How widespread are Archaeal lipids in sedimentary systems?

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Over the past fifteen years, new analytical developments in microbiological approaches have led to the identification of Archaea in almost all environments. However, comparable evidence for archaeal ubiquity from lipid biomarkers, such as dialkyl glycerol diethers (DGDs) and glycerol dialkyl glycerol tetraethers (GDGTs), has been less consistent. In part, this reflects the quantitative nature of biomarker approaches, such that they are typically found where Archaea comprise a significant portion of the biomass (e.g. sediments associated with methanogenesis or anaerobic methanotrophy (AOM); extreme environments; pelagic sediments). However, lack of attention and difficulty in analysis has also contributed to the relative lack of archaeal lipid reports. Here, we survey a range of terrestrial and marine sediments and show that both DGDs and GDGTs are highly widespread.

In sites where Archaea are important mediators of biogeochemical processes, archaeal lipids can be the most abundant compounds in total lipid extracts. These include cold seeps, characterised by AOM, and extreme geothermal systems. However, we also observe archaeal lipids, albeit at concentrations several orders of magnitude lower than observed at seeps, in marine sediments characterised by diffusive methane flux and very low AOM rates. We also observe DGDs (archaeol and sometimes hydroxy- archaeol) and GDGTs at all methanogenic settings examined, including those where rates are very low. This suggests that such biomarkers should be common in the sedimentary record, being found where sulfate is depleted and organic matter oxidation proceeds via methanogenesis. Indeed, we have found archaeol in Pleistocene Amazon Fan and Benguela Upwelling Region sediments, Holocene estuarine sediments, and Cenozoic coastal margin sediments (Tanzania). Thus, archaeal lipids are widespread and can be an important component of biomarker-based evaluation of ancient depositional environments.

Metabolic capabilities of prokaryotes in the deep ocean

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Rapid advances in molecular biological techniques have enabled a more detailed study of marine microorganisms and microbial communities in their environment. However, the microbial ecology of newly discovered phylogenetic groups and their roles in various biogeochemical cycles remain elusive. Here we employ the geochemical tracer radiocarbon (^{14}C) to assess the sources of carbon that fuel prokaryotic production in the mesopelagic ocean. The radiocarbon ages of carbon pools (DIC, total DOC, and POC/new DOC) in the sub-surface ocean are distinct, which makes ^{14}C an ideal tracer for investingating carbon flow into the dark ocean's biosphere. Radiocarbon dates of nucleic acids extracted from microorganisms living at various depths in the Subtropical North Pacific Ocean demonstrate that the fraction of ^{14}C-depleted (old) intracellular carbon increases as the supply of fresh organic carbon diminishes. Based on isotopic signatures of these nucleic acids and available carbon pools at each depth, we estimate the age of the substrate(s) fueling prokaryotic production in both surface and mesopelagic waters. Using molecular biological and lipid biomarker analyses we further estimate the depth-dependent contribution of Group I Archaea to the total prokaryotic community in our samples and the $\Delta^{14}C$ signature of carbon fueling archaeal production. This is the first in-situ investigation of the carbon metabolism of microorganisms inhabiting the sub-surface ocean and it provides direct evidence for the uptake of old carbon by prokaryotes in the deep ocean.