

## Preliminary model of hydrothermal circulation at East Pacific Rise 9°50'N constrained by thermal, chemical, and seismic data

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The East Pacific Rise 9°50' N area has been a subject of intense multidisciplinary study for two decades. Currently, numerous data sets provide strong constraints on magmatic activity, on the depth and flow geometry of hydrothermal circulation, on the thermal and chemical evolution of vent fluids, and on the evolution of biological communities. These data together provide strong constraints on acceptable mathematical models of the magma-hydrothermal system.

Using a combination of thermal, geochemical and seismic data as constraints [1, 2, 3], we develop a preliminary model hydrothermal circulation along approximately 2 km of ridge axis from TWP to the Bio9 vent complex. We first use a single-pass model [4] together with a heat flux estimate of 160MW and average vent temperature of 370°C to obtain a mass flux of  $\approx 80$  kg/s, a conductive boundary layer thickness of  $\approx 25$  m, and a permeability of the discharge zone ranging between  $3 \times 10^{-12}$  and  $3 \times 10^{-13}$  m<sup>2</sup>. Secondly, we use a two-limb single-pass model using the observed partitioning of heat flow between focused and diffuse discharge [5] and vent chemistry [2] to show that at least 80% of the total heat flow comes from magma sources. As a result of these analyses, we find that the sub-axial magma chamber must be actively replenished on a decadal time scale, which is consistent with recent petrological data. Finally, the preliminary model suggests that the seismically inferred recharge zone may not be large enough to carry all the flow without clogging as a result of anhydrite precipitation. Further analysis of this issue will require numerical modeling.

[1] Ramondenc *et al.* (2006) *EPSL* **245**, 487–497. [2] Von Damm & Lilley (2004) *Geophys. Monogr.* **144**, 245–268. [3] Tolstoy *et al.* (2008) *Nature* **451**, 181–184. [4] Lowell & Germanovich (2004) *Geophys. Monogr.* **148**, 219–244. [5] Germanovich *et al.* (2010) *J. Geophys. Res.* (in press)

## Sulfate reduction in peatlands – Does a rare keystone microorganism drive a process that mitigates global warming?

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Methane emission from peatlands contributes substantially to global warming but is significantly reduced by sulfate reduction, which is fuelled by globally increasing aerial sulfur pollution. However, the biology behind sulfate reduction in terrestrial ecosystems is not well understood and the key players for this process as well as their abundance remained unidentified. At a model peatland site, we monitored long-term temporal and spatial changes in the diversity of the marker genes *dsrAB* using microarray and quantitative PCR techniques. These genes encode subunits of dissimilatory (bi)sulfite reductase and are generally characteristic for microorganisms that reduce sulfate, sulfite or some organosulfonates for energy conservation, but can also be present in anaerobic syntrophs. Members of novel, uncultivated *dsrAB* lineages (approximately representing species-level groups) (i) dominated a temporally stable but spatially diverse *dsrAB* community and (ii) represented relatively abundant 'core' members of the autochthonous microbial community. A biogeography survey showed that several of these novel *dsrAB*-carrying microorganisms are widespread in different peatlands from various geographic locations (distance  $\sim 1$ -400 km). Surprisingly, comparative 16S rRNA gene stable isotope probing in the presence and absence of sulfate indicated that a *Desulfosporosinus* species, which constitutes only 0.006% of the total microbial community, is the major sulfate reducer in the model peatland. Parallel stable isotope probing of *dsrAB* confirmed that no other microorganisms contributed substantially to sulfate reduction. For the identified *Desulfosporosinus* species a high cell-specific sulfate reduction rate of 341 fmol SO<sub>4</sub><sup>2-</sup> cell<sup>-1</sup> day<sup>-1</sup> was determined. Thus, the small *Desulfosporosinus* population has the potential to reduce sulfate *in situ* at a rate of up to 18.5 nmol (g soil w. wt.)<sup>-1</sup> day<sup>-1</sup>, sufficient to account for the bulk of sulfate reduction in the peat soil. These data show that the identified *Desulfosporosinus* species, despite being a member of the 'rare biosphere', can drive an important biogeochemical process that diverts the carbon flow in peatlands from methane to CO<sub>2</sub> and, thus, alters their contribution to global warming.