FTICR Mass spectrometry imaging at extreme mass resolving power using a dynamically harmonized ICR cell with 1ω or 2ω detection

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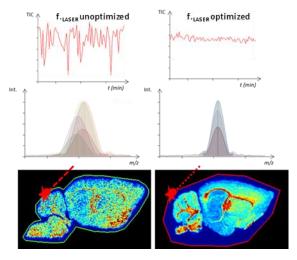
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13 Abstract

14 MALDI mass spectrometry imaging (MALDI MSI) is a 15 powerful analytical method providing the 2D 16 localization of compounds from thin sections of 17 typically but not exclusively biological samples. The 18 dynamically harmonized ICR cell (ParaCell©) was 19 recently introduced to achieve extreme spectral 20 resolution capable to provide the isotopic fine 21 structure of ions detected in complex samples. The 22 latest improvement in ICR technology also includes 23 2ω detection which significantly reduces the transient 24 time while preserving the nominal mass resolving



25 power of the ICR cell. High-resolution MS images acquired on FT-ICR instruments equipped with 7T 26 and 9.4T superconducting magnets and the dynamically harmonized ICR cell operating at suboptimal 27 parameters, suffered severely from the pixel-to-pixel shifting of m/z peaks due to space-charge effects. 28 The resulting profile average mass spectra have depreciated mass measurement accuracy and mass 29 resolving power under the instrument specifications that affect the confidence level of the identified 30 ions. Here we propose an analytical workflow based on the monitoring of the Total Ion Current to restrain 31 the pixel-to-pixel m/z shift. Adjustment of the laser parameters is proposed to maintain high spectral 32 resolution and mass accuracy measurement within the instrument specifications during MSI analyses. 33 The optimized method has been successfully employed in replicates to perform high-quality MALDI MS 34 images at resolving power (FWHM) above 1,000,000 in the lipid mass range across the whole image 35 for superconducting magnets of 7T and 9.4T using 1 and 2w detection. Our data also compare favorably 36 with MALDI MSI experiments performed on higher magnetic field superconducting magnets, including 37 the 21T MALDI FT-ICR prototype instrument of the NHMFL group at Tallahassee, Florida.

38

40 1. Introduction

41 Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Imaging (MALDI-MSI) has emerged 42 as a label-free analytical method monitoring the relative abundance (despite severe limitations due to 43 suppression effects) and spatial distribution for a wide variety of analytes, especially for biological 44 samples¹⁻³. To properly distinguish isobaric compounds⁴ inherent to the complexity of biological 45 samples, high resolving powers at full width at half maximum (R.P.FWHM > 300,000 at 400 m/z) and a 46 reliable mass measurement accuracy (MMA) are required in the absence of an upstream separation 47 method (such as ion mobility). These performances are commonly achieved by Fourier Transform mass 48 analyzer such as Fourier Transform-Ion Cyclotron Resonance (FT-ICR)⁵. The Bruker dual ion source 49 ESI/MALDI FT-ICR (solariX and scimaX) is a hybrid instrument equipped with multipoles, a quadrupole, 50 and a collision cell for precursor ion selection and fragmentation. lons produced by electrospray (ESI) 51 and MALDI are also accumulated in the multipole region to prepare the ion packet to be introduced into 52 the ICR cell. Consequently, almost any combination of MALDI laser settings are compatible with any 53 transient time for mass spectra acquisition. Recent developments introduced by E.N. Nikolaev et al.⁶⁻⁸ 54 led to the dynamically harmonized ICR cell commercialized by Bruker in the solariX XR and scimaX XR 55 brand FT-ICR mass spectrometers under the name ParaCell®. This new cell offers the highest mass 56 resolving power (R.P.) currently achievable for such instruments⁹ (around 1,000,000 in the lipid mass 57 range in broadband mode) and mass measurement accuracy typically is in the sub-ppm range. These 58 improvements drastically increase the confidence level of the precursor ions empiric formula 59 determination, especially when including the fine isotopic structure¹⁰. Moreover, the introduction^{11–13} 60 and the experimental application^{12,14} of 2ω detection drastically improved the mass R.P. and the scan 61 duration of the ICR transient signals.

