Cyclic variations of iron isotope composition during diagenesis: the Kimmeridge Clay Formation (UK)

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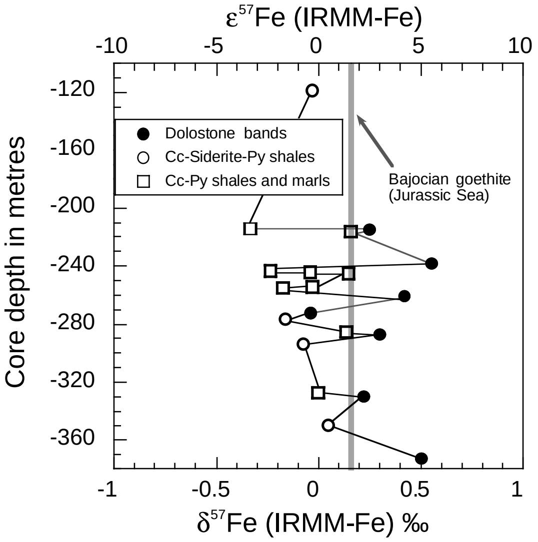
Key questions of iron isotope fractionation in low-temperature environmental systems focus on the relative roles of bacterial and inorganic redox processes. This study examines the Fe isotope composition of mineral assemblages from a core-section of the Upper Jurassic Kimmeridge Clay Formation (SQ1 borehole), located close to the type-section in Dorset. Three types of iron-bearing assemblage are defined by XRD and magnetic susceptibility data: shales/marls with (i) calcite+pyrite and (ii) calcite+pyrite+siderite; (iii) ferroan dolomite (dolostone) bands. Fe isotope measurements (made after total dissolution, ion exchange purification and MC-ICP MS analysis) show cyclic variations (Fig. 1).

Figure 1: Iron isotope results from the KCF



The epicontinental Jurassic sea source of the iron is represented by the analysis of Bajocian goethite. Relative to this value, pyrite and siderite-bearing samples are depleted in ^{57}Fe by up to 0.7 ‰, whereas the dolomite bands are ^{57}Fe-enriched. The ^{57}Fe-depleted values are consistent with the expectation of bacterially mediated reduction of iron to form pyrite and siderite, but not with the predictions of calculated iron isotope fractionation factors. The isotopic composition of dolostone bands correspondingly may reflect entrapment of residual ^{57}Fe-enriched component in the diagenetic pore waters.

Molecular approach to study microbial communities involved in modern dolomite formation

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Modern dolomite-precipitating environments, such as Lagoa Vermelha, Brazil (a hypersaline coastal lagoon) provide unique opportunities to directly investigate the microbial mechanisms involved in dolomite formation. To study the microbial community mediating dolomite precipitation, we examined the composition of bacteria entombed in sub-recent dolomite concretions and surrounding dolomitic sediment collected from the center of Lagoa Vermelha. We posed the following questions: 1) what are the molecular remains preserved inside the dolomite crystals, 2) are there differences between the microbial composition in the concretion and in the surrounding sediments, and 3) do changes occur with burial depth? To answer these questions, two dolomite concretions sampled from -15 and -40 cm below the sediment/water interface, representing respective sediment depositional ages of approx. 500 and <2,000 yr. BP, were studied together with their surrounding sediment. The microbial communities were evaluated using phospholipid fatty acids (PLFA) identification and fluorescent *in situ* hybridization (FISH). We used probes Eub338, Arch915, and SRB385, which target members of the Eubacteria and Archea domains, and sulfate reducing bacteria of the delta-subdivision of Proteobacteria, respectively. We observed both Eubacteria and Archaea in the concretions and sediment, with Eubacteria, being mostly sulfate-reducers, dominating in the concretions. Biomarkers (PLFA) for living bacteria and organisms detectable by FISH were found even in the oldest concretion. Our results indicate that a consortium of microbes is probably involved in the formation of dolomite and show that a combined molecular approach to study subsurface biomineralization is possible.