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Changes in microbial community structure by methane fluxes at arctic cold seeps

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Introduction

- **Cold seeps** are characterized by **methane** (CH_4) -rich sediments¹ and this **CH_4** provide a source of carbon for local foodwebs, forming **biological hot spots**²
- CH_4 is oxidized by different groups of methanotrophs depending of the presence of oxygen (**Aerobic Methane oxidation (MOx), Bacterial groups**)³, or its absence (**Anaerobic Methane oxidation (AOM), Archaeal groups**)⁴.
- MOx and AOM thereafter induce **new available sources of energy**, such as **sulphide** that becomes targetted by chemosynthetic bacteria⁵, **organic matter** degraded by some archaeal and bacterial groups⁶, and higher **abundances of living organisms** grazed by larger eukaryotes⁷

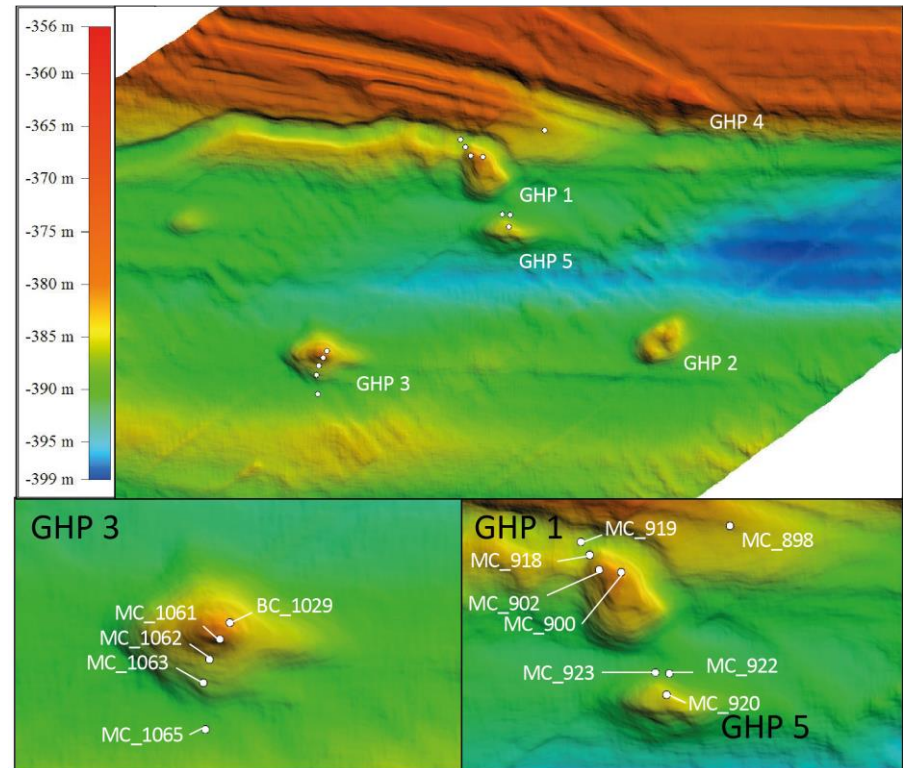
Therefore...

- we aimed for determining **spatial variation of microbial community structure** at cold seeps, addressing **key environmental factors** influencing both the **prokaryotic and eukaryotic communities**

Location of interest

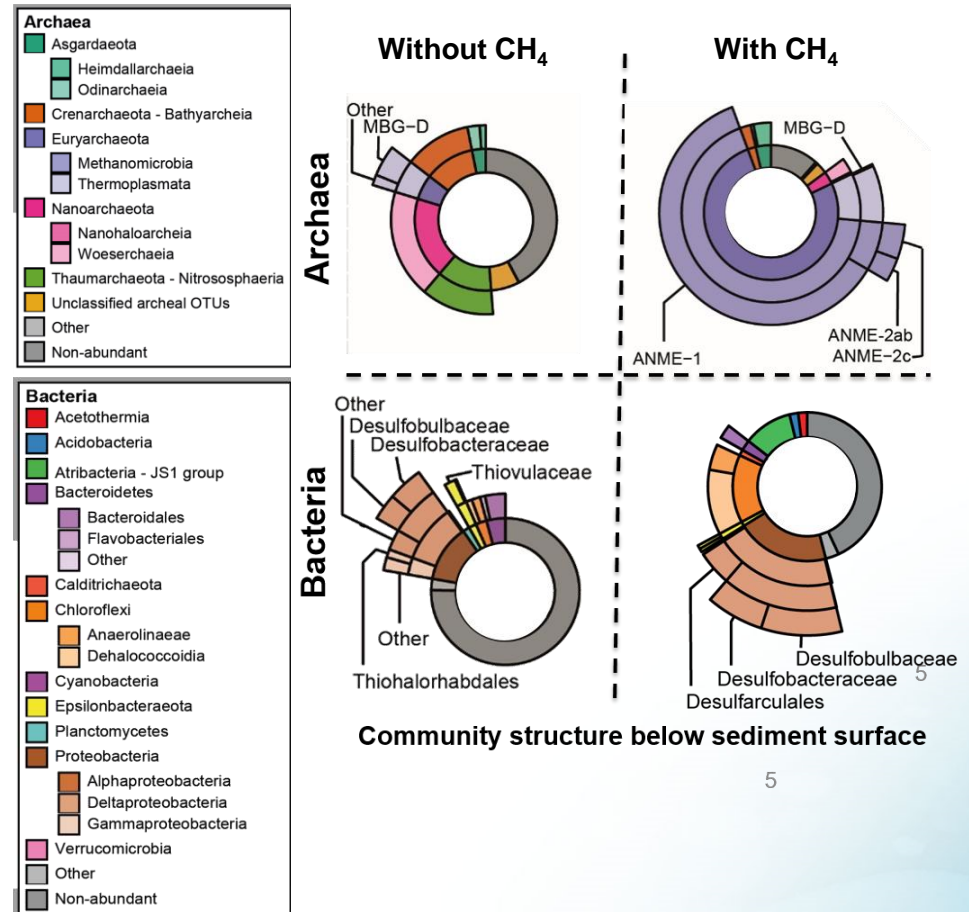
In the Arctic Ocean, south of Svalbard, were discovered recently 5 gas hydrates bearing pingos (GHPs).

