

Case Study Oil and Gas Ecology

Project Topic: Analysis of microbial process in oil and gas wells

Project Partner: National Energy Technology Laboratory (US DOE)

Location: Oil and gas wells in Pennsylvania (USA) and Texas (USA)

Sample type: Produced fluids

Target Molecule: DNA

Laboratory Analysis:

16S rRNA and metagenomic sequencing of microbial biomass retrieved from produced waters and oil and gas wells and infrastructure

Bioinformatic Analysis:

Basecalling, taxonomic classification, assembly and binning, genome quality assessment, annotation, metabolic pathway reconstruction

Summary:

Evaluation of microbial abundance and composition patterns highlighted elevated potential for biocorrosion and well fouling. Statistical assessment suggested a link between biocide usage and microbial distribution. Reconstruction and characterization of draft genomes provided insights into microbial processes in oil and gas environments.

More details:

https://journals.asm.org/doi/abs/10.1128/aem.02659-16 https://academic.oup.com/femsle/article/365/12/fny107/4982779?login=true



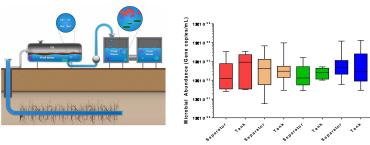


TABLE 1 Average nucleotide identity and amino acid identity between recovered produced water Halonaerobium sp. strain MDAL1 draft genome and other available Halonaerobium genomes^o

(1002) (100			
Genome	GenBank accession no.	ANI (%)	AAI (%
Halanaerobium sp. strain MDAL1 draft genome	MIJU00000000.1		
Halanaerobium sp. strain T82-1	LSBN00000000.1	98.48	93.82
Halanaerobium saccharolyticum subsp. saccharolyticum DSM 6643	NZ_CAUI00000000.1	84.62	82.04
Halanaerobium praevalens DSM 2228	CP002175.1	83.93	73.73
Halanaerobium hydrogeniformans	CP002304.1	82.65	67.59

aANI, average nucleotide identity; AAI, amino acid identity.