

Title- The cutaneous microbiomes of Appalachian salamanders and their role as an innate defense against the pathogen *Batrachochytrium dendrobatidis*

Program of Study- Biology

Presentation Type- Oral Presentation

Subtype- Basic

Mentor and Mentor Email- Dr. Matthew Becker (mbecker5@liberty.edu)

Student Name and Email- Miranda Sheridan (mjsheridan@liberty.edu)

In recent years, amphibian populations worldwide have seen unprecedented declines, which have been associated with a dramatic increase of chytridiomycosis. *Batrachochytrium dendrobatidis* (*Bd*) and *B. salamandrivorans* (*Bsal*) are two fungal pathogens that infect the skin of amphibians, leading to chytridiomycosis. Previous research suggests that the symbiotic microbial skin community of some amphibians protects them from *Bd* and *Bsal*. Considering these results, we characterized the microbial communities of two stream salamanders, *Desmognathus fuscus* and *D. monticola*, and examined interactions between the isolated microbes and the pathogen *Bd*. We captured *D. fuscus* (n=18) and *D. monticola* (n=11) individuals from a stream in Bedford County, VA. We rinsed all salamanders to remove transient microbes before swabbing them to collect microbial cells. These were transferred to R2A agar and incubated at room temperature. We identified unique morphotypes by extracting, amplifying, and sequencing the 16S rRNA gene. We co-cultured each isolate with *Bd* to determine if they promote inhibition or growth of *Bd in vitro*.

We found that *D. fuscus* and *D. monticola* had similar microbial community compositions, primarily dominated by the phyla Proteobacteria (61% of isolates), Actinobacteria (18%), Firmicutes (18%), and Bacteroides (3%). These communities were phylogenetically diverse, containing 34 genera of bacteria. The dominant genus was *Pseudomonas*. We cultured an average of 16 and 15 isolates per *D. fuscus* and *D. monticola*, respectively. In *Bd* challenge assays of 236 total *D. Fuscus* metabolites, 32.6% strongly inhibited *Bd* (inhibition score of $\geq 50\%$), 23.7% moderately inhibited it ($< 50\%$ and $\geq 0\%$), and 43.6% facilitated *Bd* growth ($< 0\%$). 148 total *D. monticola* metabolites were assayed as well: 48.6% strongly inhibited *Bd*, 23.0% moderately inhibited it, and 28.4% facilitated *Bd* growth. This data has a translational impact, as antifungal cultures isolated from this study could be used potentially as probiotics to mitigate chytridiomycosis in susceptible species.