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Review

Synthesis of *Batrachochytrium dendrobatidis* infection in South America: amphibian species under risk and areas to focus research and disease mitigation

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Amphibian chytridiomycosis, caused by *Batrachochytrium dendrobatidis* (*Bd*), has been recognized as the infectious disease causing the most catastrophic loss of biodiversity known to science, with South America being the most impacted region. We tested whether *Bd* prevalence is distributed among host taxonomy, ecoregion, conservation status and habitat preference in South America. Here we provide a synthesis on the extent of *Bd* infection across South America based on 21 648 molecular diagnostic assays, roles of certain species in the epidemiology of *Bd* and explore its association with the reported amphibian catastrophic declines in the region. We show that *Bd* is widespread, with a continental prevalence of 23.2%. Its occurrence in the region shows a phylogenetic signal and the probability of infection is determined by ecoregion, preferred habitat and extinction risk hosts' traits. The taxa exhibiting highest *Bd* occurrence were mostly aquatic amphibians, including Ranidae, Telmatobiidae, Hylodidae, Calyptocephalellidae and Pipidae. Surprisingly, families exhibiting unusually low *Bd* prevalence included species in which lethal chytridiomycosis and population declines have been described (genera *Atelopus*, *Rhinoderma* and *Eleutherodactylus*). Higher than expected prevalence of *Bd* occurred mainly in amphibians living in association with mountain environments in the Andes and Atlantic forests, reflecting highly favourable *Bd* habitats in these areas. Invasive amphibian species (e.g. *Lithobates catesbeianus* and *Xenopus laevis*) exhibited high *Bd* prevalence; thus we suggest using these as sentinels to understand their potential role as reservoirs, vectors or spreaders of *Bd* that can be subjected to management. Our results guide on the prioritization of conservation actions to prevent further biodiversity loss due to chytridiomycosis in the world's most amphibian diverse region.

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Introduction

Amphibians (+8400 spp.; Frost 2021), are the most threatened vertebrate group on earth and consequently have become one of the most representative examples of the current biodiversity crisis (Collins and Crump 2009). The chytrid fungus *Batrachochytrium dendrobatidis* (*Bd*), which causes the emerging infectious disease chytridiomycosis, has been increasingly recognized as an important driver behind alarming amphibian population declines and extinctions across the world (Berger et al. 1998, Lips et al. 2006, Bielby et al. 2008, Scheele et al. 2019). Infecting all amphibian orders (i.e. anurans, urodelans and gymnophionans), *Bd* has a wide range of hosts: so far evidence of infection comes from nearly 1400 species from all continents inhabited by amphibians (Olson et al. 2021). However, there is a large between- and within-species variability in susceptibility to *Bd* infection (Berger et al. 2016, Lips 2016) and there is an ontogenetic shift in the susceptibility to *Bd* infection during metamorphosis (Van Rooij et al. 2016, Mesquita et al. 2017). Although tadpoles and adults are usually equally susceptible to infection, they differ on susceptibility to disease (Van Rooij et al. 2016). In most species *Bd* infects tadpoles without developing clinical signs but may cause death after metamorphosis, while in other species *Bd* infection of larvae is associated with oral disc depigmentation and abnormalities, and sometimes causing death (Berger 2016). In addition, in some cases previous pathogen exposure can increase survivability and resistance to *Bd* (Stice and Briggs 2010, Cashins et al. 2013, McMahon et al. 2014).

While many species are declining, some to the point of extinction, others persist with enzootic presence of *Bd* (Bielby et al. 2008, Berger et al. 2016). The relationship between *Bd* and amphibians is complex, with a wide variability in population declines exhibited by different amphibian host species in response to *Bd*, and for which a phylogenetic signal has been demonstrated (i.e. phylogenetically related amphibians show similar patterns of chytridiomycosis susceptibility; Bielby et al. 2008, Baláž et al. 2014). Additionally, as not all areas are environmentally suitable for *Bd* persistence (e.g. *Bd* coldspots in cold and arid climates), a geographical non-random pattern in *Bd* distribution has been described in some regions of the world (Rödder et al. 2009, Liu et al. 2013, James et al. 2015, Bacigalupe et al. 2017). Therefore, by studying the geographic and taxonomic distribution of *Bd* at the continental level, relevant information for disease prevention and mitigation can arise, for instance through the recognition of hot and coldspots of pathogen occurrence; pathogen invasion routes; taxa playing important roles in disease epidemiology; and determination of groups of species at greatest risk of decline or extinction (Lips et al. 2008, James et al. 2015, Bacigalupe et al. 2017, Scheele et al. 2019).

With over a third of the world's amphibian diversity, South America has been particularly badly hit by chytridiomycosis (Bielby et al. 2008, Lips et al. 2008, Rödder et al 2009, Scheele et al. 2019). Several examples linking this emerging disease with severe population declines and extinctions have been reported in the region, notably the cases of the genera *Atelopus* (Ron et al. 2003, La Marca et al. 2005, Lampo et al. 2006), *Telmatobius* (Barrionuevo and Ponssa 2008, Burrowes and De la Riva 2017) and *Rhinoderma* (Soto-Azat et al. 2013b, Valenzuela-Sánchez et al. 2017). Also, few isolates of *Bd* have been genetically characterized in South America, with the hypervirulent Global Panzootic Lineage (*Bd*GPL) being the most widespread genotype (Schloegel et al. 2012, Flechas et al. 2013, Rosenblum et al. 2013, James et al. 2015, Jenkinson et al. 2016, Valenzuela-Sánchez et al. 2018, Burrowes et al. 2020). Based on whole genome sequencing of a global panel of *Bd*, O'Hanlon et al. (2018) revealed that a recent intercontinental expansion of *Bd*GPL from East Asia occurred within the past century. A recent introduction of *Bd*GPL into South America (Lips et al. 2008, Valenzuela-Sánchez et al. 2018) coincides with the onset of amphibian enigmatic declines in this region beginning in the late 1970s (Lips et al. 2008, Soto-Azat et al. 2013a, Carvalho et al. 2017). Also, a hypovirulent lineage of *Bd* in the Atlantic forests of Brazil, termed *Bd*ASIA-2/*Bd*BRAZIL, has been shown to hybridize with *Bd*GPL to create hypervirulent hybrid genotypes (Rosenblum et al. 2013, Rodriguez et al. 2014, Jenkinson et al. 2016, Greenspan et al. 2018, O'Hanlon et al. 2018).

Despite a large number of studies focused on the presence of *Bd* in many sites of South America, there is a lack of a compilation collecting and analysing evidence about which amphibian clades and geographic areas currently show the greatest levels of *Bd* infection and, hence, potential amphibian chytridiomycosis and population declines. Because of differences in amphibian species' susceptibility to infection, we expect that *Bd* prevalence is not randomly distributed among host taxonomy, ecoregion, conservation status and habitat preference (aquatic versus terrestrial) in South America. Therefore, the goals of this study were to provide a general overview of the patterns of occurrence of *Bd* infection in wild amphibians in South America and explore its association with the amphibian catastrophic declines recorded in the region. We also examined available evidence of the importance of certain amphibian species having roles in the persistence and spread of *Bd*, in order to give recommendations for future research and mitigation strategies.

