

# GENETIC STRUCTURE AND DISEASE PREVALENCE OF BOREAL TOADS (*BUFO BOREAS*) IN GLACIER NATIONAL PARK

Brett Addis, Division of Biological Sciences, University of Montana

Boreal toads (*Bufo boreas*) are widely distributed throughout the western United States, including Glacier National Park, Montana. They are of conservation concern because they are declining in portions of their range. The causes of these declines remain unclear, but have been linked to chytridiomycosis, an infectious disease caused by the fungal pathogen *Batrachochytrium dendrobatidis* (Bd). Additionally, complex topography (i.e., mountains) may lead to reductions in genetic variation within toad populations by restricting gene flow (genetic exchange) among populations, which may ultimately perpetuate declines. To address threats to the persistence of boreal toads in Glacier National Park, I collected DNA samples from toads throughout the park ( $n = 551$ ; Fig. 1) to identify landscape barriers to gene flow. I also tested a subsample of toads for Bd to investigate how genetic variation influences disease susceptibility.



Fig. 1. Swabbing the buccal cavity of a toad to collect DNA.

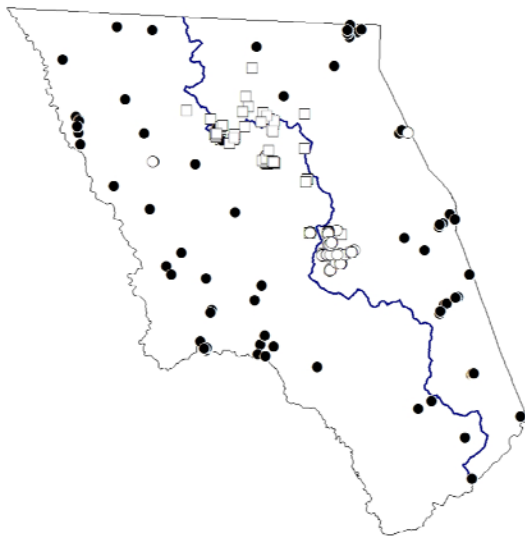


Fig. 2. Locations of boreal toad genetic samples in Glacier National Park. Symbols (see text) represent high- and low-elevation genetic groups.

I found that elevation strongly influenced the genetic structure of boreal toads in the park. There were 2 genetic groups at high elevations, clustered near the Continental Divide along a north-south gradient (white symbols in Fig. 2), and 1 low-elevation genetic group (black symbols in Fig. 2). Within the high elevations groups, mountains reduced gene flow among local populations. However, genetic variation was still high in the high elevations groups, indicating reduced gene flow will probably not facilitate future toad population declines.

Surprisingly, I found that individual toads with high heterozygosity (generally a signature of increased disease resistance) were actually *more* likely to be infected with chytridiomycosis (Fig. 3). This result suggests dispersal among populations may facilitate disease spread and may represent the greatest threat to population persistence.

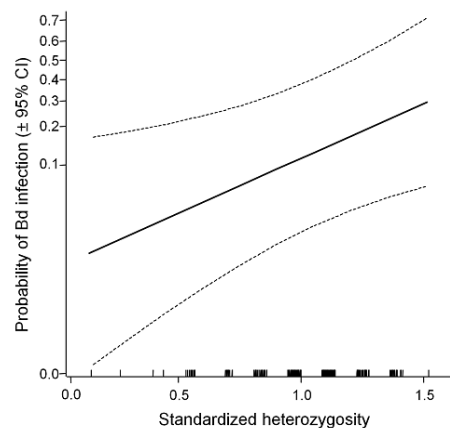


Fig. 3. Predicted probability of infection with *Batrachochytrium dendrobatidis* (Bd) relative to heterozygosity.