



Chytridiomycosis:

Identifying and understanding a global cause of amphibian decline

A mysterious threat putting amphibian species across the globe in danger

According to the International Union for the Conservation of Nature (IUCN), amphibians are currently the vertebrate class at greatest risk, with 41% of species threatened with extinction¹. This follows several decades of precipitous declines in amphibian populations on several continents. Although some of these losses were driven by habitat destruction and other direct effects of human activity, many were considered enigmatic by researchers as they occurred in environments thought to be relatively pristine². A partial solution to this mystery was found in the late 1990s, with the discovery of the pathogenic fungus *Batrachochytrium dendrobatidis* (*Bd*), and the disease it causes in amphibians: chytridiomycosis³ (fig. 1).

Bd can infect an amphibian's skin, thereby interfering with their respiration and osmoregulation functions and potentially

leading to death. Its spread has been associated with mass die-offs, rapid and sustained population declines, and the extinction of entire species⁴. It was found to have played a role in the decline of over 500 species of amphibian, including the presumed extinction of 90 species and decreases in abundance of over 90% in another 124 species. This currently represents the greatest loss of biodiversity attributable to a single species other than humans⁵⁻⁶. Many aspects of *Bd* and chytridiomycosis remain poorly understood, including how the disease is transmitted, why it affects some populations more severely than others, and how it became so geographically widespread.

¹ IUCN. *The IUCN Red List of Threatened Species*. Version 2022-2. 2022. <https://www.iucnredlist.org> Accessed on 16/02/23

² Fisher MC, Garner TWJ. *Chytrid fungi and global amphibian declines*. *Nature Reviews Microbiology*. 2020 Jun;18(6):332-343.

³ Berger L, Speare R, Daszak P, Green DE, Cunningham AA, Goggin CL, Slocombe R, Ragan MA, Hyatt AD, McDonald KR, Hines HB, Lips KR, Marantelli G, Parkes H. *Chytridiomycosis causes amphibian mortality associated with population declines in the rain forests of Australia and Central*

America. *Proceedings of the National Academy of Sciences of the U A*. 1998 Jul 21;95(15)

⁴ Lips KR. *Overview of chytrid emergence and impacts on amphibians*. *Philosophical Transactions of the Royal Society B: Biological Sciences*. 2016 Dec 5;371(1709)

⁵ Fisher MC, Garner TWJ. *Chytrid fungi and global amphibian declines*. *Nature Reviews Microbiology*. 2020 Jun;18(6):332-343.

⁶ Bellard C, Genovesi P, Jeschke JM. *Global patterns in threats to vertebrates by biological invasions*. *Proceedings of the Royal Society B: Biological Sciences*. 2016.





Using DSI to solve the mystery

Much of the modern biological and ecological research that underpins biodiversity conservation efforts depends upon the use of DSI. Among other things, it's used to explore changes in population dynamics, the mutation and evolution of pathogens over time, and host-pathogen interactions. It is necessary for designing and developing tests that can be used to identify different strains of *Bd* in the field. The use of DSI is therefore essential to resolving many of the uncertainties that still surround *Bd* and chytridiomycosis and to eventually developing ways to prevent or mitigate its impacts.

For example, early hypotheses as to its origin suggested that it first emerged in Africa, before being accidentally exported around the world as part of the global trade in live African clawed frogs and subsequently establishing feral populations in Europe and North and South America⁷. Research published in 2018, however, demonstrated that the origins of *Bd* were instead most likely in East Asia. The researchers came to this conclusion by analysing a globally representative set of 243 *Bd* genome sequences, covering all continents where *Bd* has been detected and all three

extant orders of amphibians, and comparing with existing DSI in public databases. An in-depth analysis of this comparison revealed a spot of endemism of *Bd* in Asia, from which the other infectious lineages have emerged and spread (fig. 2). The researchers concluded that the global trade of wild species is still associated with the dispersion of *Bd*⁸.

