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Biogeochemical Responses and Microbial Community Dynamics Responding to Experimental Hydrogen Storage Conditions

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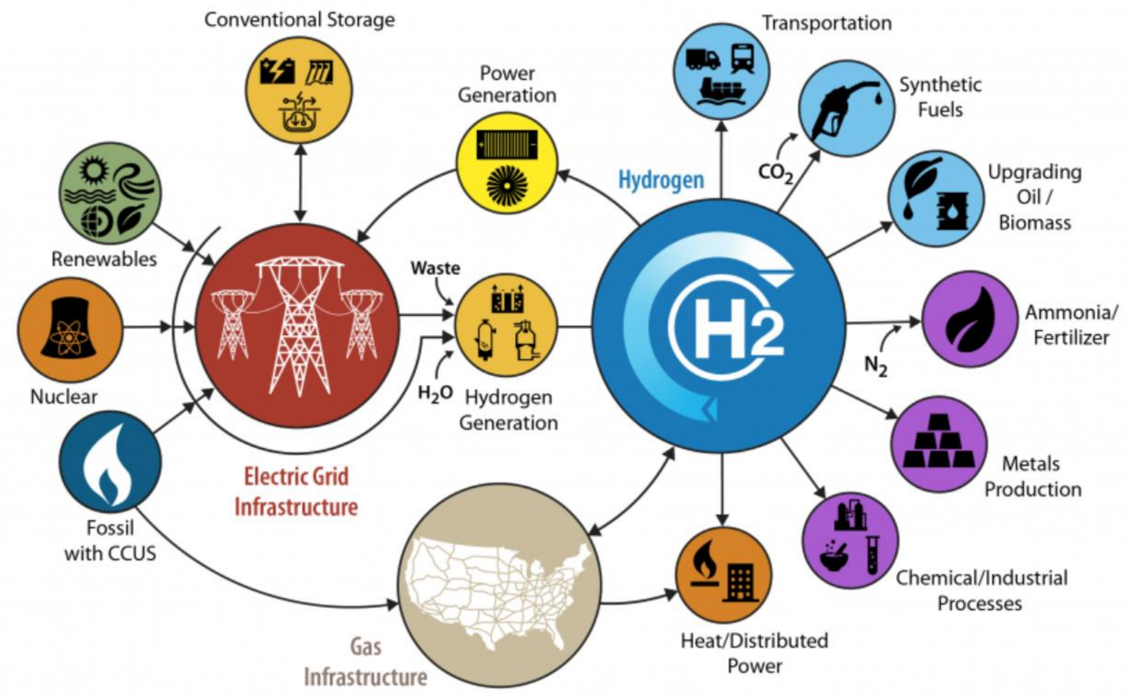
Abstract

Hydrogen has been identified as a flexible energy carrier with zero or negative carbon emission across multiple energy sectors. There is tremendous capacity for deep geologic storage of H_2 but many aspects of feasibility, reliability, safety and the potential for unintended consequences need to be examined. As part of a larger programmatic effort to address the knowledge gaps, we aim to gain a better understanding of reservoir microbial communities and their metabolic and biogeochemical responses to hydrogen storage conditions. In this study we collected and characterized reservoir brine from candidate hydrogen storage sites in the southwestern U.S. for use in a temporal reactor series under blended storage conditions (40% H_2, 40% CH_4, 20% CO_2) at reservoir temperature (60°C).

