

DISCOVERING KEY RELATIONSHIPS BETWEEN FOREST DISEASE / HEALTH AND MICROBIAL COMMUNITIES

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The forest pathology paradigm is shifting to include complex ecological interactions that contribute to disease development, such as 1) microbial communities associated with the soil or host plant that suppress or enhance disease; 2) invasive pathogens that are associated with new hosts in new environments; 3) host and pathogen populations that display different adaptation and ecological behaviors; 4) induced host resistance to disease that is derived from differential gene expression; and 5) other interacting environmental factors that influence biological processes related to plant disease.

Currently, the impacts of climate change are of paramount importance, because the behavior of forest pathosystems is changing and forest diseases are occurring in an unprecedented manner. For example, native forest pathogens could behave like invasive pathogens because of climatic influences on the abiotic/biotic environment and hosts. Thus, novel and robust approaches are needed to understand and manage forest diseases caused by endemic and invasive pathogens under changing climates (Mendes et al. 2011). Forest diseases and associated microbial processes are the result of dynamic, long-term, and complex interactions among the pathogen, host, and the biotic and abiotic environment.

Recent findings suggest that single microbes are not always the sole agent responsible for forest ecological processes, such as disease, symbiosis, decomposition, and others. Instead, many forest ecological processes are likely the result of complex interactions among microbial communities. For example, biological control activities by *Armillaria altimontana* and associated microbes may act in concert to protect western white pine (*Pinus monticola*) from Armillaria root disease (Warwell et al. 2019). Furthermore, ecological communities can be strong indicators of overall forest health. Recently developed technologies, such as metagenomics (or metabarcoding), allow analyses of complex microbial communities associated with soil, organic debris, rhizosphere, root/stem/foliar endophytes, and phyllosphere in association with forest health and ecological processes (Terhonen et al. 2019).

Innovative approaches are essential for assessing the interactions and functions of the microbial communities in forest disease processes, while integrating influences of other environmental factors. Understanding the myriad of interactions among host, pathogen, microbial community, and environment requires unprecedented integration of novel methodologies (Denman et al. 2018). Results from such integrated information will help develop novel approaches to manage forest disease and improve forest health by promoting conditions that suppress disease or enhance beneficial processes.

Literature Cited

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The image shows a woman with glasses and a purple vest standing in front of a large projection screen. The screen displays a slide titled "Meta-barcoding & Meta-genomics" which compares the two methods. The woman is gesturing with her right hand while speaking. She is wearing a name tag that says "Jane CSA".

Meta-barcoding & Meta-genomics		Applications
Community	+	-
Meta-barcoding	Fast and cost-effective identification (bacteria and eukaryotes)	- Does not capture other gene content - Amplification bias - Identification is as good as database
Metagenomics	- Captures more diversity (bacteria, archaea, viruses and eukaryotes) - Enable assembly of genomes	- Expensive - Analyses more time intensive - Many reads from host

Applications:

- Profiling what is present
- Microbial ecology
- rDNA-based phylogeny
- Detection of pathogens
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- Microbial ecology
- Phylogeny
- Detection of pathogens
- Functional genomic analyses