

Elimination of Aliasing by use of Aligned LA–ICP–MS

DR. C. ASHLEY NORRIS AND NICHOLAS R WEST

Norris Scientific

Presenting Author: an@norsci.com

The use of fast-washout ablation cell (“fast cells”, washout time to 1% < 50 ms) for LA–ICP–MS can improve spatial resolution of images, reduce measurement time, and raise peak signal intensity – which in some cases may bring signals above detection. The obvious application of fast cells is imaging/mapping, which is a powerful and useful technique with a wide range of applications in the earth, material, and biological sciences^[1]. However, other applications of fast cells include high throughput analysis and whenever there is a need for high spatial resolution in the down-hole signal, such as ablation of heterogeneous materials.

The main problem when using fast cells with a sequential mass spectrometer, such as a quadrupole, is the need to avoid certain conditions that result in aliasing. Inevitably the conditions used will be a compromise and sub-optimal for the application. An example of this is to eliminate aliasing by lengthening the response time of the ablation cell, when doing so is fundamentally at odds with the objective of collecting images that contain millions of pixels^[2].

Our new approach^[3] is to align firing of the pulsed laser with the sweep time of the single-detector mass spectrometer. We call this aligned LA–ICP–MS and the technique can be implemented by way of an external circuit that monitors the mass filter position of the mass spectrometer in real time and fires the laser as required.

To demonstrate the technique we have collected a series of images from biological and mineral samples which show that aligned LA–ICP–MS makes it feasible to use fast cells with quadrupole mass spectrometers by eliminating aliasing. We will also demonstrate further applications, such as the ability to selectively increase or decrease the signal intensity for individual masses within the sweep, and how it is now possible to perform simultaneous detection on a sequential mass spectrometer.

[1] Doble, Philip A., et al. *Chemical Reviews* 121.19 (2021): 11769-11822.

[2] Marillo-Sialer, Estephany, et al. *Journal of Analytical Atomic Spectrometry* 35.4 (2020): 671-678.

[3] Norris, C. Ashley, et al. *Journal of Analytical Atomic Spectrometry* 36.4 (2021): 733-739.

