



Comparative analysis of microbial diversity and possibilities of dispersal of microbial cells across different subterranean systems of Deccan traps

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The existence of life in the deep terrestrial subsurface is established, yet few studies have investigated the diversity and ecological role of organisms residing in deep basaltic-granitic system. Exploration of deep biosphere of subterranean crustal system provides an unprecedented opportunity to unravel the composition of microbial dark matter, limits of life, and mechanisms of microbial interaction within aphotic, oligotrophic environment with elevated pressure and temperatures. Scientific exploratory boreholes at Koyna-Warna region of Deccan traps have provided a unique window to study microbial diversity at different depths of 65 million years old basalts and its underlying Archean granitic basement. This study area has gained considerable interest owing to the occurrence of Reservoir Triggered Seismicity (RTS) due to the impoundment of Koyna-Warna dam. Though studies have shown the evidence of diverse microbial population in subsurface rock hosted microbiome, microbial diversity in the subsurface water of Deccan traps remains unknown. The present study gives us an overview of microbial diversity of the subsurface water and its comparison with surface water and rock-hosted microbiome. Three subsurface water samples were collected from different boreholes (two samples from a depth of 100 m and one from a depth of 1029 m) whereas other samples from groundwater seepage sites, Koyna river and Koyna dam were collected for comparison purposes. Culture independent, high throughput deep sequencing of V4 region of 16S rRNA gene was performed to elucidate the microbial diversity of different water samples. Distinct microbial communities were observed between the surface and subsurface water samples which were further validated by different statistical approaches. Subsurface water microbiome was marked with abundance of chemolithotrophic Comamonadaceae, biomineralizing Moraxellaceae and methylotrophic Methylophilaceae whereas presence of chemoorganotrophic Sporichthyaceae and photosynthetic Cyanobacterial members in higher numbers was observed in surface water samples. The dominating genera of Comamonadaceae (*Varivorax*), Moraxellaceae (*Perucidibaca*) and Methylophilaceae (*Methylotenera*) present in the water samples are known to harbor flagella which might enhance their motility to move toward favorable environments in the oligotrophic subsurface provinces. Though presence of similar taxonomic groups was observed across subsurface water and rock hosted microbiome, OTU (Operational Taxonomic Unit) overlap was insignificant. Non-metric multidimensional scaling on the basis of microbial diversity across subsurface water, subsurface rock core and surface water displayed three distinct clusters. This proves that microbial dispersal in the Deccan subsurface is limited or the microbes were not introduced to the Deccan subsurface in the recent past. Shotgun metagenomic studies of two subsurface and one groundwater seepage sample also showed marked differences in the genomic inventory. One of the striking differences was the presence of photosystem I and II in the groundwater seepage sample and absence of the same in the subsurface water samples. Overall it gives us a sense that microbial community in subsurface environment of Deccan traps is different from the surface microbial diversity and introduction of microbial cell from surface to subsurface environment is limited.