

Evolutionary history constrains microbial traits across environmental variation

Ember M. Morrissey^{1*}(ember.morrissey@mail.wvu.edu), Rebecca L. Mau^{2,3}, Michaela Hayer², Xiao-Jun Allen Liu^{2,4,5}, Egbert Schwartz^{2,4}, Paul Dijkstra^{2,4}, Benjamin J. Koch^{2,4}, Kara Allen⁶, Steven J. Blazewicz⁷, Kirsten Hofmockel⁸, Jennifer Pett-Ridge⁷, **Bruce A. Hungate**^{2,4}

¹Division of Plant and Soil Sciences, West Virginia University, Morgantown, WV, 26506 ²Center for Ecosystem Science and Society, Northern Arizona University, Flagstaff, AZ, 86011, USA ³Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, AZ 86004, USA ⁴Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, 86011, USA ⁵Department of Microbiology, University of Massachusetts, Amherst, MA, 01003, USA ⁶Department of Biology, West Virginia University, Morgantown, WV, 26506, USA ⁷Physical and Life Sciences Directorate, Lawrence Livermore National Lab, Livermore, CA 94551 ⁸Environmental Molecular Science Laboratory, Pacific Northwest National Laboratory, Richland, WA, 99354

Project Goals: Connecting the composition of microbial communities with biogeochemical process rates has the potential to improve our understanding of, and ability to model, ecosystem function. This project aimed to determine if the growth of prokaryotic taxa is consistent across ecosystems. This work dovetails with our larger goal to characterize *in situ* rates of biogeochemically significant microbial activity at the community scale and for specific taxa. This information will be leveraged to establish whether there is a “phylogenetic imprint” on soil carbon and nitrogen cycling processes that can facilitate better incorporation of microbial data into process-scale modeling efforts.

Organisms influence ecosystems, from element cycling to disturbance regimes, to trophic interactions, to energy partitioning. Microorganisms are part of this influence, but the field of microbiology has been historically limited to inferring functional potential from traditional pure culture investigations or genome-based, qualitative analyses. Understanding the ecology of microorganisms in nature requires studying traits of these organisms quantitatively in their natural habitats, a challenging task, but one which new approaches now make possible. Here, we show that growth rate and carbon assimilation rate of soil microorganisms are more influenced by taxonomy than by climate, even across a broad climatic gradient spanning major temperate life zones, from mixed conifer forest to high desert grassland. Taxonomy accounted for ~50% to ~90% of the explained variation in growth rate and carbon assimilation rate, and was more predictive for organisms responding to resource addition. With added carbon and nitrogen substrates, taxonomy explained ~8 times more variance in growth rate than did the ecosystem type. Taxon-specific growth and carbon assimilation rates were highly intercorrelated across the four ecosystems, constrained by the taxonomic identity of the organisms, such that plasticity driven by climate was limited across ecosystems varying as much as 4.5°C in mean annual temperature and 560 mm in mean annual precipitation. Taken together our results suggest that, similar to multicellular life, the traits of prokaryotes in their natural habitats are constrained by evolutionary history to a greater degree than environmental variation.

This research was supported by the Office of Biological and Environmental Research in the DOE Office of Science