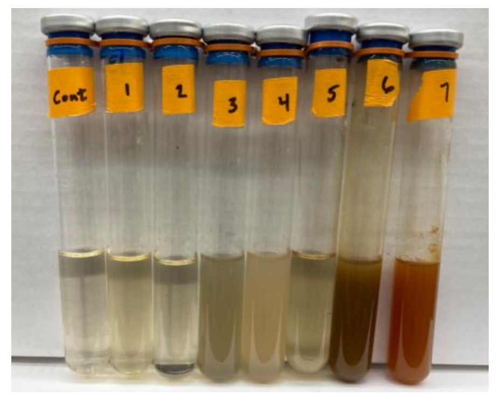
- Specific Biogeochemistry Goals:
- Quantify operational risks
- Quantify potential for resource losses
- Develop enabling tools, technologies, and recommended practices
- Develop collaborative field-scale test plans



Candidate Storage Site Compositional Study

Brine Fluid Chemistry

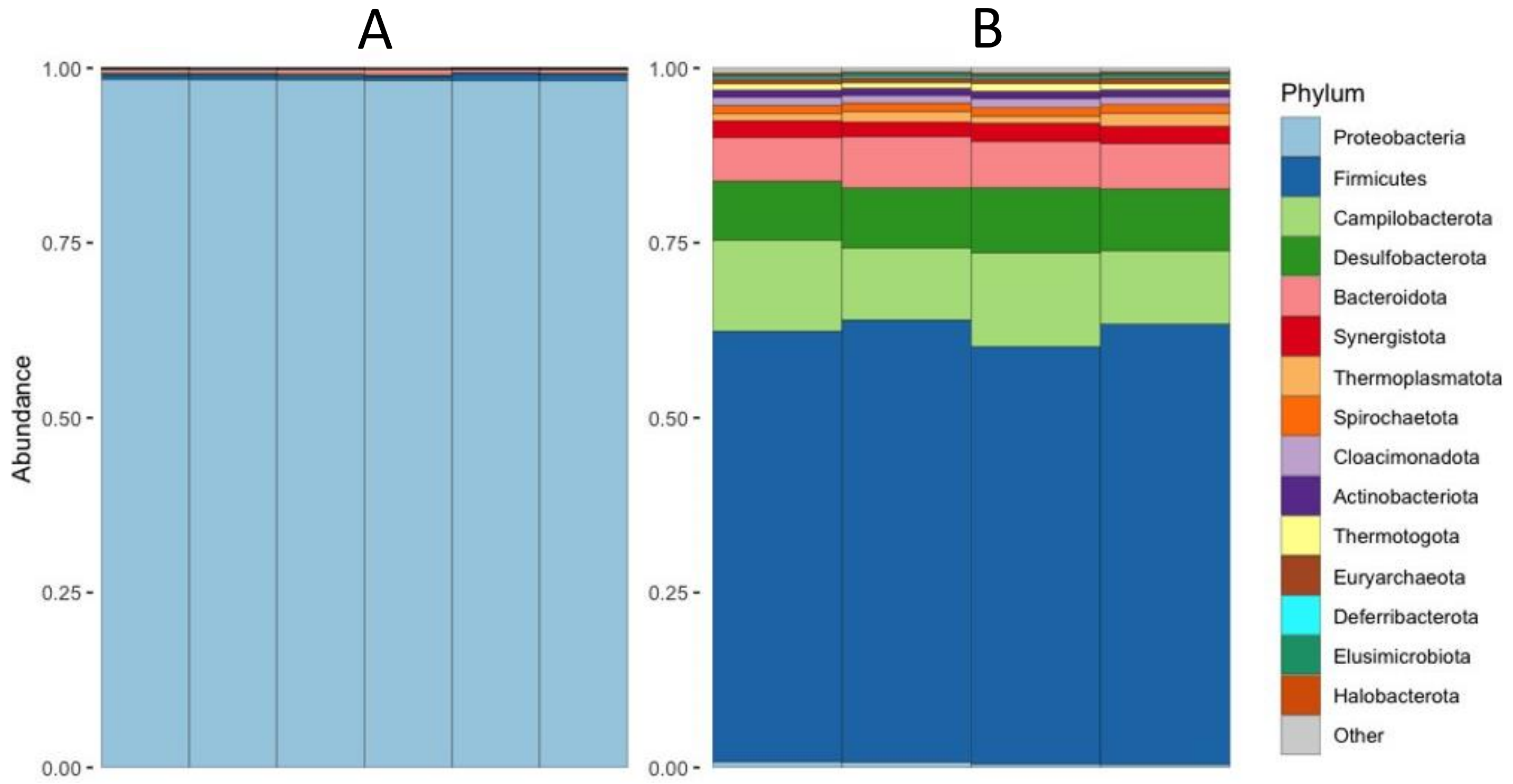
Organics (mg/L)	Formate	Acetate	Propionate	Butyrate	Succinate	Oxalate
SW1	27	1,333	326	57	41	2.1
SW1	27	1,198	257	50	41	2.1
SW2	8	3,783	843	284	158	4.0
SW2	8	3,895	853	291	163	4.3



