Fractionated refractory elements in the Allende meteorite

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Chondrites are mixtures of various components with very different chemical compositions, e.g. chondrules, matrix, metal, and rare Ca, Al-rich inclusions (CAI). Bulk analyses of different aliquots of a single meteorite thus depend on the size and distribution of these constituents. A certain sample size is consequently required to avoid compositional bias due to sample heterogeneity, and to assure a truly representative bulk composition.

Here, we investigate the effect of sample heterogeneity on the major and trace element composition of the CV3 chondrite Allende using a single 30 g slice, which is 22.5 cm² in dimension and 4 mm thick. Thirty-seven equally sized pieces with an average sample weight of 0.6 g were powdered and aliquots of 0.12 g and 0.02-0.03 g were analyzed by XRF for major and ICP-MS for trace elements.

Mg, Si and Fe are essentially isochemical (S.D. 0.9, 1.3 and 2.6%, respectively) on the mm-cm scale [1]. Al and Ca are more variable (S.D. 17 and 9%, respectively), caused by different proportions of mm-size CAIs [1], many of them with strongly fractionated group II REE patterns [2] and relative enrichment of the more volatile refractory elements (Ta, U, Nb, Sr, Tm, Nd) over the strongly refractory elements (Lu, Zr, Hf). With increasing bulk Al and Ca concentrations group II patterns become more pronounced and more variable. The total average of all 37 samples has a clear group II pattern, with Nb and U being 30% more enriched than Er and Lu relative to CI, similar to inferences by [3].

If the fractionated refractory element pattern of our 30 g Allende sample is representative of its parent body, bulk planetary bodies, including Earth-forming planetary embryos, may also have refractory element ratios different from CI chondrites. This requires large-scale removal of a superrefractory component in the solar nebula.

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[2] Mason, B. & Taylor, S.R. 1982. Smithonian Contrib. Earth Sci. 25, 1–30.
[3] Fegley B. & Kornacki A. S. 1984. Lunar Plan. Sci. Conf. XV, 262–263.

Gene expression of dissimilatory sulfite reductase in *Desulfovibrio vulgaris* as a marker for the rate of sulfate reduction in natural systems

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We tested whether the gene expression of dissimilatory sulfite reductase (dsr mRNA), a critical enzyme in the sulfate reduction pathway, can serve as an indicator of the rate of sulfate reduction in natural systems. We grew Desulfovibrio vulgaris in fed-batch reactors under electron-donor limiting conditions. To simulate conditions characteristic of oligotrophic environments such as anoxic aquifers, we constrained the rates of sulfate reduction from 0.15 μ M h⁻¹ to 19 μ M h⁻¹ by controlling the rate of formate addition into the system. We used quantitative-PCR to measure the number of dsr mRNA transcripts per cell from biomass sampled over the course of these experiments. We observed a well-defined relationship between the rate of sulfate reduction and the number of dsr mRNA transcripts per cell. Cells from experiments with the highest rate of sulfate reduction contain 36 times more dsr mRNA than those from experiments with the lowest reduction rate. These results suggest we might be able to infer rates of sulfate reduction in the field by measuring the amount of dsr mRNA per cell in biomass samples. Such estimates are difficult to make directly because the rate at which bacteria consume reactants and generate products cannot be observed readily in many environments, such as aquifers open to groundwater flow.