

Carbon fixation potential of the deep biosphere: Implications for geological CO₂ storage

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The subsurface hosts the unseen majority of microbial life on Earth. Yet, the contributions of these rock-hosted communities to global biogeochemical cycles remains unclear. As humankind looks to the subsurface to permanently dispose of captured CO₂ emissions, it is essential to understand the role of deep biosphere communities in global carbon cycling. In particular, the extent to which native communities in storage target formations can use CO₂ to drive metabolism remains to be investigated. Lithoautotrophic metabolism in these environments could help or hinder permanent storage efforts, for instance by enhanced sequestration via mediated carbonate formation or converting CO₂ to biomass (positive), or through conversion to methane (a more potent greenhouse gas) and production of corrosive by-products that threaten leaks (negative).

In attempt to predict potential microbial response to CO₂ injection, we surveyed the native carbon fixation potential of deep biosphere microbial communities recovered from multiple lithologies and settings, spanning granite-, basalt-, sandstone-, clay-hosted aquifers, oil reservoirs, mines and cold-water geysers. To identify and quantify carbon fixation pathways, raw sequencing data from 6 new and 90 published metagenomes were analysed using a bespoke pipeline. We found no strong correlations between host lithology of microbial communities and carbon fixation capacities. Results highlight that carbon fixation capacity is prevalent in the deep biosphere regardless of habitat of origin, especially via the Calvin-Benson-Bassham (CBB) cycle. Metatranscriptomics data from a granite-hosted aquifer community indicated expression of genes encoding the ribulose-1,5-bisphosphate (RuBisCO) enzyme – the key CO₂-fixing step in the CBB cycle. Further study of RuBisCO-encoding genes in metagenomic assemblies highlighted a variety of RuBisCO types spanning the known CO₂-fixing forms I, II and III, with links to a multitude of phyla of known chemoautotrophic bacteria, in addition to genomic evidence for carboxysome production. These findings suggest a previously underestimated contribution of the CBB cycle to carbon cycling in the deep biosphere. Our results also highlight that, although the capacity for CO₂-fixation is widespread, the responses of subsurface communities to CO₂ injection and storage are difficult to predict from baseline genomic data alone, and warrant application of combined geochemical and multi-omics approaches to longitudinal data.