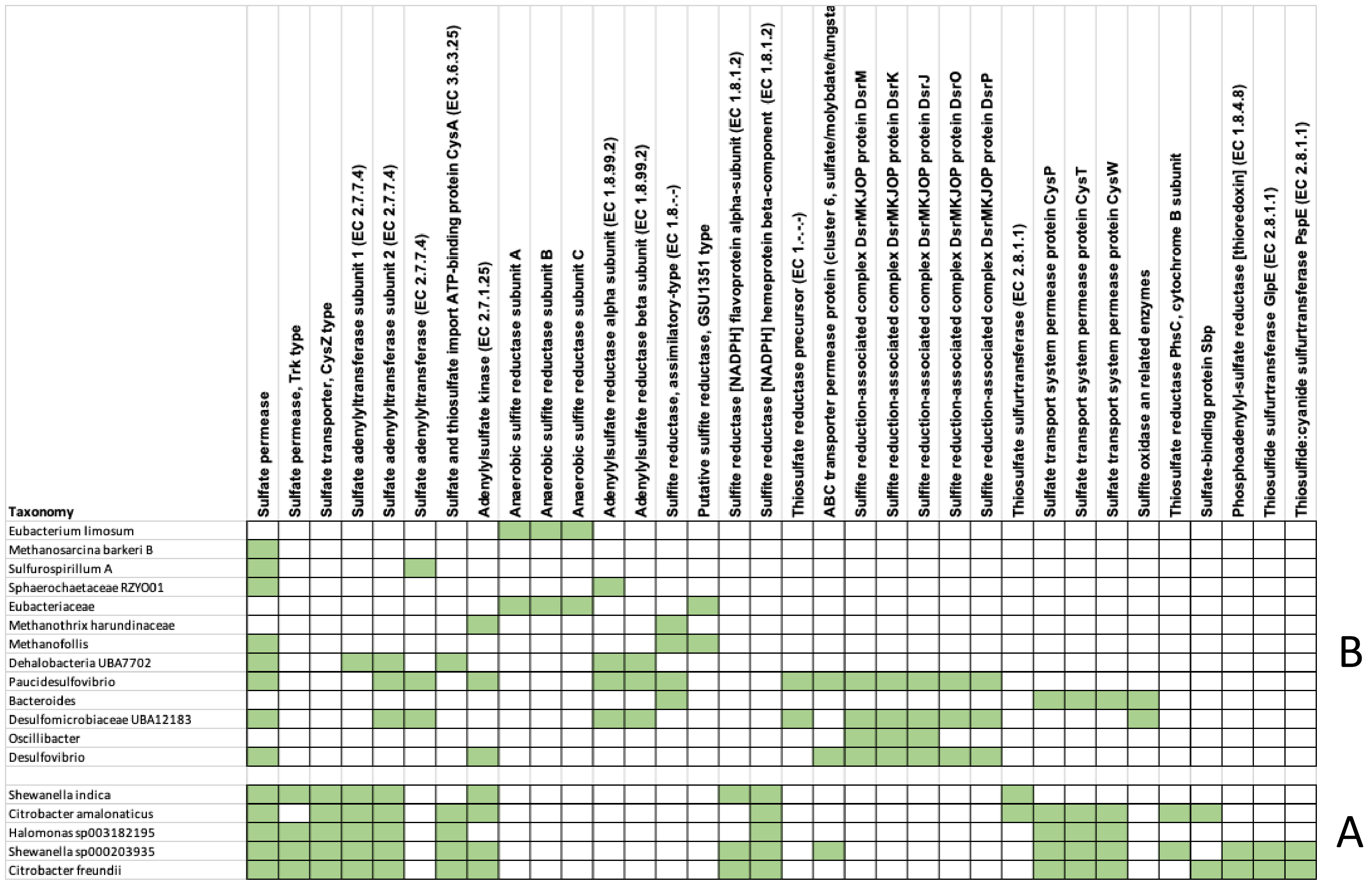
Cation/Anion (mg/L)	Ba	Ca	Cl	Fe	K	Li	Mg	Mn	Na	P	SO_4	Sr
SW1	5.2	1,033	78060	89.4	2,792	0.36	104	4.2	42,966	0.84	195	73.3
SW1	5.1	1,024	64096	83.4	2,774	0.38	100	4.2	43,592	0.85	191	77.8
SW2	1.2	250	12144	104.5	2,125	0.90	52	2.7	7,774	0.87	731	5.8
SW2	1.1	256	12258	103.7	2,139	0.91	54	2.6	7,793	0.96	754	5.7

