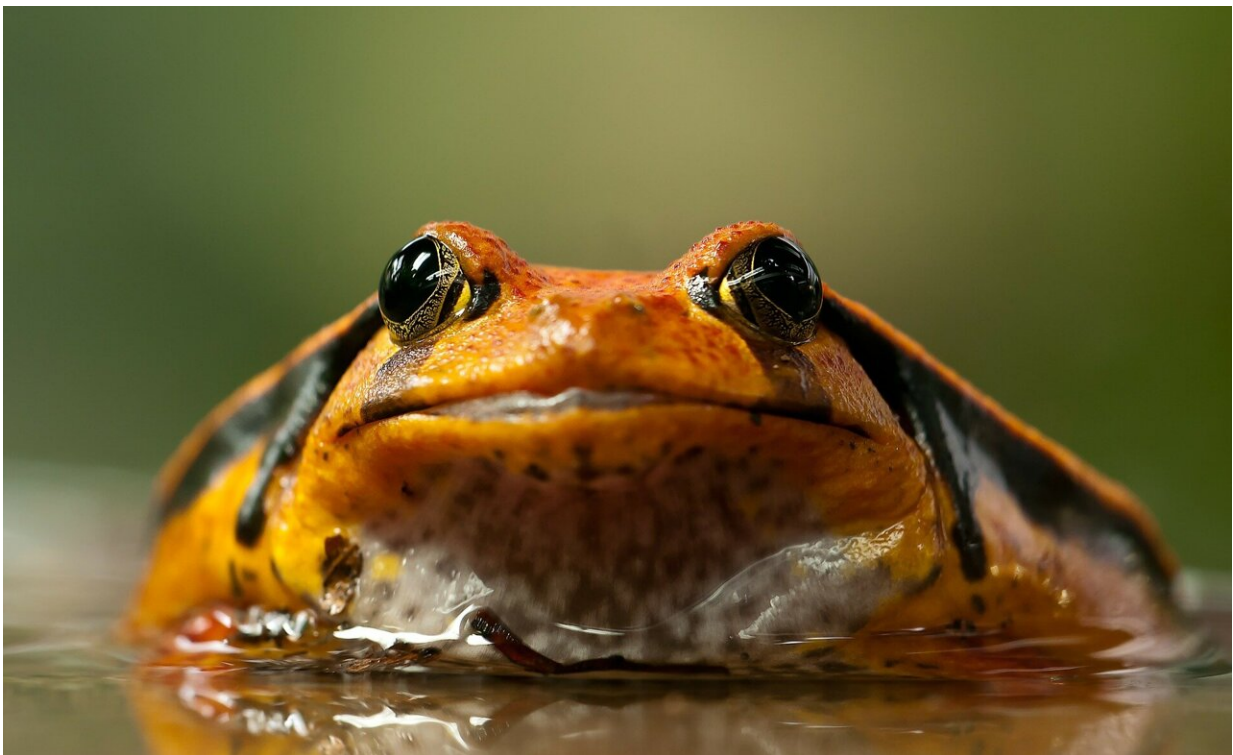


# Rapid surge in highly contagious killer fungus poses new threat to amphibians across Africa

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Mass fungus infections that drive populations worldwide to near-collapse don't just occur in science fiction. Chytridiomycosis, the worst vertebrate disease in recorded history, has already wiped out hundreds of

species of amphibians around the world. Due to a large part to this fungal disease, 41% of amphibians are currently threatened with extinction. Only species living in Africa seemed to have been relatively spared from the scourge of chytridiomycosis—at least so far.

Now, a study in *Frontiers in Conservation Science* has shown that this reprieve was likely temporary: The results show that the fungus *Batrachochytrium dendrobatidis* (Bd), the pathogen that causes [chytridiomycosis](#), is now firmly established throughout Africa. It may so far have been overlooked there, but it is likely that the pathogen will spread further and cause epizootics across Africa in the near future.

"We show that Bd has become more prevalent and widespread across the continent of Africa since the year 2000," said Dr. Vance Vredenburg, a professor at the San Francisco State University and University of California Museum of Vertebrate Zoology, Berkeley, and the study's corresponding author. "This rapid surge may signal that disease-driven declines and extinctions of amphibians may already be occurring in Africa without anyone knowing about it."

