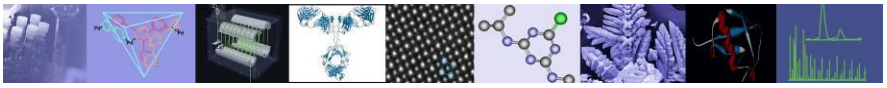


SpiralTOF™

High Mass Resolution MALDI-MS Imaging Part II
Using the "MALDIVision" from PREMIER Biosoft

Introduction

Matrix-assisted laser desorption/ionization mass spectrometry imaging (MALDI-MS Imaging) is a powerful tool for the biochemical analyses of surfaces. Previously, this technique has been used to determine the spatial distribution of hundreds of unknown compounds in thinly sliced tissue sections. The mass spectral images are generated by changing the laser irradiation point at regular intervals across the sample surface and collecting a mass spectrum for each point. Time-of-flight mass spectrometers (TOFMS) are widely used as the mass analyzer for MALDI-MS Imaging because they are well matched for the MALDI ionization process. Ultra-high mass resolution achieving isobaric peak separation is important for lipid profiling using MALDI-Imaging [1, 2]. However, the fine structure of the matrix crystals and small irregularities in the tissue surface flatness can cause peak drift in the collected mass spectra that is caused by slight differences in the starting point of the flight path for the ions at each laser irradiation point. As a result, the typical reflectron type TOFMS systems have a difficult time achieving high mass resolution from spot to spot over a thinly sliced biological surface.

Conversely, the JEOL JMS-S3000 "SpiralTOF™", which has 5-10 times longer flight path than the traditional reflectron type TOF, is able to reduce the effect of this mass drift to achieve high mass resolution and high mass accuracy [3]. The SpiralTOF is a MALDI-TOFMS that uses the unique JEOL spiral ion optical system which increases the ion flight path length to 17m. One consequence of this improvement in resolution is that there are more data points across each mass spectral peak, resulting in an overall increase in file size. This feature, along with the dimensions of the surface, the spatial resolution of each image data point, and the mass range measured, can all result in producing very large data files (10-20GB). Consequently, SpiralTOF imaging data generally requires file compression in order for the typical imaging software to reconstruct the MS images. However, a new software package called MALDIVision from PREMIER Biosoft [4] can easily handle these larger sized data files without the need for file compression. In this work, we used the SpiralTOF to collect the mass spectral data for a mouse brain section and then used MALDIVision to reconstruct the MS images using the uncompressed data files.

Experimental

A mouse brain tissue section was placed on an ITO conductive glass slide plate. The matrix compound DHB was sprayed onto the surface of the tissue and then the sample was introduced into the mass spectrometer. The MS Imaging measurements were performed on the left half of the brain tissue section (5 mm×7 mm) with 40 μm spatial resolution. The sampling interval of data acquisition system was 0.5 ns, which included 170,000 mass data points in m/z 500-1000. The total pixel was 21,125 and imaging data size was 14GB. The MALDIVision was able to handle the data without any data reduction.

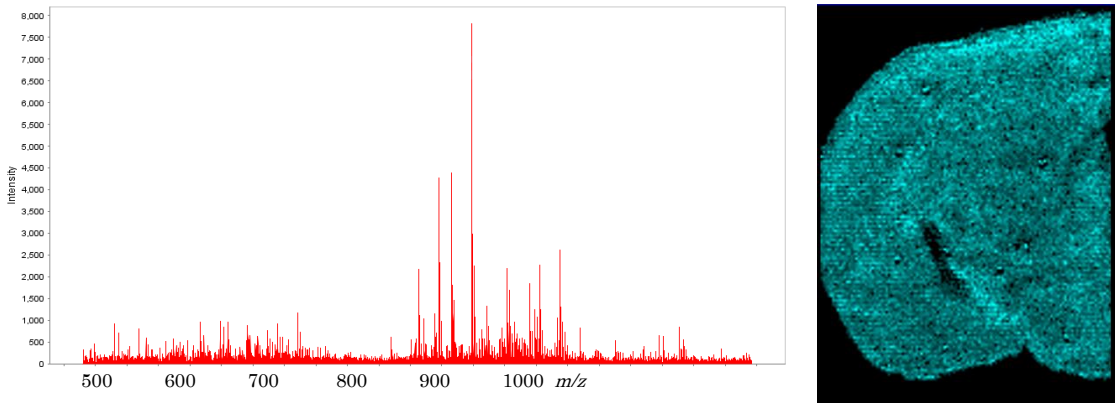
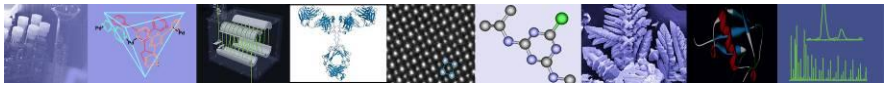


