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Seafloor Cold Seeps as Crucial Mediators of Arsenic Enrichment in Deep Sea

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Seafloor cold seepage systems are environments known for their high levels of arsenic, a prevalent and toxic metalloid in nature. However, the biogeochemical mechanisms of arsenic enrichment remain poorly understood. In this study, sediment cores recovered from the active, inactive, and reference areas of the Hama cold seep in the South China Sea were examined using geochemical and metagenomic analyses. Geochemical data revealed evident enrichment of total arsenic, sulfide-bound arsenic, and organic arsenic in the seep site sediments compared to the reference area. Metagenomic analyses identified genes involved in arsenic oxidation (*aoxA* and *arxA*) primarily present in the upper zone, while arsenic reduction genes (*arrA*) were predominantly detected in the deeper zone of the sediment cores in the active area. Moreover, 25 metagenome-Assembled Genomes possessing arsenic reduction genes were affiliated with the *Desulfobacterota*, possibly syntrophic partners of the Anaerobic Methane Oxidizing Archaea. Furthermore, a strong linear correlation was observed between the dissolved arsenic and DIC ($R^2=0.64$, $p<0.01$) and $\delta^{13}C_{DIC}$ values ($R^2=0.86$, $p<0.01$) in the active area. These results suggest a synergistic relationship between arsenate reduction and methane oxidation, possibly indicating the occurrence of AsR-AOM, within the sediment column of the active seep site. Combining this with the Fe and Mn geochemistry, we propose that arsenic was efficiently transported from the seawater column to the sediment column through rapid and continuous redox cycling of Mn and Fe, then stored in the sediment columns by HS^- , which is produced by bacterially mediated sulfate reduction. In summary, these findings indicate that cold seepage systems function as crucial sink for arsenic in the deep ocean, which would create arsenic-deficient seawater environments during the large-scale methane release events in earth history.