## Spatial variations in microbial community composition inhabitating terrestrial mud volcanoes across the Eurasian continent

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Recent estimates indicate that up to  $2-6 \times 10^{29}$  cells are present in global continental subsurface. This quantity of biomass is comparable with that for marine sediments. Yet, intense debate arises regarding which variables drive their diversity, distribution and abundance. Terresrrial mud volcanoes (MVs) represent the surface expression of conduits tapping fluid and gas reservoirs in deep subsurface. Therefore, MVs provide a direct, effective means to recover deep microbial communities and offer materials to investigate the community variations in biological hotspots fueled by geologically produced gases and fluids.

Based on the concept of metacommunity, we first hypothesize that microbiome in terrestrial MVs may be composed of specific colonists highly adapted to local environmental context and restricted with dispersal capability. Environmental selection over long timescales could result in substantial local diversification. In this regard, we analyzed microbial community structures of 14 terrestrial MVs across the Eurasian continent to test the validity of distance control and physiochemical factors in explaining biogeographic pattern. Our analyses demonstrated that community variance between geographic locations was greater than within sites. Among 30,139 OTUs recovered, no cosmopolitan member could be found. The slopes of abundance-range and distance-decay relationships were generally steeper than those for marine seafloor or seep sediments, suggesting highly spatial heterogeneity and/or isolation of terrestrial MVs. For comparison, physiochemical parameters only explained 16.34% of community variance, and specific geochemical parameters were correlated with specific taxa. Overall, our results suggest that microbial communities in terrestrial MVs are greatly controlled by distance effect rather than the geochemical variation imposed by local fluid or geological processes. While local physiochemical parameters apparently control the distribution of limited taxa, the stochastic assembly processes better accounts for the biogeographic pattern across the large spatial scale.