

Amphibian disease



The world's amphibian population is at grave risk from two deadly groups of pathogens – chytrid fungi and ranaviruses – and IoZ scientists are at the forefront of the fightback.

Amphibians are recognised as the most highly threatened vertebrate class, in no small part due to the impacts of two groups of pathogens – chytridiomycete fungi and ranaviruses. In the 1990s, research at IoZ was key to the identification of these pathogen groups as causes of amphibian mass mortality and significant population declines. IoZ continues to lead the world in understanding the impacts these pathogens have on wild and captive amphibians and identifying factors that increase the probability of infection, disease and host population decline. Last year, we played a significant role in identifying new genetic variants of these pathogens that may pose a greater threat to amphibians than previously thought. In response to the ever-increasing and global risk infectious diseases pose to amphibians, our researchers are at the forefront of efforts to control the spread, and mitigate the impacts, of chytrid fungi and ranaviruses in both wild and captive populations.

Newly described ranavirus decimates amphibian communities

Ranaviruses have long been recognised as lethal pathogens of amphibians, reptiles and fish. For amphibians, only one case of emergent ranavirosis, first described in the early 1990s by IoZ scientists, has been shown to cause amphibian declines. In the UK, infection with, and disease caused by, FV3-like variants of ranaviruses commonly result in mass death and persistent population declines of common frogs (*Rana temporaria*). Other UK native amphibians are rarely affected, even at locations where infected common frogs share ponds with them (Duffus et al. 2014a,b). In contrast, last year we showed how CMTV-like variants of the virus, first discovered by a team including IoZ staff (Balseiro et al. 2009), are decimating entire Iberian amphibian communities. Unlike the FV3-like variants causing common frog mass mortalities in the UK, CMTV-like ranaviruses emerging in amphibian communities in Spain and Portugal have the ability to infect and cause disease in all eight host amphibian species at the study sites (Price et al. 2014). Even more worryingly, the extraordinary number of host species exploited by CMTV-like ranaviruses does not stop at amphibians. A snake that ingested a diseased frog died with signs of disease consistent with ranavirosis and from which virus DNA could be isolated. The genetic code of this DNA was identical to that infecting



Main image: Amphibians worldwide are under threat from lethal pathogens. Below, inset: Midwife toad tadpole infected with a ranavirus. Opposite: European salamanders have proved vulnerable to novel infections

the frogs (Price et al. 2014). Additional research has shown CMTV-like viruses are not uncommon across Europe and are already being detected in traded and transported hosts (Stöhr et al. 2015).

As part of the Global Ranavirus Consortium, our staff work with researchers across the globe to understand why CMTV-like viruses affect so many species to such a terrifying degree. Funded by the Natural Environment Research Council, we are exploring the genetic make-up of ranaviruses to determine if CMTV-like ranaviruses contain specific genetic elements associated with broad host range and severe disease. To do this, researchers at IoZ, our partner institution UCL and long-term collaborators at Queen Mary University of London are comparing the genomes of ranaviruses isolated from amphibians, reptiles and fish to identify genes or gene variants that are unique to Iberian CMTV-like viruses. Once these have been described, we will use state-of-the-art molecular manipulation techniques to 'knock out' these novel genetic elements to see if loss of gene function leads to decreased infectivity and virulence.



Find out more about the
Global Ranavirus Consortium
at ranavirus.org



*We continue to investigate where, how and why the fungus *Batrachochytrium dendrobatidis* causes amphibian population and species declines.*

Ancient chytrid fungus poses a severe threat to Europe's amphibians

At the end of the last century, IoZ researchers were part of an international consortium that first described how a fungal infectious disease was responsible for amphibian declines in the New World, Australia and beyond. We continue to investigate where, how and why the fungus *Batrachochytrium dendrobatidis* causes amphibian population and species declines.

Last year, we showed how, unlike in the Americas and Australia, infection is relatively rare in Europe (Baláž et al. 2014). In some cases this could be attributed to resistance to infection (Bielby et al. 2015). However, even highly susceptible European species can avoid lethal infections through the efforts of the aquatic microorganisms that inhabit amphibian breeding ponds. If the population densities of these microorganisms are high enough, they can reduce the amount of fungus and reduce the risk of infection and disease by eating the



aquatic zoospores that lead to infection (Schmeller et al. 2014).

At the same time, colleagues in Belgium were describing a newly discovered species of *Batrachochytrium*, *B. salamandrivorans*. Unlike the genetic lineages that have been identified as variants of *B. dendrobatidis*, a recently evolved species (Farrer et al. 2011), *B. salamandrivorans* appears to be a distinct and ancient species.

We collaborated with this group and others to show that this novel chytrid fungus has newly emerged in Europe, infects and kills

salamanders and newts, but not frogs and toads, and likely evolved as a parasite of Asian newts millions of years ago (Martel et al. 2014).

So why the sudden and devastating emergence of lethal chytridiomycosis in wild European

salamanders caused by an ancient Asian fungus? We hypothesised that emergence in Europe was the result of movement of infected, but tolerant Asian newt species to Europe via the amphibian pet trade (Martel et al. 2014).

Less than a year later, our researchers described new cases of this disease caused by the Asian fungus in animals involved in the amphibian trade, showing conclusively how infected animals in the trade may be moved among facilities and transmit chytrid infections on arrival (Cunningham et al. 2015).



IoZ works in many locations, including Madagascar, home to many rare amphibian species including these frogs from the Boophis genus (this image and below)

IoZ research is conserving species threatened by disease

The combined evidence of ongoing emergence of novel and highly lethal viruses and fungi presents a compelling case arguing for immediate effort to control dangerous pathogens in the amphibian trade. Again, IoZ researchers lead in this, developing strategies for chemical disinfection, application of antifungals and strategies for biosecurity to control pathogen transmission in nature and captivity. We seek to understand how amphibians respond immunologically to exposure and infection (Price et al. 2015) and how microbial communities that inhabit the skin of amphibians may afford resistance to infection (Antwis et al. 2015). We work at various locations across the globe – Chile, Dominica, Montserrat, Mallorca, the French Pyrenees, Sardinia, Madagascar (Bletz et al. 2015) and wherever novel and threatened amphibian populations, species and communities may be threatened by these and other parasites – to develop local capacity to conserve amphibian biodiversity in captivity and return species threatened by disease safely to the wild. This is an enormous and daunting task, requiring international efforts to coordinate research and implement conservation strategies guided by the evidence we produce.



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