

Title - Microbiome Characterization of the Cave Salamander as Potential Defense Against Emerging Infectious Diseases

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Abstract:

Recent global amphibian population decreases have prompted inquiry into possible causes, and scientists have implicated the fungal pathogens *Batrachochytrium dendrobatidis* (*Bd*) and *Batrachochytrium salamandrivorans* (*Bsal*) as key causes. These fungi infect the skin of many amphibian species which can result in the pathogenesis of chytridiomycosis, a fatal disease. While some amphibian populations have been shown to be resistant to chytridiomycosis others are susceptible to the disease; resistance against *Bd* infection has been linked to the production of anti-fungal biomolecules by symbiotic cutaneous bacteria. The cave salamander *Eurycea lucifuga*, also known as the Spotted Tail salamander, is a brook salamander species that resides in regions of the Southeast and Ohio Valley. As its susceptibility to *Bd* is yet unknown, we sought to characterize the microbiome of *E. lucifuga*, which may lead to discerning its host-symbiont-pathogen interactions. Twelve *E. lucifuga* individuals were captured using gloves and rinsed with sterile water to remove transient microbes. The skin of each specimen was then swabbed to collect microbial cells. Cells were transferred to R2A agar plates and incubated at room temperature. Bacterial and fungal colonies were examined for morphology and were isolated by streaking. The DNA of pure cultures was extracted and subsequent 16S rRNA Sanger sequencing will identify the species of each isolate. Co-culture assays will be employed to test the *in vitro* efficacy of each

bacteria in inhibiting the growth of *Bd*. It is suspected that the healthy microbiome of the *E. lucifuga* will confer some anti-fungal properties, and this finding will prompt exploration into possible bioaugmentation strategies for conservation purposes.