Microbial cycling of sulfur and other redox-sensitive elements in porewaters of San Clemente Basin, California, and Cocos Ridge, Costa Rica

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Motivation

WHAT DRIVES THE MARINE SULFUR CYCLE?

- Since sulfate is the most important electron acceptor in marine sediments after oxygen, its reduction products are readily available electron donors for autotrophic microbes.
- The biogenic oxidation of reduced sulfur back to sulfate is mediated by a wide variety of metabolic pathways, which generate sulfur with intermediate oxidation states.

WHY ARE WE INTERESTED?

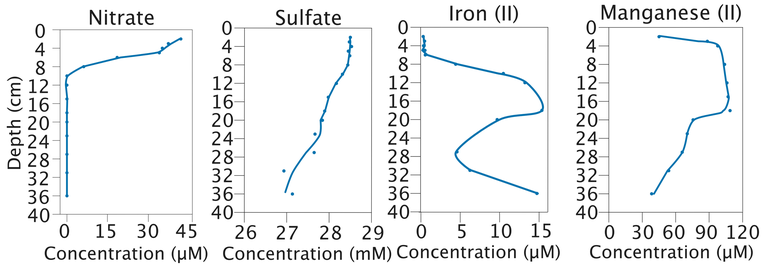
- Quantifying sulfur intermediates in porewaters is a critical first step towards achieving a better understanding of the oxidative sulfur cycle.
- Since very few studies have accomplished this, we provide here the first profiles of sulfur intermediates for the San Clemente Basin and Cocos Ridge.

WHAT IS THE GOAL OF OUR RESEARCH?

We integrate porewater depth profiles of sulfur intermediates, major ions, and redox-sensitive elements with 16S rRNA data of of the sediment microbial community composition to constrain the cycling of C and S.

Redox-sensitive elements profiles

San Clemente Basin (SCB)

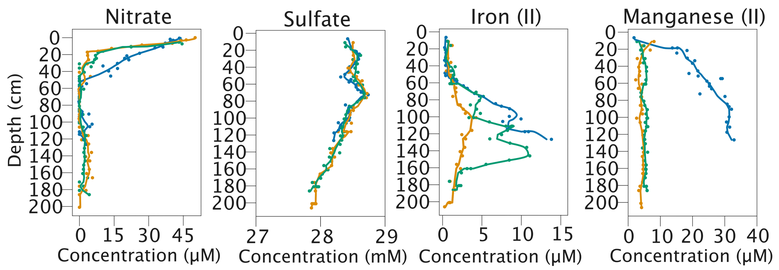


Dissolved iron and manganese are high in SCB at much lower depths than CR. Nitrate also gets depleted at shallower depths in SCB. All these are evidence of higher organic matter at SCB.

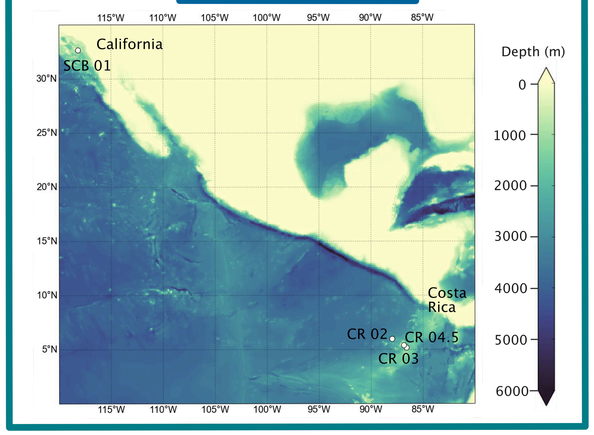
Manganese (II) and magnesium (not shown) both increase with depth only at CR02.

Sulfate doesn't get depleted in the sediments in CR at over 2 m depth.

Cocos Ridge (CR)



Study site

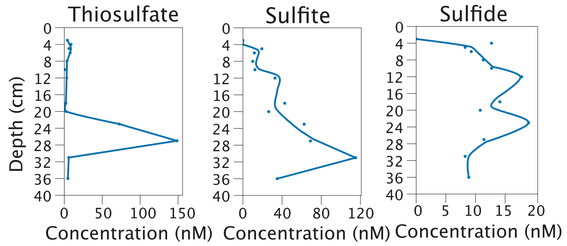


At **San Clemente Basin**, nitrate is depleted at shallow depths where ammonium-oxidizing bacteria dominate. Dissolved iron, manganese, and sulfur intermediates at further depths correlate with the presence of bacteria that can oxidize them.

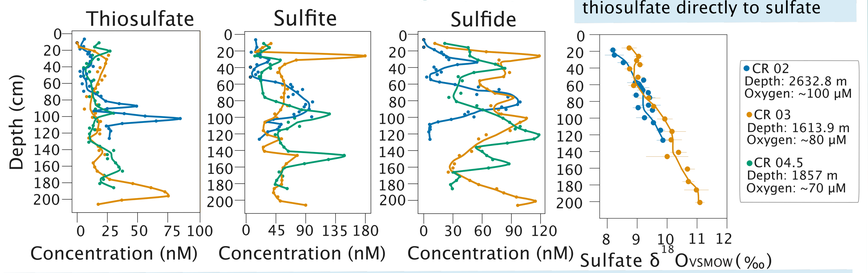
At **Cocos Ridge**, [nM] of reduced S species and O isotopes remaining stable at some depths are evidence of an active sulfur cycle and potential O isotope exchange between sulfate and S intermediates. Abundance of specific genes in the microbial community must be addressed to constrain which microbes are driving the S cycle at this location.

