Sr and Nd isotopes of modern cold seep carbonates from the northern South China Sea

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Methane-derived carbonate precipitation, a well-known phenomenon at hydrocarbon seeps on active and passive continental margins worldwide, forms as a result of microbial oxidation of methane and bacterial sulphate reduction. Seep carbonates are generally well preserved in the sedimentary and geological records, and hence can supply information about fluid compositions, fluid sources, and fluid migration pathways over geologic time. In cold seep related studies, it is important to identify the origin of methane-rich fluids. The determination is generally inferred from stable isotopes and rare earth elements. In addition, isotopic tracers have been used for investigating the origin of fluids in continental margin sediments (Sr, Li, B and I isotopes, e.g.).

In this study, we report the Sr and Nd isotopic compositions on a series of modern cold seep carbonate chimneys from the northern South China Sea. $^{87}Sr/^{86}Sr$ ratios of cold seep carbonates vary from 0.709171 to 0.709269, which are indistinguishable from modern seawater (mean 0.709175), reflecting a shallow marine Sr source.

ε_{Nd} values of cold seep carbonates are between -8.60 and -5.38, which lie within the range of modern sea water and sediments in the northern South China Sea. The Nd isotopic characteristics imply a mixed Nd source from two end members, but different proportions of mixture.

We conclude that the Sr and Nd isotopes can be used to identify the origin of fluids at cold seep sites.

This research is funded by the National Science Foundation of China (Grant No. 41203021) and the Jiangsu Postdoctoral Sustentation Fund, China (Grant No. 1201061C) and the State Key Laboratory for Mineral Deposits Research Fund of China (Grant No. 17-1112-2).

Microbial iron reduction in marine intertidal sediments

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Oxidized iron compounds may be important electron acceptors for anaerobic respiration, in particular in marine intertidal sediments. Tidal cycles generate changes in the position of the chemocline and may drive rapid cycling of iron between oxidized and reduced iron species. The possible mechanisms for iron(III) reduction include microbial iron reduction by respiratory microorganisms, use of iron(III) as electron sink by fermentative microorganisms and the indirect reduction of iron with sulfide that is generated by sulfate-reducing microorganisms. Using geochemical and omics methods we aim to identify the microorganisms responsible for iron(III) reduction and the pathways involved.

We have incubated the microbial community from the surface layer of a marine intertidal flat using medium that contains both iron, as sparingly soluble iron(III) hydroxide, and sulfate as electron acceptors in anaerobic continuous culture with different electron donors. Batch incubations with the enriched microbial community using labelled sulfate were carried out to evaluate the importance of the production of sulfide by sulfate-reducing bacteria for the indirect reduction of iron(III).

The development of the enriched microbial community was analyzed using automated rRNA intergenic spacer analysis (ARISA), and the metagenome of this enriched community was sequenced. Sequences denoting 16S rRNA genes and universal single copy genes were used to analyse the microbial community composition. The metagenome, together with metatranscriptomic and/or metaproteomic analyses, also gives insight into substrate utilization and the pathways involved in the reduction of iron and sulfate. Based on our data, a model for carbon, sulfate and iron(III) utilization in this system is presented.

DOI:10.1180/minmag.2013.077.5.7