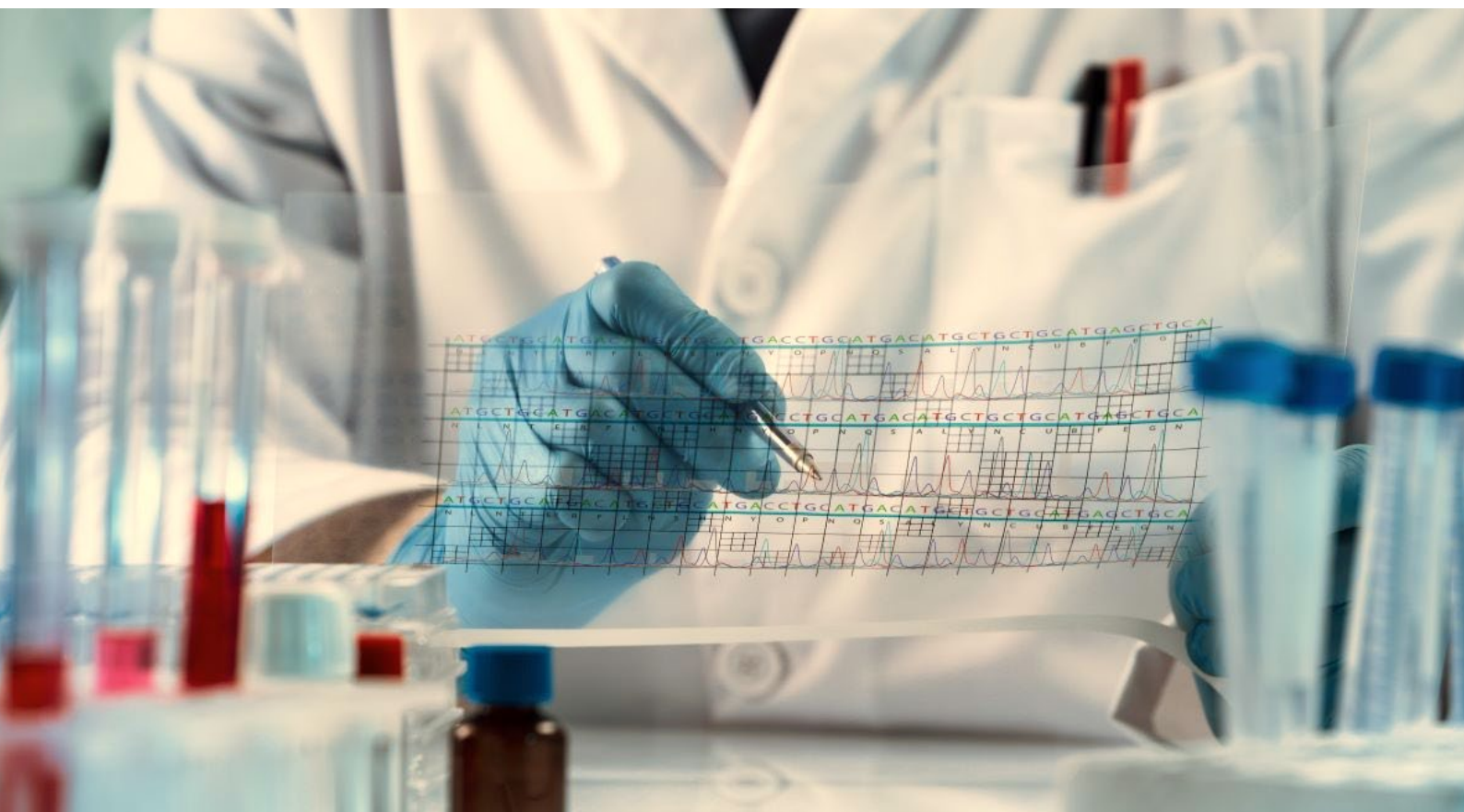
Discovering the point of origin of the pathogen has important implications for understanding how to prevent its spread, how it has evolved over time, and which populations are most at risk. It would not have been possible without the widespread sharing of, and open access to, DSI. The sequence information used by those researchers is currently available to anyone through public repositories. It can be used to perform further analyses, and help track the evolution and spread of different strains of *Bd*. The more sequence information is collected and made accessible, the better and more complete researchers' picture of what strains are present where and how they relate to each other will be. And the clearer this picture is, the more effective efforts to prevent amphibian biodiversity loss will be.

⁷Weldon C, du Preez LH, Hyatt AD, Muller R, Spears R. *Origin of the amphibian chytrid fungus*. *Emerging Infectious Diseases*. 2004 Dec;10(12)

⁸O'Hanlon SJ, Rieux A, Farrer RA, Rosa GM, Waldman B, Bataille A, Kosch TA, Murray KA, Brankovics B, Fumagalli M, Martin MD, Wales N, Alvarado-Rybak M, Bates KA, Berger L, Böll S, Brookes L, Clare F, Courtois EA, Cunningham AA, Doherty-Bone TM, Ghosh P, Gower DJ, Hintz WE, Höglund J, Jenkinson TS, Lin CF, Laurila A, Loyau A,

