

## **Exposure History Dependence of Microbial Mediated Substrate Transformation Rates in Groundwater**

Charles J. Paradis<sup>1,\*</sup> (charlesjparadis@gmail.com), Terry C. Hazen<sup>1,2</sup>, Adam P. Arkin<sup>3</sup>, and Paul D. Adams<sup>3</sup>

<sup>1</sup>University of Tennessee, Knoxville, TN, <sup>2</sup>Oak Ridge National Laboratory, Oak Ridge, TN,

<sup>3</sup>Lawrence Berkeley National Laboratory, Berkeley, CA, \*Presenting author

<http://enigma.lbl.gov/research/environmental-microbiology/>

**Project Goals: The goals of this project are to: (1) demonstrate the exposure history dependence of microbial mediated substrate transformation rates in groundwater at the field scale and (2) elucidate the microbial mechanism(s) which control the exposure history dependence of microbial mediated substrate transformation rates**

The rates at which natural microbial communities can transform a substrate in groundwater have been shown to increase after repeated exposures to the substrate; herein referred to as the “memory effect”. The objectives of this study were to determine: (1) how long the memory effect can last and (2) how the memory effect can alter the structure and function of natural microbial communities. Ethanol substrate was injected into a single groundwater test well for six consecutive weeks in order to establish a memory effect. The groundwater control well, located up-gradient of the test well, was not injected with ethanol during this time. The rate of ethanol removal in the test well was negligible the first week whereas subsequent rates were significant. The test and control wells will be monitored for six additional weeks under ambient conditions. Ethanol substrate will then be injected into both test and control wells in order to determine: (1) if the test well retained its memory effect and (2) if the rate of ethanol removal in the control well is negligible.

Here we present the hydrological, geochemical, and microbiological data and analyses in hand from the study site and the experimental well pair. This includes: (1) the direction and magnitude of groundwater velocity, (2) the effective porosity of the groundwater system, (3) diffusive mass transport in the experimental well pair, (4) the rates of ethanol removal in the test well, (5) the extent of nitrate, sulfate, and uranium removal in the test well, (6) the extent of limiting metal nutrient and/or co-factor removal in the test well, (7) microbial community structure (16S rRNA sequencing) at the study site, and (8) microbial community function (GeoChip) at the study site.

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