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Connecting population genomics and the microbiome in the endangered rock gnome lichen (*Cetradonia linearis*, Cladoniaceae)

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The population genetic structure of species is shaped by their intrinsic biological characteristics, including reproductive biology, dispersal modes, and other life history traits, ecological adaptation, and landscape-level processes on geological and anthropogenic time scales. Similarly, bacterial microbiomes may be influenced by the environment, geographic location, and co-evolutionary processes. In this presentation I will discuss the population genomics and microbiome of the rock gnome lichen (*Cetradonia linearis*), a rock-dwelling species endemic to the southern Appalachian Mountains. *Cetradonia linearis* is one of two fungal species protected by the Endangered Species Act in the United States of America, and is one of the earliest diverging lineages in the family Cladoniaceae. Based on analyses of genome-wide single nucleotide polymorphisms, populations are genetically diverse and unique, and rates of gene flow among populations are low. The microbiome similarly shows some correlation with location. There was no evidence for ecological adaptation of *C. linearis* based on the environment variables selected. Conversely, there is a significant correlation between the microbiome community and two environmental variables, habitat and the mean temperature of the warmest quarter. Finally, I place my findings in the context of other recent studies of lichen population genomics and microbiomes, as researchers worldwide continue to unravel the complex interactions among lichenized fungi, their holobiomes, and the environment.

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