Microbial community structures associated with deep sedimentary rocks from an active tectonic region

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Abstract

The Taiwan Chelungpu Drilling Project (TCDP) has provided an unprecedented opportunity to probe terrestrial subsurface microbial ecosystem that may have experienced constant disturbance by the arc-continent collision since 5 Ma. The drilling penetrated through the Pleistocene-Pliocene sedimentary rocks to a depth of 2000m below land surface (mbls). Two major fracture zones with ~100 m thickness were encountered at depths of ~1100 and ~1750 mbls, respectively.

Among 40 samples retrieved from rock formations or within fracture zones, thirty were ground to powders, inoculated to media designed for fermenter, iron reducer, sulfate reducer and methanogen, and incubated at temperatures ranging from 30 to 70^{o}C. Mesophilic and thermophilic fermenters and organotrophic sulfate reducers are ubiquitously present in most samples, whereas iron reducers and methanogens appear only in the samples retrieved from the upper (400-700 mbls) and lower depths (1800-1900 mbls).

Analyses of 16S rRNA genes for samples along the depth profile reveal that microbial communities were dominated by *Proteobacteria* at depths shallower than 1300m and by *Firmicutes* at great depths (>1900m). The diversity of community decreases as the depth increases. At great depths (1906m and 1979m), the communities of the consolidated siltstone were almost identical and primarily composed of sequences affiliated with a deep-branching environmental clone within *Clostridia* (92% similarity) by more than 50% of the clone libraries. The community of the fracture

zone at 1810m, however, exhibited much greater diversity and primarily consists of *Proteobacteria*. Of the phylotypes identified from 1810m, one is similar with an iron reducing bacterium isolated from 545m and the other is similar with one known thermophilic heterotroph, suggesting that fluid carrying various nutrients may channel either upward or downward along the fracture zone and support diverse community structure. The pore throat of the consolidated siltstone is generally less than 0.5 μm, inhibiting the migration of microbes across geological strata. The consistent dominance of *Firmicutes* clones suggests that microbes residing within the pore space at 1906m and 1979m are imposed by similar environmental stress.