

## NEWS AND VIEWS

## PERSPECTIVE

**Dr Jekyll and Mrs Hyde: Risky hybrid sex by amphibian-parasitizing chytrids in the Brazilian Atlantic Forests**

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In their article in this issue of *Molecular Ecology*, Jenkinson *et al.* (2016) and colleagues address a worrying question—how could arguably the most dangerous pathogen known to science, *Batrachochytrium dendrobatidis* (*Bd*), become even more virulent? The answer: start having sex. Jenkinson *et al.* present a case for how the introduction into Brazil of the globally invasive lineage of *Bd*, *BdGPL*, has disrupted the relationship between native amphibians and an endemic *Bd* lineage, *BdBrazil*. *BdBrazil* is hypothesized to be native to the Atlantic Forest and so have a long co-evolutionary history with biodiverse Atlantic Forest amphibian community. The authors suggest that this has resulted in a zone of hybrid *Bd* genotypes which are potentially more likely to cause fatal chytridiomycosis than either parent lineage. The endemic–nonendemic *Bd* hybrid genotypes described in this study, and the evidence for pathogen translocation via the global amphibian trade presented, highlights the danger of anthropogenic pathogen dispersal. This research emphasizes that biosecurity regulations may have to refocus on lineages within species if we are to mitigate against the danger of new, possibly hypervirulent genotypes of pathogens emerging as phylogeographic barriers are breached.

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*Batrachochytrium dendrobatidis*, the causative agent of the disease chytridiomycosis in amphibians, is now known to comprise of at least five phenotypically and phylogenetically deeply diverged lineages (Bataille *et al.* 2013; Farrer *et al.* 2011). In Robert Louis Stevenson's creation 'The Strange Case of Dr Jekyll and Mr Hyde', the good side of one man's character, the benign Dr Jekyll, becomes entirely physically separated and conflicts with the evil side of his character, the violent Mr Hyde. Analogous to this tale, the

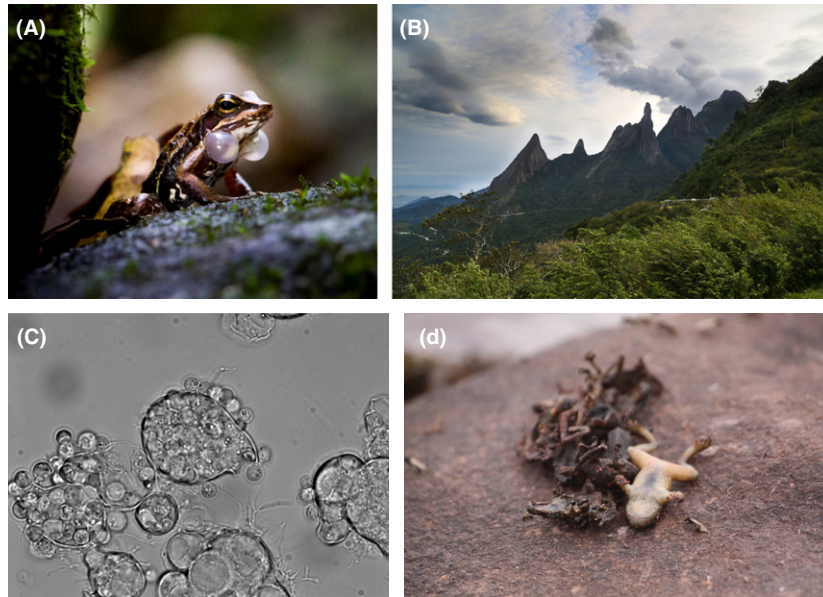
five described lineages each present very different faces of the chytrid species, *Bd*.

One lineage, *BdGPL*, has expanded recently to achieve its current worldwide distribution and this lineage underpins all known chytrid-driven amphibian mass mortalities to date. Three lineages, *BdCH* from Switzerland, *BdCape* from Southern Africa and *BdBrazil* from the Brazilian Atlantic Forest, exhibit a much lower virulence than *BdGPL* and are restricted in their distributions. A fifth lineage of unknown virulence level, *BdKorea*, appears to be endemic to Asia (Bataille *et al.* 2013). It has been hypothesized that the hypervirulent *BdGPL* arose through recombination of previously isolated (allopatric) lineages and has subsequently been spread around the world by anthropogenic means. Evidence for recombination in *Bd* was first described in 2007 (Morgan *et al.* 2007), but the fungus has never been observed to reproduce sexually and it was not until Schloegel *et al.*'s paper in 2012 that any potential hybrids of known lineages were described.

