



Contribution ID: 1002

Type: **Poster Presentation**

Archaea community in gas hydrate-bearing sediments in the South China Sea

Monday, 13 May 2024 09:55 (1h 30m)

The South China Sea, endowed with abundant natural gas hydrate resources, presents exceptional conditions for gas hydrate formation and exploration prospects. Gas hydrate-bearing sediments are characterized by methane saturation in pore waters, fostering rich and distinctive microbial ecosystems. These microorganisms play crucial roles in methane production, consumption, and global carbon cycling. This study focuses on 117 sediment samples from 11 sites across the Qiongdongnan Basin, Shenhu area, and Xisha Trough of the South China Sea, employing high-throughput MiSeq sequencing of the 16S rRNA gene to investigate the archaeal community structures and diversity. Our findings highlight significant microbial diversity variance across samples from the three geographic regions, with distinct differences noted between samples from the Qiongdongnan Basin and Shenhu area. The archaeal population is dominated by Halobacterota, Hadarchaeota, Lokiarchaeota, Euryarchaeota, and Woesearchaeota. Notably, methane-metabolizing taxa are prevalent, with a significant abundance of methanogenic archaea over anaerobic methane-oxidizing archaea (ANME). Additionally, the structure of methane-metabolizing groups varies significantly across the three regions, with ANME predominantly identified in the Qiongdongnan Basin. Methanogens show differing dominance in the Shenhu area compared to the Qiongdongnan Basin, and only a few methanogenic groups were observed in the Xisha Trough samples. This study provides the characteristics of archaeal community diversity within sediment cores from gas hydrate-bearing sediments in the South China Sea, contributing to our understanding of microbial group characteristics in these regions. Understanding these microbial populations and their functions is crucial for the comprehension of the biogeochemical processes involved in the formation of natural gas hydrates in the South China Sea.

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Session Classification: Poster

Track Classification: (MS05) Microbial Processes in Porous Media: Risks and Advances