

Non-chondritic sulfur isotope composition of the Earth's mantle: Implications on planetary differentiation

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Sulfur (S) is a siderophile and moderately volatile element. Its abundance and isotope composition in accessible parts of the terrestrial mantle can therefore provide constraints on both accretion and planetary differentiation. We have investigated the ³⁴S/³²S ratio of 23 glasses dredged on the south-Atlantic ridge between 40° and 55°S. Several of the typical mantle end-members feed the source mantle of the two plumes and analyzed samples have been chosen to reflect this geochemical variability, hence offering a unique opportunity to address ³⁴S/³²S variations with respect to various mantle heterogeneities.

We show that south-Atlantic MORB display ³⁴S/³²S ratios directly correlated to ⁸⁷Sr/⁸⁶Sr and ¹⁴³Nd/¹⁴⁴Nd. These isotope trends are compatible with a binary mixing between two extreme components: The depleted mantle, having a δ³⁴S of -1.28±0.33‰, and a S-rich component with a δ³⁴S > 1.05 ± 0.10‰, that we infer to be subducted sediments (i.e. neither sub-continental lithospheric mantle nor lower continental crust) variably distributed in the sources of two local plumes. Our dataset imply that substantial amount of S survives slab devolatilization and thereby support efficient recycling of S via sediment subduction.

As the chondritic average δ³⁴S is constrained at +0.04 ± 0.31‰ [1,2], the negative value of depleted end-member consistently illustrates a non-chondritic feature. Furthermore, the amount and isotope composition of surficial S cannot balance out the depleted mantle to a chondritic value. Such distinctly non-chondritic ³⁴S/³²S ratio for the depleted mantle can only be reconciled with a core-mantle differentiation record, implying that most of the sulfur and elements of comparable volatilities have been delivered to the Earth before such planetary differentiation event.

[1] Gao *et al.*. (1993) GCA **57**, 3159-3169. [2] Gao *et al.*. (1993) GCA **57** 3171-3176.

Frequent bacteria-phage interactions in deep biosphere

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Recent discoveries suggest that subsurface microorganisms constitute a significant fraction of the living biomass on our planet, but little is known so far about their life histories and interactions. Here, we employed single cell genomics to obtain cultivation-independent information about *in situ* bacteria-phage interactions in 0.6 to 3.8 km deep fractures in the 2.9 byr old Witwaterstrand Basin, South Africa.

Genomic sequencing of 17 single amplified genomes (SAGs) revealed viral sequences in nine SAGs, suggesting that viral infections are prevalent in these isolated communities. We recovered partial genomes of Mu-like transposable phages, retrons, and lambda-like prophages from SAGs of Firmicutes *Desulforudis* and *Thermincola*, which are known to be indigenous to deep subsurface environments. The discovered phages, while sharing some conserved genes, are highly divergent from known viruses.

Our results suggest prevalence of lysogenic host-phage systems in the studied subsurface fractures, which may be more sustainable in these extremely isolated and simple microbial communities, as compared to lytic infections. The types and genome content of the discovered phages also suggest involvement in host DNA shuffling, which may be an important mechanism for deep subsurface microbial evolution.