Patterns in microbial community composition and functional capacity associated with methane cycling in terrestrial mud volcano

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Terrestrial mud volcanoes (MVs) representing prominent surface geological features in compressional tectonics regimes are formed by expulsions of muddy fluids, hydrocarbons, and gases from deeply buried subsurface sources. Unlike the enormous buffering capacity of seawater above marine MVs, terrestrial MVs directly emit methane into the atmosphere. As microbial communities play a key role in governing methane fluxes in MVs [1, 2], we are interested in how microbial community compositions and functions could be correlated with *in situ* geochemical characteristics and therefore, control the flux of methane across redox transitions. Here, we coupled sequence-based methods with geochemical analyses of sediments, gases, and pore and surface fluids to characterize community assemblages, functions and activities in a methane-emitting MV of southeastern Taiwan. Multiple lines of evidence indicated that aerobic / anaerobic oxidation of methane, metal reduction, methanogenesis, and fermentation were active and compartmentalized into discrete and stratified niches. A number of microbial populations and functions showed strong correlations with the types and the availability of specific electron acceptors, and concentration of methane. Although methanotrophs, methanogens, and nitrate-, sulfate-, and metal-reducing bacteria were observed in all samples along the core, functional marker genes related with anaerobic oxidation of methane and metal reduction were more enriched at shallower intervals, whereas those associated with methanogenesis and fermentation were more abundant at depth, indicating the existence of spatial heterogeneity. Conspicuously, both molecular and geochemical evidence indicated that microbial communities inhabiting in the bubbling pool and near surface region have the strongest ability to consume methane.

[1] Cheng *et al.* (2012) *ISME J.*, **6**, 2280-2290.
[2] Wang *et al.* (2014) *Front. Microbiol.*, **5**.