Ion kinetic energies' influence on mass bias in (MC)ICPMS

B. HATTENDORF[1]*, G.H. FONTAINE[1], F. OBERLI[2], B. BOURDON[2] AND D. GÜNTHER[1]

[1]ETH Zurich, Laboratory for Inorganic Chemistry, Wolfgang Pauli Str. 10, 8093 Zurich (*bodo@inorg.chem.ethz.ch)
[2]ETH Zurich, Isotope Geochemistry and Mineral Resources, Clausiusstr. 25, 8092 Zurich (bourdon@erdw.ethz.ch)

The variability of mass bias imposes a severe limitation on the accuracy and precision of isotope ratio measurements achievable by multi collector inductively coupled plasma mass spectrometry (MCICPMS). There are a number of processes that affect not only the magnitude of mass fractionation but also its stability with respect to subtle changes in the operating conditions. Space charge effects and diffusion processes are most likely the dominating sources but cannot fully explain the dependence of mass fractionation changes on subtle variation of the operating conditions within the ICP [1].

This study investigated the dependence of the mass discrimination on the operating conditions of MCICPMS instruments. Variation of the carrier gas flow rates revealed that mass fractionation is not monotonously depending on the temperature in the ion source, which would be expected from changes in the respective ion mobilities and mean kinetic energies.

The respective changes are however well explained by energy- and thus mass-dependent changes of ion transmission inside the ion optics of the ICPMS. The mean ion kinetic energies were found to be generally correlated with the gas temperature inside the ion source, which may thus be considered a significant contribution to variation of mass bias with changes in the physical properties of the ICP source.

A reduction of mass bias variability can be achieved by adjusting the operating conditions of the ion source in a way that small changes in the respective ion energies have similar instead of opposite effects on the relative trasnmission of different isotopes. For example, this approach reduced the mass bias variation of Nd, in the presence of a 10 fold excess of Ho, by a factor of six.

[1] Fontaine G.H. et al. *J Anal. At. Spectrom*., 2009, DOI: 10.1039/b816948a

Novel tools for *in situ* detection of biodiversity and function of dechlorinating and uranium-reducing bacteria in contaminated environments

K. HAUER[1], D.B. MEISINGER[1], M. PAVLEKOVIC[1], S.H. THOMAS[2]; A.K. KNIGGENDORF[3], J. CHEE-SANFORD[4], R. SANFORD[5], C.A. LEBRÓN[6], W. LIEBL[1], F.E. LOEFFLER[2] AND N.M. LEE[1]

[1]TUM, Technische Universität München, Freising, Germany (nlee@msecol.net)
[2]Georgia Institute of Technology, Atlanta, GA, USA (frank.loeffler@ce.gatech.edu)
[3]Leibniz Universität Hannover, Hannover, Germany (kniggendorf@biophysik.uni-hannover.de)
[4]USDA Agricultural Research Service, Goodwin, Urbana, IL, USA (cheesanf@uiuc.edu)
[5]University of Illinois at Urbana-Champaign, Urbana, IL, USA (rsanford@uiuc.edu)
[6]NFESC, Port Hueneme, CA, USA (carmen.lebron@navy.mil)

The combination of chlorinated and radioactive compounds impose a serious, long-lasting threat to our environment that demand a holistic approach for successful bioremediation. During the last years, several different species have been discovered that can degrade or transform these compounds to a less hazardous state. However, in order to fully exploit their potential, it is necessary to develop reliable and quick analytical tools for real time *in situ* detection of target cells and their activities. To achieve this, we developed and compared different types of *in situ* detection tools: i) a hierarchic set of 16S rRNA oligonucleotide probes to detect highly active species, targeting relevant genera and key species on different taxonomical levels; ii) a 16S rRNA ribosomal based CARD-FISH probe set to detect cells that evade detection with standard FISH procedures; iii) a functional gene FISH approach, to target single copy genes encoding degradative traits; and iv) RAMAN microscopy, to develop a probe-independent and non-invasive alternative to the FISH protocols. All tools were applied to pure cultures, enrichment cultures and samples from contaminated environments, and the results retrieved with these tools were compared with other analytical tools such as PCR and degradation kinetics. Interestingly, we often observed discrepancies between the results produced with the different tools, which most likely reflect the inherent biases of each respective tool. Hence, for a full mapping of microbial ecological parameters, a combined approach is best suited for providing a better understanding of *in situ* activities and overall systems ecology in environmental systems.