

Challenging GDGT proxies' assumptions of archaea ecology: compound-specific δ C and genetic insights from Orca Basin, Gulf of Mexico

SAMANTHA LICHTIN , COURTNEY WARREN , ANN PEARSON , THOMAS NEAR , MARK PAGANI

Geology & Geophysics, Yale University, New Haven, CT 06520, USA (*correspondence: samantha.lichtin@yale.edu)

Earth & Planetary Sciences, Harvard University, Cambridge, MA, 02138, USA

Ecology & Evolutionary Biology, Yale University, New Haven, CT 06520, USA

Over the last decade and a half, glycerol dialkyl glycerol tetraethers (GDGTs) have increasingly been used to reconstruct environmental temperatures; proxies like TEX that correlate the relative abundance of these archaeal cell membrane lipids to sea surface temperature are omnipresent in paleoclimatology literature. While it has become common to make claims about past temperatures using GDGTs, our present understanding of the organisms that synthesize the compounds is still quite limited. The generally accepted theory states that microorganisms like the Thaumarchaeota modify the structure of membrane lipids to increase intermolecular interactions, strengthening the membrane at higher temperatures. Yet to date, culture experiments have been largely restricted to a single species, *Nitrosopumilus maritimes*, and recent studies on oceanic archaeal rRNA have revealed that these biomarkers are produced in diverse, heterogeneous, and site-specific communities. This brings up questions as to whether different subclasses of GDGTs, and all subsequent proxies, represent adaptation within a single organismal group or a shift in community composition. To investigate whether GDGTs with different chain structures, from the simple isoprenoidal GDGT-0 to Crenarchaeol with its many cyclopentane groups, are sourced from archaea with similar or disparate metabolic pathways—and if that information is inherited in GDGTs trapped in marine sediments—this study examines the stable carbon isotope values (δ C) of GDGTs extracted from the uppermost meters of sediment in the Orca Basin, Gulf of Mexico, using spooling-wire microcombustion isotope-ratio mass spectrometer (SWiM-IRMS). The homogeneity of GDGT δ C through the sediment profile contrasts with a heterogeneous biological community represented in archaea ribosomal genetic sequences, challenging fundamental assumptions of archaeal lipid based proxies that influence the way we perceive the veracity of existing temperature records.