Methods

Bd database

We built a database of the *Bd* infection status of wild South American amphibians that had been tested for this pathogen using molecular diagnostic assays and which had

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been sampled between 1 January 2000 and 31 April 2020 (Supporting information). To this end, we carried out a literature search in Google Scholar and Web of Science, using the search term combination: ('*Batrachochytrium dendrobatidis*' OR 'chytrid*') AND ('name' of each South American country), to find scientific publications, grey literature and other sources providing relevant data. The bibliographies in all retrieved articles were screened for further relevant publications. Additionally, an unpublished data set of *Bd* quantitative real-time PCR (qPCR) assays from Chile was included. For each reference obtained, the title was scanned; if relevant, the abstract was read; and, if relevant, the full article was read. A filter for inclusion in the analysis was the diagnostic method used: only data obtained using standard PCR or qPCR as a means of *Bd* detection was included, due to their high sensitivity, repeatability, comparability and today's widespread use (Scheele et al. 2019). Data based on museum specimens was not included as time and method of preservation can interfere with the likelihood of *Bd* detection (Soto-Azat et al. 2009).

Species, conservation status and geographic data

From each selected article, we obtained the name of each studied amphibian species, the latitude and longitude of the sampled population, the total number of individuals sampled and the number of individuals that tested positive for *Bd*. Hereafter we assume that an animal that tested positive for the pathogen was infected with *Bd*. Each species was assigned its preferred habitat (between aquatic and terrestrial) and conservation status, information that was obtained from the IUCN Red List (IUCN 2021). When a species was listed in both aquatic and terrestrial habitats, further information was examined, and the preferred habitat of adults was used. Finally, from each geographic coordinate record we obtained the level II ecoregion classification (Griffith et al. 1998). The conservation category 'extinct' was not included in further analyses as it only had one individual record (i.e. *Atelopus longirostris*). Similarly, age status was not included in the analyses since the vast majority of records were from adults.

Statistical analyses

To reduce the heterogeneous distribution of the sampling effort and to increase the spatial independence between sites, all populations from the same species within 5.5 km of each other were grouped, summing up their numbers of *Bd*-positive individuals and total sample size and assigning the centroid of each grouped site as the new georeferenced location. This resulted in a reduction of the original database from 2224 to 1624 locality records, ranging from 1 to 458 sampled individuals per site (median = 4). For operational purposes, the prevalence of *Bd* for each species per sampling site was quantified as the number of positives/total samples. As our final database (Supporting information) is highly disparate in the evaluated total numbers of individuals, all analyses were repeated using 1, 2, 5, 10, 20 and 30 individuals as the minimum sample size per species. Thus, the number of species considered when using those cut-off points was 522, 458, 337, 254, 173 and 125, respectively (Supporting information).

We carried out weighted phylogenetic generalized least squares (PGLS) to evaluate the role of ecoregion, conservation status and habitat preference in the prevalence of *Bd* across species and sites. To account for phylogenetic relatedness, we used a time-calibrated phylogeny based on the hypotheses of Jetz and Pyron (2018). Multiple sampled localities per species were included with branch lengths equal to zero (Felsenstein 2008). Prior to all analyses, *Bd* prevalence was arcsine square root transformed (details in Bacigalupe et al. 2017). To control for the uncertainty surrounding estimates of *Bd* prevalence when sample sizes were small, we assumed a variance of $1/n^2$ around each estimate of prevalence, where n corresponds to the total number of individuals measured in each site per species.

We employed a model selection with an information–theoretic approach (Burnham and Anderson 2002) to contrast the adequacy of the following five working hypotheses explaining the geographic occurrence of *Bd* in South America: 1) null model with no predictors; 2) minimum model with habitat (aquatic versus terrestrial); 3) habitat + conservation status; 4) habitat + ecoregion; and 5) habitat + conservation status + ecoregion. Conservation status was transformed in a numerical variable with values ranging from 1 = least concern (LC) to 6 = critically endangered (CR) with increasing levels of threat (i.e. 2 = near threatened (NT), 3 = data deficient (DD), 4 = vulnerable (VU), 5 = endangered (EN)). Because models included different fixed effects, Pagel's λ was estimated with restricted maximum likelihood in the minimum model (i.e. including only habitat) and set to the respective estimated value in subsequent model comparisons employing maximum likelihood (ML). All analyses were performed in R employing packages *ape* ver. 5.4 (Paradis et al. 2004; <https://cran.r-project.org/web/packages/ape/ape.pdf>), *picante* ver. 1.8.2 (Kembel et al. 2010; <https://cran.r-project.org/web/packages/picante/index.html>) and *nlme* ver. 3.1 (Pinheiro et al. 2020; <https://cran.r-project.org/web/packages/nlme/index.html>).

As *Bd* prevalence was not randomly distributed (Results), we used a randomization procedure to evaluate which families, ecoregions, conservation status and habitats deviated from the average continental prevalence. For each category, we calculated a weighted continental mean to account for the highly different sample sizes, and a 95% confidence interval using a permutation procedure. Those levels within each category that fell above or below the confidence interval were considered to have unusually high or low levels of *Bd* prevalence, respectively. Before the analyses, data for those species with more than one sampling locality was first pooled into a single species estimate of the number of *Bd*+ individuals and total sample size. This procedure was carried out for families, conservation status and habitats, and within each ecoregion (i.e. species that inhabit different ecoregion were considered as statistically independent). The confidence interval was

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calculated as follows. First, for each of the evaluated cut-offs (above), the *Bd* prevalence of each species was calculated, and an n × 1 matrix was constructed, with species identity as rows and prevalence as the single column. Then, rows of that matrix were randomized with replacement and the average prevalence of that run was estimated. We repeated this procedure 10 000 times and estimated the 95% confidence interval of the null distribution of those means. All analyses were carried out using R base package ver. 3.6.3.

Results

Bd database

Our literature review resulted in 94 initial references, of which 73 met the required criteria for subsequent analyses (Supporting information). We obtained the results of 21 648 individual *Bd*-specific molecular diagnostic assays, of which 17 621 records were obtained from the literature and 4027 corresponded to our unpublished data from Chile. A total of 5019 individual samples showed evidence of *Bd* infection, giving an overall continental *Bd* prevalence of 23.2%. Samples came from all countries in South America but Paraguay, and all ecoregions except the Humid Chaco (Fig. 1). Details of *Bd* prevalence by families, ecoregions, conservation status and preferred habitat are shown in Fig. 2, Fig. 3 and Fig. 4, respectively.

Data of *Bd* infection was obtained for 522 amphibian species from 28 families (from a total of 30 present in South America), 519 of which were native and 3 were introduced species: the North American bullfrog *Lithobates catesbeianus*, the African clawed frog *Xenopus laevis* and the whistling frog *Eleutherodactylus johnstonei*. Two introduced species (*L. catesbeianus* and *X. laevis*) and 342 native species showed evidence of infection. Of the samples tested for *Bd*, 2594 were from tadpoles and 19 054 from postmetamorphic frogs. The taxonomic representation was also skewed at the family level for sample size, ranging from 1 (Ceuthomantidae) to 3714 (Craugastoridae; Fig. 2).

