

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

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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<sub>2</sub> 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<sub>2</sub>, 40% CH<sub>4</sub>, 20% CO<sub>2</sub>) at reservoir temperature (60°C). The subsurface brine collected from the reservoir was replete in organic carbon (>1.0 g/L), including products (acetate, propionate, butyrate) suggestive of active fermentation. Two sites, part of the same geologic formation, displayed characteristically unique microbial communities. One site was dominated by *Shewanella spp.* and the second was composed of a variety of taxa corresponding to sulfate reducing bacteria, acetogens, and methanogens. Brine communities were concentrated and incubated under blended H<sub>2</sub> gas for 1.5 months and analyses were performed weekly. Gas analysis showed a consistent 5 – 10% alteration in starting gas composition relative to the abiotic controls, providing evidence for hydrogenotrophic and chemoautotrophic metabolisms. On average 10 mg / L H<sub>2</sub>S production was detected from incubated samples from both sites. Organic carbon content initially decreased 14 – 29% over the course of these incubations. *Archaeal* and *Eubacterial* biomass estimations (QPCR) were stable, implying that microbial growth was negligible. Temporal analyses of 16S rRNA gene amplicon data showed that the distinct, site-specific microbial communities eventually converged to a common core of approximately 16 OTUs, including salt tolerant *Aerococcaceae* and *Corynebacteriaceae*, as well as *Enterobacteriaceae* and *Comamonadaceae*. Subsurface characterization and laboratory experimentation with representative reservoir samples is needed to achieve a predictive understanding of reservoir responses to storage conditions and ultimately enable the H<sub>2</sub> economy by de-risking geologic storage of this energy asset.