



# Environmental Science Graduate Program Seminar Series

## Investigating the American Beech Microbiome to Identify the Causal Agent of Beech Leaf Disease

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**Smith Laboratory, Room 3150**



### Abstract

Beech leaf disease (BLD) is a recently discovered disease that is causing severe damage to American beech (*Fagus grandifolia*) in northeastern North America. The recently described nematode *Litylenchus crenatae* ssp. *mccannii* was detected in BLD affected foliage and may be associated with the disease. However, speculation on the direct role of the nematode in infection still remains. In this study we profiled the microbial communities associated with asymptomatic, symptomatic, and naïve (control) American beech foliage by using a high throughput sequence-based metabarcoding analysis of all plant pathogen types. We then used both a differential abundance analysis and indicator species analysis as well as several diversity metrics to try and discover microbes associated only with symptomatic foliage. To do so we amplified the organism-specific phylogenetic informative regions of the 16S, 18S, and internal transcribed spacer (ITS1) regions to explore bacterial and phytoplasma, nematode, and fungal pathogens, respectively, and extracted RNA to explore viral pathogens using high-throughput sequencing. Our results detected the amplicon sequence variant (ASV) associated with the nematode *L. crenatae* ssp. *mccannii*, but in all symptom types. However, four ASVs associated with the bacterial genera *Wolbachia*, *Erwinia*, *Paenibacillus*, and *Pseudomonas* and one ASV associated with the fungal genus *Paraphaeosphaeria* were detected only in symptomatic samples. In addition, we identified significant differences based on symptom type in both the alpha and beta diversity indices for the bacterial and fungal communities. These results suggest that *L. crenatae* ssp. *mccannii* may not be fully responsible for BLD, but rather that other microbe(s), may be contributing to the syndrome, including the putative nematode endosymbiont *Wolbachia* sp.