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

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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
1. This work is currently in review in the journal, ISME.

Funding Statement
This work was supported by the US Department of Energy, Program in Genomic Sciences,
Award Number: DE-SC0016207. We thank Jingrun Sun for assistance in the laboratory and Alicia
Purcell for intellectual contributions.