Fig.1 (a) Averaged mass spectrum and (b) MS image for base peak *m/z* 798



Results and Discussion

The averaged mass spectrum for all of the image pixels is shown in Fig. 1a. The base peak ion *m/z* 798 was estimated as Phosphatidylcholine (PC) (34:1) [M+K]+. The mass image of *m/z* 798 with ±0.1 u mass window is also shown in Fig.1b. The mass spectrum for *m/z* 820 – 825, which showed several doublet and triplet peaks for minor components, is shown in Fig. 2a. The mass resolving power is approximately 30,000 (FWHM) for this region of the mass spectrum. Phosphatidylcholine (PC), phosphatidylethanolamine (PE), and galactosylceramide (GarCer) and their corresponding isotopic peaks, indicated by colored arrows, were all observed within 3 u of their theoretical masses. The enlarged *m/z* 822 – 823 mass spectrum plotted with the measured mass points is shown in Fig. 2b. The number of points across these peaks is much larger than for a traditional high-resolution reflectron TOF, resulting in a better representation of each closely related peak, an advantage realized by extending the flight path. The mass images of the three peaks are shown in Fig. 3. Each peak showed a distinctly different distribution across the surface of the mouse brain.

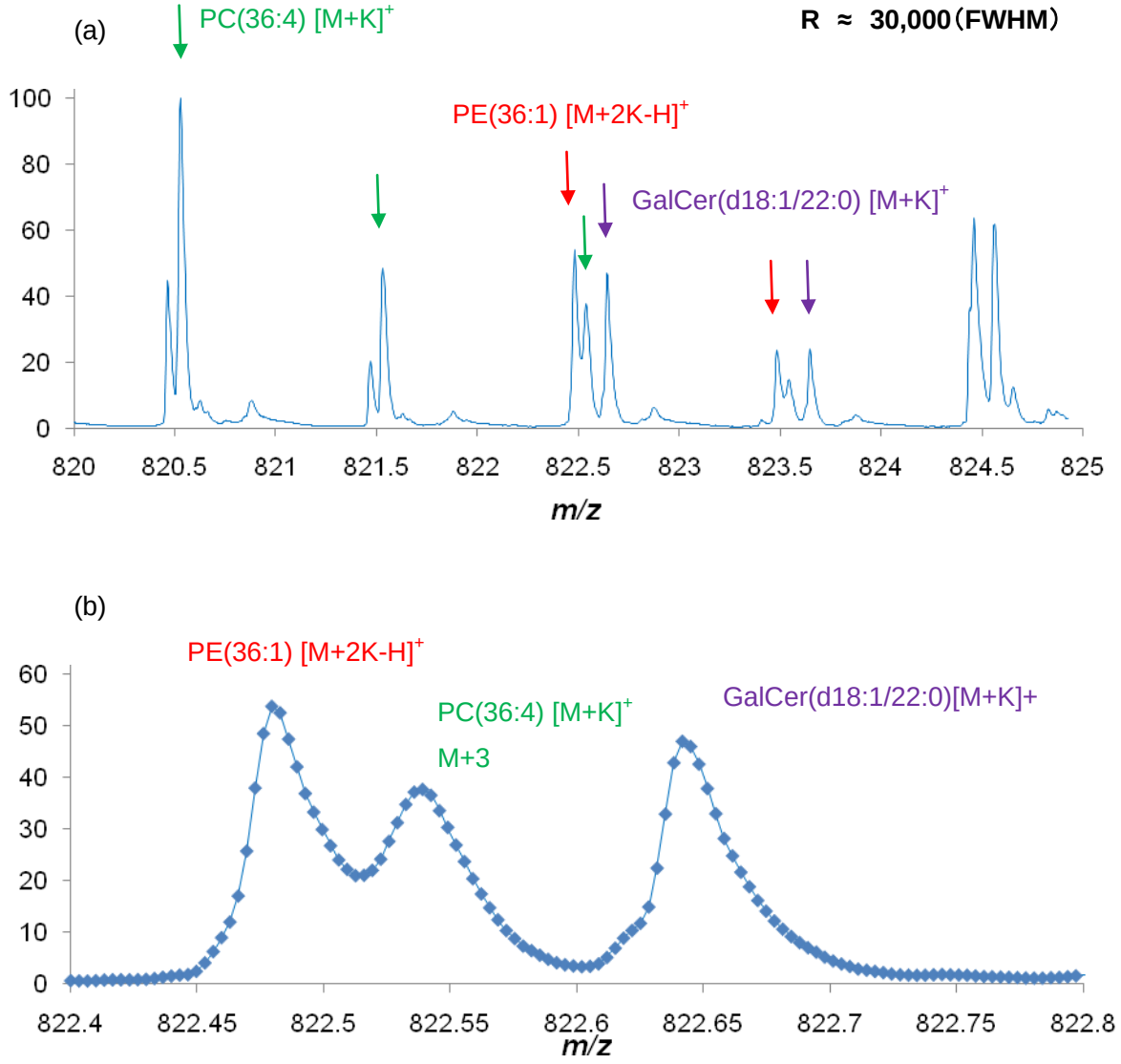
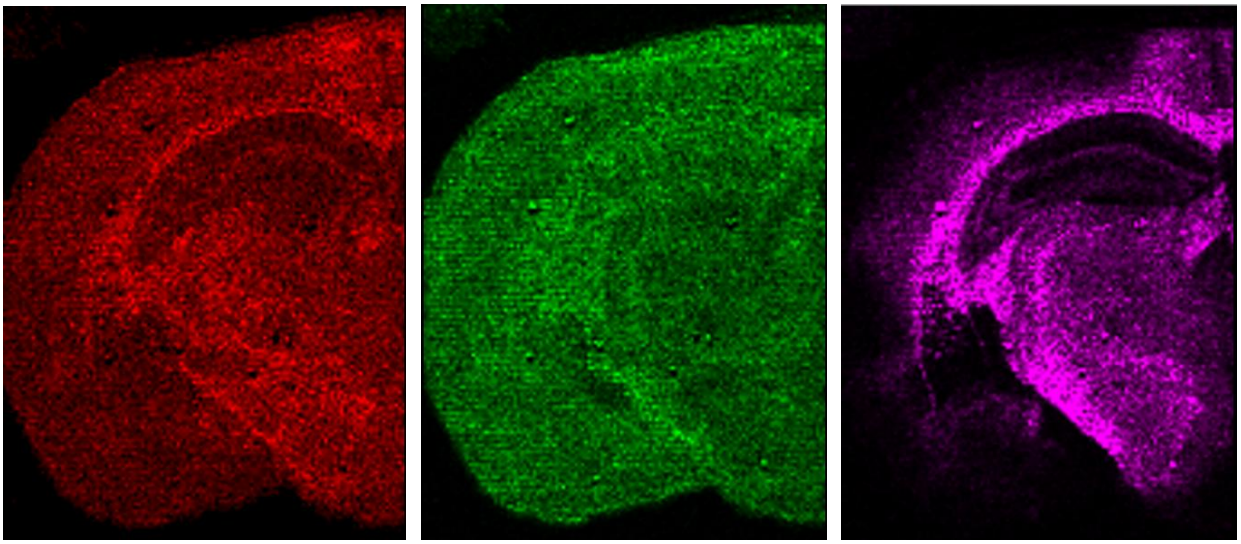


Fig. 2 (a) Enlarged mass spectrum at *m/z* 820-825 and (b) at *m/z* 822.4-822.8



(a) *m/z* 822.48 (b) *m/z* 822.53 (c) *m/z* 822.64

Figure 3. Mass images of three peaks around *m/z* 822.5

Conclusions

The ultra-high mass resolving power for separating isobaric peaks are necessary for lipid profiling using imaging mass spectrometry. The large data handling ability of MALDIVision could make the analysis more efficiently.

Acknowledgment

We thank Mr. N. Moriguchi, Assistant Professor Dr. H. Hazama and Professor Dr. K. Awazu for providing the mouse brain tissue specimens.

References

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