



Insights into microbial population dynamics and DNA cycling in sediments from extracellular DNA pools

Andrea Torti (1), Bo Barker Jørgensen (1), Mark Alexander Lever (1,2)

(1) Center for Geomicrobiology, Aarhus University, Aarhus, Denmark, (2) Department of Environmental Systems Science, ETH Zurich, Zurich, Switzerland

Marine sediments harbor DNA not associated with currently living organisms. Including this extracellular DNA in genetic surveys may distort abundance and diversity estimates of living microbial communities. We separated soluble DNA (sDNA) of extracellular origin, extracted using a mildly alkaline phosphate buffer, from initially non-soluble DNA (nsDNA), extractable only by chemical lysis treatment and likely from living cells, from the top 10m of sediment in Aarhus Bay (Denmark). We compare the phylogenetic compositions of both DNA pools at the 16S rRNA gene level and examine trends in relation to biogeochemical zonation, time of deposition, and lithology. Below the depth of bioturbation, the two DNA pools display high phylogenetic similarity, suggesting that sDNA largely reflects the currently living microbial community. In contrast, the phylogenetic similarity of sDNA and nsDNA in bioturbated surface sediments is lower. Here the majority of Operational Taxonomic Units from sDNA was absent from nsDNA, representing genetic signatures from microorganisms that were not alive at the time of sampling. We discuss possible explanations for the depth trends in relation to macrofaunal activity along with general implications for the time scales and controls on DNA cycling and DNA preservation in sediment.