Automated Processing of Seawater Samples for Iron Isotope Ratio Determination

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Bioactive metals such as iron act as important nutrients in the ocean, often present as such low concentrations to limit phytoplankton growth. In recent years, measurement of the dissolved stable isotope ratio of bioactive metals in seawater has provided insight into the biogeochemical cycling of these elements. Iron isotope ratios, in particular, have been shown to be useful tracers of iron source across the open oceans [1].

High precision isotope ratio analysis requires sample amounts ranging from 2 to >100 ng (depending on the element and isotopes of interest). Trace and bioactive metals at low natural concentrations (1-100 ng L⁻¹) in seawater pose a significant challenge with respect to sample volume requirements (~1-4 L), the seasalt matrix and sample processing. Currently, twostep manual processes are employed to, first preconcentrate (a suite of metals, batch mode) and then purify (chromatographic isolate) the metal(s) of interest for isotopic analysis (e.g. [2]), with methods often only optimized for 1 or 2 elements at a time.

Here we investigate a fully automated complete sample processing procedure using a newly developed, large volume (up to 2L), seawater preconcentration system in conjunction with a commercially available chromatography system (prep*FAST* MC). The first automation system uses a 200uL sea*FAST* column to perform a 1000x (400mL to 400 \Box L) preconcentration/matrix removal step for a suite of transition row and REEs. The prep*FAST* MC is then used to purify discrete Cu, Fe and Zn fractions for isotopic analysis.

Elemental concentrations determined using HR-ICP-MS (Element 2) are used to calculate total procedural blank, recovery, and carry over. Fe isotope ratios for seawater samples processed by both methods are measured using a HR-MC-ICP-MS (Neptune *Plus*) and compared for precision and accuracy with samples measured using a published batch extraction and column purification method [2].

[1] Conway and John, (2014), Nature, 511, 212-215.

[2] Conway et al., (2013), ACA, 793, 44-52.

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