Martel A, Meurling S, Miaud C, Minting P, Pasmans F, Schmeller DS, Schmidt BR, Shelton JMG, Skerratt LF, Smith F, Soto-Azat C, Spagnoletti M, Tessa G, Toledo LF, Valenzuela-Sánchez A, Verster R, Vörös J, Webb RJ, Wierzbicki C, Wombwell E, Zamudio KR, Aanensen DM, James TY, Gilbert MTP, Weldon C, Bosch J, Balloux F, Garner TWJ, Fisher MC. *Recent Asian origin of chytrid fungi causing global amphibian declines*. *Science*. 2018 May 11;360(6389)





Key takeaways

- **Open access** to DSI is vital to efforts to conserve biodiversity. DSI is a powerful tool for understanding threats to biodiversity and public health and thereby taking effective action to address them. The multilateral mechanism must protect open access and **avoid triggers for benefit sharing at the point of access to DSI** in public databases like subscription models, or paywalls.
- As more DSI is available in open access databases, more in-depth analysis can be performed and more accurate knowledge will be generated. The benefit sharing mechanism should **encourage the scientific practice of sharing sequences in open access databases** that are accessible for everyone, and contributing to the common good.
- The knowledge generated from the use of DSI is a **non-monetary benefit**. Research results from large-scale analysis can guide actions to fight the causes of biodiversity loss, e.g. invasive species, and contribute to achieving the Kunming-Montreal Global Biodiversity Framework goals and targets. Indicators that can measure the contribution of the use of DSI to conservation, as a non-monetary benefit, are urgently needed.
- **Capacity development is necessary to increase the use of DSI for conservation in Low- and Middle-Income Countries.** Although the access to DSI is open and free, the capacity to use and analyse the sequences is uneven around the world. The exchange of scientific expertise, joint international research, together with funds from the multilateral mechanism, will help to even out the capacities to produce and use DSI.



