PMI SFA Publication Highlight

U.S. DEPARTMENT OF ENERGY | Office of Science

High-impact publication: Harnessing the hemlock microbiome: a potential defender against the hemlock woolly adelgid

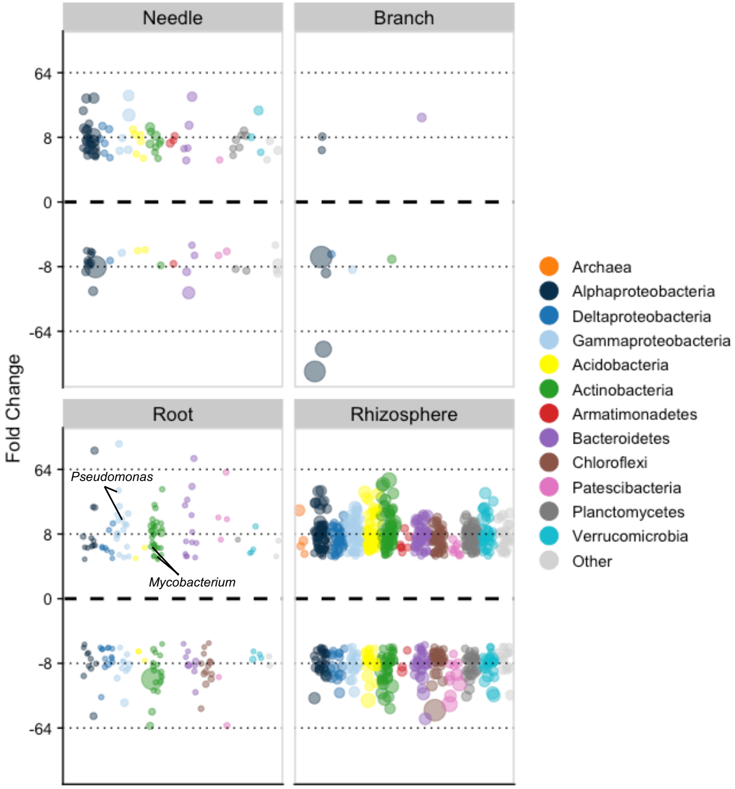
Objective	Describe the hemlock microbiome across plant tissues and host species and to identify microbial taxa associated with different Hemlock Woolly Adelgid (HWA) population levels that might subsequently be considered in HWA control.
New science	Both archaeal/bacterial and fungal needle communities, as well as the archaeal/bacterial branch and root communities, varied in composition in both hemlock species relative to HWA population levels. High HWA populations were associated with enrichment of 100 likely fungal pathogen sequence variants across the four plant-associated habitats (e.g., needle, branch, root, rhizosphere) compared to trees with lower HWA populations. Host species and plant-associated habitat (e.g., needle, branch, root, rhizosphere) explained a relatively large proportion of the variance in the microbiome.
Impact	This work contributes to a growing body of literature linking plant pathogens and pests with the changes in the associated plant microbiome and host health. Furthermore, this work demonstrates the need to further investigate plant microbiome effects across multiple plant tissues to understand their influences on host health.

Microbiome variation across two hemlock species with hemlock woolly adelgid infestation

Nicholas C. Dove1, Timothy J. Rogers, Christy Leppanen, Daniel Simberloff, James A. Fordyce, Veronica A. Brown, Anthony V. LeBude, Thomas G. Ranney, and Melissa A. Cregger

Frontiers in Microbiology.

DOI: 10.3389/fmicb.2020.01528



Differentially abundant ($p < 0.05$) archaeal/bacterial sequence variants colored and spread by taxonomic group in low compared to high hemlock woolly adelgid population levels across plant-associated habitats and host species. The x-axis is dimensionless and is used to spread apart microbial taxa. Sizes of points represent the average relative abundance of the sequence variant in the low hemlock woolly adelgid population levels.

PMI

OAK RIDGE
National Laboratory