Species, conservation status and geographic data

The use of six cut-off points for sample sizes did not produce different results, and therefore we only present the results using all the database (i.e. $n \geq 1$; Supporting information) for the remaining analyses. As *Bd* prevalence showed phylogenetic structure (Pagel's $\lambda = 0.233$, $p < 0.001$), the five evaluated models included the phylogenetic relatedness among species. The model selection procedure indicated that, from the five candidate models tested, the best one was the most complete, including habitat preference, conservation status and ecoregion, having a relative support of 100% given by its Akaike weight w_i (Table 1). This result did not change when we used IUCN categories instead of the numeric variable we created (results not shown). Families exhibiting disproportionally high (10) and low (12) prevalence of *Bd* relative to the background continental average are shown in Fig. 2. Prevalence was also affected by ecoregion, with eight and ten ecoregions having disproportionally high and low levels of *Bd* prevalence, respectively (Fig. 3). Conservation categories of highest threat (CR and EN) showed disproportionally lower levels of *Bd* prevalence, while VU category showed disproportionally higher levels of *Bd* infection than the continental average (Fig. 4). As expected, in comparison with the continental average, terrestrial species have disproportionally lower levels of *Bd* prevalence while aquatic species show disproportionally higher levels (Fig. 4).

Discussion

South America has experienced a devastating biodiversity loss due to amphibian chytridiomycosis, but although a considerable amount of *Bd* research has been conducted during the past decade, there has been no synthetic analysis linking *Bd* infection with amphibian host traits for this region. Using the results of > 21 000 molecular assays for the detection of *Bd* infection across South America, we found that probability of infection is determined by host taxonomy, ecoregion, preferred habitat and extinction risk. These results identify where in South America and on which groups of species should future research and conservation efforts be focused.

Taxonomic pattern of *Bd* occurrence

Disproportionally high Bd *prevalence*

The taxa exhibiting high *Bd* prevalence were in most cases associated with aquatic environments (Fig. 2 and Fig. 4). For instance, Telmatobiidae, Ranidae, Calyptocephalellidae, Hylodidae and Pipidae are all highly dependent on aquatic habitats, making species within these families likely to have high contact rates with aquatic *Bd* zoospores in areas where the pathogen occurs (Bielby et al. 2008, Van Rooij et al. 2016). The high *Bd* prevalence found in Calyptocephalellidae and Telmatobiidae are of special concern because the vast majority (> 80%) of the species within these families are declining and categorized as being at high risk of extinction (i.e. vulnerable, endangered and critically endangered; IUCN 2021). Recently, Alvarado-Rybak et al. (2021) described a lethal chytridiomycosis outbreak in postmetamorphic Chilean giant frogs *Calyptocephalella gayi* from a captive breeding programme. Although many studies have described *Bd* infection in *Telmatobius* (63 spp.), only a few have provided evidence linking *Bd* infection with disease, mass mortalities or population declines (Burrowes and De la Riva 2017). Chytridiomycosis due to *Bd* infection has been associated with mortality in *T. pisanoi* and *T. atacamensis* from northern Argentina (Barrionuevo and Mangione 2006) and in *T. marmoratus* in Peru (Seimon et al. 2007, Catenazzi et al. 2011). Also, the disappearance of two species of *Telmatobius* from the Upper Manu National Park in southeastern Peru has been linked with chytridiomycosis (Catenazzi et al. 2011). Burrowes and De la Riva (2017) studied nearly 600 wild

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Figure 1. Total sampled individuals across South America. The size of the circles is proportional to the numbers of individuals sampled. Red and green coloured circles represent *Batrachochytrium dendrobatidis* positive and negative sites, respectively.

amphibians (museum and live specimens) from the cloud forests of Bolivia, and found an association between *Bd* infection and severe population declines since the 1990s, particularly in *Telmatobius* spp.

Terrestrial frogs in the families Odontophrynidae and Phyllomedusidae also showed a high proportion of infection compared to the continental average; however, the small sample size in both groups prevented conclusions being made (Fig. 2). Other amphibian families exhibiting higher than expected prevalence of *Bd* infection were Hylidae, Brachycephalidae and Hemiphractidae. Species in these groups represent tropical and subtropical anurans, with a variety of life histories and reproductive modes, including terrestrial and semiaquatic frogs. Particularly surprising is the high occurrence of *Bd* in Brachycephalidae (33.0%), a group of frogs with terrestrial habits that breed by direct development. Perhaps the high suitability of *Bd* identified in the humid tropical forests of southeastern Brazil, where

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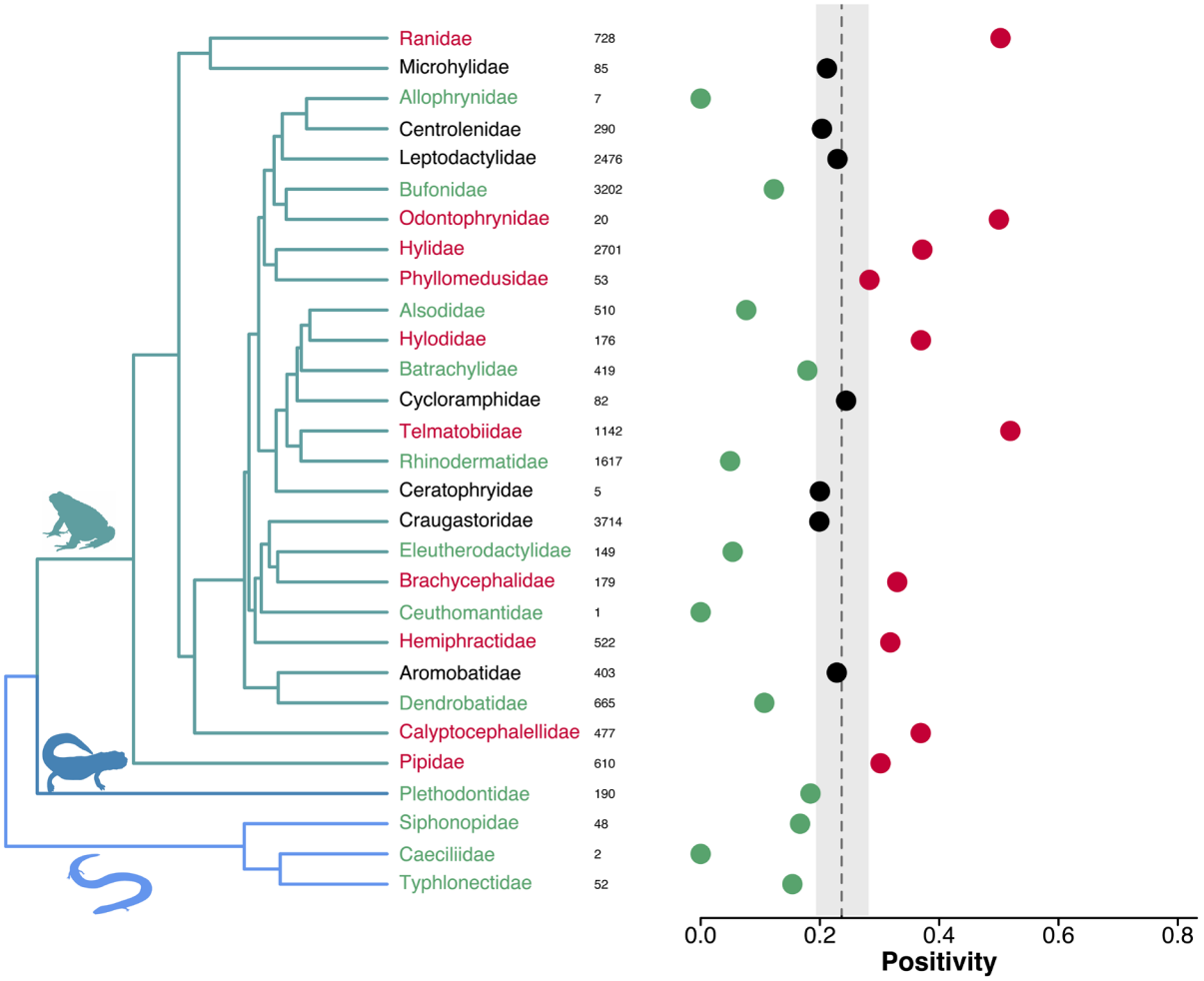

