Photoferrotrophy and Fe-cycling in a freshwater column

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Ferruginous (anoxic and iron-rich) conditions dominated ocean chemistry throughout much of the first 3.5 billion years of Earth history. Modern ferruginous water masses are rare, but detailed examination of these oddities, especially of photoferrotrophs and their Fe-reducing respiratory counterparts, could yield important insights into the early evolution of life on Earth. Here, we report pelagic photoferrotrophs from Kabuno Bay, DR Congo. Based on 16S rDNA, the Kabuno Bay photoferrotrophs are similar to laboratory cultures of *Chlorobium ferrooxidans*, the only member of the Chlorobi previously known to conduct photoferrotrophy. Photoferrotrophs comprised up to 38.3%, of the total microbial communinty and exhibited high rates of phototrophic ferrous Fe oxidation. Up to 60% of total depth integrated bacterial production was carried out at depths where photoferrotrophic GSB dominate. Microbial groups involved in methanogenesis and Fe-reduction also comprised large fractions of the microbial community within depth intervals domminated by photoferrtrophs. Microorganisms typically implicated in the sulfur cycle were only present at low relative abundances, and this is consitent with low measured rates of sulfate reduction and sulfide oxidation. Our findings in Kabuno Bay support models for early ocean ecosytems with primary production driven by photoferrotrophy and organic matter degradation channeled through both Fe-reduction and methanogenesis.

A meta-analysis reveals biases in methods to quantify marine microorganisms

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There is no universally-accepted method for quantifying specific microbial taxa in the marine subsurface, but this is a crucial first step in any analysis of sedimentary microbial ecology. The two most common methods are fluorescent in situ hybridization (FISH), often with catalyzed reporter deposition (CARD-FISH), and quantitative PCR (qPCR). We compiled sediment cell quantifications from published papers and defined yield as the sum of bacterial and archaeal FISH/CARD-FISH counts divided by total cell counts. We found that permeabilization with proteinase K results in higher yield, as well as higher percent archaea, than permeabilization with lysozyme or other methods, which may be explained by the fact that lysozyme hydrolyses peptidoglycan, which does not exist in archaeal cell walls. Studies in which the absence or near-absence of archaeal CARD-FISH signals have been used to argue for the dominance of bacterial activity in the deep subsurface (e.g. [1], [2]) used lysozyme, suggesting that the low abundance of Archaea in those studies may be artifactual. The ratio of qPCR-determined 16s rDNA copy numbers to directly-counted cells is highly variable, and is often outside of physiologically reasonable range of 1-10, suggesting that qPCR does not provide absolute quantification of specific taxa.

[1] Schippers, *et al*.. (2005), Nature, 433: 861-864. [2] Webster, *et al*.., (2009), Environmental Microbiology, 11:239-257.

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