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

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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. By combining field survey data and. high-throughput laboratory cultivation data we found that 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. Our results clarify which ions are causal factors that impact the microbial community at this field site and are not merely correlated with taxonomic shifts, and we have leveraged our results to classify isolates and determine genetic mechanisms of adaptation to field relevant selective pressures.