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Biogeochemical Activities and Associated Biodiversity at the Gigantic Pockmark Regab - A Multidisciplinary Study

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The Regab pockmark cold seep ecosystem off the West coast of Africa at a water depth of 3000 m harbours a high benthic biomass and biodiversity of chemosynthetic organisms. The establishment of these chemosynthetic communities is promoted by discharges of fluids and gasses rich in methane - a potentially potent greenhouse gas. The chemosynthetic communities are dominated by bivalves of the Mytilidae or Vesicomyidae, or by syboglinid polychaetes, contributing to the high heterogeneity of Regab. Different from most other active seep systems, mats of sulfide oxidizing bacteria were mostly absent. The distribution of these indicator communities and the associated biogeochemical processes were studied in order to better understand the mechanisms governing the interactions between the chemosynthetic communities and the abiotic environment.
Main aims of this study were to determine the spatial scales on which the sediment biogeochemistry varied and to investigate if these variations were also reflected in the distribution of the bacterial and megafaunal communities. Microbial community analysis, ROV-operated in situ payloads (Microprofiler and Benthic Chamber), ex situ techniques (radiotracer incubations) and pore water analyses were used to investigate the micro-heterogeneity of the chemosynthetic habitats, their associated fluxes and the underlying biogeochemical processes.
Here we present data on bacterial diversity, in situ geochemical characterization, microbial turnover rates and benthic fluxes of the different seep habitats. Different chemosynthetic communities were associated with different sulphide fluxes, produced by AOM coupled to SR. Conversely, the characteristic behaviour of certain chemosynthetic organisms influenced the depth distribution of chemical species, promoting sediment patchiness of this ecosystem. Methane effluxes and sediment AOM rates differed by an order of magnitude between different communities located away from each other on scales of tenths to hundreds of meters. Furthermore, differences in the methane budget could also be detected among locations only decimetres apart indicating a high lateral heterogeneity of subsurface methane fluxes. Methane, and moreover, the fluid flow intensity could mostly explain the variations in the bacterial community structure. Due to steep geochemical gradients, which provide contrasting living conditions, the bacterial community structure also varied with sediment depth. In situ microsensor measurements showed substantially shallower oxygen penetration depth (2 mm) in the vicinity of a Vesicomyidae patch compared to a methane-poor reference site, revealing locally restricted geochemical hotspots. The results of this study therefore show that the sediment biogeochemistry at the Regab pockmark varies among different habitats and differences exist on a scale of decimetres to hundreds of meters. These variations are reflected in the sediment bacterial community structure as well as in the megafaunal distribution. Moreover, this study confirms that the establishment of different chemosynthetic communities is associated to variations in fluid flow, biogeochemical processes and consequently methane emissions.
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