

Fluid flow and redox metal cycling in Cayman Trough hydrothermal sediments

RACHEL A. MILLS^{1*}, WILLIAM B. HOMOKY¹
AND THE DEEPESTVENTS SHIPBOARD SCIENTIFIC TEAM

¹Ocean and Earth Science, University of Southampton,
National Oceanography Centre Southampton, SO14 3ZH,
UK (*correspondence: rachel.mills@soton.ac.uk,
w.homoky@soton.ac.uk)

Metalliferous sediments accumulate adjacent to active hydrothermal vent sites via mass wasting of mound debris and fall-out of particles from hydrothermal plumes. Continued redox reactions at the limit of oxygen penetration lead to 'zone refining' of the sediment pile and metal enrichment around the active redox front [1]. Diffusive processes and active circulation of dilute hydrothermal fluids through the sediments may lead to significant fluxes of some elements into and out of the seafloor, though this is poorly constrained and not included in evaluations of ocean budgets for these elements.

We present dissolved micro-nutrient trace metal pore-fluid data for representative sediments from the Beebe Vent Field [2]. The Beebe Vent Field fluids are extremely deep (5000 m), high temperature (>400°C) and metal-rich. Fragile sulfide chimneys topple readily to form metalliferous sediments which are oxygen depleted within 3-7 mm of the seawater interface. The deep sedimentary setting precludes significant carbonate accumulation at the seafloor and pelagic sedimentation is minimal leaving weathered sulfide exposed to seawater. Primary chimney mineral phases which dominate the sediment, break down during seafloor weathering and there is a flux of reduced metals to the overlying water column associated with this sedimentary reprocessing. Therefore, secondary processing of hydrothermal material during active weathering of seafloor deposits can lead to enhanced fluxes of trace metals to the ocean which are then transported out of the benthic boundary layer via plume entrainment and dispersal over significant distances.

[1] Severmann, S., *et al.*, (2006) *Geochim. Cosmochim. Acta*, 70, 1677-1694. [2] Connelly, D.P. *et al.*, (2012) *Nature Comms.*, 3, doi:10.1038/ncomms1636.

Biomass residues from different classes of soil microorganisms are a significant source of soil organic matter

A. MILTNER*, J. ACHTENHAGEN, C. HOFFMANN-JÄNICHE, M. SCHWEIGERT, M. BRAECKEVELT, F.-A. HERBST, J. SEIFERT, T. FESTER AND M. KÄSTNER
UFZ - Helmholtz Centre for Environmental Research, Leipzig,
Germany (*correspondence: anja.miltner@ufz.de)

Introduction

Cell envelope fragments originating from soil microorganisms were demonstrated to contribute significantly to the formation of soil organic matter (SOM) [1]. This hypothesis was supported by chemical and microscopic analyses [1] as well as by NMR spectroscopy [2]. Different classes of soil microorganisms have different chemical compositions of their cell envelopes and thus may contribute to SOM formation to a different extent. We compared the fate of *Escherichia coli* (Gram-negative bacterium), *Bacillus subtilis* (Gram-positive bacterium) and *Laccaria bicolor* (ectomycorrhizal fungus) in soil to estimate their relative contributions to SOM formation.

Material and Methods

¹³C-labeled organisms produced by culturing them on labeled glucose were mixed with soil and incubated for up to 224 days. Isotopic data of soil and CO₂ released by respiration were used to set up mass balances. Additional information about the fate of the biomass C was derived from quantitative and isotopic analyses of fatty acids and amino acids. Selected samples were also analysed by scanning electron microscopy.

Results and Discussion

For all classes of microorganisms, substantial amounts of the label remained in the soil. Fungal biomass was mineralised slower than bacterial biomass, with Gram-negative bacteria being mineralised slightly slower than Gram-positive ones. The amount and isotopic composition of the biomolecules showed that substantial amounts of the bacterial biomass-derived C were incorporated into non-living SOM. Proteins seemed to be particularly prone to stabilisation in soil: Highly labeled *B. subtilis* proteins were detected until the end of the experiment. Biomass residues of all types of soil organisms thus contribute to SOM formation, and proteins seem to be involved significantly in this process.

[1] Miltner *et al.* (2012) *Biogeochemistry* **111**, 41-55. [2] Simpson *et al.* (2007) *Environ Sci Technol* **41**, 8070-8076.