

2024_81_ZSL_TG: How do pathogen genotype climate envelopes dictate opportunities for coinfections and recombination of a multihost pathogen?

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B dendrobatidis (Bd) is a globally emerged pathogen responsible for the greatest loss of biodiversity attributable to infectious disease. The fungus is composed of a suite of highly diverged lineages that have been distributed through human activities. Only two lineage contact zones have been detected, one in South Africa, which involving the lineages most responsible for global amphibian declines. Our field data indicate distinct but overlapping environmental envelopes for these two lineages, envelopes that do not completely exclude opportunities for cocirculation, coinfection and recombination. This in turn offers opportunities for radical restructuring of pathogen genotypes and the potential for the emergence of new and highly virulent variants.

South Africa is predicted to be one of the regions worst affected by human-incurred climate variation. A serious drought has been affecting the country since 2015, driven by warming temperatures and unpredictable rainfall. Both these parameters directly affect Bd lineage growth rates and amphibian host distributions and availability. Thus the current pattern of lineage distribution will change, and we have no understanding if this will increase or decrease the interactions between these genotypes. This uncertainty is the basis of this project. The student, working with our partners in South Africa, will expand our current knowledge of lineage distributional overlaps using established methods for collecting and genotyping samples and isolates collected in South Africa. Our partners are already monitoring ongoing patterns of climate change for a related project on impacts on pollination, thus offering access to the key data sets required to explore climate-driven lineage interactions at a fine scale. ZSL offers the ex situ experimental setting to use isolates collected during the project and housed in the Imperial live Bd archive to test hypotheses generated from field data and ascertain empirically what conditions facilitate or restrict lineage co-circulation and coinfections.

We expect the student to develop a suite of hypotheses that together address the over-arching question: how will ongoing climate change drive the genetic structure of the world's worst wildlife disease?

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