Microbial communities in ultra-deep sedimentary rocks of a foreland basin in Taiwan

LI-HUNG LIN[1], LI-WEI WU[1] AND PEI-LING WANG[2]

[1]Department of Geosciences, National Taiwan University, Taipei, Taiwan
[2]Institute of Oceanography, National Taiwan University, Taipei, Taiwan

The deep biosphere is the largest habitat on Earth. Previous studies have suggested that microorganisms inhabiting the deep subsurface environments metabolize at extremely slow rates and constitute up to 30% of the total biomass, exerting a profound impact on global elemental cycling among different reservoirs over geological time. Most previous efforts are, however, diverted to examine microbial ecosystems associated with unconsolidated marine sediments at relatively shallower depths (<1 km below seafloor). In contrast, terrestrial settings are composed of primarily crystalline or consolidated sedimentary rocks with hydrological circulation and substrate availability distinct from those in marine sediments. While most groundwater in consolidated rock settings is confined in the fracture network, the distribution and assemblage of microbial communities in pore space with limited nutrient exchange and fluid transport are largely unexplored. Furthermore, the retrieval of terrestrial samples dedicated to geomicrobiology research remains to be a rare opportunity. In this study, we collected a suite of rock samples distributed from 1500 to 3000 meters below land surface in a foreland basin of Taiwan through a coring operation designed to retrieve the formation property for CO_2 sequestration. Contamination assessment, cell abundances, community assemblages and geochemistry of sediments and porewater will be presented and discussed.