

Microbial diversity and functions in a deep and old terrestrial subsurface aquifer ecosystem

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The deep biosphere remains one of the last unexplored territories on Earth. The terrestrial deep subsurface is composed of aquifer systems and bedrock layers deep below our feet and hosts a large fraction of prokaryotes on Earth, which play an important role in key element biogeochemical cycling (C, N and P), as well as in the shaping and transformations of this habitat. Nonetheless, the interactions of this subsurface microbiota with their geochemical and geological environments remain poorly understood. Subterranean microbial communities are composed of not only a motile fraction, living in the groundwater, but also an endolithic fraction living in the rocks. Thus, in this project we studied the diversity of archaeal and bacterial communities living in a deep (900 m) aquifer (groundwater and rock samples) located in the Becancour region (Quebec, Canada), as well as deep rock samples from the Gaspésie region (Quebec, >600 m), using 16S amplicon and shotgun sequencing. The Becancour aquifer is estimated to be 350 million years old. Our results show that endolithic communities differ between regions (different ages), and between the specific stratigraphic depths. Atomic composition of the rocks was correlated with community structure, with calcium showing a positive correlation. Thus, our results suggest that microorganisms in deep subsurface aquifers interact with the rocks they live in. Metagenomic reconstruction of the groundwater communities showed the presence of pathways belonging to both heterotrophic and autotrophic microorganisms. Autotrophic pathways included the reductive acetyl-CoA pathway, reductive citric acid, reductive pentose phosphate, and dicarboxylate-hydroxybutyrate cycles. We also found genes involved in the dissimilatory reduction of sulfate and nitrate. These genomes also contained genes involved in glycolysis, and hydrocarbon degradation (xylan, chitin, benzoate), indicating potential for both carbon fixation and utilization. Microbial source tracking analyses showed that less than 2% of the groundwater taxa colonized the rock matrices, especially in the deeper layers, highlighting the small taxon overlap between both habitats and thus the distinct abiotic conditions characterizing both ecosystems.