

Microbial communities imposed by different geochemical contexts in Sicilian mud volcanoes

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Mud volcanoes and seeps are prominent surface manifestation of fluid channels connected to fluid/gas reservoirs in deep subsurface environments. While methane and carbon dioxide constitute the main components of exsolved gases, the discharge of these gases into the atmosphere have been estimated to exert profound effects on greenhouse over contemporary and geological time scales. How microbial processes and what community compositions imposed by different geochemical contexts near surface regulate the exact quantity of gas emission remain poorly constrained. In this study, porewater, gas and sediment geochemistry, and 16S rRNA genes for samples collected from mud volcanoes in Sicily of Italy were analyzed to investigate the changes of methane cycling and compositions of methanotrophic populations in response to different methane/ CO_2 ratios and other geochemical characteristics in gas bubbling environments. The analyses yielded contrast patterns of solute and gas geochemistry, and gene assemblages and abundances between sites related to different tectonic regimes. For sites located at the southern flank of Mt. Etna, methane and other hydrocarbons were low (less than tens of μ M) in concentrations, whereas fluids were more saline than seawater and enriched with various solutes. No apparent methane consumption could be identified from geochemical profiles. Cell abundances were low, varying between $10^4 - 10^6$ cells g⁻¹ with anaerobic methanotrophs being generally less than 10^4 cells g⁻¹. Communities were primarily composed of Halobacteriales, Gamma-Proteobacteria, Defferibacteres, Chloroflexi, and Delta-Proteobacteria. The dominant OTUs were related to heterotrophic halophiles, and sulfide oxidizers. While a fraction of sequences related to aerobic methanotrophs were detected, anaerobic methanotrophs and methanogens were rarely present. In contrast, methane and other hydrocarbons were high (generally more than 0.4 mM) at sites located within accretionary wedge. Fluids were relatively depleted in solutes (with chloride concentrations ranging about 40% of seawater). Transition of methane abundances indicative of methane consumption could be equivocally identified. Cell abundances were high, varying between $10^8 - 10^9$ cells g⁻¹ with anaerobic methanotrophs ranging around 10^7 cells g⁻¹. Communities were primarily composed of Halobacteriales, ANME, Delta-Proteobacteria, Bacteroidetes, and Chloroflexi. The dominant OTUs were related to uncultured DHVEG-6, ANME-2, sulfate reducers and S/Fe reducers. A small fraction of sequences related to aerobic methanotrophs and methanogens were recovered from samples near surface and at depth, respectively. Overall, our results combined with previous studies conducted elsewhere demonstrate that anaerobic methanotrophy and methanogenesis were prevalent in terrestrial mud volcanoes characterized by low salinity and high methane. Their in situ activities and interactions with other metabolisms would be vital in determining the quantity of methane produced within sediments and released into the atmosphere. Moreover, aerobic heterotrophy and sulfur oxidation dominated over other metabolisms in mud volcanoes fed with fluids potentially circulating through evaporites and low-methane volcanic gases. The effectiveness of biological methane filtration is therefore strongly controlled by geochemical contexts imposed by geological frameworks.