

The characterization of the microbiome for the Northern two-lined salamander (*Eurycea bislineata*) and its ecological interactions with the pathogen *Batrachochytrium dendrobatidis*

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Fungal pathogens are a major threat to amphibians worldwide, but the most prevalent fungal pathogen seen today is *Batrachochytrium dendrobatidis* (Bd). Bd is a chytrid fungus that is highly virulent and has been linked to population decline in numerous amphibian populations across the world due to the development of chytridiomycosis (Voyles et al., 2009). Bd infects the amphibian's skin by rooting their spherical thalli into the amphibian's keratinized epidermal layer of their skin, disrupting the exchange of many vital molecules such as oxygen, carbon dioxide, and ions (Pessier, Nichols, Longcore, & Fuller, 1999).

For this research project, the focus will be on the skin microbiome of the Northern two-lined salamander. The resident microbiome of an individual is intricately linked to its survival and overall health due to its role in metabolism, the immune system, and in defense (McFall-Ngai et al., 2013). It has been demonstrated that the microbiome plays a vital role in pathogen-host interactions so it is vital to better understand the role that the microbiome plays when it comes to preventing pathogens, such as Bd (Bletz et al., 2018).

This project focused on characterizing the microbiome of the Northern two-lined salamander by collecting swabs from individuals caught along the Blue Ridge Parkway. All bacterial samples were isolated on R2A media and DNA was extracted using freeze-thaw technique. Once the DNA was extracted, a PCR was run, and samples were sent off for sequencing. The hope is that this project is to act as springboard for the future when bacterial isolates can be used in a challenge assay against Bd in hopes of finding bacterial strains that inhibit the fungal pathogen.

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