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## Recent Work

### Title

The complete genome of the uncultivated bacterium *Desulforudis audaxviator* from 2.8 km beneath earth's surface

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#### TITLE

The Complete Genome of the Uncultivated Bacterium *Desulforudis audaxviator*  
from 2.8 km Beneath Earth's Surface

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## ABSTRACT

A more complete picture of life on Earth, and even life *in* the Earth, has recently become possible through the application of environmental genomics. We have obtained the complete genome sequence of a new genus of the *Firmicutes*, the uncultivated sulfate reducing bacterium *Desulforudis audaxviator*, by filtering fracture water from a borehole at 2.8 km depth in a South African gold mine. The DNA was sequenced using a combination of Sanger sequencing and 454 pyrosequencing, and assembled into just one genome, indicating the planktonic community is extremely low in diversity. We analyzed the genome of *D. audaxviator* using the MicrobesOnline annotation pipeline and toolkit (<http://www.microbesonline.org>), which offers powerful resources for comparative genome analysis, including operon predictions and tree-based comparative genome browsing. MicrobesOnline allowed us to compare the *D. audaxviator* genome with other sequenced members of the *Firmicutes* in the same clade (primarily *Pelotomaculum thermopropionicum*, *Desulfotomaculum reducens*, *Carboxydotherrmus hydrogenoformans*, and *Moorella thermoacetica*), as well as other known sulfate reducers and thermophilic organisms. *D. audaxviator* gives a view to the set of tools necessary for what appears to be a self-contained, independent lifestyle deep in the Earth's crust. The genome is not very streamlined, and indicates a motile, endospore forming sulfate reducer with pili that can fix its own nitrogen and carbon. *D. audaxviator* is an obligate anaerobe, and lacks obvious homologs of many of the traditional O<sub>2</sub> tolerance genes, consistent with the low concentration of O<sub>2</sub> in the fracture water and its long-term isolation from the surface. *D. audaxviator* provides a complete genome representative of the Gram-positive bacteria to further our understanding of dissimilatory sulfate reducing bacteria and archaea. Additionally, study of the deep subsurface has offered access to the simplest community yet studied by environmental genomics, perhaps consisting of just a single species that is capable of performing all of the tasks necessary for life.