U isotope variations in CAIs: Implications for the age of the Solar System

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Uranium has two primordial isotopes, ^{238}U and ^{235}U, which were produced by r-process nucleosynthesis. The isotope composition in meteoritc materials is generally considered to be constant, which is an essential prerequisite for U-Pb and Pb-Pb dating. The absolute age of the Solar System is mainly based on Pb-Pb ages of CAIs (e.g. [1]), which are considered to be the oldest solid condensates from the protoplanetary disk. Here we present high precision analyses of ^{238}U/^{235}U in bulk Allende, Allende matrix-CAI mixtures and individual CAIs that were determined relative to the SRM 950a U standard (^{238}U/^{235}U = 137.88) with a double spike technique [2, 3] on two Thermo-Neptune MC-ICP-MS instruments at Frankfurt and ASU. Bulk Allende displays ^{238}U/^{235}U that are only slightly lower (by 0.15‰ ± 0.05‰, 2SD) than those of terrestrial basalts. In contrast, Allende CAIs display significant U isotope variations, ranging between ^{238}U/^{235}U = 137.49 and 137.88, i.e. 2.4‰ (± 0.2‰, 2SD) lower and 0.4‰ (± 0.1‰, 2SD) high than that of bulk Allende.

There are 3 possible explanations for these isotope variations: (1) nucleosynthetic anomalies preserved in CAIs, (2) decay of extant ^{247}Cm to ^{235}U ($T_{1/2}$ ~ 15.6 Myrs) and fractionated Cm/U in CAIs or (3) isotope fractionation during chemical reactions, as recently observed on Earth [3, 4]. Particularly low ^{238}U/^{235}U (but no correlation with Nd/U or Th/U as proxy for Cm/U (e.g. [2])) was observed for two group-II CAIs. Allende matrix-CAI mixtures, consisting of ~ 30% group-II CAIs (as modeled by their REE pattern), also display slightly lower ^{238}U/^{235}U relative to that of bulk Allende. Possibly, the U isotope composition in the protoplanetary disk was still heterogeneous when these very primitive CAIs formed. Notably, our results demonstrate that a constant value for ^{238}U/^{235}U can not generally be assumed for Pb-Pb dating of CAIs; e.g. using the CAI with the lowest ^{238}U/^{235}U of this study for Pb-Pb dating would require a ~ 4 Myr age adjustment towards a younger age.

[1] Amelin *et al.* (2002) Science **297**, 1678-1683. [2] Stirling *et al.* (2005) GCA **69**, 1059-1071. [3] Weyer *et al.* (2008) GCA **72**, 345-359. [4] Stirling *et al.* (2007) EPSL **264**, 208-225.

Biodegradation of naphthenic acids

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The vast heavy oil fields and tar sands in North America represent a 6 trillion barrel resource that has not yet been fully exploited. In addition to the oily bitumen, these tar sands also contain complex mixtures of mainly alicyclic carboxylic acids known as 'Naphthenic Acids' (NAs). NAs cause severe environmental and economic problems as they are recalcitrant, corrosive and are acutely toxic to a wide range of organisms. Aromatic compounds make up a small, but so far unexplored fraction of the NA mix.

We adopted a novel approach; combining analytical and molecular techniques to characterise and quantify aromatic NA-degrading microorganisms in relation to NA biodegradation rates. Environmental samples from a hydrocarbon impacted site were inoculated into minimal media containing individual synthetic aromatic carboxylic acids as the sole carbon and energy source. GC-MS analysis demonstrated complete biodegradation had occurred on enrichments grown on the least-branched alkyl side chain whilst the acids with more-branched side chains were recalcitrant. Identification of metabolites suggested that degradation involved β-oxidation of the alkanoate side chain.

Molecular analysis of the 16S rRNA genes revealed shifts in the community structure during enrichment and identified putative NA-degrading communities. In addition, an aromatic NA-degrading isolate with high 16S rRNA gene sequence identity to *Mycobacterium fluoranthenivorans* was also able to degrade the aromatic acids tested. This isolate will allow further mechanistic studies to be undertaken to identify the genes involved in the NA degradation pathways. These key findings are a major advance towards the ultimate goal of bioremediating recalcitrant NAs.