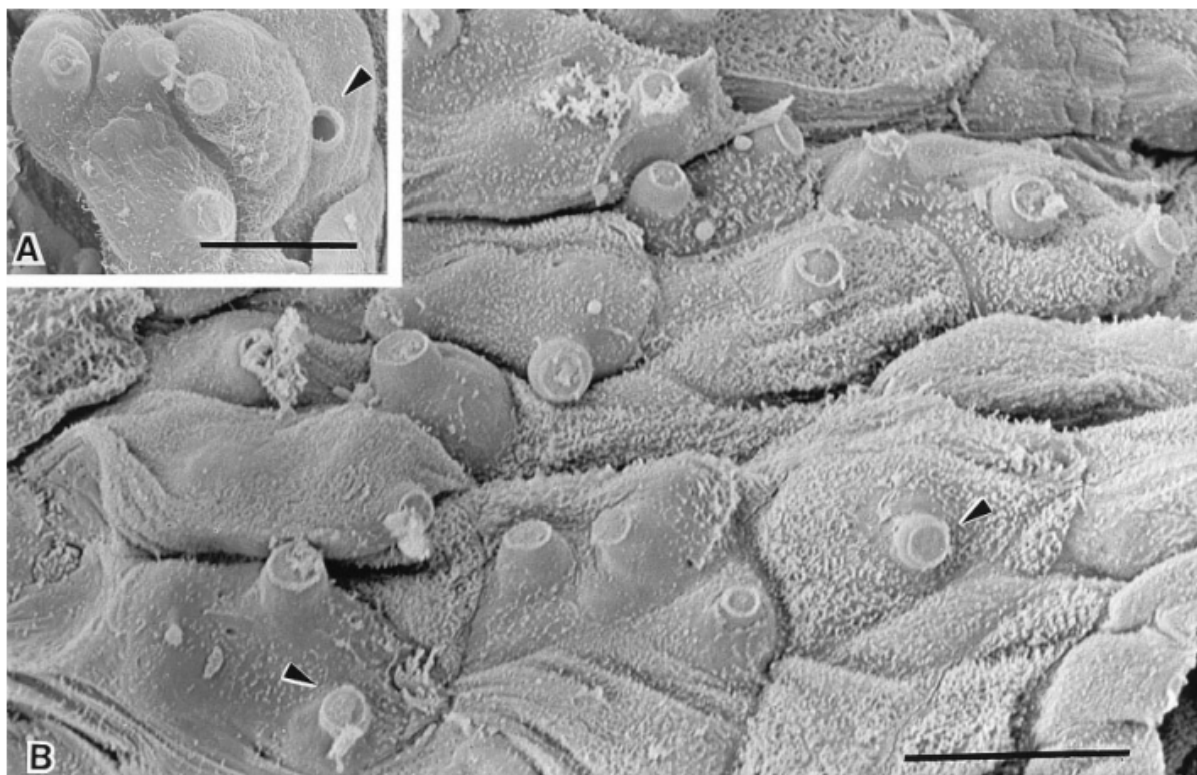
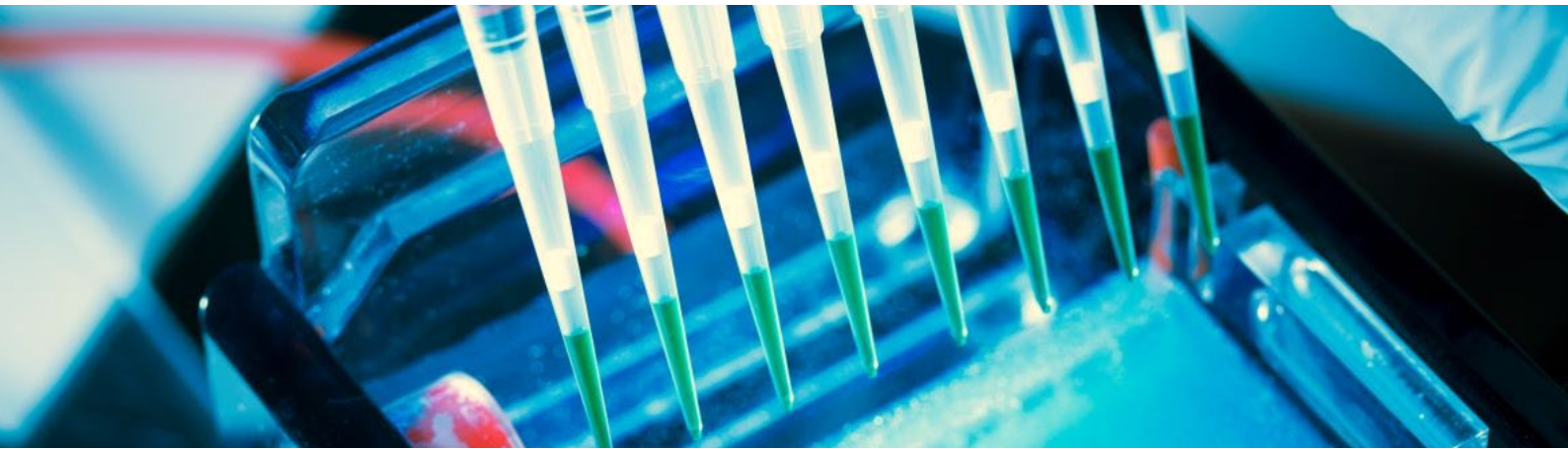
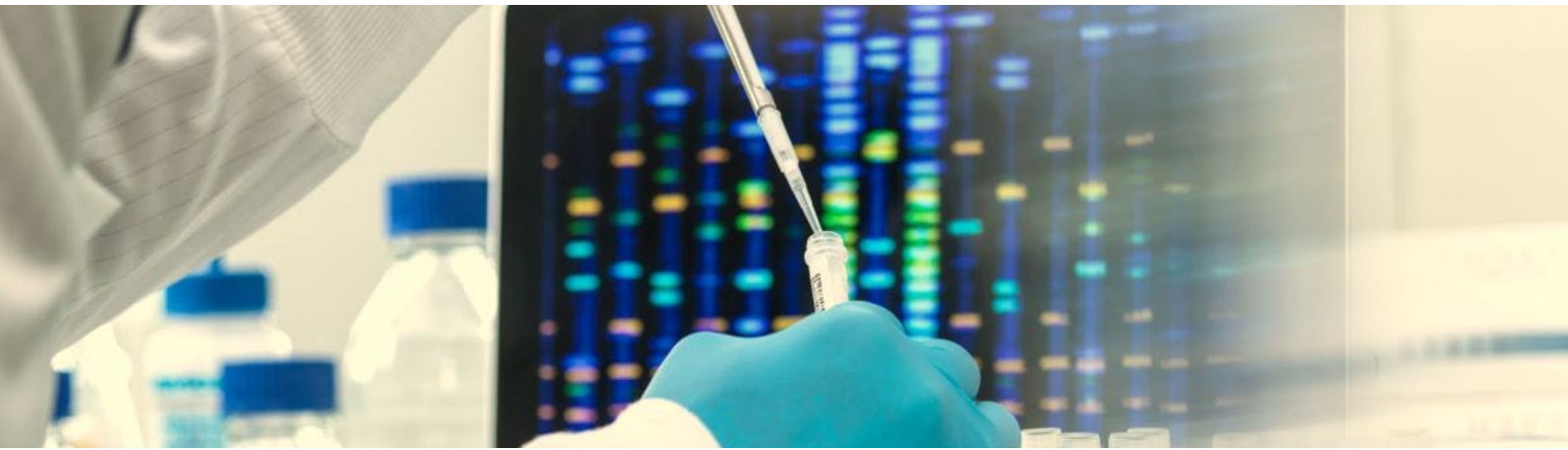