## **Exceptionally contagious**

Bd is a chytridiomycid fungus, a basic group of fungi that produces asexual "swarm spores," which use a whip-like flagellum to swim. Bd spores thrive in cool, moist habitats, and become embedded and multiply in the keratinized mouthparts and skin of salamanders, newts, and caecilians, but especially frogs and toads. Chytridiomycosis is exceptionally contagious, since it doesn't need an animal vector to spread, while the spores can infect at least 1,000 distantly related species. The disease rarely kills tadpoles, but often kills adults, in which it causes the sloughing off of skin, lethargy, weight loss, and ultimately cardiac arrest.

The first known chytridiomycosis epizootics occurred in the late 1970s and early 1980s in western North America, in the late 1990s in Central America and Australia, and in the early 2000s in South America. Genetic analysis has shown that besides the strain Bd-GPL ("Global Pandemic Lineage"), thought to be responsible for most chytridiomycosis epizootics, at least four other (possibly less virulent) strains from South Korea, Switzerland, South America, and southern Africa exist today.

Some species, for example the marine toad and the American bullfrog, seem relatively immune, while there is also evidence that previously devastated populations may currently be evolving a degree of resistance to the pathogen.

## **Study covering 171 years**

Here, Vredenburg and colleagues first used quantitative real-time PCR to determine whether 2,972 museum specimens were infected with any known strain of Bd. These had been collected from Cameroon, Ethiopia, Kenya, Lesotho, Tanzania, and Uganda between 1908 and 2013 and were kept at the California Academy of Sciences, the Museum of Vertebrate Zoology in Berkeley, and Harvard University's Museum of Comparative Zoology.

The researchers also tested the skin swabs from 1,651 live amphibians caught between 2011 and 2013 in Burundi, Equatorial Guinea, Cameroon, and the Democratic Republic of Congo for infection with Bd. Finally, they looked through the scientific literature from between 1852 and 2017 for records of the presence or absence of visible chytridiomycosis infection in amphibians from across Africa. All told, the study analyzed patterns of pathogen presence in over 16,900 amphibians.

In this study, they present estimates for the prevalence of Bd infection over time for Africa as a whole, and for individual countries and regions.

## Millennium bug

The results show that the earliest Bd-positive [amphibian](#) in the dataset dated from 1933 in Cameroon. The infection prevalence across Africa as a whole stayed below 5% for every decade between the 1930s and 2000. But that same year, the infection prevalence suddenly jumped to 17.2%, and increased further to 21.6% during the 2010s. In countries for which more data are available, such as Cameroon, Kenya, Equatorial Guinea, and Burundi, this jump after 2000 in prevalence was even more pronounced: for example, up to 73.7% of samples were infected in Burundi.

An exception was South Africa, where positive samples were found as far back as 1943, and the infection prevalence was relatively steady (approximately 23.3%, including the local strain Bd-CAPE) from the 1970s through the end of the study.

The authors conclude that since 2000, there has been a largely overlooked but major increase in the prevalence of Bd, which poses a new threat to amphibians across Africa. The regions most at risk are eastern, central, and western Africa.

"We don't have a good idea of why the change seems most evident around 2000 in Africa, that is later than on other continents. This could be due to chance," said Vredenburg.

"But there is also a hypothesis that climate change-induced stress could make amphibians more susceptible to pathogens, or that the climate may be changing such that the climate envelope for the pathogen is becoming more common. It's likely that increased air travel of humans and cargo is

also a culprit."

"The first thing that needs to be done is that we need to find out whether amphibians in the areas we identified as high Bd prevalence are experiencing epizootics. What we need is a dynamic picture of the pathogen-host interaction," said Vredenburg.

"Eliminating this microscopic pathogen in the wild is not possible, but we know that if given the opportunity, many host species can survive. Since this pathogen appears to be moved globally by humans, we have a moral imperative to get involved and try to manage and mitigate whenever possible."

**More information:** Continent-wide recent emergence of a global pathogen in African amphibians, *Frontiers in Conservation Science* (2023). DOI: [10.3389/fcosc.2023.1069490](https://doi.org/10.3389/fcosc.2023.1069490) , [www.frontiersin.org/articles/10.3389/fcosc.2023.1069490/full](https://www.frontiersin.org/articles/10.3389/fcosc.2023.1069490/full)

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