Japan Geoscience Union Meeting 2014
(28 April - 02 May 2014 at Pacifico YOKOHAMA, Kanagawa, Japan)
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BPT26-12 Room:421 Time:May 2 12:00-12:15

Development for new hyphenated analytical technologies for paleogenomics research

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Cytometry is the analytical technique, basically applied for quantitative analysis of cells and cell systems. In general, cytometry measures optical properties of cells, and most often uses fluorescence to measure specific antigen molecules, intracellular ions and DNA/RNA. Cells may be live or fixed, depending on the application, and individual cells can often be physically sorted. ? Other optical signals can be measured, including light scatter. The cytometry has blossomed to become the key technique to evaluate the nutritional status or to understand the elemental metabolism for animals. Several advantages can be derived by the cytometry, such as analysis speed, detection sensitivity, the ability to measure many parameters simultaneously, and the ability to sort individual cells (i.e., single cell spectroscopy). Recently, new generation cytometry utilizing the sensitive mass spectrometers (i.e., mass cytometry) was described. With the mass cytometry, further sensitive detection of ions or proteins and higher capability for the multiparameter analysis of individual adherent cells (e.g.,; Benfall et al., Science, 2011; Bodenmiller et al., Nature Biotechnology, 2012). With the extensive number of information collected from cells or samples through the cytometry, reliable and objective evaluation for the changes in biochemical functions could be achieved. This approach can also be applied to understand the solar system evolution based on the numerous number of age data. In recent ten years, we have demonstrated the unique study approach using the distribution pattern of sample ages based on the series of precise age data collected from large number of samples (i.e., age-cytometry) (e.g., Rino et al., PEPI, 2008; Iizuka et al., Geology, 2008; Iizuka et al., Iizuka et al., Chem. Geol., 2009; Iizuka et al., GCA, 2010). The mass cytometry will become a powerful tool to promote the big-data science for various research fields such as metallomics, medical sciences or the geochemistry. For elemental or isotopic analysis of trace- or ultratrace-elements, plasma ion source mass spectrometry (ICP-MS) has been widely employed because of its high analytical capabilities such as high-elemental sensitivities, minimal sample preparation procedures, high-analysis throughput or user-friendly operations (Bandura et al., Anal. Chem., 2009). With the laser ablation sample introduction technique, distribution of both the elemental and isotopic data for trace- or ultratrace-elements can be successfully derived directly from large-sized solid samples (>10cm). Despite the obvious success in obtaining elemental and isotopic data (age data), it should be noted that stable isotope ratio data for light elements (e.g., C and O) could not be derived by the present LA-ICPMS technique because of serious contribution mass spectrometric interferences on C and O isotopes, which provides key information concerning the physico-chemical conditions for the sample formation. To overcome this, we would like to develop a new analytical technique to measured the C isotopes, at a same time with elemental analysis using the LA-ICPMS technique. Newly developed spectroscopy technique combined to the LA-ICPMS technique can become a major analytical tool to expand the analytical capability for mass cytomery for biochemical samples and geochemical samples through precise, reliable and uniform quality data. The analytical technique develop here will promote the big-data science for various research fields including geochemistry and biochemistry.

Keywords: mass spectrometry, laser ablation, paleogenomics, hyphenated technology, analytical chemistry, geochemistry