

Enhanced Stratigraphic Correlations in Shales Sequences Using Extract DNA from Endolithic Microorganisms, Quebec, Canada

Cassandre Lazar¹, Jean-Sebastien Marcil², Julia Meyer¹, J- Gagnon²

¹Universite du Quebec a Montreal (UQAM); ²Dereena Geosciences

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Abstract

The deep biosphere remains one of the last uncharted territories on Earth. The search for what is called intra-terrestrial life is an ongoing quest. Although the deep biosphere is often characterized by dark, anoxic, oligotrophic, hot, saline, and highly pressurized conditions, life extends more extensively into the subsurface than it was presumed only 20 years ago. The major fraction of organisms living in the deep subsurface are prokaryotes (Bacteria and Archaea), surviving and adapting in ways we know only little of. Subsurface microbes can be found living in either the aquatic fraction of aquifers (motile microbes), or in the immobile fraction of aquifers colonizing rock matrices (endolithic microbes). Endolithic microbes have developed biochemical strategies to scavenge limiting nutrients like phosphorus contained in feldspar minerals. These "rock-eating" microbes can destroy minerals through dissolution or weathering of the rock, by producing strong acids such as ferric iron or sulfuric acid. New evidence suggests that the endolithic fraction could be even more abundant and active than the motile organisms in the terrestrial subsurface. Nonetheless, few studies have focused on this portion of the microbes in deep aquifer systems. In this study, we use molecular tools to extract DNA from endolithic microorganisms dwelling in rock samples collected during drilling of wells in the Becancour, Lotbiniere and Gaspesie regions of Quebec. In order to check for a correlation between the geological formations and the diversity of the microbial communities, the rock samples were recovered from different formations, and different aquifer systems. Because the number of microbial genera in one sample can range from 50 to 400,

specific communities or populations could be linked to distinct geological formations. Therefore, analysis of the endolithic microbial diversity in rock samples recovered from one exploratory well could help pinpoint areas of interest, like reservoir zones, sealing units or favorable facies. From a broader geological point of view, the use of genetic sequencing makes it possible to improve the stratigraphic correlation of a similar mineralogically but, temporally different geological units. Tests to demonstrate the utility of this approach have been performed in complex geological environments such as thrust and fold belts.