

JASMINE LAFFERTY, AIDA JIMENEZ ESQUILIN, & DESIREE EVANS, Dept. of Natural Science and Mathematics, University of Charleston, Charleston, WV, 25304. Microbiome associated with the Haustorium of *Epifagus virginiana*.

*Epifagus virginiana* is a holoparasitic plant whose only host is the American Beech tree, *Fagus grandifolia*. Currently, little is known about the specific mechanism used by *Epifagus* to colonize the tree. It is thought that lignin-like or lignin degradation by-products are needed to signal the colonization process for other members of Orobanchaceae. Knowing that microbial communities that inhabit eukaryotic hosts can influence their function and development, we aimed to describe the microbial community structure of *Epifagus*, in particular the communities inhabiting the haustorium, (the organ used to parasitize). Using community-level physiological profiling, selective culture media, and metabarcoding we found that microbial communities in *Epifagus* haustorium were active and diverse and structurally similar to those from adjacent bulk soil in Fall (MRPP A= -0.004, p=0.509), but different in Summer (MRPP A= 0.169, p=0.003). Metabarcoding shows increase in the Rhizobiales, Betaproteobacteriales and Flavobacteriales in the haustorium associated soil compare to the beech tree bulk soil. We found that a larger number of endophytic isolates showed lignolytic activity compared to the haustorium associated microorganisms (HAMs). Finally, we were able to isolate bacterial isolates that use cellulose as their only carbon source. Altogether these findings lead us to further hypothesize that microbes associated with the haustorium could be involved in the production of the lignin-like haustorium inducing factors that are thought to facilitate the parasitism of other parasitic plants. These are, to our knowledge, the first published descriptions of the microorganisms inhabiting this holoparasite. Funding from the Appalachian Colleges Association Ledford Scholars Program.