Fast TOF-MSI combined to high resolution FT-ICR-MSI for lipidomic studies of rat brain slices

M. Tiquet[a], D. van Kruining[b], P. Martinez[b], E. De Pauw[a]

[a] Laboratoire de spectrométrie de masse, ULiège, Liège, Belgique.

[b] MHeNS School for Mental Health and Neuroscience, Maastricht University, Maastricht, Netherlands.

Introduction

Lipidomics studies, among others, shows interest in the localization of molecules in a biological sample. In the recent years, Mass Spectrometry Imaging (MSI) has emerged as a label-free method of choice to obtain this type of information.

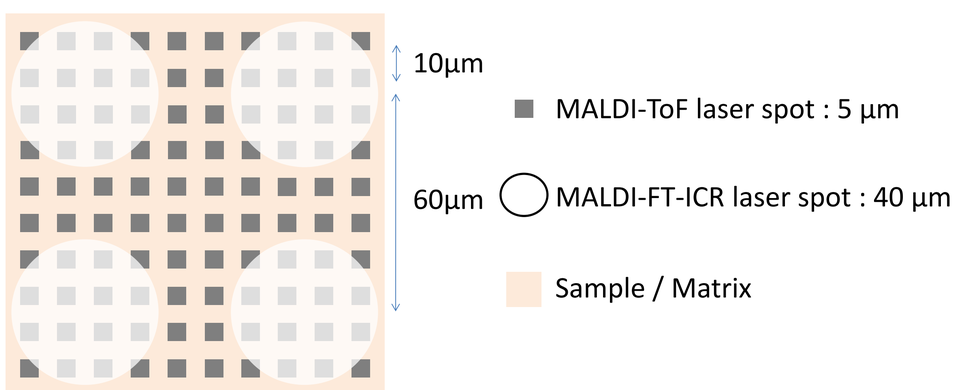
Unfortunately, MSI is time consuming and underperforming methods are often willingly used in order to keep the acquisition time under reasonable margins. Thus, this work proposes a workflow designed to obtain the best possible results, localization and identification wise, on single sample while keeping the shortest possible acquisition time.

Method

Samples :	*Rat brain sagittal cuts*
Matrix :	*1,5-DHB*
	4-HCCA
Auto. sprayer :	*SunCollect*
Mass spectrometer:	*FT-ICR (solariX XR)*
	ToF (rapifleX)
Data Analysis :	*SCiLS Lab 2016b*

Workflow

The workflow starts with a MALDI-ToF-MSI acquisition with the best spatial parameters possible. The same sample is then analyzed by MALDI-FT-ICR-MSI with a wider spacing and laser focus while boosting the spectral resolution.



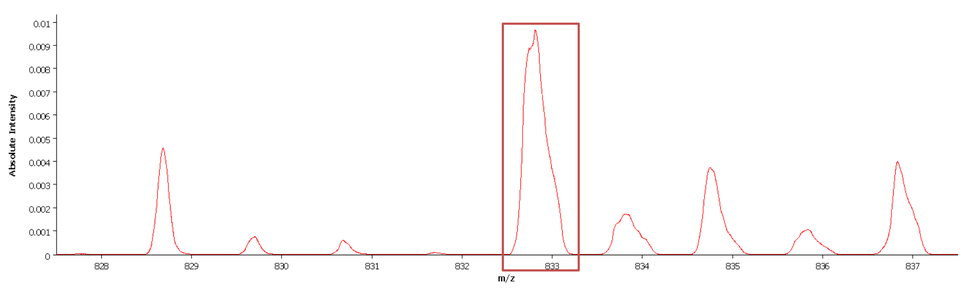
Analyzer	FT-ICR	ToF	FT-ICR
Spatial resolution	80 µm	10 µm	25µm
Laser focus	~40 µm	5 µm	~25 µm
Spectral resolution	800.000 at mass 400	10.000 to 25.000	800.000 at mass 400
Acquisition time	**8 hours**	**3 hours**	**150+ hours**

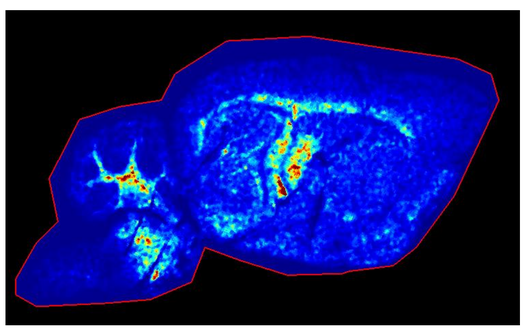
The table lists different MSI methods and their respective acquisition time for the same sample. The first two columns correspond to the combined methods in the presented workflow. For the sake of comparison, a third method parameterized to obtain similar results in a single acquisition is shown.

Results

MALDI-ToF-MSI

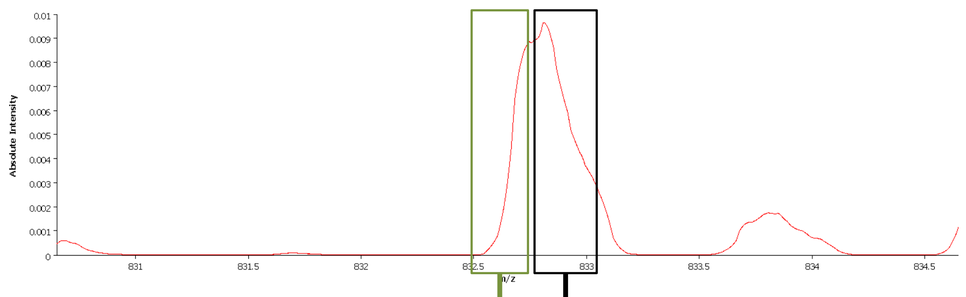
1.

