Petrography and composition of iron formation from the ca. 3.8 Ga Nulliak Supracrustal Association (northern Labrador, Canada)

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Banded iron formations (BIFs) are important sources of information on the composition of ancient seawater [1,2]. Eoarchean BIFs in particular may disclose information on the nutrient levels bracketing the evolution of early microbial metallo-enzymes. Only a limited amount of pre-3.6 Ga year old BIFs are know, and chemical sediments from the ca. 3.8 Ga year old Nulliak Supracrustal Association of northern Labrador (Canada) [3] offer an exciting opportunity to expand our data base.

We present new petrographic and geochemical data on these Fe- and Si-facies iron formations, by integrating geochemical relationships observed between minerals in thin section and whole rock chemistry. This approach provides an important framework for studying the chemical variations in these sediments, on several scales. Preliminary results show that the Nulliak sediments are relatively aluminous (Al_2O_3>1 wt%), with correspondingly high abundances of Zr (up to 20 ppm) and other high-field strenght elements (e.g., Nb, Hf), suggesting a non-trivial detrital component. These chemical sediments contain noteworthy abundances of Cr, Ni, Zn, Sr, and Ba, while other elements tend to be <25 ppm. The high Ni and Zn abundances correlate well with previous studies on Eoarchean-aged iron formations, suggesting that these metals were found globally in high concentrations during the Eoarchean [3,4]. Rare earth element and yttrium profiles tend to show seawater-like anomalies (LREE<MREE<HREE; positive La and Eu anomalies, and superchondritic Y/Ho ratios) despite granulite-facies metamorphic overprinting. Collectively, these findings indicate that at least some of the original seawater signature has been preserved. Neverthless, these sediments may not be an accurate seawater proxy, as detrital material tends to obscure seawater signals. Instead, they may provide a measure of balanace between hydrothermal- and terrestrial inputs affecting the composition of Eoarchean seawater composition as reflected in BIFs.

[1] Bjerrum and Canfield (2002) *Nature* 417, 159-162
[2] Konhauser et al. (2009) *Nature* **458**, 750-753
[3] Nutman et al. (1989) *Canadian Journal of Earth Sciences* **26**, 2159-2168
[4] Mloszewska et al. (2012) *Earth and Planetary Science Letters* 317-318, 341-342.

GOLIATH: A systems biology, geochemical and physiological approach to discern microbial transformations of Mercury and Methylmercury.

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BACKGROUND: Mercury (Hg) contamination is a global concern. Hg methylation is an important biogeochemical process, which generates the potent neurotoxin monomethylmercury (MeHg). Net MeHg production in aquatic ecosystems is linked to environmental and geochemical parameters along with electron donor and acceptor availability. Recently we found that methylating communities contained high populations of Desulfobulbus and Geobacter spp. To gain a deeper understanding of the microbial community populations invlolved in, and geochemical influences on, Hg methylation, physiological and meta-omic analyses were performed. **METHODS**: Intact sediment cores from two methylating sites (NOAA, upstream; New Horizon, downstream) and a background site were collected and used to construct sediment microcosms from different depths with 6 different carbon/electron sources. All microcosms were spiked with Hg stable isotope tracers to enable quantification of both Hg methylation and MeHg demethylation and incubated under anaerobic conditions in the dark for 48 hours at room temperature. DNA from the original core material and incubations were hybridized to functional gene arrays and sequenced via 454 16S rRNA gene pyrosequencing. **RESULTS**: Functional gene array results revealed a greater relative abundance of Hg(II)-reduction genes at NOAA while actual methylation was higher downstream at New Horizon. Each of the latter two sites displayed ~15X more methylation than the background site. Upstream at NOAA, methylation was moderately stimulated by methanol and ethanol but not by acetate, lactate, propionate or cellobiose, while downstream at New Horizon cellobiose stimulated methylation relative to unamended controls. Meta -genomic, -transcriptomic, and -proteomic analyses as well as 454 pyrosequencing are currently underway. **CONCLUSIONS**: The multidisciplinary combination of the above approaches are being employed together for the first time in order to more comprehensively ascertain the influence of geochemistry on the microorganisms, genes, and gene products that are differentially present, abundant and expressed in active MeHg generating ecosystems.