We sampled brine fluid chemistry to gain an understanding of the baseline geochemical composition of a candidate hydrogen storage site in the Southwestern United States. Geochemistry principally provides clues about the types of metabolic reactions that can occur, or limitations to key pathways or total microbial activity. A key driver is sulfate reduction and the potential to produce hydrogen sulfide. Results demonstrate an abundance of organic carbon in this system and detection of numerous volatile organic carbon species suggests active fermentation.

Bioreactor modeling of microbial metabolism

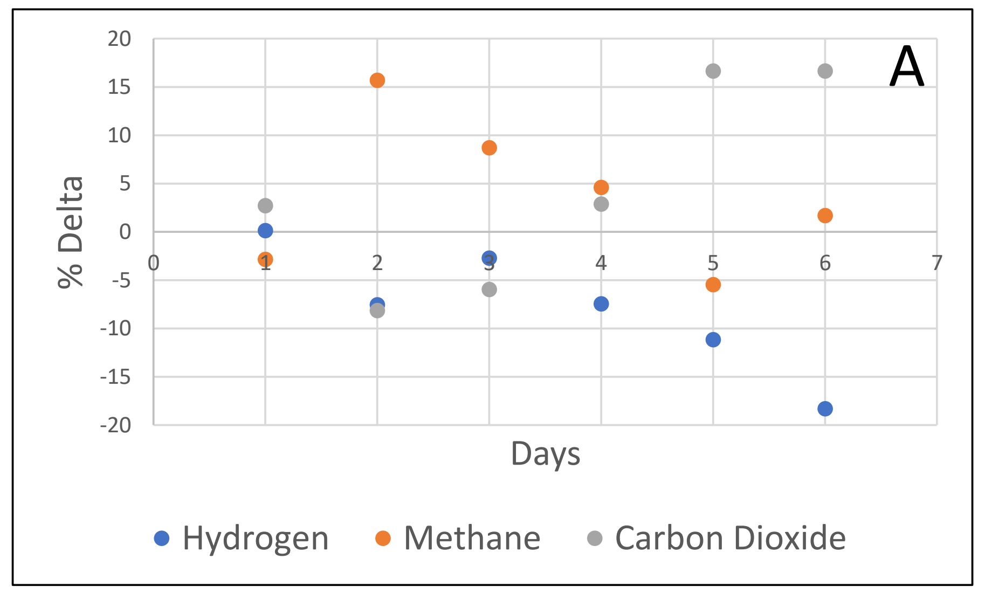


Microbial Composition

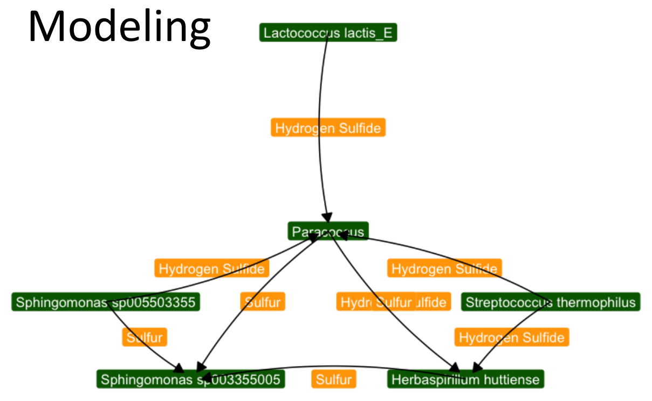


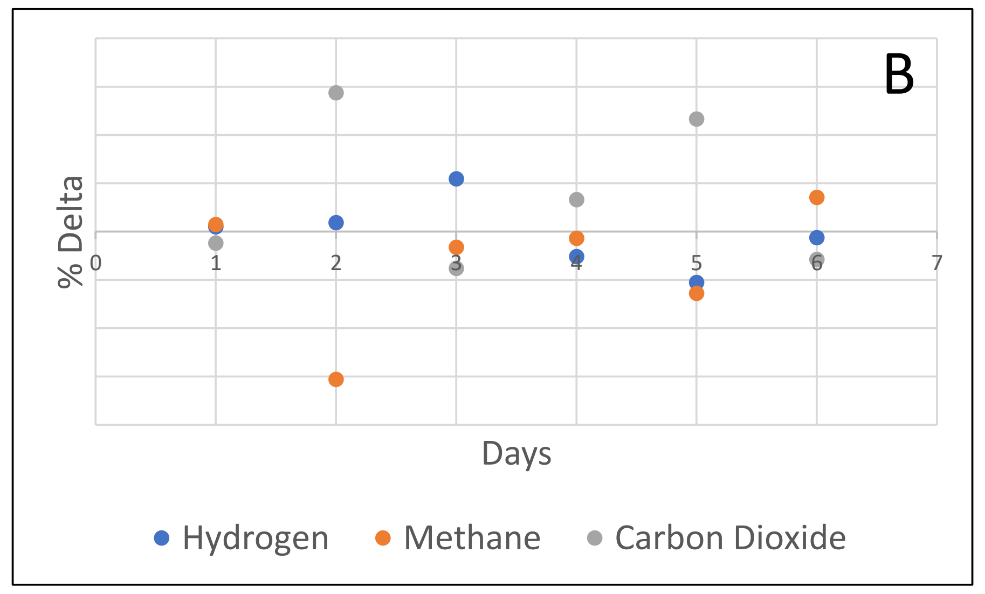
Taxonomy	Sulfate permease	Sulfate permease, Trk type	Sulfate transporter, CysZ type	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	Sulfate adenylyltransferase (EC 2.7.7.4)	Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)	Adenylylsulfate kinase (EC 2.7.1.25)	Anaerobic sulfite reductase subunit A	Anaerobic sulfite reductase subunit B	Anaerobic sulfite reductase subunit C	Adenylylsulfate reductase alpha subunit (EC 1.8.99.2)	Adenylylsulfate reductase beta subunit (EC 1.8.99.2)	Sulfite reductase, assimilatory-type (EC 1.8.-.-)	Putative sulfite reductase, GSU1351 type	Sulfite reductase [NADPH] flavoprotein alpha-subunit (EC 1.8.1.2)	Sulfite reductase [NADPH] hemeprotein beta-component (EC 1.8.1.2)	Thiosulfate reductase precursor (EC 1.-.-.