Figure 2. Prevalence of *Batrachochytrium dendrobatidis* (*Bd*) in amphibian host families from South America presented in a phylogenetic tree based on Jetz and Pyron (2018). Prevalence was calculated as the number of individuals positive for *Bd*/the total number of amphibians tested. The numbers next to each name show the total sample size for each family. The dashed line and grey band correspond to the continental mean and 95% confidence band, and the points represent the prevalence of each family. Families depicted in red and green show disproportionally higher and lower prevalence values than the continental average, respectively (details in Results). All silhouettes were obtained from phylopic (<http://phylopic.org/>). The Anura silhouette (*Bufo gargarizans*) was created by Steven Traven. The Caudata silhouette (*Pseudoeurycea boneti*) was created by C. Camilo Julián-Caballero. The Gymnophiona silhouette (*Eocaecilia micropodia*) was created by Nobu Tamura (vectorized by T. Michael Keesey).

this group of frogs lives, helps to explain such unexpectedly high prevalence (James et al. 2015). Evidence of any impact of *Bd* infection at the population level among these taxa is scarce, but chytridiomycosis has been implicated in population declines of the horned marsupial frog *Gastrotheca cornuta* (Hemiphractidae) and of three species of *Hyloscirtus* spp. (Hylidae) treefrogs (Lips et al. 2006). Whether low or high *Bd* prevalence is indicative of relative resistance to infection or susceptibility to disease should be interpreted with caution, and when possible confronted with available evidence, population monitoring data and experimental studies (Scheele et al. 2014, Mesquita et al. 2017, Valenzuela-Sánchez et al. 2017).

Disproportionally low Bd *prevalence*

The species within families identified with significantly lower than expected *Bd* prevalence were predominantly terrestrial (Fig. 2), including many with direct development. This is a situation that prevents these species from making frequent contact with aquatic habitats, and hence potentially high amounts of *Bd* (Fig. 4). *Atelopus*, however, live near small streams in the tropical wet forests and humid paramos of Central and South America, and they have aquatic larvae, thus depending on water bodies for reproduction (La Marca et al. 2005). Within families with low *Bd* prevalence are Harlequin toads (*Atelopus* spp. (Bufonidae)), Darwin's frogs (*Rhinoderma* spp. (Rhinodermatidae)) and coquis (*Eleutherodactylus* spp. (Eleutherodactylidae)). The first two are known to be highly threatened groups that have been severely impacted by chytridiomycosis (Lampo et al. 2017, Valenzuela-Sánchez et al. 2017). In Puerto Rico, *Bd* has been associated with the severe decline of *E. coqui* and *E. portoricensis*, and the presumed extinction of *E. karlschmidti*, *E. jasper* and *E. eneidae* (Longo and Burrowes 2010). Unless

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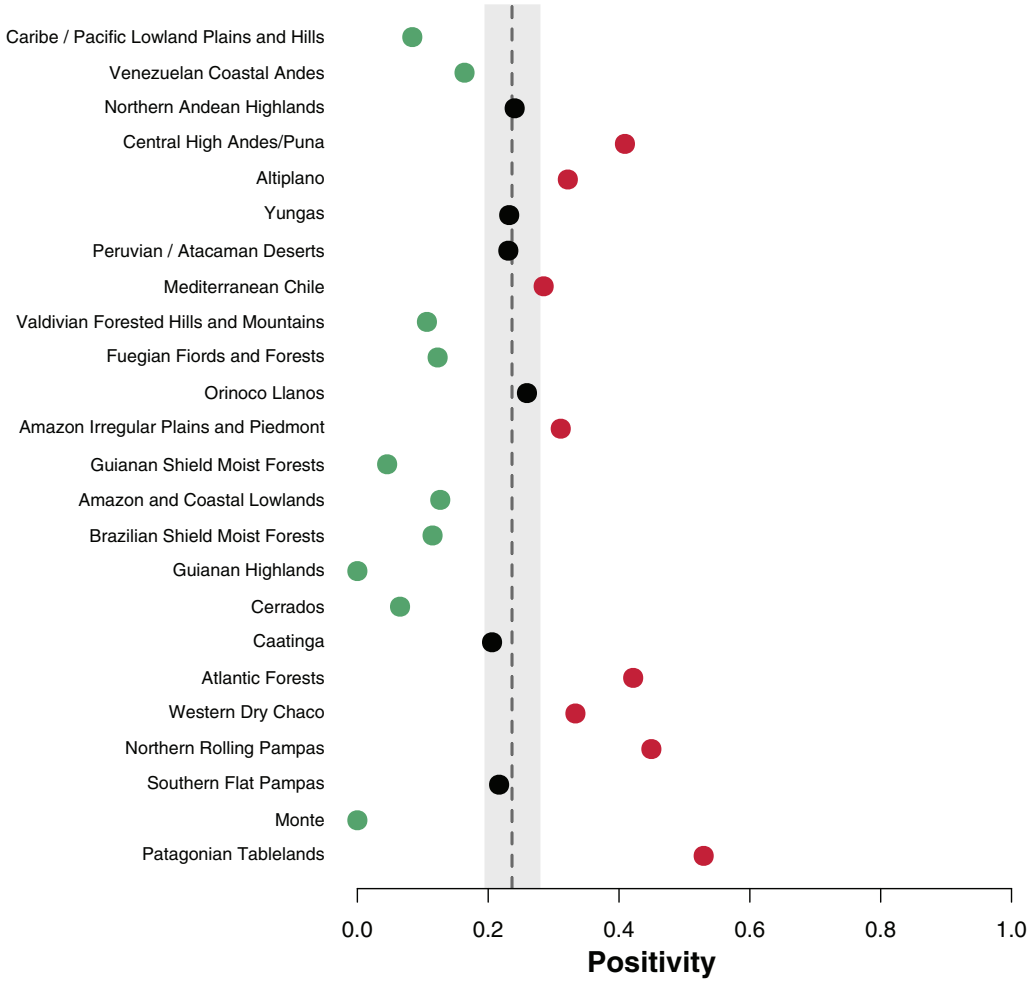

Figure 3. Prevalence of *Batrachochytrium dendrobatidis* (*Bd*) in South America ecoregions (Griffith et al. 1998). Prevalence was calculated as the number of individuals positive for *Bd*/the total number of amphibians tested. The dashed line and grey band correspond to the continental mean and 95% confidence band, and the points represent the prevalence of each ecoregion. Ecoregions to the right of the confidence band showed disproportionally higher prevalence values than the continental average, while ecoregions to the left showed disproportionally lower values.

