

Host-pathogen dynamics of mycoses in reptiles and amphibians

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The negative impacts of mycoses (diseases caused by fungi) affecting humans, plants, and wildlife have increased over the last few decades, yet host-pathogen interactions remain poorly understood because fungal biodiversity is also critically understudied. In wildlife, prominent examples include the decimation of bat populations owing to white-nose syndrome, and the recent spread and emergence of Snake Fungal Disease (SFD), which causes disfiguring lesions and mortality in snakes. However, no other fungal pathogens have been more destructive to wildlife than the amphibian chytrids (Genus *Batrachochytrium*). Focusing on the latter two diseases, our research aims to disentangle host-pathogen dynamics in reptiles and amphibians on the landscape, experimentally testing infection outcomes, and measuring diversity in both the host and the pathogen. Using quantitative PCR, we have detected *Ophidiomyces ophiodiicola*, the causative agent of ophidiomycosis or SFD, contemporaneously and historically in snakes occupying the Brazos river drainage (Texas). Our results have implications on the management and conservation of the Brazos water snake (*Nerodia harteri harteri*), which is endemic and characterized by low population sizes and low genetic diversity. Invasion of *Batrachochytrium dendrobatidis* (*Bd*) into naïve amphibian populations has led to outbreaks of chytridiomycosis, a skin disease that has caused amphibian declines across the world. Using isolates of *Bd* from Texas, we have investigated the population genetics of this introduced pathogen and found higher heterozygosity compared to other invaded regions. We also experimentally confirmed that Cricket frogs (*Acris crepitans*), a wide-ranging host species, can be asymptomatic and carry high loads of *Bd*, potentially facilitating spread. Despite intensive and increased study since its

discovery, understanding of host specificity (when specific strains infect specific hosts) at the population level is still lacking for many regions invaded by *Bd*. Population-scale genotyping studies of *Bd* itself are critically needed to address this lack of resolution. Thus, our approaches contribute to the development of new tools leveraging emerging, portable genetic technologies to sequence or genotype *Bd* strains and amphibian hosts at the population scale across continental sites.