

Understanding the fate of hydrogen in subsurface and anoxic storage reservoirs

LAURA FABLET¹, DR. SETAREH RAD¹, NICOLE DOPFFEL², CAROLINE MICHEL³, KATERINA CERNA⁴, JAKUB RIHA⁵, BIWEN AN-STEPEC², JOACHIM TREMOSA⁶ AND SYLVAIN STEPHANT¹

¹BRGM, French Geological Survey

²NORCE

³BRGM

⁴Technical University of Liberec, Institute for Nanomaterials, Advanced Technologies and Innovations, Bendlova 1407/7, 461 17 Liberec 1, Czech Republic

⁵TUL

⁶GEOSTOCK

Hydrogen (H₂) storage supports the decarbonization of society by enabling the use of green hydrogen produced from renewable energy sources. Subsurface reservoirs like deep aquifers (AQ), (depleted) hydrocarbon reservoirs (HR), and salt caverns (SC) provide large-scale and long-term storage solutions that help balance supply and demand. These anoxic environments host diverse microbial communities that can consume H₂ for their metabolisms. This microbial H₂ consumption poses risks, such as the loss of stored H₂, lower quality due to the production of other gases (H₂S, CH₄) and alterations in the physicochemical properties of the reservoirs. Yet, the general presence (taxonomy and occurrence), activities and metabolism rates of the microbial communities are insufficiently explored. To better understand the potential fate of H₂ in the different storage types, 25 sampling and microbial enrichments were performed to characterize the natural microbial communities and monitor H₂ concentration changes over time, using natural underground water samples. For each sample, initial microbial communities were identified using 16S rRNA amplicon sequencing. Enrichments were set up under various conditions: with H₂ or N₂ input, with or without nutrients addition, at field or standard (30°C) temperature. Negative controls were also carried out under the following conditions: autoclaved brine solution with H₂, brine solution with N₂, and anoxic distilled water with H₂. Gas concentration and pH were monitored over time. As expected, the first results highlight a high diversity of the natural microbial communities and metabolisms. However, enrichment tests results show that H₂ consumption is only present in a few samples. H₂ consumption is more significant in HR compared to SC and AQ. Methanogenesis was recognized as the key microbial metabolism responsible for the observed hydrogen loss. Production of CH₄ together with the presence of methanogenic archaea was observed in the brine during incubation. These preliminary findings underscore the importance of characterizing microbial communities in potential H₂ storage sites and to determine the associated risks for each site.