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Microbial processes and diversity at cold seeps in the Nile Deep Sea Fan

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The Nile Deep Sea Fan (NDSF) hosts numerous cold seeps, which emit fluids, gases and muds. Compounds contained within cold seep emissions are often capable of supporting diverse microbial metabolisms. Using a combination of molecular and microbiological techniques such as 16S rDNA sequencing, fluorescence in situ hybridization, and enrichment cultures, we examined the bacterial communities present in highly active methane-oxidizing and sulfate reducing sediments overlying cold seeps in the NDSF. Our results revealed a large diversity of archaea and bacterial phylotypes endemic to many seep, vent and polluted ecosystems. Among the 16S rDNA phylotypes detected were methanotrophic archaea closely related to ANME 2 and 3, as well as their syntrophic bacterial partners belonging to the Desulfococcus and Desulfosarcina cluster. Anaerobic enrichments using methane and sulfate as sole electron donor and acceptor, respectively, produced hydrogen sulfide, indicating that these consortia were indeed active within the sediments. We also detected a many more phylotypes closely related to known autotrophs and heterotrophs, as well as many unidentified bacterial phylotypes. We conclude that the cold seep sediments of the NDSF, contain highly active and phylogenetically diverse bacterial populations that are capable of a wide variety of microbial processes, some of which are relevant in the control of greenhouse gas emission. In the framework of the ESF EUROMARGIN program MEDIFLUX we will further investigate the dominant microbial communities, and how fluid flow affects their metabolic activities.