Sneaky sulfate signals: Isotope fingerprints reveal *cryptic* pathways

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The presence of sulfate in deeply buried methanic marine sediments traditionally considered to be sulfate-free (e.g. Holmkvist *et al* [1]) implies that sulfur (S) cycling is an ongoing process in the deep biosphere, reflecting catabolic pathways where S constituents act as shuttles between compounds that are being oxidized on the one side and reduced on the other side. The pivotal role of the S constituents in such processes often remains hidden or 'cryptic' because while the S compounds are continuously reduced and re-oxidized, the overall inventory of the S constituents remains constant. Exploring cryptic S cycling is of importance for two reasons. First, it provides insight into how microbial processes under energy limitation work, and if/how, specialized microorganisms share the already small amount of available energy to carry out different biochemical reactions. Second, it potentially challenges or at least transforms the paradigm that there is a sequential cascade of electron accepting processes in the environment across redox gradients, with the energetically most favorable electron acceptor consumed first and the least attractive process carried out last. In other words, dissimilatory sulfate reduction could occur in presence of Mn(IV) or Fe(III), or in the methanogenic zone.

We elucidate deep sulfate cycling in the Aarhus Bay sediments and at other sites by looking at both the S and oxygen (O) isotope composition of sulfate, which is affected by sulfate generation and consumption in combination with a numerical model. The combined S and O isotope singature of sulfate allow us to disentangle the processes responsible for sulfate production, such as oxidation of reduced organic and inorganic S and dissolution of barite from processes that consume sulfate, such as sulfate reduction.

Whereas cryptic sulfate generation is evident from the observation of sulfate in the methanic zone, where sulfate has canonically been presumed not to be present, this is not the case for the main sulfate reduction zone in marine sediments. Here, only the analysis of the combination of concentration and S and O isotope composition profiles of sulfate reveals the hidden intricacies of S cycling.

[1] Holmkvist *et al* (2011) *Geochim. Cosmochim. Acta* **75**, 3581-3599.

Functional contrasts and functional redundancy in Arctic bacterial communities in the oxic water column and anoxic sediments

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Investigation of enzymatic activities and bacterial community composition in the water column and sediments of an Arctic fjord of Svalbard during two summers captured the transition from a fully oxidized water column to anoxic, sulfate-reducing sediments. In 2008, water column bacterial clone libraries were dominated by members of the phylum *Verrucomicrobia* and the subphylum *Flavobacteria* (Fig. 1), known as aerobic degraders of polysaccharides. Some Svalbard phylotypes were specifically related to single cells attaching to and presumably taking up laminarin and xylan [1]. In addition to these substrates, chondrotin sulfate and fucoidan were hydrolyzed in the water column. In sediments, phylotypes of the anaerobic *Bacteroidetes* and sulfate-reducing *Deltaproteobacteria* were prominent, and a greater range of polysaccharides were hydrolyzed. Despite considerable diffences in water column community composition between 2007 [2] and 2008, patterns of enzyme activities were largely constant. We therefore have evidence of functional redundancy among water column communities of differing composition, which nonetheless use the same comparatively narrow spectrum of substrates relative to their benthic counterparts.

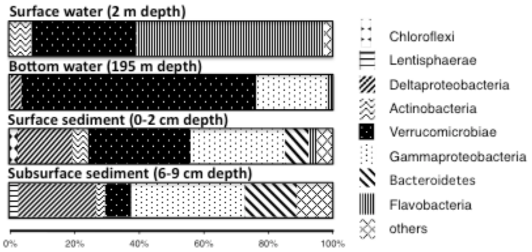

Figure 1. Bacterial 16S rRNA gene clone library composition of water column and sediment samples.

[1] Martinez-Garcia *et al* (2012). *PLoS* One 7:335314. [2] Teske *et al* (2011). *AEM* 77:2008.

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