16S and 18S rDNA were amplified from sediments samples taken at 2 active and 1 inactive GHPs⁸



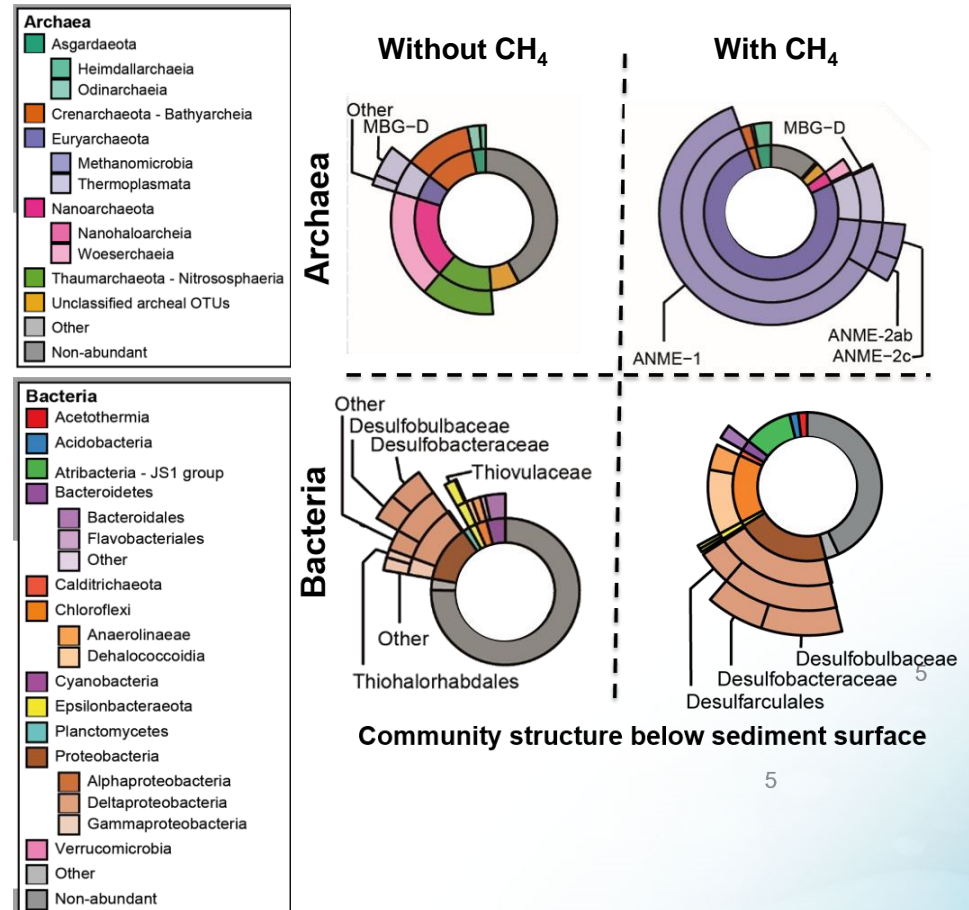
Results – community changes with and without CH₄

- Beta-diversity revealed community changes in the composition of bacterial and archaeal groups
- Groups across the domains had strong co-occurrence, where the abundance of some archaeal groups are commonly associated to particular bacterial and eukaryotic groups (and vice versa).



Results – taxa groups influenced by CH₄

- ANME-1 was the most dominant methanotroph at all locations, and MOx bacteria were barely detected
- In addition to the sulphate-reducing bacteria, other groups, especially groups belonging to Thermoplasmata, Chloroflexi and Atribacteria, dominated CH₄-rich sediments
- In the vicinity of ANME dominated communities, bacterial groups were also dominated by sulphide oxidizers (not shown)
- Eukaryotic communities contrasted with higher abundances of heterotrophic ciliates and cercozoa, and parasitic Apicomplexa and Holozoa



Conclusion

- Our study demonstrated that both prokaryotic and eukaryotic communities at arctic cold seeps formed a unique structure influenced by the distribution of CH₄ seepage
- In addition to ANME-1, CH₄-rich sediments presented the emergence of several taxonomic groups, including Epsilonbactareota, Thermoplasmata, and the heterotrophic Cercozoa and Ciliates, suggesting a complex functional microbial system supported by, or contributing to, the local oxidation of CH₄
- Manuscript is under review and will likely be published soon

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CAGE – Centre for Arctic Gas Hydrate,
Environment and Climate research work was
supported by the Research Council of Norway
through its Centres of Excellence funding scheme
grant 287 no. 223259.

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