a population has undergone long-term *Bd* monitoring, this suggests not only that prevalence is not a good predictor of chytridiomycosis susceptibility, but also may reflect a biased sampling towards healthy animals (particularly in populations sampled only once), given the rapid mortality experienced by infected individuals of these groups (Valenzuela-Sánchez et al. 2017). By using *Bd* prevalence together with *Bd* infection loads, two recent studies – one across amphibian hosts from the Atlantic forests of Brazil (Lambertini et al. 2021), and another in amphibian communities from several regions of the world (Greenberg et al. 2017) – have identified predictors of patterns of infection such as species life history, amphibian richness, habitat use and climatic niche. With many species having disappeared and others having suffered drastic declines across their whole distribution (from Costa Rica to Bolivia), the situation of genus *Atelopus* is possibly the most dramatic example of biodiversity loss due to an infectious disease (La Marca et al. 2005, Lips et al. 2008, Catenazzi et al. 2011, Scheele et al. 2019). Of 94 *Atelopus* spp. listed in the IUCN Red List, 3% are currently categorized as extinct, 69% as critically endangered and 13% as endangered (IUCN 2021). Population crashes of *Atelopus* spp. were first recognized in the 1980s in South America and in the 1990s in southern Central America, coincident with the hypothesized arrival and subsequent epidemic wave of *Bd* (Lips et al. 2008). Severe chytridiomycosis-associated declines have been well described in *A. chiriquensis*, *A. varius* and *A. zeteki* in Panama and Costa Rica (La Marca et al. 2005, Lips et al. 2006), and the combined effects of chytridiomycosis and climate change have been implicated in the disappearances of *A. ignescens* from Ecuador (Ron et al. 2003) and *A. carbonerensis*, *A. mucubajiensis* and *A. sorianoi* from Venezuela (Lampo et al. 2006). Believed extinct for 30 years, surviving populations of *A. ignescens*, *A. longirostris* and *A. mindoensis* have been recently rediscovered and individuals of the first two species translocated to a captive breeding programme in Ecuador (Tapia et al. 2017, Barrio Amorós et al. 2020). Contemporaneously, the golden toad (*Incilius periglenes*

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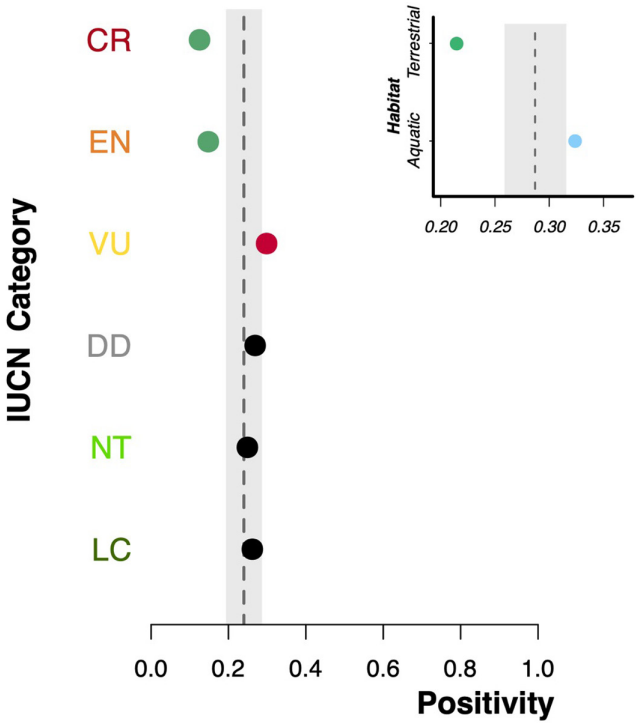

Figure 4. Prevalence of *Batrachochytrium dendrobatidis* (*Bd*) for IUCN conservation categories and habitat prevalence (inset). Prevalence was calculated as the number of individuals positive for *Bd*/the total number of amphibians tested. In both plots, the dashed line and grey band correspond to the continental mean and 95% confidence band, and the points represent the prevalence of each IUCN category (left) and habitat (right). Points to the right of the confidence band showed disproportionally higher prevalence values than the continental average, while points to the left showed disproportionally lower values. CR = critically endangered, EN = endangered, VU = vulnerable, DD = data deficient, NT = near threatened, LC = least concern.

[Bufonidae]) from Costa Rica became an iconic example of the amphibian biodiversity crisis (Collins and Crump 2009) with its extinction due to chytridiomycosis reported in 1989. While the effect of *Bd* on this species might have been exacerbated by climate change (Pounds et al. 2006), the role of climate in the decline of neotropical amphibian communities is still uncertain.

Native to southern Chile and Argentina, both species of *Rhinoderma* have undergone severe population declines (Soto-Azat et al. 2013a). Once abundant, *R. rufum* is thought to have become extinct around 1982, while *R. darwinii* has recently disappeared from much of its range (Soto-Azat et al. 2013a). In both cases, chytridiomycosis due to *Bd* infection has been proposed as a driver of these population declines (Soto-Azat et al. 2013b). Studies of wild populations have found significantly reduced survival probabilities of *Bd*-infected versus *Bd*-uninfected frogs for *A. cruciger* in Venezuela (Lampo et al. 2017) and *R. darwinii* in Chile (Valenzuela-Sánchez et al. 2017). Lampo et al. (2017) estimated that infected *A. cruciger* individuals were, on average, four times more likely to die during the study period (six years) than uninfected individuals. Similarly, Valenzuela-Sánchez et al. (2017) used empirical evidence to model slow declines to extinction of infected *R. darwinii* populations in the absence of mass mortality and despite low *Bd* prevalence. There is experimental evidence that some terrestrial direct-developing frog species lack adaptive responses against chytrid fungi when compared to species with aquatic larvae, possibly because the former are less likely to be exposed to such waterborne pathogens during their ontogeny (Mesquita et al. 2017).

Role of invasive species in the epidemiology of *Bd*

The high *Bd* infection prevalence exhibited by *L. catesbeianus* (44.2%) and *X. laevis* (29.9%) indicates that these species can act as important reservoirs of *Bd* (Schloegel et al. 2010, Soto-Azat et al. 2016). Originally from North America, *L. catesbeianus* is the most commonly farmed amphibian species worldwide; intensive farming of this species also occurs in South America (Garner et al. 2006). For example, it has been estimated that 2000 bullfrog farms were operational in Brazil alone by 1988 (Schloegel et al. 2010). In South America, invasive populations of *L. catesbeianus* are known to be established in Venezuela, Colombia, Ecuador, Peru, Brazil, Uruguay and Argentina (IUCN 2021). Evidence for transmission of *Bd* between farmed *L. catesbeianus* and wild amphibians exists in Central and South America (Schloegel et al. 2010). Likewise, introduced *L. catesbeianus* has been found to be associated with an increase in *Bd* prevalence in Korean treefrogs (Borzée et al. 2017). Similarly, *X. laevis* is a widely distributed invasive species, often as a result of escapes or releases from research laboratories in which it has been widely used as a model for biological research since the early 1900s (Measey et al. 2012). In South America,

Table 1. Evaluated models for the prevalence of *Batrachochytrium dendrobatidis* (*Bd*) infection among amphibians in South America.

