

Subsurface microbial hydrogen cycling: implications for Underground Hydrogen Storage projects

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ABSTRACT

Hydrogen is considered a crucial energy carrier in energy transition roadmaps. It can be used to store surplus electricity from intermittent solar and wind energy sources thus providing crucial flexibility and stability to the electricity grid. Hydrogen will also help decarbonize other sectors characterised by high energy demand, such as industry, heavy transport and the built environment, which are hard to electrify. **Underground hydrogen storage (UHS)** will be a critical enabler of a future hydrogen economy because it provides cost-effective large-scale and long-duration storage solution for managing supply and demand.

Microorganisms in anaerobic environments, such as underground systems, can use hydrogen for their metabolism. These hydrogen-fueled microbes, known as **hydrogenotrophic microbes**, can cause several problems in UHS projects including the direct loss of gas volume, decreasing H_2 purity due to CH_4 and H_2S production, corrosion and eventually reduced storage capacity. Here, we conducted a sensitivity analysis to understand how environmental parameters affect H_2 consumption by a pure culture of the hydrogenotrophic methanogen, *Methanobacterium subterraneum* (Archaea), isolated from deep subsurface environments. We also studied H_2 consumption by an environmental microbial consortium sampled from a UHS site (aquifer) prior to H_2 injection.

The optimum pH for H_2 consumption by *Methanobacterium subterraneum* was examined by testing its kinetics at pH 7, 7.5, 8.5, and 9. Our experiments showed that this archaeon can grow -and consume H_2 - only at pH 7 and 7.5, with the former being the optimal one. *M. subterraneum* consumed H_2 at low salinity (0.5M NaCl) and this ability increased with increasing temperature. No activity was observed at 0.75M and 1M NaCl. CH_4 production, growth rate, and changes in the pH during cultivation, were also monitored for all different conditions.

The environmental consortium was acclimatised in sequential cultures to specific conditions prior to the experiment. The microbial consortium produced H_2S in the presence of H_2 in the gas phase. We found a correlation between H_2 and sulphate consumption and the production of H_2S . The diversity of the microbial community was studied by Next Generation Sequencing (NGS) of the V3-V4 region of 16S rRNA gene (\approx 450 bp) for the characterisation of bacterial communities. The highly variable ITS1 subregion was targeted for the characterisation of fungi without any outcome. Three main bacterial genera were identified in all cultures, *Terrisporobacter*, *Clostridium*, and *Aeromonas* sp. (two of them at species level, *Terrisporobacter petrolearius* and *Clostridium huakuii*). *Terrisporobacter* and *Aeromonas* sp. are sulfur-reducing microbes while *Clostridium* sp. is an acetogen.

Microbial activity data can be used in geochemical models to evaluate hydrogen reactivity in UHS sites and improve the safety, efficiency, and longevity of the storage systems. Growth kinetic data from pure cultures of isolated microorganisms are used in these models, while results from environmental consortia, like the one studied here, serve for cross-referencing and model calibration. Based on our results and the fact that hydrogenotrophic microorganisms are ubiquitous, we emphasise the need for microbial analysis at potential UHS sites before H₂ injection.

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