Fig 1. Scanning electron micrographs of infected digital skin of a wild frog, *Litoria lesueuri*, from Queensland, Australia, which died with cutaneous chytridiomycosis. Fungi sporangia are evident within the cells of the epidermis (their discharge tubes are indicated by the arrows). (Scale bars = 10 μ m.)⁹

⁹ Berger L, Speare R, Daszak P, Green DE, Cunningham AA, Goggin CL, Slocombe R, Ragan MA, Hyatt AD, McDonald KR, Hines HB, Lips KR, Marantelli G, Parkes H. *Chytridiomycosis causes amphibian mortality associated with population declines in the rain forests of Australia and Central America*. Proceedings of the National Academy of Sciences of the U A. 1998 Jul 21;95(15)





A

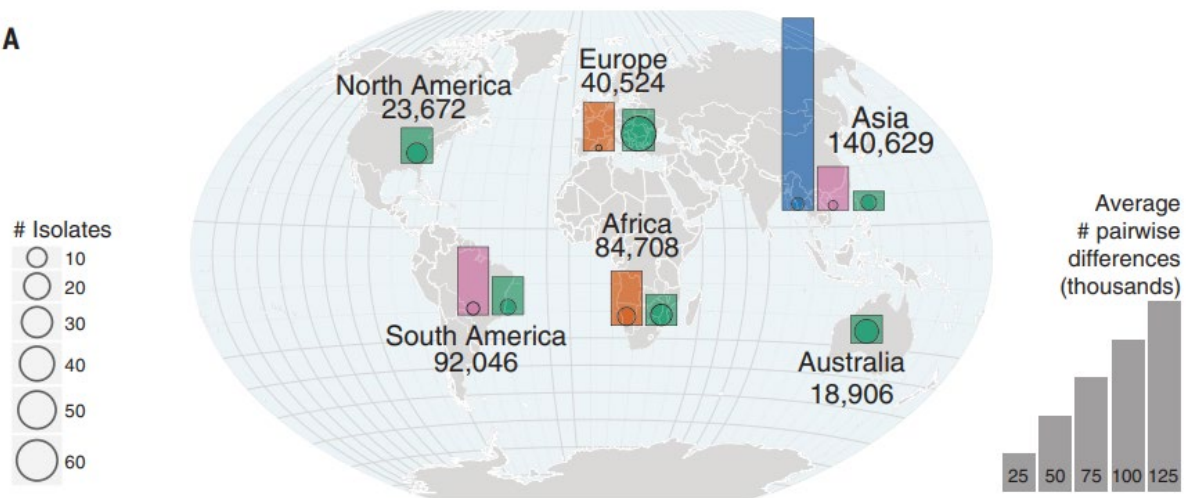


Fig 2. Genetic diversity of a global panel of 234 *B. dendrobatidis* isolates. Map overlaid with bar charts showing the number of isolates (circle size) and diversity of isolates (bar height) per major lineage (colours). Asian sequences showed the highest diversity of isolates. In-depth analysis identified East Asia as the likely source of the strains killing amphibians around the world.¹⁰

¹⁰ O'Hanlon SJ, Rieux A, Farrer RA, Rosa GM, Waldman B, Bataille A, Kosch TA, Murray KA, Brankovics B, Fumagalli M, Martin MD, Wales N, Alvarado-Rybak M, Bates KA, Berger L, Böll S, Brookes L, Clare F, Courtois EA, Cunningham AA, Doherty-Bone TM, Ghosh P, Gower DJ, Hintz WE, Höglund J, Jenkinson TS, Lin CF, Laurila A, Loyau A, Martel A, Meurling S, Miaud C, Minting P, Pasmans F, Schmeller DS, Schmidt BR, Shelton JMG, Skerratt LF, Smith F, Soto-Azat C, Spagnoletti M, Tessa G, Toledo LF, Valenzuela-Sánchez A, Verster R, Vörös J, Webb RJ, Wierzbicki C, Wombwell E, Zamudio KR, Aanensen DM, James TY, Gilbert MTP, Weldon C, Bosch J, Balloux F, Garner TWJ, Fisher MC. Recent Asian origin of chytrid fungi causing global amphibian declines. *Science*. 2018 May 11;360(6389)

