

Variations in microbial community composition in methane enriched sediments across a tectonic transition offshore southwestern Taiwan

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Variations of microbial communities in seafloor are commonly attributed to the control imposed by factors, such as environmental selection and microbial dispersal, exerted over modern and geological time scales. How these intertwined factors shape microbial community composition and activity in methane-rich sediments across a tectonic transition remains poorly understood. In this study, we conducted geochemical, DNA-based gene abundance and diversity analyses for sediments extending to a depth of 120 mbsf through the MeBo drilling technology from active (FWCR) and passive (FR) margins off southwestern Taiwan. Geochemical analyses yielded typical marine sediment profiles at both sites, with the sulfate-methane transition occurring at depths <20 mbsf. Cell abundances and community diversities decreased with depth. However, the variation magnitudes were much greater at FWCR. Community patterns showed that the communities clustered likely in accordance with depth variation for individual sites even though scattering for some communities in NMDS plot. The communities from two sites were less distinct from each other but much more distinct from communities retrieved from the overlying seawater, surface sediments (<0.3 mbsf), and abyssal regions in the South China Sea. Pairwise comparisons revealed that the majority of community dissimilarities weakly increased with depth separation for individual sites (>0.69 for FR; >0.88 for FWCR) and between sites (0.86; $p < 0.001$). Detailed examination indicated that dissimilarities were less than an arbitrary threshold (0.6) for few depth pairs shallower than SMI. Comprehensively, the results suggested that while sediment communities were inoculated from particulates sunken from the overlying seawater that could be traced back to up to hundreds of thousands of years, they also represented the consequence of interactions between burial history, fluid circulation, and biogeochemical processes (e.g., sulfate reduction, methanotrophy, and organotrophy as predominant metabolisms). As the seed inoculants were relatively homogenized, the sediment communities shifted and diversified as burial progressed with niche isolation imposed by compaction and the

predominance of specific community members or functions diminished as the counteracting redox gradients became marginalized. Overall, our finding indicated that the assembly of microbial communities in marine sediments across a tectonic transition was affected by intertwined factors terrestrially and meanwhile developed independently.