

Visualizing Spatial Metabolic Interactions Within a Soil Microbiome

Christopher R. Anderton¹ (christopher.anderton@pnnl.gov), Natalie C. Sadler², Sheryl L. Bell¹, Dušan Veličković¹, Rosalie K. Chu¹, Thomas W. Wietsma¹, Pubudu P. R. Handakumbura¹, **Kirsten S. Hofmockel¹, Janet K. Jansson²**

¹Environmental Molecular Sciences Division; ²Biological Sciences Division, Earth and Biological Sciences Directorate, Pacific Northwest National Laboratory, Richland, WA

<https://www.pnnl.gov/biology/programs/>

Project Goals: PNNL's Soil Microbiome SFA aims to achieve a systems-level understanding of the soil microbiome's phenotypic response to changing moisture through spatially explicit examination of the molecular and ecological interactions occurring within and between members of microbial consortia. Integrated experiments will be designed to confront both the scaling challenges and inter-kingdom interactions that regulate networks of biochemical reactions. Individual- and population-based models for predicting interspecies and inter-kingdom interactions will be parameterized using experimental data, and predictions will be tested in soil to reveal spatially explicit microbial interactions. Discoveries from controlled experiments will be tested and validated in the field, using moisture gradient experiments at a new local field site. Data will be captured and shared through the establishment of a Soil Microbiome Knowledgebase (SMK). Knowledge gained will provide fundamental understanding of how soil microbes interact to decompose organic carbon and enable prediction of how biochemical reaction networks shift in response to changing moisture regimes.

Abstract:

Understanding the basic biology that underpins soil microbiome interactions is required in order to predict the metapenome response to environmental shifts, such as changing moisture content. A significant knowledge gap is how such changes will affect microbial community structure and its metabolic landscape. We aim to visualize the metabolome of interacting organisms within the soil habitat by attaining high resolution multidimensional maps of the compositional and functional state of soil microbial communities. This entails mapping the metabolic exchanges that occur within soil microbiomes, wherein historically it has been exceedingly difficult to measure the biochemical currency among interacting community members within a soil system.¹ For example, traditional metabolomic approaches are often limited in their ability to distinguish between molecules that remain localized within microbes and exuded molecules that are in proximity, and thus often disregard the multifaceted chemical exchange within and between interacting

species. However, visualizing metabolic interactions between interacting organisms within environmental microbiomes with unmatched sensitivity and specificity can now be accomplished using mass spectrometry imaging (MSI) methodologies we recently developed.^{2,3} We are able to attain high confidence in both molecular identification and localization, offering unprecedented insights into the metabolic interactions of an inter-kingdom interaction (e.g., changes in disaccharide synthesis).³ We will utilize these methods in a multimodal fashion with optical microscopy approaches, capable of visualizing desired taxa, in order to understand how change in soil moisture content will modify the soil microbiome community organization and its spatial metabolome.

References

1. D. Veličković, C. R. Anderton, "Mass spectrometry imaging: Towards mapping the elemental and molecular composition of the rhizosphere," *Rhizosphere* **2017**, 3, 254
2. C.R. Anderton, R.K. Chu, N. Tolic, A.V. Creissen, L Pasa-Tolic, "Utilizing a Robotic Sprayer for High Lateral and Mass Resolution MALDI FT-ICR MSI of Microbial Cultures," *J. Am. Soc. Mass Spectrom.* **2016**, 27, 556
3. D. Veličković, R. K. Chu, A. A. Carrell, M. Thomas, L. Paša-Tolić, D. J. Weston, C. R. Anderton, "Multimodal MSI in conjunction with broad coverage spatially resolved MS² increases confidence in both molecular identification and localization," *Anal. Chem.* **2018**, 90, 702

Funding statement: *This research was supported by the U.S. Department of Energy (DOE), Office of Biological and Environmental Research (OBER), as part of BER's Genomic Science Program (GSP), and is a contribution of the Pacific Northwest National Laboratory (PNNL) Soil Microbiome Scientific Focus Area "Phenotypic Response of the Soil Microbiome to Environmental Perturbations." A portion of this work was performed in the William R. Wiley Environmental Molecular Sciences Laboratory (EMSL), a national scientific user facility sponsored by OBER and located at PNNL. PNNL is a multi-program national laboratory operated by Battelle for the DOE under Contract DE-AC05-76RLO 1830.*