

How can environmental DNA help understanding chemosynthetic communities evolution and ecology?

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Chemosynthetic environments in the deep sea harbor highly specialised communities. Those communities are often dominated by a few characteristic species. While the dominant macrofaunal species received lots of attention from the scientific community, other groups such as the meiofauna remain largely unknown. Benthic meiofauna groups organisms between 500 (1000) and 44 (31)micrometers living on or in the sediments. Meiofauna has been reported to be rare or less diverse in chemosynthetic environments such as hydrothermal vents compared to bathyal or abyssal plains. This is likely explained by the little availability of sediments samples as well as environmental characteristics of hydrothermal vents ecosystem. In shallow environments, meiobenthic communities have been shown to be sensitive to a variety of environmental parameters. In response to the steep gradients in multiple environmental parameters encountered in hydrothermal vents fields, it is expected that the patterns of chemosynthetic communities will be complex and meiobenthos will be reflecting such environmental changes accurately. However, low abundance of organisms and difficulty to collect samples from these environments are a major issue towards the investigation of meiofaunal diversity and biogeographical patterns.

Metagenetics is the part of metagenomics consisting in sequencing one homologous marker from environmental DNA. This method offers new perspectives to investigate the taxonomic composition of the communities inhabiting ocean seafloor. In comparison to more traditional methods based on sorting of organisms, environmental DNA allows to detect rare species in an environment, even if only fragment of organisms or DNA are present in the sampled sediments. Moreover, metagenetics approach allows the estimation of taxonomic richness and distribution across multiple phyla in parallel.

Our study focused on environmental DNA extracted from sediments samples collected in the Iheya North hydrothermal vent field in the Okinawa Trough. In the research cruise NT12-27, eight sediment cores were obtained from 3 sites within the vent field. One is located near a site of active hydrothermal venting, while the other two sites are distant from the active vent. The core samples were sliced in five layers of 1cm thickness, and three replicates were sub-sampled from each layer. Environmental DNA was extracted independently from less than 1 g sediments from each replicate.

Large amounts of DNA were obtained from the core sample from the active area covered by white matter, while the samples collected in inactive zones yielded very low amounts of DNA. Here we will present the preliminary results obtained from the sequence data of this environmental DNA, and discuss on the usefulness of this metagenetic protocol to determine the diversity of meiobenthic community.

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