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Effects of Nitrate, pH and Uranium on the Subsurface Microbial Communities Revealed by Functional Gene Arrays

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Abstract

To understand how contaminants affect microbial community structure, five ground-water samples with varying nitrate, pH and uranium concentrations obtained from the Field Research Center (FRC) site of the U.S. DOE ERSP (Environmental Remediation Science Program) program at Oak Ridge Reservation, Oak Ridge, Tennessee, were analyzed with a comprehensive functional gene arrays containing more than 24,000 gene probes. An uncontaminated background site was also processed in the same manner. Signal intensity was measured for genes involved in the nitrogen cycle, metal reduction, organic carbon degradation and sulfate reduction. Gene diversity and prevalence was correlated to the geochemistry of each well. Wells that were highly contaminated with nitrate had elevated numbers of genes involved in nitrate reduction and denitrification, most likely as a result from the selective pressure exerted by nitrate stress. The well with the highest concentrations of uranium and nitrate and the lowest pH also had the fewest total number of genes reported, indicating that stress from uranium and low pH are likely factors in reducing microbial community diversity. Analysis of the gene diversity from these wells is ongoing.

Presenter
Waldron, P. J.

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