A new methodology for precise cadmium isotope analyses of seawater

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Previous studies have shown that biological uptake of Cd from seawater is associated with considerable isotope fractionation [1,2]. The most fractionated isotope compositions were determined for nutrient-depleted surface waters, which exhibit $\varepsilon^{114/110}$Cd values of up to about +40 [1]. In contrast, seawater from the deep oceans was found to display a nearly constant Cd isotope composition of $\varepsilon^{114/110}$Cd $\approx$ +3 [1], roughly similar to results obtained for the silicate Earth [3]. The origin and distribution of these distinct Cd isotope signatures will be further investigated as part of the GEOTRACES research initiative, to gain a better understanding of the biogeochemical cycling of Cd in the oceans, and to verify whether Cd isotopes can be employed to study past and present variations in marine nutrient utilization.

The low Cd concentrations (<10-20 pmol/L) that are commonly encountered in nutrient-depleted surface seawater pose a particular challenge for precise Cd isotope analyses. To cope with this problem, we have developed a new method for the determination of Cd isotope compositions that is suitable for the processing of seawater samples as large as 10 to 20 L. The procedure involves the use of a Cd double spike, co-precipitation of Cd from seawater using $Al(OH)_3$, and subsequent Cd purification by anion-exchange chroma-tography. The Cd isotope analyses are then carried out by MC-ICPMS [4].

The performance of the technique was verified by analyzing multiple aliquots of a large seawater sample that was collected in the English Channel. The overall Cd yield of the procedure is consistently >85%, when the co-precipitation is carried out at optimized conditions (pH value, Al^{3+} concentration). Analyses that were carried with the new method were furthermore found to yield data, which are identical to results that were obtained with a previously published double spike methodology [4] but which is not suitable for the processing of large samples.

[1] Ripperger *et al.* (2007) *EPSL* **261**, 670. [2] Lacon *et al.* (2006) *GCA* **70**, 5105. [3] Schmitt *et al.* (2009) *EPSL* **277**, 262. [4] Ripperger & Rehkämper (2007) *GCA* **71**, 631.

Molecular fossils extracted from an Ediacaran/Cambrian boundary section in the Three Gorge area, South China

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The Ediacaran/Cambrian boundary is one of the most important intervals for the evolution of life. It is essential to understand link between the global environmental changes and early animal evolution. Pristine drill core samples collected from the Three Gorge area, South China, was used for the systematic biomarker extraction in this study. A white dolostone without detectable TOC did not yield any biomarker molecules, indicating contaminations during drilling procedure and in laboratory extraction should be negligibly small. Acyclic isoprenoids (pristane and phytane) and n-alkanes were identified in almost samples. The distributions of n-alkanes often show bimodal distributions with two peaks at around $_nC_{17}$ and $_nC_{27}$. This distribution pattern suggests the presence of two different source of hydrocarbon. Furthermore, in some samples, the long-chain n-alkanes with a peak around $_nC_{27}$ predominate over short-chain ones having a maximum at $_nC_{27}$. The predominance of the long-chain n-alkane occurs particularly across the Pc/C and Nemakit-Daldynian/Tomotian boundaries, where major biological diversifications have been known to occur. The long-chain hydrocarbons could have been originated from some specific eukaryotic algae, and thus their predominant occurrences biostratigraphic boundaries may suggest blooming of single or a few species. The decline of biodiversity is likely to have occured due to severe environmental stress like oceanic anoxia (Pc/C) and global cooling (Nd/T) [1]. The observed $_nC_{16\text{-}18}/_nC_{26\text{-}28}$ anomalies may witness the bioligical turnover.

[1] Ishikawa T. *et al*. *Gondwana Res.* **14**, 193-208.