

Proposal

Title- Characterization of the interactions between the resident microbial flora and chytridiomycoses in *Desmognathus fuscus* communities of Central Virginia

Program of Study- Biology

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Category- Basic

Abstract:

In recent years, amphibian populations worldwide have seen unprecedented declines, including the extinction of a few species¹. These declines have been closely associated with a dramatic increase in the incidence of chytridiomycosis and ranavirus, which are known amphibian diseases^{2,3}. Chytridiomycosis is caused by two pathogens, *Batrachochytrium dendrobatidis* (*Bd*) and *B. salamandrivorans* (*Bsal*). Both are fungal pathogens of the skin in amphibians and are unique in that they have been shown to infect organisms across three different orders of vertebrates (Anura, Caudata, and Gymnophiona)⁶. Ranaviral disease is caused by several species of virus within the genus *Ranavirus* and has been seen as a cause of mass die-offs across the Southeastern United States⁷. It has been demonstrated that both ranaviral disease and chytridiomycosis are present in amphibian species of the Southeast, with widespread distribution and low levels of occurrence, suggesting that they may be endemic⁵. However, the interaction between these pathogens and the microbiome of the host organisms has yet to be fully established. Previous studies have indicated that the microbial community of some amphibians protects them from *Bd*.⁸ This study seeks to characterize the microbial communities of the local salamander species *Desmognathus fuscus* and to identify interactions between the host microbiome and well-known pathogens. This will be done by culturing the cutaneous bacteria of *D. fuscus* and identifying these isolates through Sanger sequencing of the 16s ribosomal RNA gene. Isolates from the same amphibians will also be tested for *Bd*, *Bsal*, and ranavirus through skin swabs and quantitative PCR. The data from both portions of the study will be compared to identify relationships between beneficial microbes and those that are pathogenic. We expect that the resident microbial flora isolated from *D. fuscus* will inhibit the growth of the *Bd* and *Bsal* pathogens.

Literature cited:

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