

## **Genomic traits predict microbial growth in culture but fail in soils, except during resource pulses**

Junhui Li<sup>1</sup>, Benjamin J. Koch<sup>1,2\*</sup> (Benjamin.Koch@nau.edu), Rebecca L. Mau<sup>1</sup>, Paul Dijkstra<sup>1,2</sup>, Egbert Schwartz<sup>1,2</sup>, Xiao-Jun Allen Liu<sup>1,2</sup>, Ember M. Morrissey<sup>3</sup>, Steven J. Blazewicz<sup>4</sup>, Jennifer Pett-Ridge<sup>4</sup>, Bram W. Stone<sup>1</sup>, Michaela Hayer<sup>1</sup>, **Bruce A. Hungate**<sup>1,2</sup>

<sup>1</sup>Center for Ecosystem Science and Society, Northern Arizona University, Flagstaff, AZ, 86011, USA; <sup>2</sup>Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ, 86011, USA; <sup>3</sup>Department of Biology, West Virginia University, Morgantown, WV, 26506, USA; <sup>4</sup>Physical and Life Sciences Directorate, Lawrence Livermore National Laboratory, Livermore, CA, 94550, USA

### **Project Goals: Short statement of goals. (Limit to 1000 characters)**

The objectives of the proposed work are to 1) develop a quantitative SIP targeted –omics-based framework to infer taxon-specific rates of growth, mortality, and associated carbon (C) fluxes in soil microbial communities, a framework that will scale from individual microbial taxa to the integrated soil system; 2) develop a new means to quantify taxon-specific C-use and growth efficiency in order to quantify taxon-specific contributions to soil C loss; and 3) apply newly developed quantitative tools to test key hypotheses about responses of the soil microbial community to experimental warming and to latitudinal variation in temperature. This work will push the frontier of –omics enabled techniques by demonstrating their applicability at the ecosystem scale, and by relating taxon-specific isotope assimilation to dissimilatory processes in the C cycle, thereby enabling the identification of organisms especially responsible for soil C loss.

The genomic revolution in microbial ecology has encouraged optimism that genomic traits of microorganisms will coalesce into coherent ecological strategies which enable predictions of the ecosystem processes that soil microorganisms perform in nature. Relationships between microbial genes and performance are evaluated in the laboratory in pure cultures, with little validation in nature. Here, we show that genomic traits related to maximum growth potential failed to predict the growth rates of bacteria in unamended soil, but successfully predicted growth responses to resource pulses: growth increased with 16S rRNA gene copy number and declined with genome size after substrate addition to soils, responses that were repeated in four different ecosystems. Genome size best predicted growth rate in response to addition of glucose alone; adding ammonium with glucose weakened the relationship, and the relationship was absent in nutrient-replete pure cultures, consistent with the idea that reduced genome size is a mechanism of nutrient conservation. Our findings demonstrate that genomic traits of soil bacteria can map to their ecological performance in nature when resources are abundant, but not when scarce, when genomic traits related to stress tolerance may prove more predictive. These results remind that the phenotype depends on environmental context, underscoring the importance of verifying proposed schemes of trait-based strategies through direct

measurement of performance in nature, an important and currently missing foundation for translating microbial processes from genes to ecosystems.

Microbiology has advanced by studying microorganisms in culture, and improved culturing strategies will undoubtedly support new insights about quantitative variation in important traits of microorganisms. Ecology has advanced by studying organisms in nature, accepting environmental heterogeneity and community interactions as essential features of the world organisms inhabit. Microbial ecology should bridge these approaches, but the frequency of speculation in the field based on principles derived from pure culture laboratory studies is belied by the paucity of direct tests of those principles in nature, where community interactions are intact, resource availability is native, and environmental stressors apply. Results presented here show how microbial ecology can advance beyond the pure culture paradigm by measuring quantitative trait variation of microorganisms in the habitats where they naturally occur. Techniques like quantitative stable isotope probing can evaluate where principles derived from the laboratory apply to microorganisms in nature, and where they fail. It is not surprising that growth responses to resource pulses corresponded with traits derived from studies of resource-rich laboratory cultures, and that the translation of genomic traits related to high resource abundance failed in unamended soils. At the same time, the high variation in growth rates observed without resource amendment points to important phenotypic variation in growth, even under resource-limited conditions, and the need to explore the genomic traits and environmental conditions that drive that variation.

Assigning ecological strategies based on taxonomy is a common approach for interpreting microbiome data, but this effort to date is largely divorced from measurements testing whether the organisms actually utilize their assigned strategies in nature. Growth is a useful metric for evaluating ecological strategies, because it integrates ecological and evolutionary processes, from metabolism, to resource uptake and use and thus the imprint of biology on element cycles, to fitness, the ultimate result of variation in genomic traits. Assessing growth in natural microbial communities, combined with molecular tools, provides access to a richer suite of ecological mechanisms influencing organismal performance than can be assessed in laboratory cultures. Findings presented here show that it is now possible to pair genomic traits of microorganisms with their growth rates in nature. Such efforts hold promise for a refined and evidence-based foundation for proposed ecological strategies, whether best defined by a single axis of copiotrophic to oligotrophic, by a triangle of competitive, ruderal, and tolerance, or by multi-dimensional spectra of traits and tradeoffs.

## **Notes**

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