ENIGMA: The selective pressures on the microbial community in a metal-contaminated aquifer

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Project Goals: ENIGMA -Ecosystems and Networks Integrated with Genes and Molecular Assemblies mission is to support the development of laboratory and computational tools that link the molecular functions within individual microbes to the integrated activities of microbial communities as they interact with their environment. Our goal is to understand how human activity associated with energetic processes - in particular, contamination and climate change - is affecting the ecology of critical soil, groundwater, and aquifer systems.

Abstract: In many environments, toxic compounds restrict which microorganisms persist. However, in complex mixtures of inhibitory compounds, it is challenging to determine which specific compounds cause changes in abundance and prevent some microorganisms from growing. We focused on a contaminated aquifer in Oak Ridge, Tennessee, U.S.A. that has large gradients of pH and widely varying concentrations of uranium, nitrate and many other inorganic ions. In the most contaminated wells, the microbial community is enriched in the *Rhodanobacter* genus. *Rhodanobacter* abundance is positively correlated with low pH and high concentrations of uranium and 13 other ions and we sought to determine which of these ions are selective pressures that favor the growth of *Rhodanobacter* over other taxa. Of these ions, low pH and high UO_2^{2+}, Mn^{2+}, Al^{3+}, Cd^{2+}, Zn^{2+}, Co^{2+}, and Ni^{2+} are both (a) selectively inhibitory of a *Pseudomonas* isolate from an uncontaminated well versus a *Rhodanobacter* isolate from a contaminated well, and (b) reach toxic concentrations (for the *Pseudomonas* isolate) in the *Rhodanobacter*-dominated wells. We used mixtures of ions to simulate the groundwater conditions in the most contaminated wells and verified that few isolates aside from *Rhodanobacter* can tolerate these 8 ions. These results clarify which ions are likely causal factors that impact the microbial community at this field site and are not merely correlated with taxonomic shifts. Furthermore, our general high-throughput approach can be applied to other environments, isolates and conditions to systematically help identify selective pressures on microbial communities. We are currently extending our approach to identify selective nutrients and carbon sources that influence community composition at our field site. We are leveraging the results of these efforts to classify isolates and determine genetic mechanisms of adaptation to field relevant selective pressures.

References/Publications:

1. Carlson, H. K.; Price, M. N.; Callaghan, M.; Aaring, A.; Chakraborty, R.; Liu, H.; Kuehl, J. V.; Arkin, A. P.; Deutschbauer, A. M. The ISME Journal 2018, 1–13. doi:10.1038/s41396-018-0328-1