In Stevenson's story, Jekyll and Hyde alternately inhabit one body, never existing simultaneously. *Bd* lineages, however, are able to meet and interact as they are transported and expand in distribution around the world. What is unknown is what happens when these meetings occur. Do the Jekyll and Hyde lineages coexist or compete? If they do compete, which side wins? Could we have Dr Jekylls and Mrs Hydes, where lineages hybridize *via* sexual processes and give rise to mixed genotypes? How dangerous will these hybrids be?

Significant progress in the field of *Bd* research has been made by comparative genomic analysis of the lineages, revealing expansions in genes associated with virulence compared with nonpathogenic chytrids as well as significant evolutionary divergence between lineages of *Bd*. It has also been shown that different lineages of *Bd* are associated with the variation in phenotype and levels of virulence (Fisher 2008; Farrer *et al.* 2011). However, there are two major areas of research that need to be tackled when it comes to unravelling the evolutionary history and future trajectory of *Bd*: first, the marrying of extensive mapping work around the world with the genomics data, and the placing of this information in the public domain. This information is crucial to enable potential contact zones between different lineages to be identified, highlighting areas which should be watched especially closely for emergence of new lineages. This is because new lineages may also exhibit novel traits that present a risk to biodiversity, such as hypervirulence. Second, investigations into what happens when two lineages do meet in nature are needed. As Jenkinson *et al.* show, there is now convincing evidence that different *Bd* lineages are capable of hybridizing with each other. The frequency with which different *Bd*

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**Fig. 1** (A) The Boraceia tree toad (*Hylodes phyllodes*), one of the Brazilian Atlantic Forest species infected with *Batrachochytrium dendrobatidis*. Photo Credit: David Rodriguez; (B) Serra dos Órgãos National Park in Rio de Janeiro State, Brazil, one of the study sites in Jenkinson *et al.* (2016). Photo Credit: C. Guilherme Becker; (C) Mature *B. dendrobatidis* sporangia releasing infective zoospores into its environment (1000 $\times$ ). Photo Credit: Thomas Jenkinson; (D) Mass mortalities caused by the 'Hyde' lineage BdGPL in Europe. Photo Credit: Matthew Fisher.

genotypes hybridize in contact zones; the long-term viability of offspring genotypes; and whether lineages compete, coexist or influence host survival differentially when in contact, are all extremely poorly understood. In demonstrating a clear hybrid zone, Jenkinson *et al.* have made a base from which to address these important questions in the context of the Brazilian Atlantic Forest (Fig. 1).

In a wider context, the evolution of virulence in mycoses is becoming a truly urgent issue to tackle. With emerging fungal pathogens on the rise in animals and plants, global wildlife health, food security and ecosystem stability are threatened (Fisher *et al.* 2012). To control these mycoses, we need to understand the factors leading to (and to be able to accurately reconstruct) their geographical expansion and emergence. This is an area which to date has been poorly addressed and this study is a step forward in investigating this much wider issue. Research into how to mitigate these diseases is hampered by disproportionately low levels of funding. Fungi, as illustrated by the hybridization described here, have extremely plastic genomes and an extraordinary ability to adapt to changing environments or hosts, making them formidable targets for disease control. Understanding how fungal pathogens interact with each other, with their hosts, and the environment will be crucial for sustaining biodiversity, human health and food security in the future.

This study points towards the next frontiers in chytrid and emerging mycoses research more generally. The next tasks for the research community are as follows: (i) understand the evolutionary nuances of lineage within species; (ii) trying to predict whether, when and how

lineages will interact with each other; and (iii) whether these interactions will ultimately impact host survival and onwards pathogen spread. Emerging fungal infections are a global, omnipresent threat not only to wildlife but also to crops and human health. To manage these threats, it will be necessary to delve deep into their evolutionary history and to understand what the factors were that drove them to become threats in the first place. It will be necessary to go beyond simple documentation of what is present now into the much more complex questions of where these pathogens came from, and how to predict where the next generations of Jekyll and Hyde hybrids will emerge in the future.

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