Reduced sulfur profiles

San Clemente Basin (SCB)



Cocos Ridge (CR)



In general, the concs. of the 3 reduced sulfur species quantified here increase with depth, but are 3 orders of magnitude lower than those in euxinic basins.

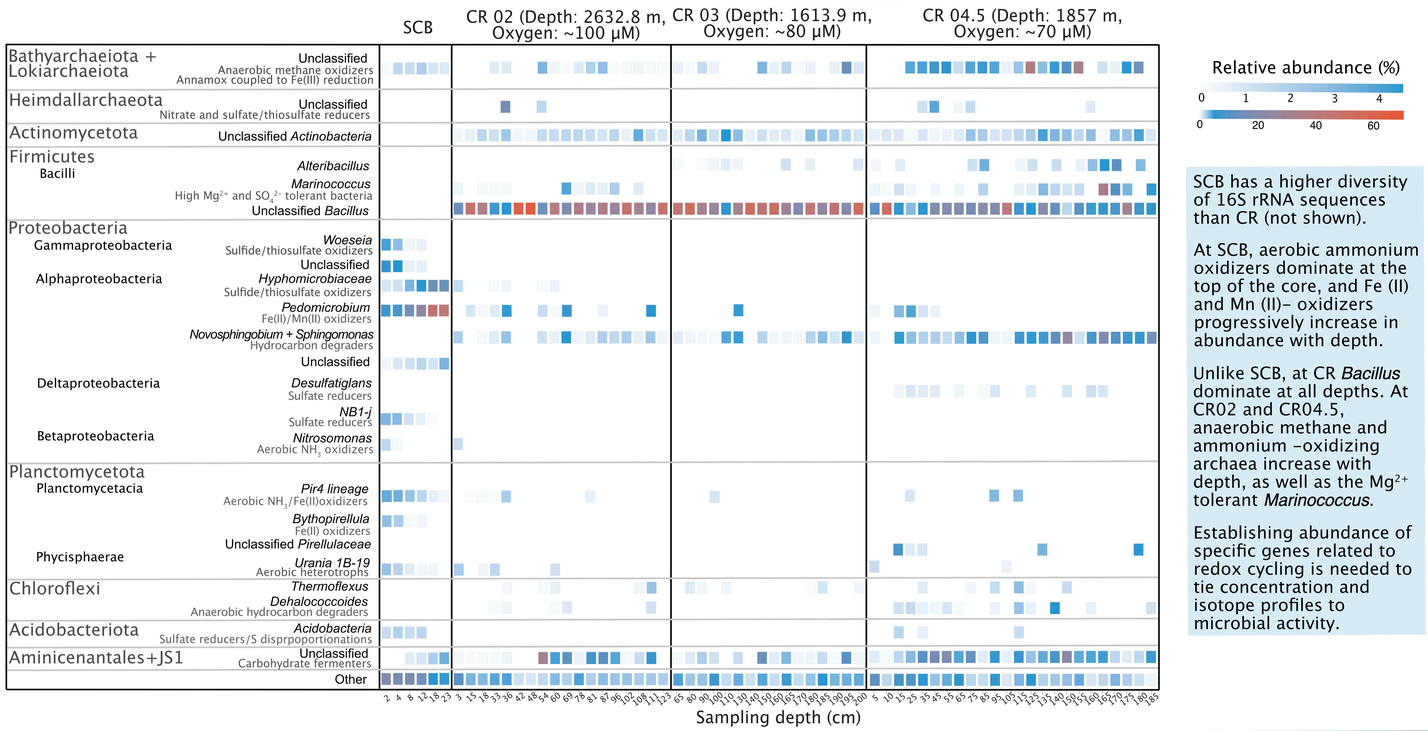
Sulfide and sulfite profiles seem to be coupled, indicating that there might be a spatial separation between:

- Microbes that oxidize sulfide with sulfite as intermediate
- Microbes that oxidize thiosulfate directly to sulfate

The $\delta^{18}O$ of porewater sulfate increases with depth in both of the CR cores analyzed.

- This is consistent with a normal kinetic isotope effect, as sulfate reduction increases with depth.
- There might be oxygen exchange between S intermediates and sulfate at depth ranges where the $\delta^{18}O$ remains constant.

Microbial community composition



SCB has a higher diversity of 16S rRNA sequences than CR (not shown).

At SCB, aerobic ammonium oxidizers dominate at the top of the core, and Fe (II) and Mn (II)- oxidizers progressively increase in abundance with depth.

Unlike SCB, at CR *Bacillus* dominate at all depths. At CR02 and CR04.5, anaerobic methane and ammonium -oxidizing archaea increase with depth, as well as the Mg^{2+} tolerant *Marinococcus*.

Establishing abundance of specific genes related to redox cycling is needed to tie concentration and isotope profiles to microbial activity.

Acknowledgements

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