Model[a]	K	AICc	ΔAICc	w_i	LogLik
Null	2	7908.90	1591.57	0	−3952.45
Habitat	3	7126.47	809.14	0	−3560.23
Habitat + conservation	4	6845.28	527.95	0	−3418.63
Habitat + ecoregion	26	6522.31	204.97	0	−3234.71
Habitat + ecoregion + conservation	27	6317.33	0.00	1	−3131.18

Estimates of *Bd* prevalence are weighed for sample size n by specifying a heterogeneous variance = $1/n^2$. Pagel's $\lambda = 0.232$ for all models, n = 1624. K = number of parameters. AICc: Akaike information criterion values corrected for small sample sizes. w_i: Akaike weights (the probability that the model is the correct one of those tested).

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invasive populations are only known from central and northern Chile (Soto-Azat et al. 2016, Mora et al. 2019). Tolerant to *Bd* infection, but resistant to chytridiomycosis, these two invasive species are important vectors of this pathogen, maintaining and spreading *Bd* as they colonize new areas (Soto-Azat et al. 2016, Borzée et al. 2017). Furthermore, both species have been implicated in the intercontinental spread of *Bd* (Garner et al. 2006, Schloegel et al. 2012, Carvalho et al. 2017, Valenzuela-Sánchez et al. 2018).

Geographic distribution of *Bd*

We found a non-random geographic pattern of *Bd* infection across South America, with some ecoregions showing a particularly high occurrence of *Bd* (Fig. 1 and Fig. 3). Ecoregions showing significantly higher *Bd* prevalence in relation to the continental average were mainly located at moderate to high altitudes associated with the Andes and the Atlantic forests (e.g. central high Andes, Altiplano, Mediterranean Chile, Atlantic forests). Habitat suitability of *Bd* is largely dependent on temperature and water (Liu et al. 2013), and mountainous areas have been identified of high environmental suitability for *Bd* (Ron 2005, Rödder et al. 2009, Liu et al. 2013, James et al. 2015). This is coincident with most documented declines and extinctions attributed to chytridiomycosis in South America involving Andean amphibians (La Marca 2005, Ron 2005, Lampo et al. 2006, Barrionuevo and Ponssa 2008, Lips et al. 2008, Catenazzi et al. 2011, Soto-Azat et al. 2013b, Burrowes and De la Riva 2017, Flechas et al. 2017, Lampo et al. 2017, Valenzuela-Sánchez et al. 2017). While amphibian population declines in the Atlantic Forests were initially not linked to chytridiomycosis (Eterovick et al. 2005, James et al. 2015, Becker et al. 2016, Lambertini et al. 2017), recently Carvalho et al. (2017) showed a spatiotemporal association between *Bd* and amphibian declines in this region.

In contrast, significantly low prevalence of *Bd* was associated with ecoregions at low altitudes, such as the Caribbean and Pacific lowlands, Amazon and coastal lowlands, Valdivian forests and Fuegian fjords (Fig. 3). *Batrachochytrium dendrobatidis* was detected in all ecoregions where *Bd* analyses were available, apart from the Monte and Guianan highlands (Fig. 1 and Fig. 3). Although Mathie et al. (2018) analysed 247 samples from the Kanuku Mountauns in south-western Guyana, no evidence of *Bd* infection was found. Similarly, an absence of *Bd* from an extensive survey in Suriname has been corroborated (Jairam 2020). The absence or low occurrence of *Bd* in large areas of the Amazon basin, Caribbean lowlands and the southern cone of South America represent coldspots of *Bd* (i.e. very low prevalence or absence of *Bd*; James et al. 2015, Becker et al. 2016, Carvalho et al. 2017, Bacigalupe et al. 2019). This might be because these areas contain unsuitable habitats for *Bd* or are protected by barriers to its spread (e.g. remote areas with reduced human presence) or a combination of both (Lips et al. 2008). Only two (of 24) analysed ecoregions had small sample sizes (< 60 records): Western dry Chaco (n = 3) and Monte (n = 11), a situation that prevents conclusions being drawn from those areas. Further investigation of the *Bd* status of amphibians in the under-surveyed areas is recommended to help understand the drivers of *Bd* as a conservation threat and on any factors limiting *Bd* establishment that might be relevant for conservation management in South America and elsewhere.

Bd and conservation categories

The patterns of *Bd* prevalence in amphibian hosts according to their extinction risk should be interpreted with caution (Fig. 4). Only species in the vulnerable category exhibited a higher occurrence of *Bd* compared to the regional average. In contrast, species under the greatest risk of extinction (i.e. endangered and critically endangered) showed lower *Bd* prevalence compared to the continental average. It is possible that a lower occurrence of *Bd* may be masked by a bias sampling towards healthy animals, following high mortality after *Bd* infection (Lampo et al. 2017, Valenzuela-Sánchez et al. 2017). Also, it is possible that less threatened species (near threatened and least concern) are less likely to suffer declines due to chytridiomycosis, although they may play important roles maintaining and vectoring *Bd* to other sympatric species (Bacigalupe et al. 2017). For example, Scheele et al. (2016) demonstrated how the abundant and least concern Australian eastern froglet (*Crinia signifera*), which maintains a high *Bd* prevalence (78.7%) in the wild, acts as a competent pathogen reservoir for the endangered northern corroboree frog (*Pseudoprhyne pengilleyi*). Therefore, efforts to monitor *Bd* in species exhibiting high prevalence are recommended, either to evaluate the possible effects of chytridiomycosis on these species, or to assess their potential role in the maintenance and spread of *Bd*.

Conclusions

Evidence that chytridiomycosis is having a devastating effect on South American amphibians is overwhelming (Scheele et al. 2019). Our research focuses on taxonomic groups, ecoregions, habitats and conservation categories, to identify amphibian families playing key roles in the epidemiology of *Bd*, as well as some taxa and regions that are particularly at risk of the consequences of chytridiomycosis. Our results guide research, such as identifying under-surveyed areas (e.g. Guianan region, Orinoco Llanos, Gran Chaco, Monte-Patagonia), where further work is required if we are to understand the distribution of *Bd* in South America and the factors driving this. Efforts are also required to genotype *Bd* isolates from across South America to fill gaps in our knowledge of the genetic diversity of *Bd* and evolutionary history, and whether *Bd* lineages may influence *Bd* occurrence and impacts to amphibian populations (Azat 2021). Conducting long-term amphibian population monitoring and *Bd* infection surveillance is vital to assess the effects of chytridiomycosis. It seems also appropriate to target abundant species (native and invasive) as sentinels for *Bd* monitoring, and to identify *Bd* reservoirs,

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vectors or spreaders that can be subjected to management (Scheele et al. 2014, Soto-Azat et al. 2016). Nevertheless, taxonomic groups showing low prevalence of *Bd* should not be disregarded, as some may be driven to extinction by chytridiomycosis even in the absence of obvious mortalities (Lampo et al. 2017, Valenzuela-Sánchez et al. 2017). A better understanding of the patterns of *Bd* distribution, and the effects of the chytrid fungus on South American amphibians, will guide the prioritization of conservation actions to minimize further biodiversity loss in the world's greatest amphibian megadiverse region.

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Data availability statement

Data is available from the Dryad Digital Repository: <https://doi.org/10.5061/dryad.n5tb2rbxd> (Azat et al. 2022).

