

The deep biosphere in Bengal Fan sediments (IODP Exp. 354)

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The deep biosphere in the Indian Ocean has not been studied in detail so far. We collected sediment samples along a 8°N transect across the Bengal Fan drilled during International Ocean Discovery Program Expedition 354 (February – March 2015, Singapore – Colombo, Sri Lanka) to explore subseafloor microbial processes and to understand their significance in a global context [1]. It is specifically aimed to determine (i) prokaryotic cell concentrations using flow cytometry, (ii) endospores abundance based on dipicolinic acid concentration, (iii) potential hydrogenase enzyme activity using a radiotracer based assay, and (iv) microbial community composition using ultra-high-throughput analysis of DNA on the Illumina MiSeq platform.

We present preliminary observations on prokaryotic cell concentrations and microbial community compositions from selected sites; and depth profiles of microbial activity and endospore concentrations from all sites. We identified various bacterial and archaeal communities based on DNA sequencing. Prokaryotic cell densities exponentially decrease by three orders of magnitude over depth. In contrast endospore concentrations vary between 2.6×10^4 and 7.9×10^6 g⁻¹ sediment, which are relatively lower than in previous studies [2, 3], and appear to depend more strongly on lithology and total organic carbon contents than on sediment age/depth. Potential enzyme activity varies by about three orders of magnitudes along depths that span a wide range of biogeochemical zones e.g. sulfate reduction, methanogenesis etc. Similar to other environments, per-cell hydrogen utilization depends on vertical biogeochemical zones [4].

We conclude that the deep biosphere in Bengal Fan is active and due to its large volume contributes substantially to global subsurface biomass.

[1] France-Lanord *et al.* (2016) *International Ocean Discovery Program Proceedings* **354**. [2] Fichtel *et al.* (2008) *Geomicrobiology Journal* **25**, 371-380. [3] Lomstein *et al.* (2012) *Nature* **484**, 101-104. [4] Adhikari *et al.* (2016) *Frontiers in Microbiology* **7**.