Sulfur cycling in the sediments affected by high aeolian fluxes of reactive iron

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Biogeochemical cycling of redox-sensitive elements in the sediments of the Red Sea and of its northeastern extention, the Gulf of Aqaba, is strongly affected by high fluxes of reactive iron(III) (hydr)oxides. Sources of these minerals include direct aeolian deposition of desert dust and transport from creek beds by seasonal flash floods. Dust is relatively rich in highly reactive iron minerals, especially in its dithionite-extractable fraction, which includes hematite and goethite. Creek bed material, which is preferentially deposited in the coastal areas, is relatively poor in reactive iron(III) (hydr)oxides due to alteration during transport and dilution of dust deposited on land by material from weathering of local rocks. These settings result in three important consequences for biogeochemical cycling of redox-sensitive elements in the sediments of the Gulf of Aqaba:

First, sharp horizontal gradient of redox conditions is established in the sediments. Pore-waters of the upper 30 cm of near-shores sediments are sulfidic, while at intermediate water depths pore-waters are iron-rich. Sediments overlaid by deep waters are characterized by both iron- and manganese-rich pore-waters [1]. Secondly, high concentrations of reactive iron(III) (hydr)oxides at the deep-water sites result in cryptic sulfur cycle, e.g. sulfate reduction followed by nearly quantitative reoxidation of sulfide. Thirdly, sinking of the dust particles bearing high reactive iron to total iron ratios is associated with only minor alteration in the water column. This process results in translation of these high ratios directly to the surface sediments followed by further preservation during the early diagenesis. Such sequence of processes results in iron speciation, which is anomalously high for sediments overlaid by oxygen-rich water column.

[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.