Supporting information

The supporting information associated with this article is available from the online version.

References

Alvarado-Rybak, M. et al. 2021. Chytridiomycosis outbreak in a Chilean giant frog *Calyptocephalella gayi* captive breeding program: genomic characterization and pathological findings. – Front. Vet. Sci. 8: 733357.
Azat, C. 2021. Not just a pathogen: the importance of recognizing genetic variability to mitigate a wildlife pandemic. – Mol. Ecol. Res. 21: 1410–1412.
Azat, C. et al. 2022. Data from: Synthesis of *Batrachochytrium dendrobatidis* infection in South America: amphibian species under risk and areas to focus research and disease mitigation. – Dryad Digital Repository, <https://doi.org/10.5061/dryad.n5tb2rbxd>.
Bacigalupe, L. et al. 2017. Effects of amphibian phylogeny, climate and human impact on the occurrence of the amphibian-killing chytrid fungus. – Global Change Biol. 23: 3543–3553.
Bacigalupe, L. et al. 2019. *Batrachochytrium dendrobatidis* in a biodiversity hotspot: identifying and validating high-risk areas and refugia. – Ecosphere 10: e02724.
Baláž, V. et al. 2014. Assessing risk and guidance on monitoring of *Batrachochytrium dendrobatidis* in Europe through identification of taxonomic selectivity of infection. – Conserv. Biol. 28: 213–223.
Barrio Amorós, C. L. et al. 2020. Back from extinction: rediscovery of the harlequin toad *Atelopus mindoensis* Peters, 1973 in Ecuador. – Herpetol. Notes 13: 325–328.
Barrionuevo, S. and Mangione, S. 2006. Chytridiomycosis in two species of *Telmatobius* (Anura: Leptodactylidae) from Argentina. – Dis. Aquat. Org. 73: 171–174.
Barrionuevo, S. and Ponssa, L. 2008. Decline of three species of the genus *Telmatobius* (Anura: Leptodactylidae) from Tucumán Province, Argentina. – Herpetologica 64: 47–62.
Becker, C. G. et al. 2016. Historical dynamics of *Batrachochytrium dendrobatidis* in Amazonia. – Ecography 39: 954–960.
Berger, L. et al. 1998. Chytridiomycosis causes amphibian mortality associated with population declines in the rain forests of Australia and Central America. – Proc. Natl Acad. Sci. USA 95: 9031–9036.
Berger, L. et al. 2016. History and recent progress on chytridiomycosis in amphibians. – Fungal Ecol. 19: 89–99.
Bielby, J. et al. 2008. Predicting susceptibility to rapid declines in the world's frogs. – Conserv. Lett. 1: 82–90.
Borzée, A. et al. 2017. Introduced bullfrogs are associated with increased *Batrachochytrium dendrobatidis* prevalence and reduced occurrence of Korean treefrogs. – PLoS One 12: e0190551.
Burnham, K. P. and Anderson, D. R. 2002. Model selection and multimodel inference: a practical information–theoretic approach, 2nd edn. – Springer.
Burrowes, P. A. and De la Riva, I. 2017. Unravelling the historical prevalence of the invasive chytrid fungus in the Bolivian Andes: implications in recent amphibian declines. – Biol. Invas. 19: 1781–1794.
Burrowes, P. A. et al. 2020 Genetic analysis of post-epizootic amphibian chytrid strains in Bolivia: adding a piece to the puzzle. – Transb. Emerg. Dis. 67: 2163–2171.

