

Nucleic acid insights into present and past microbial activities in subseafloor sediment

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Subseafloor sediment contain the largest reservoir of reactive Carbon on Earth, which represents a potentially vast habitat for microbial life. Microbial life in subseafloor sediment has been confirmed through cultivation and cultivation independent approaches, yet there is a dearth of data on which microbes are active in situ and which biochemical activities dominate in different marine subsurface habitats. Messenger RNA (mRNA) and ribosomal RNA (rRNA) are relatively labile molecules that are rich in biological information, and thus can serve as useful proxies for high-resolution reconstruction of present microbial activities. While RNA-based approaches are challenging in the subseafloor due to relatively low levels of activity, recent work has successfully optimized mRNA and rRNA proxies for subseafloor samples. Here, several studies utilizing RNA proxies will be presented that investigated distributions and metabolisms of active subseafloor microbes in the context of the geochemical environment. This work supports biogeochemical calculations and models of subseafloor microbial activity and has helped to refine our understanding of subseafloor microbiology by elucidating key active microbial players and their metabolic strategies for adapting and surviving under varying geochemical conditions. Compared to RNA however, DNA is much less labile. DNA is preserved over geological timescales under certain sedimentary and geochemical conditions (the “paleome”), and can be used as a paleoproxy for reconstructing the response of plankton to past climate change with high (genus and species level) resolution. Recent paleome studies from the Black Sea have elucidated the historical response of virioplankton, microzooplankton, and zooplankton to historical climate change and will also be discussed.