Microbial Biogeographic Patterns of Terrestrial Mud Volcanoes across Eurasian Continent

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Biogeography studies provide an insight to unravelling the coevolution of geology and ecology. Compared to the marine counterparts, microbial dispersal across terrestrial mud volcanoes is essentially impossible due to the limited fluid exchange. Whether such geographic isolation leads to greater divergence of community compositions or the geochemical contexts control similarity of communities remain unknown. In this study, we examined environmental factors and similarities of microbial community structures of mud volcanoes using samples collected from six countries across the Eurasian continent. A total of 279 samples distributed at 13 sites were collected, from which 109 samples were sequenced on the Illumina platform. A total of 3,614,981 reads targeting the V3-V4 region of 16S rRNA genes were obtained and subject to OTU (Operational Taxonomy Unit) clustering. The analysis yielded 104,059 OTUs with the Shannon indexes ranging from 2.11 to 6.73 over sites. Although ten most abundant OTUs taxonomically classified into lineages affiliated with ANME-2a/2b, Thiobacillus, Anaerolineaceae, Cyanobacteria, Thiohalorhabdus, Sva1033 and Desulfobacca constituted 12.8% of the total reads, their abundances varied considerably across all sites and along depth. For example, the ANME-2a/2b lineage has been commonly recovered from marine seeps and mud volcanoes, and known to play a major role in removing methane syntrophically with sulfate reducers. However, the ANME-2a/2b members were mostly recovered from three sites separated by a distance of >9,000 km in this study. The other most abundant OTU related to Thiobacillus was mostly confined to two sites several km apart from each other. In contrast, the Cyanobacteria was present at much more sites when compared with the major OTUs described above. Their abundances, however, decreased substantially with depth. Overall, a wide range of oxygen affinities and substrate preferences potentially possessed by these major community members suggests that a strong redox and geochemical gradient offers a great variety of niches for microbial colonization.