

Microbial Hydrogen Transformation During Underground Hydrogen Storage

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Underground hydrogen (H₂) storage (UHS) could be an alternative or important supplement to energy storage. However, there is still lack of knowledge about fundamental biogeochemical aspects. This work addresses the potential of microbial H₂ consumption and the involved microorganisms at possible UHS sites.

Microbial reactions that consume H₂ are still a major uncertainty factor for UHS. Microbial life is widespread in the crust of the earth and geological formations suitable for UHS need to be seen as a habitat for microorganisms. Microbial activity at the UHS site might affect the stored H₂ as well as the integrity of the storage site itself. A specific interest is to gain information about microbial activity that might result in a loss of stored H₂ as well as the production of unwanted metabolic products e.g. H₂S. The importance of specific conditions with relevance for UHS i.e. elevated pressure, high temperature, fluid chemistry and mineralogy, will be addressed.

Depleted gas fields in porous rock reservoirs are one option of future UHS. To simulate UHS in depleted gas fields incubation experiments were performed and microbial H₂ transformation activity was studied. Formation fluids from seven boreholes within one gas field were obtained during gas production. Five fluids showed immediate H₂ consumption without the need of adding any supplements, while one needed sulfate addition for activity and one remained inactive. The fluid from one borehole was studied in more detail: Microorganisms oxidized H₂ at relevant UHS *in situ* pressure conditions (100 bar) and tolerated dynamically changing pressure conditions, reflecting multiple cycles of H₂ injection and withdrawal during UHS. A temperature shift experiment indicated the recovery of microbial H₂ oxidation at 30°C after a period of inactivity at 60°C. The microbial H₂ oxidation rate was affected by H₂ partial pressure and the availability of sulfate as a terminal electron acceptor. High-throughput sequencing of 16S rRNA gene amplicons indicates H₂ oxidation by sulfate reducing bacteria as responsible process in these porous rock reservoir fluids.