

PRF# 57417-DNI2

Project Title: The role of sulfate reduction in microbial carbonate formation across a restricted lagoonal carbonate facies: A modern analog investigation

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Research Goals

This project aims to identify microbial drivers of carbonate precipitation using molecular DNA techniques, biomarkers, petrographic, and geochemical methods. The geographical locus for this research question are the brackish to hypersaline microbial mats and carbonate lake sediments of Kiritimati, Republic of Kiribati (2°N, 157°W). This research is useful in the context of petroleum research given the importance of ‘microbialite’ carbonate reservoirs in recent oil discoveries, but the limited understanding of how these reservoirs formed.

Research Activities

We have published our first paper, in *The Depositional Record* (Schmitt et al., 2019). This paper assesses the relationship between carbonate mineralogy, water chemistry, and bacterial and archaeal communities across a suite of brackish to hypersaline, carbonate precipitating lakes on Kiritimati.

We have also continued to develop a down-core analysis of from ‘Lake 1,’ a hypersaline lake on Kiritimati. We completed analyses of the age (via radiocarbon measurements), mineralogy, carbonate morphology, microbial communities, and stable isotopes of carbonate and organic matter in a 2000 year-long core, as well as a metagenomic analysis.

We completed fieldwork on Kiritimati in July 2019, and have presented our findings at the AGU Fall Meeting in 2018 and the Midwest Geobiology Symposium.

Main findings

- Distinct communities of bacteria and archaea vary with salinity and carbonate and evaporite mineralogy across brackish to hypersaline lakes (Schmitt et al. 2019)
- In a 1600-year old sediment core from Lake 1, both $\delta_{15}\text{N}$ and the taxonomy annotations from 5 unique metagenomes vary with depth, with $\delta_{15}\text{N}$ increasing toward the top of the core
- The relative abundance of *Cyanobacteria*, *Gammaproteobacteria*, and *Zixibacteria* show a significant correlation with downcore $\delta_{15}\text{N}$ variability.
- Functional annotations suggest that genes related to nitrogen fixation (NifDHK), followed by denitrification (narGHI) are more abundant in the surface sediment, while dissimilatory nitrate reduction to ammonium (NirBD) is the predominant N-related pathway in the deep sediment (Figure 1).

Future work

We plan to submit a manuscript on the downcore Lake 1 metagenomic-stable isotope analysis for publication. We then plan to measure high resolution stable oxygen and carbon isotope analysis from Lake 1 carbonate spherules at the University of Wisconsin WiscSIMS lab in order to understand how this unique carbonate morphology forms. We will also attempt to extract DNA

from super-cleaned spherules in order to investigate what microbes and microbial processes drive the precipitation of this distinct carbonate morphology.

Education/Training

PhD student Mingfei Chen has worked on this project since August 2017. In the last two years, Mingfei has learned a suite of new molecular and geochemical techniques, and has gained expertise in geobiology and geochemistry through his training at UIUC and as a selected participant at the International Geobiology Course. He has presented his results at the Fall 2018 AGU meeting and 2019 Midwest Geobiology Symposium, and will also present his work at the Fall 2019 AGU meeting.

Publications

1 Student author

1Schmitt, S.J., Conroy, J.L., Flynn, T., Sanford, R., 1Chen, M. 1Higley, M.C., and Fouke, B.W. 2019. Salinity, microbe, and carbonate mineral relationships in brackish to hypersaline lake sediments: a case study from the tropical Pacific coral atoll of Kiritimati. *The Depositional Record*, 5:212-229.

1Chen, M., Conroy, J.L., Sanford, R.A., Chee-Sanford, J.C., Connor, L.M. Interpreting lacustrine bulk sediment $\delta^{15}\text{N}$ values using metagenomics in a tropical hypersaline lake system. In preparation for submission to *Journal of Paleolimnology*

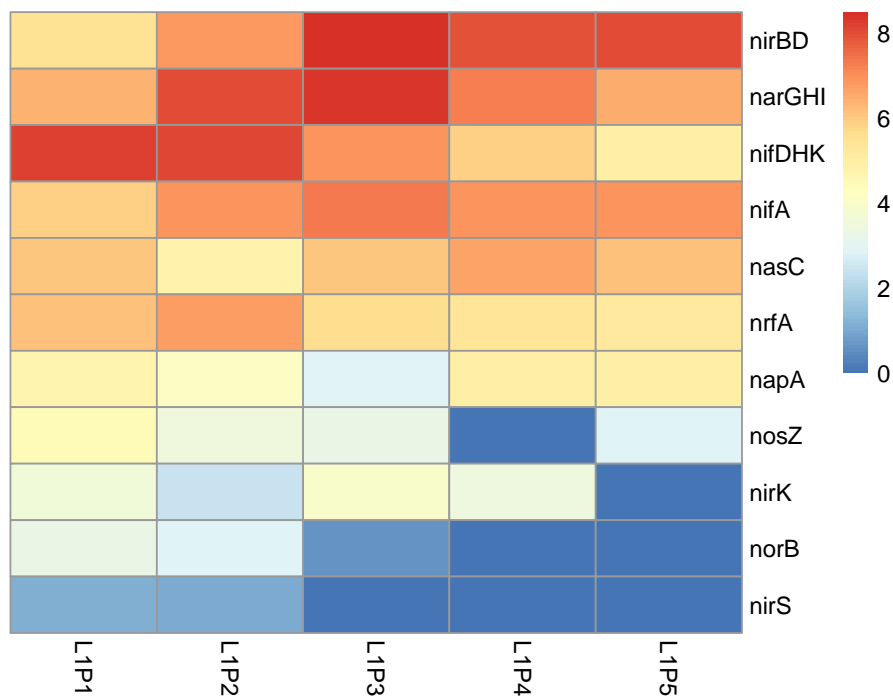


Figure 1: Heatmap of N-related functional genes annotated from five metagenomes. Pool 1 represents the surface sediment, and pool number increases with depth. The color bar is log₂fold scale, and the raw counts of genes are normalized by the normalization function in DESeq2 package in R.