-)	ABC transporter permease protein (cluster 6, sulfate/molybdate/tungsta	Sulfite reduction-associated complex DsrMKJOP protein DsrM	Sulfite reduction-associated complex DsrMKJOP protein DsrK	Sulfite reduction-associated complex DsrMKJOP protein DsrJ	Sulfite reduction-associated complex DsrMKJOP protein DsrO	Sulfite reduction-associated complex DsrMKJOP protein DsrP	Thiosulfate sulfurtransferase (EC 2.8.1.1)	Sulfate transport system permease protein CysP	Sulfate transport system permease protein CysT	Sulfate transport system permease protein CysW	Sulfite oxidase an related enzymes	Thiosulfate reductase PhsC, cytochrome B subunit	Sulfate-binding protein Sbp	Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)	Thiosulfide sulfurtransferase GlpE (EC 2.8.1.1)	Thiosulfide:cyanide sulfurtransferase PspE (EC 2.8.1.1)
Eubacterium limosum									🟩	🟩	🟩																							
Methanosarcina barkeri B	🟩																																	
Sulfurospirillum A	🟩					🟩																												
Sphaerochaetaceae RZYO01	🟩											🟩																						
Eubacteriaceae									🟩	🟩	🟩				🟩																			
Methanothrix harundinaceae								🟩						🟩																				
Methanofollis	🟩													🟩	🟩																			
Dehalobacteria UBA7702	🟩			🟩	🟩		🟩					🟩	🟩																					
Paucidesulfovibrio	🟩				🟩	🟩		🟩				🟩	🟩	🟩				🟩	🟩	🟩	🟩	🟩	🟩	🟩										
Bacteroides														🟩												🟩	🟩	🟩	🟩					
Desulfomicrobiaceae UBA12183	🟩				🟩	🟩						🟩	🟩					🟩		🟩	🟩	🟩	🟩	🟩					🟩					
Oscillibacter																				🟩	🟩	🟩												
Desulfovibrio	🟩							🟩											🟩	🟩	🟩	🟩	🟩	🟩										
Shewanella indica	🟩	🟩	🟩	🟩	🟩			🟩								🟩	🟩								🟩									
Citrobacter amalonaticus	🟩		🟩	🟩	🟩		🟩	🟩									🟩								🟩	🟩	🟩	🟩		🟩	🟩			
Halomonas sp003182195	🟩	🟩	🟩	🟩	🟩		🟩										🟩									🟩	🟩	🟩						
