Spatial information analysis using a desktop size MALDI Digital Ion Trap Mass Spectrometer based on MS imaging information

Kosuke Hosoi[1]. 1 SHIMADZU Corporation, MS Business Unit, Kyoto, Japan.

1. Introduction

Mass spectrometry imaging (MSI) technique is widely applied to study pathologies and utilized to develop drugs. However, to promote the technique to be used in general clinical sites, demands for size-reduced instrument which can be installed close to the field and can be used in simple protocol are increased, for existing apparatus is not suitable for that application.

We perform MS/MS analysis at specific position on tissue surface using iMScope™ QT and MALDImini™-1 to demonstrate that spatial MS information can be obtained even by a desktop MS instrument by specifying the position to be analyzed based on the result from preceding MSI experiment.

2. Methods

Frozen sections of mouse brain were longitudinally sectioned at a thickness of 10 µm using cryostat microtome, then vapor-deposited 9-Aminoacridine (9-AA) at a thickness of 1.0 µm on an ITO-coated slide glass using iMLayer™ apparatus.

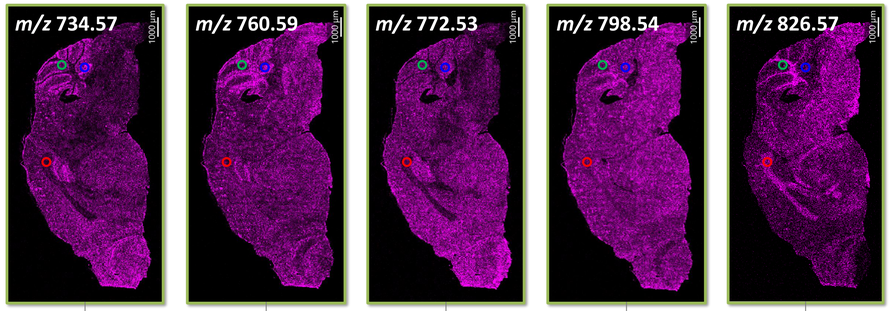
One of the consecutive tissue samples was imaged with MS by iMScope QT in positive ion mode. Laser pulse was irradiated 50shots per position, the laser diameter was approx. 10 µm. Scanned area was 500 x 260 points with 30 µm pitch. Mass spectra were acquired at range of *m/z* 680 to 900. Then the MS-image were generated by IMAGEREVEAL™ MS software.

Other tissue samples were analyzed for MS and MS/MS by MALDImini-1 with mass range of *m/z* 650 to 5000, scanning speed 4000 Da/sec.

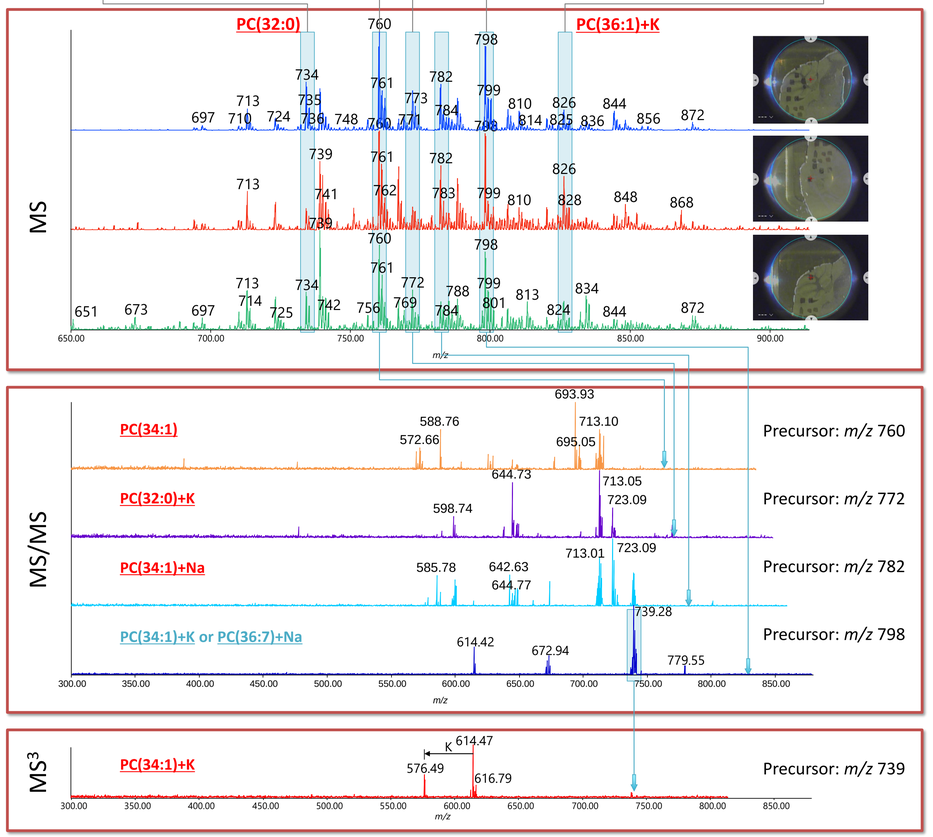
3. Results

Imaging data of the whole brain acquired with iMScope QT show that, when focusing on the cerebellar medulla and corpus callosum, the compound of *m/z* 826 is distributed more than the other region, *m/z* 734 and *m/z* 772 are relatively less, and *m/z* 760 and *m/z* 798 are distributed as much as the other region.

MS images using iMScope QT



Spectra using MALDImini-1



MALDImini-1

- **Easy to install close to the field**
- **Low Throughput**

iMScope QT

- **High-speed and high-resolution MSI**

The same position was measured using MALDImini-1 and compared with the surrounding region, showing a similar tendency to that of imaging. From the *m/z* value of the MS and MS/MS spectrum, they are estimated to be $[M+K]^+$ of PC(36:1) (*m/z* 826), $[M+H]^+$ of PC(32:0) (*m/z* 734), $[M+K]^+$ of PC(33:0) (*m/z* 772), and $[M+H]^+$ of PC(34:1) (*m/z* 760), respectively. At *m/z* 798, there are several possible candidates, $[M+K]^+$ for PC (34:1), $[M+Na]^+$ for PC(36:7), and $[M+H]^+$ for PE(40:3).

We confirmed that this is$[M+K]^+$ for PC (34:1), because fragment peaks of -59 Da and -183 Da showing neutral loss of choline and phosphocholine were detected by performing MS/MS measurement, and because by performing MS^3 measurement on this peak, fragment peaks showing elimination of potassium were detected.

4. Conclusion

These results show that MS^n analysis can be performed by selectively detecting the substance on a tissue section with MALDImini-1 using the distribution information acquired in advance. Slow throughput is not an issue because regions to be measured are specific. Considering that MALDImini-1 is a compact and lightweight product that is easy to install in the vicinity of a clinical site, it is suitable as an apparatus for widely and practically utilizing distribution information of a target substance obtained by MSI.