



## Characterizing Fungal Community on Blue-gray Gnatcatchers (*Polioptila caerulea*)

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The fungal kingdom is a highly diverse group of eukaryotic organisms, containing a multifarious set of life cycles, morphologies, and ecologies. Many species of fungi produce propagules, or structures that facilitate an organism's transition between stages of its life cycle. While fungal propagules are mainly transferred by wind, animals have been shown to serve as dispersal vectors. Birds acting as vectors are of particular interest, given the varied behavior among species and the ability to travel over long distances. Understanding bird-propagule dispersal is essential for modeling the spread of fungal pathogens and understanding fungi distribution, plant-pollinator interactions, and fungi phenological trends. However, tracking and identifying microscopic propagules is difficult. Light microscopy is a common method for identifying propagules, but can be laborious and inaccurate, especially when dealing with small quantities. Growing fungi cultures to make identification easier only yields culturable taxa. It has not been until recently researchers are able to survey the microbiome with incredible accuracy and resolution with the use of Next Generation Sequencing (NGS).

Using NGS, we conducted a marker gene survey to characterize the fungal community on bird feathers from Rio Mesa, Utah. Three different primer pairs were used to capture the widest range of fungal taxa. The relative abundances of assigned taxonomy generated from our ITS sequence primers is pictured below, using a Krona charts template (<https://github.com/marbl/Krona>).