Shewanella sp000203935	🟩	🟩	🟩	🟩	🟩		🟩	🟩								🟩	🟩		🟩							🟩	🟩	🟩		🟩		🟩	🟩	🟩
Citrobacter freundii	🟩	🟩	🟩	🟩	🟩		🟩	🟩								🟩	🟩									🟩	🟩	🟩			🟩	🟩	🟩	🟩

Sulfur metabolism in site MAGs



Metabolite Interaction Modeling





Headspace gas composition

To try and understand the effect of stored hydrogen on the microbial community present at the site, we first used 16S metagenomics to estimate the microbial composition. This revealed large differences in the taxonomic composition of the two sites, with A harboring mostly taxa within the Proteobacteria and B mostly Firmicutes phyla, respectively. To gain a deeper understanding of the community dynamics, we used short read shotgun metagenomics to assemble microbial genomes found at both sites. These MAGs exhibit wide variation in the sulfur metabolic pathways present, but sulfite reduction and sulfate transporters are present in both communities, suggesting that while the overall production of the toxic compound hydrogen sulfide could vary between both sites, pathways associated with sulfur metabolism are present in both communities.

To model the effects of hydrogen storage, we conducted incubation kinetics experiments. We inoculated bioreactors with concentrated biomass sampled from a potential hydrogen storage site in brine simulant with lactate (20 mM) and a gas mixture headspace (40% H_2, 40% CH_4, 20% CO_2, 60°C, 1 atm) and sampled weekly. The observed gas kinetics will inform modeling of the metabolite interactions among the biological community within the site using sequencing data from biological samples. This work is still ongoing.

Link to abstract

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