; Berman, J. et al. Tackling the emerging threat of antifungal resistance to human health. Nat. Rev. Microbiol., v. 20, p. 557–571, 2022.

Fisher, M. C.; Garner, T. W. J.; Walker, S. F. Global emergence of *Batrachochytrium dendrobatidis* and amphibian chytridiomycosis in space, time, and host. Annu. Rev. Microbiol., v. 64, p. 291–310, 2020.

Fisher, M. C.; Gurr, S. J.; Cuomo, C. A. et al. Threats posed by the fungal kingdom to humans, wildlife, and agriculture. mBio, v. 11, n. 3, e00449-20, 2020.

Fisher, M. C.; Gurr, S.; Gow, N. A. R. et al. Tackling emerging fungal threats to animal health, food security, and ecosystem resilience. Philos. Trans. R. Soc. B, v. 371, 20160332, 2016.

Fisher, M. C.; Henk, D. A.; Briggs, C. J. et al. Emerging fungal threats to animal, plant and ecosystem health. Nature, v. 484, n. 7393, p. 186–194, 2012.

Fisher, M. C. et al. A One Health roadmap towards understanding and mitigating emerging fungal antimicrobial resistance. npj Antimicrob. Resist., v. 2, n. 1, 2024.

Franklinos, L. H. V. et al. Emerging fungal pathogen *Ophidiomyces ophiodiicola* in wild European snakes. Sci. Rep., v. 7, 3844, 2017.

Frick, W. F.; Pollock, J. F.; Hicks, A. C. et al. An emerging disease causes regional population collapse of a common North American bat species. Science, v. 329, n. 5992, p. 679–682, 2010.

Frick, W. F.; Cheng, T. L.; Langwig, K. E. et al. Pathogen dynamics during invasion and establishment of white-nose syndrome explain mechanisms of host persistence. Ecology, v. 98, n. 3, p. 624–631, 2017.

Garcia-Solache, M. A.; Casadevall, A. Global warming will bring new fungal diseases for mammals. mBio, v. 1, n. 1, e00061-10, 2010.

Gibb, R. et al. Zoonotic host diversity increases in human-dominated ecosystems. Nature, v. 584, n. 7821, p. 398–402, 2020.

Grisnik, M.; Gray, M. J.; Piovia-Scott, J. et al. Incorporating caudate species susceptibilities and climate change into models of *Batrachochytrium salamandrivorans* risk in the United States. Biol. Conserv., v. 284, 110181, 2023.

Haddaway, N. R.; Page, M. J.; Pritchard, C. C.; McGuinness, L. A. PRISMA 2020: R package and ShinyApp for producing PRISMA 2020 compliant flow diagrams. Syst. Rev., v. 11, n. 1, 43, 2022.

Hui, M. et al. Emerging antifungal resistance: mechanisms and management strategies. Front. Cell. Infect. Microbiol., v. 14, 2024.

Jenkinson, T. S. et al. Amphibian-killing chytrid in Brazil comprises both locally endemic and globally expanding populations. Mol. Ecol., v. 25, n. 13, p. 2978–2996, 2016.

Lambertini, C. et al. Amphibian chytrid fungus in the Brazilian Amazon: prevalence, species richness and lineage diversity. Sci. Rep., v. 12, n. 1, 1489, 2022.

Langwig, K. E.; Frick, W. F.; Reynolds, R. et al. Host and pathogen ecology drive the seasonal dynamics of white-nose syndrome. Proc. R. Soc. B, v. 282, 20142335, 2015.

Lorch, J. M. et al. Snake fungal disease: an emerging threat to wild snakes. Philos. Trans. R. Soc. B, v. 371, 20150457, 2016.

Martel, A. et al. *Batrachochytrium salamandrivorans* sp. nov. causes lethal chytridiomycosis in amphibians. Proc. Natl. Acad. Sci. U.S.A., v. 110, n. 38, p. 15325–15329, 2013.

Martel, A.; Blooi, M.; Adriaensen, C. et al. Recent introduction of a chytrid fungus endangers Western Palearctic salamanders. Science, v. 346, n. 6209, p. 630–631, 2014.

Martel, A.; Blooi, M.; Pasmans, F. Transcontinental spread of the emerging amphibian pathogen *Batrachochytrium salamandrivorans*. Emerg. Infect. Dis., v. 26, n. 9, p. 2122–2124, 2020.

McClure, M. L.; Hranac, C. R.; Haase, C. G. et al. Projecting the compound effects of climate change and white-nose syndrome on North American bat species. Clim. Change Ecol., v. 3, 100047, 2022.

Müller, L.; Martel, A.; Praet, S.; Pasmans, F. Ophidiomycosis in a European snake: case report and review of literature. Vet. Rec. Case Rep., v. 6, n. 4, e000730, 2018.

Page, M. J. et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ, v. 372, n. 71, 2021.

Peters, M. D. J. et al. Chapter 11: Scoping Reviews. In: Aromataris, E.; Munn, Z. (eds.). JBI Manual for Evidence Synthesis. Adelaide: JBI, 2020.

Rodriguez, D.; Becker, C. G.; Pupin, N. C.; Haddad, C. F. B.; Zamudio, K. R. Long-term endemism of the amphibian chytrid fungus *Batrachochytrium dendrobatidis* in the Brazilian Atlantic Forest. Mol. Ecol., v. 23, n. 4, p. 774–787, 2014.

Scheele, B. C. et al. Amphibian fungal panzootic causes catastrophic and ongoing loss of biodiversity. Science, v. 363, n. 6434, p. 1459–1463, 2019.

Sigler, L.; Hambleton, S.; Paré, J. A. Molecular characterization of reptile pathogens currently known as members of the *Chrysosporium* anamorph of *Nannizziopsis vriesii* complex. Mycologia, v. 105, n. 2, p. 469–492, 2013.

Thomas, P. et al. Point-of-care diagnostics for emerging wildlife fungal pathogens. EcoHealth, v. 21, n. 1, p. 25–36, 2024.

Ugochukwu, E. I.; Osakwe, O. N.; Oragwa, A. O.; Nnadi, N. E.; Onyekwere, E. C. Emerging fungal diseases of wildlife: diagnostic challenges and control strategies. Vet. World, v. 15, n. 3, p. 563–573, 2022.

Voyles, J. et al. Shifts in disease dynamics in a tropical amphibian assemblage are not due to pathogen attenuation. Science, v. 359, n. 6383, p. 1517–1519, 2018.

Waddle, A. W.; Refsnider, J. M.; Adams, C. et al. Global patterns of emerging fungal pathogens in reptiles. Fungal Ecol., v. 47, 100956, 2020.

Walker, D. M.; Raudabaugh, D. B.; Miller, A. N. Environmental DNA as a tool for monitoring fungal pathogens. Fungal Ecol., v. 54, 101115, 2022.

Wiederhold, N. P. Antifungal resistance: current trends and future strategies to combat. Infect. Dis. Clin. N. Am., v. 37, n. 2, p. 271–288, 2023.

Woodhams, D. C. et al. Antifungal isolates database of amphibian skin-associated bacteria and function against emerging fungal pathogens. Ecology, v. 101, n. 1, e02918, 2020.

Woods, M.; Ashraf, N.; Bromley, M. et al. A One Health approach to overcoming fungal disease and antifungal resistance. WIREs Mech. Dis., v. 15, e1610, 2023.