

Geobacter daltonii strain FRC-32^T (Prakash et al., IJSEM, in press)

- Isolated from the highly contaminated OR-IFRC source zone
- Gene sequences indicate that the strain is abundant and active in OR-IFRC sediments undergoing U(VI) bioremediation
- Reduces U(VI) and grows by Fe(III) respiration
- Genome sequence is quite distinct from all other *Geobacters*
- Genome contains genes for degradation of aromatic hydrocarbons

Morphological details of strain FRC-32^T as observed by scanning electron microscopy. Long (i.e. >1 μm) pili-like structures can be seen radiating from the cells. Bar, 0.2 μm . Image by Greg Wanger of the J. Craig Venter Inst.



A new *Geobacter* species was isolated from the OR-IFRC contaminant source zone that has a distinct metabolic and genetic signature

Few metal-respiring microorganisms have been isolated from the contaminated subsurface of U.S. DOE sites. An iron(III)- and uranium(VI)-reducing bacterium, strain FRC-32^T, was isolated by the Kostka laboratory at Florida State University from the highly contaminated subsurface source zone of the U.S. Department of Energy Oak Ridge Integrated Field-Scale Subsurface Research Challenge (OR-IFRC) in Oak Ridge, Tennessee, where the sediments are exposed to mixed waste contamination of radionuclides and hydrocarbons. Analyses of gene sequences retrieved from subsurface sediments indicate that this strain is abundant and active in the OR-IFRC subsurface undergoing uranium(VI) bioremediation. Based on phylogenetic analysis and metabolic differences, strain FRC-32^T is validly described as a new species of the subsurface clade of genus *Geobacter* and proposed as *Geobacter daltonii* sp. nov with strain FRC-32^T (DSM22248, JCM15807) as the type strain (Prakash et al., 2009, IJSEM, in press). Comparison to other species within the subsurface *Geobacter* clade illustrates the remarkable genetic and physiological plasticity of *Geobacter*. Though *G. daltonii* shares 98% 16S rRNA gene sequence identity to *G. uraniireducens*, whole genome comparisons and DNA-DNA hybridization studies indicate that few genes other than the ribosomal RNAs share greater than 90% DNA sequence similarity. In addition, *G. daltonii* exhibits substantial metabolic versatility and traits that are not found in other members of the subsurface *Geobacter* clade, including growth on aromatic compounds such as benzoate and toluene.