High precision mass-independent Cr isotope compositions by MC-ICPMS: application to terrestrial and meteorite samples

ROBERT C. J. STEELE* AND MARIA SCHÖNBÄCHLER

Institute for Geochemistry and Petrology, ETH Zürich, 8092 Zürich, Switzerland.
(*r.steele@uclmail.net)

Chromium isotope compositions are measured in a variety of natural materials to investigate questions ranging from tracing the mixing of nucleosynthetic sources in the early Solar System[1] to the records of changes in oxygenation of seawater in Earth's past[2]. Chromium has been measured to high precision by both MC-ICPMS[2,3] and TIMS[4].

In the last fifteen years, the limits of precision achievable for isotope ratios measured by MC-ICPMS have steadily increased[5]. For some elements, especially those with a high work function, e.g. W, MC-ICPMS offers obvious advantages over TIMS. Other elements, e.g. Cr, are ionised easily by TIMS and require high mass resolution in MC-ICPMS to resolve molecuar interferences resulting in signifcant loss of transmition. For these elements TIMS has remained the highest precision technique. In a recent contribution, Schiller et al. 2014[3] described a technique by which Cr isotope compositions are determined by MC-ICPMS to precision which rivals, or even exceeds, that achievable by TIMS.

In this study, we obtained Cr isotope compositions both by TIMS and MC-ICPMS. We compare new measurements performed at ETH with the most precise data available in the literature. The data are assessed both in terms of ultimate precision, where Cr is not limited, but also precision achievable per µg of Cr. Our results demonstrate that for sample masses of <5 µg, TIMS achieves the highest precision. However, when Cr available for analysis is not limited, preliminary results indicate MC-ICPMS yields higher precision of ~2-3 ppm for $\varepsilon^{53}Cr_{50/52}$ and ~8-10 ppm for $\varepsilon^{54}Cr_{50/52}$. We tentatively attribute this crossover in achievable precision to the more stable analytical conditions in MC-ICPMS from sample to sample. These stable conditions allow a more precise correction for non-exponential mass bias by sample-standard bracketing. These findings have implications for the choice of analytical technique for future studies and may expand the range of questions which can be investigated.

[1] A. Trinquier, et al. 2008, *JAAS,* **23,** 1565–1574. [2] P. Bonnand, et al. 2013, *EPSL,* **382** 10–20. [3] M. Schiller, et al. 2014, *JAAS*, **29**, 1406–1416. [4] A. Trinquier, et al. 2008, *GCA*, **72**, 5146–5163. [5] R. C. J. Steele, et al. 2011, *GCA* , **75**, 7906–7925.