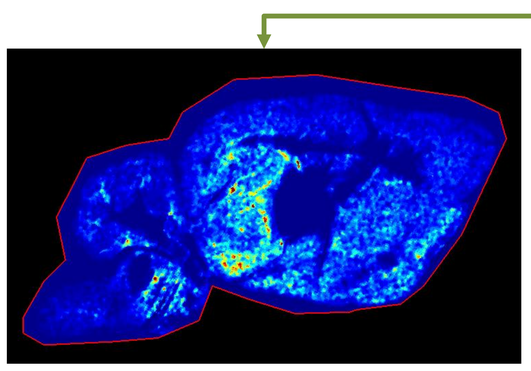




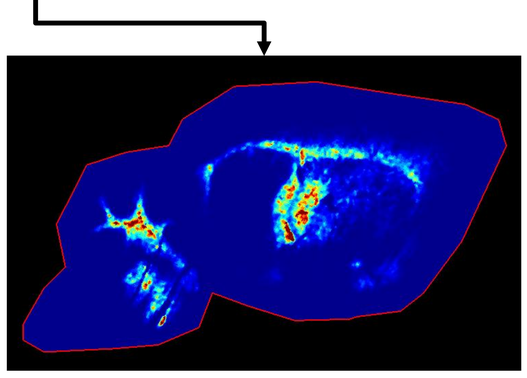
Ion 832,851 ± 334 mDa

3.





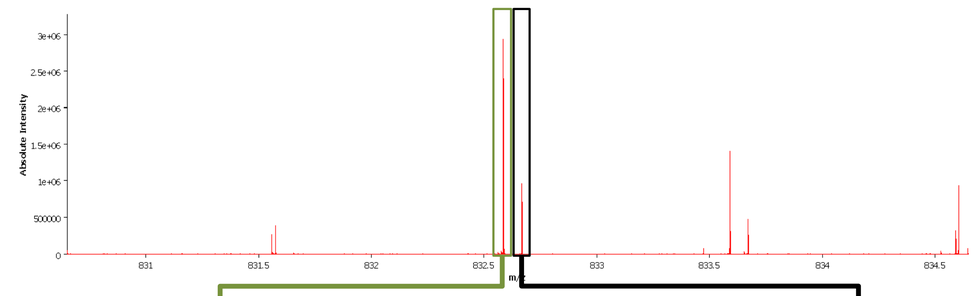
Ion 832,671 ± 114 mDa

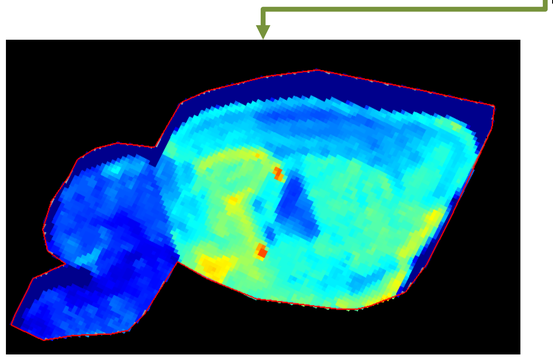


Ion 832,951 ± 154 mDa

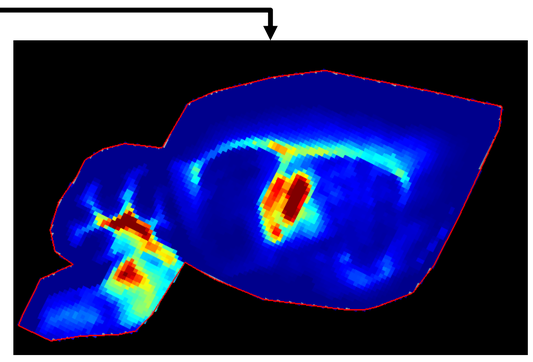
MALDI-FT-ICR-MSI

2.





Ion 832,5854 ± 0,73 mDa



Ion 832,6667 ± 0,61 mDa

Identification :

- 832,5854 *m/z* → Glycerophosphocholine (err. 0,42ppm)
- 832,6645 *m/z* → Glycosphingolipid (err. 0,97ppm)

1. MALDI-ToF-MSI shows nice images but the poor spectral resolution can lead to unknowingly select several ions.
2. The high spectral resolution of the FT-ICR method shows that in reality two ions with distinct localization are present in the previously selected window. Futhermore, the mass accuracy allowed the identification of those two ions.
3. The peak in the ToF dataset is subdivided in two windows resulting in the two correct localizations.

Conclusion

The workflow does two sequential images focused on spatial resolution first then on spectral precision. By doing so, the MSI acquisition of a sample has been done in a workday worth of time compared to several days if done in a single acquisition with similar parameters. The parallel analysis of the datasets used ToF to generates the precise localizations of ions which were discernable and identifiable thanks to the resolution and accuracy of FT-ICR.