62 To obtain the highest quality of mass spectrometry images (MSI) in terms of mass R.P. and lateral resolution, each step of the imaging workflow has to be properly optimized. The experimental 63 optimization of the FT-ICR-MS(I) instrument¹⁵ was studied by Carlos Afonso and Abdellah Tebani's 64 65 group. The sample preparation affects the ionization efficiency as well as the local diffusion of the 66 analytes in tissue sections. Different experimental parameters were evaluated extensively in the literature including slice thickness¹⁶⁻¹⁸, matrix and solvent selection¹⁹⁻²³, and optimization of the 67 68 automatized matrix deposition²⁴. When using the recommended parameters and optimized methods 69 intended for the previous ICR design, the "Infinity Cell®", the best performance in terms of R.P. FWHM 70 and mass accuracy was far from instrument specifications due to abnormally large mass shifts. From 71 an instrumental point of view, significant deviations of the amount of injected ions between scan events 72 heavily affect the global performance of the Paracell. Pixel-to-pixel fluctuations of the ion current during 73 the MSI experiments cause a non-repeatable space charge effect between pixels in regards to the 74 MALDI-MS calibration procedure. In general, this phenomenon can be corrected using a lock-mass 75 calibration during acquisition^{25,26} which would ideally require several homogeneously distributed analytes. These targets could be added before matrix deposition at the risk of inducing more or less 76 77 severe ion suppression effect(s) and lateral diffusion. An alternative is to use post-acquisition 78 recalibration software²⁷, which however can be time-consuming due to format conversion and 79 computational steps depending on the size and format of the dataset.

This study reports optimized instrument conditions to mitigate the abnormal mass shifts observed during high/extreme resolution MALDI FT-ICR MSI fitted with the ParaCell®. We present here such an optimization on sample preparation and acquisition parameters to produce MS images at R.P. FWHM at least better than 500,000 at m/z 800 (better than 1 million at m/z: 400) in broadband mode using a solariX XR 9.4T and a scimaX 7T 2XR.

85 2. Material and methods

86 2.1. Chemicals

Acetone and methanol HPLC grade were obtained from Biosolve (Valkenswaard, Netherlands).
Trifluoroacetic acid (TFA, 99%) α-cyano-4-hydroxycinnamic acid (α-HCCA, purity 97%), and red
phosphorus (>97%) were purchased from Sigma-Aldrich (Taufkirchen, Germany). The internal standard
SPLASH LipidoMIXTM containing deuterated lipids from different families was purchased from Avanti
Polar Lipids (Alabaster, Alabama, USA) via Sigma Aldrich.

92 2.2. Animal handling

Transgenic mice were purchased from Dr. Mary Jo LaDu (University of Illinois at Chicago) and bred in-house at MHeNs at Maastricht University as described elsewhere²⁸. In short, human-APOE4 knockin mice in which the mouse APOE gene was replaced by human APOE were crossbred with 5xFAD mice (Jackson laboratory) carrying human familial Alzheimer disease mutations PSEN1 and APP to obtain E4FAD mice with increased Aβ peptide production^{28,29}. Female E4FAD mice over 6 months of age were sacrificed by CO2 inhalation then brains were extracted. Mice brains were cut across the sagittal midline and immediately fresh-frozen in liquid nitrogen and subsequently stored at -80 °C. For transportation, samples were placed on dry ice and transferred to the University of Liège to be longterm stored conserved again at -80°C before further handling. All procedures were approved by the Animal Welfare Committee of Maastricht University (n° AVD107002015177) and were performed according to Dutch federal regulations for animal protection.

