

***Acidovorax* species reveal potential for oxidation of H₂ coupled to reduction of O₂, NO₃⁻, and radionuclides across a subsurface redox gradient**

A.E. PLYMALE^{1*}, J-H. LEE^{1,2}, J.K. FREDRICKSON¹,
A.C. DOHNALKOVA¹, J.J. MORAN¹, C.T. RESCH¹,
J.P. MCKINLEY¹, L. SHI¹, E.E. RODEN³,
AND B.J. CONVERSE³

¹Pacific Northwest National Laboratory, Richland, WA, USA
(*correspondance: plymale@pnl.gov)

²Korea Institute of Geoscience and Mineral Resources,
Daejeon, Republic of Korea

³University of Wisconsin, Madison, WI, USA

In the aquifer at the 300 Area of the Hanford Site in south-central Washington, we observed increasing H₂ at depth, along with decreasing O₂ and NO₃⁻, within the fine grained Ringold formation, near its interface with the overlying coarse-grained Hanford formation. To characterize the microorganisms influencing this chemical gradient, we incubated sterile sand, in-well, across the redox transition.

We detected H₂-driven ⁹⁹TcO₄⁻ reduction in laboratory microcosms constructed from colonized sand from all depths, with a reduction maximum just below an observed interface between oxidized and reduced sediments within the Ringold formation (17 m bgs). From this depth, which was coincident with the highest in-situ NO₂⁻ concentration, we isolated 11 bacterial strains, including 5 *Acidovorax* species, from H₂ + NO₃⁻ enrichments.

A representative *Acidovorax* strain, JHL-9, was selected for further experiments and genome sequencing. Under denitrifying conditions, JHL-9 could couple the oxidation of H₂ to the reduction of pertechnetate (⁹⁹TcO₄⁻), consistent with the presence of two NiFe hydrogenase genes in the genome [1]. Strain JHL-9, whose genome contains Rubisco CO₂ fixation genes, also grew lithoautotrophically on bicarbonate and H₂, using either NO₃⁻ or O₂ as an electron acceptor, and was shown to harbor the genes necessary for full reduction of NO₃⁻ to N₂.

The results suggested that H₂-oxidizing bacteria such as *Acidovorax* could contribute to the maintenance of the redox gradient in the Hanford/Ringold transition zone and influence the migration of contaminants in the Hanford subsurface [2].

[1] Shi *et al* (2011) *Appl. Environ. Microbiol.* **77**, 5584-5590.

[2] Lin *et al* (2012) *Environ. Microbiol.* **14**, 414-425.