Geophysical Research Abstracts
Vol. 20, EGU2018-11627, 2018
EGU General Assembly 2018
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Taxon-Specific Carbon Use Efficiency in Natural Microbial Communities

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Biological diversity – the variety of life – has profound influence on ecosystems, yet our ability to describe that influence for microbial biodiversity is weak. For example, a key parameter of biogeochemical models, microbial carbon use efficiency, is only considered in aggregate, and we have virtually no understanding of how carbon use efficiency might vary among taxa in natural communities. Given the tremendous diversity of microorganisms in evolutionary history and physiological traits, variation in carbon use efficiency among microbial taxa seems very likely. Carbon use efficiency is known to differ among bacterial species in culture. While the evidence is scarce, microbial community composition has frequently been posited as a potential driver of carbon use efficiency. Carbon use efficiency captures processes that influence growth, survival, and thus fitness, so it should be subject to selective pressure. Ecological strategies may underlie differences in carbon use efficiency. Slow growing organisms, typically present in low nutrient environments, are expected to exhibit high carbon use efficiency, whereas fast growing organisms that are top competitors in high nutrient environments will have lower carbon use efficiency, potentially due to physiological tradeoffs between growth efficiency and maximum growth rate.
Still, even if it is important, how could we possibly measure it for individual taxa in complex assemblages? The idea is challenging. On the one hand, isotopic tags on the elements assimilated and recovered in nucleic acids provide a way to discern which organisms use what resources at what rates for biomass growth. On the other hand, carbon use efficiency is about the balance of growth and respiration, or dissimilation, where the product, carbon dioxide, cannot be traced back to the taxon that produced it. Metabolic flux analysis can, in principal, be used to develop taxon-specific estimates of carbon use efficiency: using position-specific 13C-labeled substrates such as glucose and pyruvate, monitoring the isotope incorporation into nucleotides and DNA and RNA combines the measurement of metabolic efficiency while retaining information about the organisms that produced them. The atom mapping logic for this approach can be understood from the biochemistry of glucose anabolism and catabolism, in glycolysis, the Krebs cycle, the pentose phosphate pathway, and gluconeogenesis, pathways most important for energy production and biosynthesis, including the biosynthesis of nucleic acids. In this talk, I will present the model for determining carbon use efficiency of individual bacterial taxa in complex communities, and evaluate the sensitivity with respect to two proposed methods of measuring taxon-specific isotope composition: ChipSIP/NanoSIMS, and quantitative stable isotope probing (qSIP). The critical concept in this work is that the target molecules for the recovery of these isotope tracers are nucleic acids, the very molecules that convey the identities of the organisms. This will enable calculating the CUE of individual organisms in complex communities, with all the taxonomic resolution achievable through modern sequencing.