Multiple sulfur isotopes in pyrite and barite-rich sediments from the Barberton Greenstone Belt: Evidence for microbial sulfur cycling?

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The appearance as early as 3.4 Ga of microbial SO_4^{2-} reduction [1, 2] and S^0 reduction or disproportionation [3] has been suggested by stable S isotope variations in sulfide minerals from Archaean greenstone belts. Here we attempt to identify traces of these metabolisms in previously unstudied exceptionally fresh drill core material from the Lower Mapepe formation (3.26 to 3.23 Ga), Barberton Greenstone Belt, South Africa. The core was drilled into the main workings in the Baryte Valley Syncline on farm Heemsteede 378 JU. Samples are taken from a 100 m section of shales, cherts, tuffs and conglomerate that cuts four barite horizons of syn-sedimentary origin [4]. Rare earth element and Y data in cherts and dolomitic units support a pervasive marine influence. Trace elements in pyrite indicate a low temperature sedimentary origin (Co/Ni= 0.1-1, Se/S <5 x 10^{-5}).

We report individual mineral multiple S isotope data (^{32}S, ^{33}S, ^{34}S, determined by SIMS) for: (1) interstitial grains and inclusions of pyrite from massive barite beds, (2) syn-sedimentary microcrystalline pyrite layers in chert and reworked barite sand deposits, and (3) isolated euhedral pyrites in massive chert and barite rich units. $\Delta^{34}S$ in bedded barite and barite sands varies between +4 and +6‰, whilst pyrites show a greater range from +5 to -8 ‰. Pyrite $\Delta^{33}S$ (-1 to +4 ‰) is extremely heterogeneous on a scale of micrometers, but individual laminations and petrographic associations of pyrite define much more limited values of $\Delta^{33}S$ (within 0.5 ‰) over a range of $\Delta^{34}S$. Our results are consistent with models for combined microbial S^0 disproportionation and S^0 reduction [3], although microbial versus inorganic fractionation remains difficult to resolve.

[1] Ohmoto *et al.* (1993) *Science* **262**, 555-557. [2] Shen *et al.* (2001) *Nature* **410**, 77-81. [3] Phillippot *et al.* (2007) *Science* **317**, 1534-1537. [4] Bao *et al*. (2007) *GCA* **71**, 4868-4879.

Microbiological characteristics of circulation mud fluids during the first operation of riser drilling by the deep-sea drilling vessel "*Chikyu*"

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Quality assurance and control is significant for the scientific drilling in order to accurately characterize physical, geochemical, and biological properties in the cored deep subseafloor materials. To explore deep subseafloor life and its biosphere, identification and control of microbial contamination in drilling cores is critical for highly sensitive molecular analyses as well as cultivations, especially for the evaluation of low biomass and/or extremely harsh deep environments.

We studied some microbiological characteristics of circulation mud fluids before and after the first riser drilling operation by the newly constructed deep-sea drilling research vessel *"Chikyu"*. During the *"Chikyu"* shakedown expedition CK06-06 in 2006, we used the riser system for drilling 547 to 647 meter below the seafloor into the sediments offshore the Shimokita Peninsula of Japan. Cultivation experiments showed that no microbial growth was observed in the pre-circulation mud fluid, while 4×10^5 colonies per 1 ml were observed in the post-circulation mud fluid; all cultured bacterial isolates were found to be *Halomonas*. Using culture-independent molecular analysis, 16S rRNA gene sequences of *Xanthomonas*, which is used for industrial production of the mud fluid viscosifier 'xanthan gum', were predominantly detected in the pre-circulation mud fluid, while *Halomonas* sequences consistently dominated the clone library constructed from the post-circulation mud fluid. Archaeal 16S rRNA genes were amplified only from the post-circulation mud fluid; these archaeal clone sequences were affiliated to the Marine Crenarchaeota Group I (MGI), Marine Euryarchaeota Group II (MGII), Miscellaneous Crenarchaeotic Group (MCG), South African Gold Mine Euryarchaeotic Group (SAGMEG), Soil Group, and *Methanococcus aeolicus*. These results suggest that *Halomonas* contaminated and grew in the tank of circulation mud fluids, and other indigenous deep subseafloor microbial components, especially deep subsurface archaea, were also mixed into the post-circulation mud fluid.