Cryptic sulfur cycle in the sediments of the Gulf of Aqaba (Red Sea)

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The Gulf of Aqaba is an oligotrophic marine system with oxygen-rich water column and organic carbon-poor sediments. Microbial sulfate reduction in sediments is inferred from the presence of traces of hydrogen sulfide, sulfide oxidation intermediates, pyrite (although at relatively low concentrations), and by the sulfur isotopic composition of sulfate and solid-phase sulfides. The concentration of hydrogen sulfide in the pore-water decreased with an increase in water column depth from 12 μmol L^{-1} at the shallow-water sites to ≤30 nmol L^{-1} at 694 m water depth. Although the concentrations of thiosulfate and sulfite in the sediments decrease with increase in water column depth, the ratio of sulfur oxoanions and hydrogen sulfide concentrations increases and becomes >1 at 694 m water depth. Pyrite sulfur content at 20-30 cm bsf depth decreases from 6-16 mmol kg^{-1} at 21 m to <0.2 mmol kg^{-1} at 694 m. Isotopic fractionation between pyrite and sulfate is -50±1‰ at 21 m depth and -60±1‰ in four samples from deeper sites, in which amount of pyrite was sufficient for sulfur isotope composition analysis. Although pyrite content in the majority of samples of deep-water sediment was too low for isotopic analysis, oxygen isotopic composition of sulfate is consistent with sulfate reduction followed by hydrogen sulfide reoxidation [1].

We suggest that observed trends may be explained by an impact of high fluxes of reactive iron(III) (hydr)oxides, which facilitate fast re-oxidation of hydrogen sulfide produced during microbial sulfate reduction and limits preservation of reduced sulfur in the form of pyrite. Reactive iron minerals are derived from two sources. The first source is dry precipitation of Saharan dust, which is characterized by high contents of iron minerals such as hematite and goethite. The second source is material transported by rare seasonal flash floods. Relative impact of flash floods-transported reactive iron decreases with depth.

[1] Blonder, B., Boyko, V., Turchyn, A.V., Antler, G., Sinichkin, U., Knossow, N., Klein, R., Kamyshny Jr., A. (2017) Frontiers in Microbiology, 8:1131.