

Selective Carbon Sources Influence the End-Products of Microbial Nitrate Respiration

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Project Goals: ENIGMA -Ecosystems and Networks Integrated with Genes and Molecular Assemblies use a systems biology approach to understand the interaction between microbial communities and the ecosystems that they inhabit. To link genetic, ecological, and environmental factors to the structure and function of microbial communities, ENIGMA integrates and develops laboratory, field, and computational methods.

Abstract: Respiratory and catabolic pathways are differentially distributed in microbial genomes. Thus, specific carbon sources may favor different respiratory processes. We profiled the influence of 94 carbon sources on the end-products of nitrate respiration in microbial enrichment cultures from diverse terrestrial environments. We found that some carbon sources consistently favor dissimilatory nitrate reduction to ammonium (DNRA/nitrate ammonification) while other carbon sources favor nitrite accumulation or denitrification. For an enrichment culture from aquatic sediment, we sequenced the genomes of the most abundant strains, matched these genomes to 16S rDNA exact sequence variants (ESVs), and used 16S rDNA amplicon sequencing to track the differential enrichment of functionally distinct ESVs on different carbon sources. We found that changes in the abundances of strains with different genetic potentials for nitrite accumulation, DNRA or denitrification were correlated with the nitrite or ammonium concentrations in the enrichment cultures recovered on different carbon sources. Specifically, we found that either L-sorbose or D-cellobiose enriched for a *Klebsiella* nitrite accumulator, other sugars enriched for an *Escherichia* nitrate ammonifier, and citrate or formate enriched for a *Pseudomonas* denitrifier and a *Sulfurospirillum* nitrate ammonifier. Our results add important nuance to the current paradigm that higher concentrations of carbon will always favor DNRA over denitrification or nitrite accumulation, and we propose that, in some cases, carbon composition can be as important as carbon concentration in determining nitrate respiratory end-products. Furthermore, our approach can be extended to other environments and metabolisms to characterize how selective parameters influence microbial community composition, gene content and function.

References

1. Selective carbon sources influence the end-products of microbial nitrate respiration; Hans K. Carlson, Lauren M. Lui, Morgan N. Price, Alexey E. Kazakov, Alex V. Carr, Jennifer V. Kuehl, Trenton K. Owens, Torben Nielsen, Adam P. Arkin, Adam M. Deutschbauer
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