

## **Methane supply drives prokaryotic community assembly and networks at cold seeps of the South China Sea**

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Marine cold seeps are unique chemosynthetic habitats fuelled by deeply sourced hydrocarbon-rich fluids discharged at the seafloor. Through oxidizing methane and other hydrocarbons, microorganisms inhabiting cold seeps supply subsurface-derived energy to higher trophic levels, sustaining highly productive oases of life in the deep sea. Despite the central role of microbiota in mediating biogeochemical cycles, the factors that govern the assembly and network of prokaryotic communities in cold seeps remain poorly understood. Here we analysed the geochemical and microbiological profiles of 11 different sediment cores from two spatially distant cold seeps of the South China Sea. We show that prokaryotic communities belonging to the same methane-supply regimes (high-methane-supply, low-methane-supply and nonseep control sediments) had a highly similar community structure, regardless of geographical location, seep-associated biota (mussel, clam, microbial mat) and sediment depth. Methane supply appeared to drive the niche partitioning of anaerobic methanotrophic archaea (ANME) at the regional scale, with ANME-1 accounting for >60% sequence abundance of ANME in the high-methane-supply sediments, while ANME-2 dominated (>90%) the low-methane-supply sediments. Increasing methane supply enhanced the contribution of environmental selection but lessened the contributions of dispersal limitation and drift to overall community assembly. High methane supply, moreover, promoted a more tightly connected, less stable prokaryotic network dominated by positive correlations. Together, these results provide a potentially new framework for understanding the niches and network interplay of prokaryotic communities across different methane seepage regimes in cold-seep sediments.