

Deadly amphibian fungus has its origins in East Asia

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Lithobates sylvaticus found in southern Quebec. Credit: Wikipedia/CC BY 3.0

Batrachochytrium dendrobatidis (Bd), known as chytrid fungus, has long

been known to cause the decline and extinction of numerous species of frogs, toads, salamanders and other amphibians on several continents. Chytrid is found around the world, but until recently, it has been unclear where the pathogen originated. New research has now traced its source to East Asia.

The results were published in the journal *Science*. Researchers at Imperial College London and several partners, including the Norwegian University of Science and Technology's NTNU University Museum, carried out the study. The researchers highlight the need for more stringent biosafety guidelines across national borders, including a possible ban on trade in amphibians as pets to ensure the survival of vulnerable species.

"Biologists have known since the 1990s that Bd is behind the decline for many amphibian species. But until now, we haven't been able to identify exactly where it came from," says first author Simon O'Hanlon of Imperial College London. "In our article we solve this problem and show that the lineage that has caused this devastation can be traced back to East Asia."

Chytrid spreads rapidly in the wild and travels from animal to animal. The fungus causes catastrophic mortality and decline in some species, while others are less affected. The fungus causes a disease called chytridiomycosis. The disease attacks the animal's skin, which affects its ability to regulate water and electrolyte levels and leads to heart failure.

In this latest study, 38 institutions formed an international team that gathered pathogen samples from all over the world. They sequenced the genomes of the samples and combined the new data with the genomes of previous Bd studies to make a collection of 234 samples. The researchers analysed the data and looked at differences between the genomes. From the samples, they identified four main genetic lineages

of the fungus, of which three were found globally. A fourth line was found only in Korea, on frogs that were native to the region.

The researchers' finding supports the hypothesis that instead of dating back thousands of years, as previously thought, the disease range has greatly expanded only in the last 50 to 120 years. This coincides with the rapid global expansion of intercontinental trade. They believe that human movement of amphibians through the pet trade has directly contributed to spreading the pathogen around the world. They add that the paper provides a strong argument for banning trade in amphibians from Asia, due to the high risk associated with exporting previously unknown strains of chytrid out of this region.

The group highlights the threat of another [amphibian](#) pathogen that also emerged from Asia (*B. salamandrivorans* or BSal), which affects salamanders in Europe. The spread of this pathogen is also connected to the global trade in pet amphibians from Asia. "The NTNU University Museum contributed to the study by sequencing the genes of frogs infected by the chytrid bacteria found in the museum collections," says associate professor Michael D. Martin in NTNU's Department of Natural History.

Martin notes that the museum's scientific collections provide valuable historical material that allows researchers to look back in time and carry out genetic studies of evolution. These collections are also an extremely valuable source of genetic information from places that are otherwise difficult to travel to and gather fieldwork samples from.

More information: Simon J. O'Hanlon et al, Recent Asian origin of chytrid fungi causing global amphibian declines, *Science* (2018). [DOI: 10.1126/science.aar1965](https://doi.org/10.1126/science.aar1965)

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