16000587, 2022, 7, Downloaded from https://nsojournals.onlinelibrary.wiley.com/doi/10.1111/ecog.05977 by Cochrane Chile, Wiley Online Library on [27/05/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Carvalho, T. et al. 2017. Historical amphibian declines and extinctions in Brazil linked to chytridiomycosis. – Proc. R. Soc. B 284: 20162254.
Cashins, S. D. et al. 2013. Prior infection does not improve survival against the amphibian disease chytridiomycosis. – PLoS One 8: e56747.
Catenazzi, A. et al. 2011. *Batrachochytrium dendrobatidis* and the collapse of anuran species richness and abundance in the upper Manu National Park, southeastern Peru. – Conserv. Biol. 25: 382–391.
Collins, J. P. and Crump, M. L. 2009. Extinction in our times. Global amphibian decline. – Oxford Univ. Press.
Eterovick, P. C. et al. 2005. Amphibian declines in Brazil: an overview. – Biotropica 37: 166–179.
Felsenstein, J. 2008. Comparative methods with sampling error and within-species variation: contrasts revisited and revised. – Am. Nat. 171: 713–725.
Flechas, S. V. et al. 2013. Characterization of the first *Batrachochytrium dendrobatidis* isolate from the Colombian Andes, an amphibian biodiversity hotspot. – EcoHealth 10: 72–76.
Flechas, S. V. et al. 2017. Current and predicted distribution of the pathogenic fungus *Batrachochytrium dendrobatidis* in Colombia, a hotspot of amphibian biodiversity. – Biotropica 49: 685–694.
Frost, D. 2021. Amphibian species of the world: an online reference. Ver. 6.0 (date of access 16 June 2021). – American Museum of Natural History, <https://amphibiansoftheworld.amnh.org/index.html>.
Garner, T. W. J. et al. 2006. The emerging amphibian pathogen *Batrachochytrium dendrobatidis* globally infects introduced populations of the North American bullfrog, *Rana catesbeiana*. – Biol. Lett. 2: 455–459.
Greenberg, D. A. et al. 2017. Amphibian species traits, evolutionary history and environment predict *Batrachochytrium dendrobatidis* infection patterns, but not extinction risk. – Evol. Appl. 10: 1130–1145.
Greenspan, S. E. et al. 2018. Hybrids of amphibian chytrid show high virulence in native hosts. – Sci. Rep. 8: 9600.
Griffith, G. E. et al. 1998. Ecological classification of the Western Hemisphere. Unpublished report. – U.S. Environmental Protection Agency, Western Ecology Division, <http://ecologicalregions.info/htm/sa_eco.htm>.
IUCN 2021. The IUCN Red List of threatened species. Ver. 2021-1. – <www.iucnredlist.org>. Date of access 16 June 2021.
Jairam, R. 2020. A historical overview of *Batrachochytrium dendrobatidis* infection from specimens at the National Zoological Collection Suriname. – PLoS One 15: e0239220.
James, T. Y. et al. 2015. Disentangling host, pathogen and environmental determinants of a recently emerged wildlife disease: lessons from the first 15 years of amphibian chytridiomycosis. – Ecol. Evol. 5: 4079–4097.
Jenkinson, T. S. et al. 2016. Amphibian-killing chytrid in Brazil comprises both locally endemic and globally expanding populations. – Mol. Ecol. 25: 2978–2996.
Jetz, W. and Pyron, R. A. 2018. The interplay of past diversification and evolutionary isolation with present imperilment across the amphibian tree of life. – Nat. Ecol. Evol. 2: 850–858.
Kembel, S. W. et al. 2010. Picante: R tools for integrating phylogenies and ecology. – Bioinformatics 26: 1463–1464.
La Marca, E. et al. 2005. Catastrophic population declines and extinctions in Neotropical Harlequin frogs (Bufonidae: *Atelopus*). – Biotropica 37: 190–201.
Lambertini, C. et al. 2017. Spatial distribution of *Batrachochytrium dendrobatidis* in South American caecilians. – Dis. Aquat. Org. 124: 109–116.
Lambertini, C. et al. 2021. Biotic and abiotic determinants of *Batrachochytrium dendrobatidis* infections in amphibians of the Brazilian Atlantic Forest. – Fungal Ecol. 49: 100995.
Lampo, M. et al. 2006. Chytridiomycosis epidemic and a severe dry season precede the disappearance of *Atelopus* species from the Venezuelan Andes. – Herpetol. J. 16: 395–402.
Lampo, M. et al. 2017. Population dynamics of the critically endangered toad *Atelopus cruciger* and the fungal disease chytridiomycosis. – PLoS One 12: e0179007.
Lips, K. R. 2016. Overview of chytrid emergence and impacts on amphibians. – Proc. R. Soc. B 371: 20150465.
Lips, K. R. et al. 2006. Emerging infectious disease and the loss of biodiversity in a Neotropical amphibian community. – Proc. Natl Acad. Sci. USA 103: 3165–3170.
Lips, K. R. et al. 2008. Riding the wave: reconciling the roles of disease and climate change in amphibian declines. – PLoS Biol. 3: e72.
Liu, X. et al. 2013. Climate, vegetation, introduced hosts and trade shape a global wildlife pandemic. – Proc. R. Soc. B 280: 20122506.
Longo, A. V. and Burrowes, P. A. 2010. Persistence with chytridiomycosis does not assure survival of direct-developing frogs. – EcoHealth 7: 185–195.
Mathie, A. H. et al. 2018. The first assessment of *Batrachochytrium dendrobatidis* in amphibian populations in the Kanuku Mountains protected area of Guyana. – Herpetol. Bull. 146: 18–24.
McMahon, T. A. et al. 2014. Amphibians acquire resistance to live and dead fungus overcoming fungal immunosuppression. – Nature 511: 224–227.
Measey, G. J. et al. 2012. Ongoing invasions of the African clawed frog, *Xenopus laevis*: a global review. – Biol. Invas. 14: 2255–2270.
Mesquita, A. F. C. et al. 2017. Low resistance to chytridiomycosis in direct-developing amphibians. – Sci. Rep. 7: 16605.
Mora, M. et al. 2019. High abundance of invasive African clawed frog *Xenopus laevis* in Chile: challenges for their control and updated invasive distribution. – Manage. Biol. Invas. 10: 377–388.
O'Hanlon, S. et al. 2018. Recent Asian origin of chytrid fungi causing global amphibian declines. – Science 360: 621–627.
Olson, D. H. et al. 2021. Global patterns of the fungal pathogen *Batrachochytrium dendrobatidis* support conservation urgency. – Front. Vet. Sci. 8: 685877.
Paradis, E. et al. 2004. APE: analyses of phylogenetics and evolution in R language. – Bioinformatics 20: 289–290.
Pinheiro, J. et al. 2020. nlme: linear and nonlinear mixed effects models. – R package ver. 3.1-148, <https://cran.r-project.org/web/packages/nlme/nlme.pdf>.
Pounds, A. J. et al. 2006. Widespread amphibian extinctions from epidemic disease driven by global warming. – Nature 439: 161–167.
Rödder, D. et al. 2009. Global amphibian extinction risk assessment for the panzootic chytrid fungus. – Diversity 1: 52–66.
Rodriguez, D. et al. 2014. Long-term endemism of two highly divergent lineages of the amphibian-killing fungus in the Atlantic Forest of Brazil. – Mol. Ecol. 23: 774–787.
Ron, S. 2005. Predicting the distribution of the amphibian pathogen *Batrachochytrium dendrobatidis* in the New World. – Biotropica 37: 209–221.

16000587, 2022, 7, Downloaded from https://nsojournals.onlinelibrary.wiley.com/doi/10.1111/ecog.05977 by Cochrane Chile, Wiley Online Library on [27/05/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Ron, S. et al. 2003. Population decline of the Jambato toad *Atelopus ignescens* (Anura: Bufonidae) in the Andes of Ecuador. – J. Herpetol. 37: 116–126.
Rosenblum, E. B. et al. 2013. Complex history of the amphibian-killing chytrid fungus revealed with genome resequencing data. – Proc. Natl Acad. Sci. USA 110: 9385–9390.
Scheele, B. C. et al. 2014. Interventions for reducing extinction risk in chytridiomycosis-threatened amphibians. – Conserv. Biol. 28: 1195–1205.
Scheele, B. C. et al. 2016. Reservoir-host amplification of disease impact in an endangered amphibian. – Conserv. Biol. 31: 592–600.
Scheele, B. C. et al. 2019. Amphibian fungal panzootic causes catastrophic and ongoing loss of biodiversity. – Science 363: 1459–1463.
Schloegel, L. M. et al. 2010. The North American bullfrog as a reservoir for the spread of *Batrachochytrium dendrobatidis*. – Anim. Conserv. 13: 53–61.
Schloegel, L. M. et al. 2012. Novel, panzootic and hybrid genotypes of amphibian chytridiomycosis associated with the bullfrog trade. – Mol. Ecol. 21: 5162–5177.
Seimon, T. A. et al. 2007. Upward range extension of Andean anurans and chytridiomycosis to extreme elevations in response to tropical deglaciation. – Global Change Biol. 13: 288–299.
Soto-Azat, C. et al. 2009. Non-invasive sampling methods for the detection of *Batrachochytrium dendrobatidis* in archived amphibians. – Dis. Aquat. Org. 84: 163–166.
Soto-Azat, C. et al. 2013a. The population decline and extinction of Darwin's frogs. – PLoS One 8: e66957.
Soto-Azat, C. et al. 2013b. Is chytridiomycosis driving Darwin's frogs to extinction? – PLoS One 8: e79862.
Soto-Azat, C. et al. 2016. *Xenopus laevis* and emerging amphibian pathogens in Chile. – EcoHealth 13: 775–783.
Stice, M. J. and Briggs, C. J. 2010. Immunization is ineffective against preventing infection and mortality due to the amphibian fungus *Batrachochytrium dendrobatidis*. – J. Wildl. Dis. 46: 70–77.
Tapia, E. E. et al. 2017. Rediscovery of the nearly extinct longnose harlequin frog *Atelopus longirostris* (Bufonidae) in Junín, Imbabura, Ecuador. – Neotrop. Biodivers. 3: 157–167.
Valenzuela-Sánchez, A. et al. 2017. Cryptic disease-induced mortality may cause host extinction in an apparently stable host–parasite system. – Proc. R. Soc. B 284: 20171176.
Valenzuela-Sánchez, A. et al. 2018. Genomic epidemiology of the emerging pathogen *Batrachochytrium dendrobatidis* from native and invasive amphibian species in Chile. – Transbound. Emerg. Dis. 65: 309–314.
Van Rooij, P. et al. 2016. Amphibian chytridiomycosis: a review with focus on fungus–host interactions. – Vet. Res. 46: 137.

16000587, 2022, 7, Downloaded from https://nsojournals.onlinelibrary.wiley.com/doi/10.1111/ecog.05977 by Cochrane Chile, Wiley Online Library on [27/05/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License