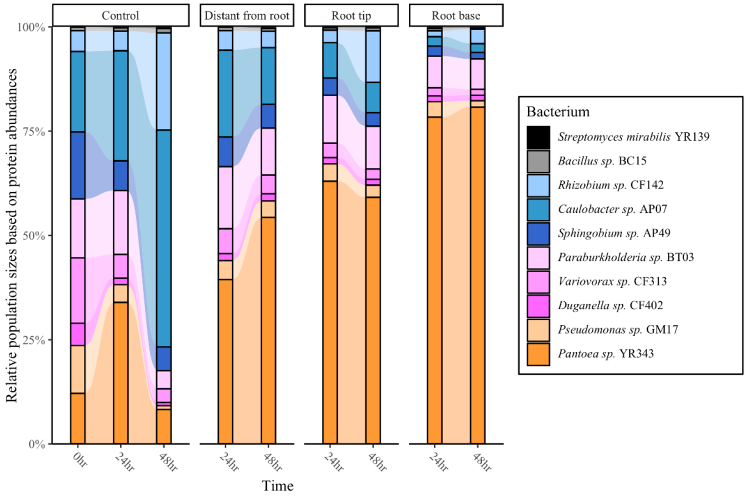
Foundational Genomics Research, Plant-Microbe Interfaces SFA

Novel Result: A novel peptide extraction method to spatially quantify plant-root associated microbiome composition and function using metaproteomics

Objective	• Develop a novel method for metaproteomic analysis of plant root exudates in root regions of *P. trichocarpa* to spatially and temporally determine the microbial communities and functions associated with these regions.
New science	• Spatial regions of *P. trichocarpa* roots were collected at different time points after being incubated with a 10-member microbial community on an agar plate. • These regions of interest were processed using a novel peptide extraction method for metaproteome sequencing. • Organism relative abundances and proteome expression profiles were obtained by coupling ultra-high performance liquid chromatography with high-resolution tandem mass spectrometry measurements.
Impact	• This novel method is an important advancement for metaproteomic measurements, as the increased depth of the proteome measurement can substantially improve the interrogation of complex microbial communities both spatially and temporally.



Estimates of microbiome composition without plant roots (control) at 0-h, 24-h, 48-h and with plant roots for three discrete locations surrounding the plant root system (root tip and base and a region distant from the root) at 24-h and 48-h.

Development of an experimental approach to achieve spatially resolved plant root-associated metaproteomics using an agar-plate system. Appidi MR et al., 2022. MPMI; https://doi.org/10.109/MPMI-01-22-0011-TA