

Convective Dissolution of CO₂ in Saline Aquifers

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Dissolution of CO₂ into the brine is one of the major trapping mechanisms that increases storage security. The increase in density of the brine that occurs when CO₂ dissolves drives convective motion that enhances the dissolution rate of CO₂. We present the results of a hydrodynamic stability analysis that describes the onset of convective motion. We have obtained expressions for the critical time necessary for the onset and the initial wavelength of the fastest growing disturbance. In high permeability aquifers onset of convection will be rapid (<1 yr), but wavelength are very small (~1 m). Resolution of these small length scales is a challenge standard reservoir simulators.

We present numerical results of the long term evolution of the convection in the brine and the dissolution rate of the CO₂. The numerical simulations show three mass transport regimes, an early diffusive regime, followed by an infinite-acting convective regime, and finally a finite-acting convective regime. The infinite acting convection regime is characterised by a constant dissolution rate. The depth of the aquifer determines the duration of this highly efficient convective mass transfer regime. As the plumes of CO₂-rich brine reach the bottom of the aquifer mass transfer decays rapidly, despite continued convective motion (finite acting convection).

We conclude that dissolution trapping will be an important mechanism in high permeability aquifers, because the onset time is short, the dissolution rate is high. In large aquifers the high infinite-acting dissolution rate can be maintained longer and therefore dissolution trapping will be more important in large aquifers.

Reference

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Microbial life in a hydrothermal spring rich in arsenic compounds

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The geothermal spring Champagne Pool in Waiotapu, New Zealand has an estimated volume of 50,000 m³ and discharges fluid at 75° C, which is oversaturated with arsenic and antimony compounds such as orpiment (As₂S₃) and stibnite (Sb₂S₃) that precipitate and form orange deposits. Although Champagne Pool is geochemically well characterized only few studies addressed its role as a potential habitat for microbial life. In the current investigation, a combined approach of first culture-independent studies followed by culturing experiments was applied to describe microbial density and diversity within Champagne Pool. ATP measurements and epifluorescence microscopy showed relatively low biomass in Champagne Pool compare to other terrestrial hot springs within New Zealand and relatively low cell numbers of $5.6 \pm 0.5 \times 10^6$ cells per ml. Denaturing Gradient Gel Electrophoresis and 16S rRNA gene clone libraries analyses indicated low microbial diversity and the abundance of hydrogen-oxidizing and sulfur-dependent populations, which were dominated by members belonging to the order *Aquificales*. On account of the results culture media were designed and two novel bacteria and a novel archaeon were successfully isolated. Experiments suggested that the observed relatively low biomass and biodiversity might be due to the presence of volatile components (H₂S, methyl and hydride derivatives of arsenic and antimony) within the spring which are inhibiting microbial growth.