104 Natural AB-type zebrafish were bred by the Groupement Interdisciplinaire de Génoprotéomique 105 Appliquée (GIGA) at ULiège under the supervision of Pr. Marc Muller. The aquarium water was 106 thermostated at 28°C with a circadian cycle of 14 hours of light and 10 hours of darkness. One-month-107 old fish were first anesthetized by adding tricaine mesylate to a concentration of 0.04% then increased 108 to 0.16% to induce cardiac arrest. Fish were then embedded in gelatin (350mg.mL⁻¹) and stored at -109 80°C for at least 24 hours. All procedures were approved by the Animal Welfare Committee of the 110 University of Liège (n° 20-2284) and were performed according to Belgian federal regulations for animal 111 protection.

112 2.3. Tissue sectioning

Sectioning was performed on a CryoStar NX70 (Thermo Fisher Scientific, Massachusetts, USA) set at -20°C. SEC35e low profile razor blades (Thermo Fisher Scientific, Massachusetts, USA) were employed at -15°C during the sectioning. Mouse brain and zebrafish whole-body sagittal slices were sectioned at a medium thickness of 14 µm and 8 µm to keep a good amount of material for ionization³⁰ while easing the collection of seriated slices. Cryosections were thaw-mounted onto indium-tin-oxide (ITO) coated conductive glass slides (Bruker Daltonics, Bremen, Germany).

119 2.4. Matrix coating

120 Prior to matrix deposition, samples were dried in a vacuum desiccator for 15 minutes or until no 121 visible wetness was observable. Dried samples were coated with matrix using the automatic sprayer 122 SunCollect MALDI spotter (SunChrom, Friedrichsdorf, Germany). Matrix solution contained 5mg.mL⁻¹ 123 of α-HCCA dissolved in methanol and milli-Q water acidified with TriFluoroacetic Acid (MeOH:H2O:TFA 124 9:0.99:0.01 v:v:v). During the spraying procedure, the nozzle was positioned to its lowest setting and 125 its moving speeds in the X and Y axis were set at medium 10 (1540 mm.min⁻¹). Matrix flow rates started from 5µL.min⁻¹ up to the 4th layer for which flow rates were increased to 10µL.min⁻¹ until the last 126 127 deposition layer. The number of layers required to obtain a homogenous coating of roughly 10nmol.mm⁻ 128 ² of matrix was calculated for each spray deposition. The amount of matrix sprayed is confirmed by 129 weight comparison of the ITO glass slide before and after the spray process. Later in this study, the

130 optimized amount of deposited matrix is 5nmol.mm⁻².

131 2.5. MALDI mass spectrometry imaging

Mass spectrometry acquisitions were performed on ESI/MALDI dual-source MALDI FT-ICRs 132 equipped with the ParaCell® (solariX XR 9.4T and scimaX 2XR 7T, Bruker Daltonics, Bremen, 133 134 Germany) operating in MALDI positive mode with a data point size of 2, 4, and 8M, or 16M for the 135 scimaX 2XR in the 300 to 1200 m/z mass range using the Amplitude mode. Other relevant parameters for the solariX XR 9.4T and the scimaX 7T 2XR are listed in Table 1. The shimming of the ICR cells 136 137 was performed using the recommended procedure by the manufacturer based on the infusion of sodium 138 trifluoroacetic solution in 50% acetonitrile. Before m/z calibration, the tissue to be analyzed, or a seriated 139 tissue test section, was first probed to determine the minimum required laser power and monitor the ion 140 current to set the laser parameters. Then, the m/z calibration of the spectrometer was performed using 141 the odd-numbered clusters of red phosphorus spotted close to the analyzed samples³¹. During 142 calibration, a TIC as close as possible to the value obtained on tissue was targeted with the help of 143 selective accumulation upper and lower cutoff set at maximum $\pm 20\%$ of the probed TIC on the sample. 144 In our case, the laser powers of the solariX XR and the scimaX 2XR were adjusted from 10 to 16% 145 depending on the number of ions to be injected in the ICR cell. The laser power could be higher depending on the rate of wear of the laser. Typical high vacuum values of the ICR cells were about 146 2.5×10^{-10} mbar and the targeted TIC with a data size of 4M was 5×10^8 cps. 147

Automated acquisitions were performed using the software FlexImaging 5.0 (Bruker Daltonics,
Bremen, Germany) with a raster of 50µm in both (x,y) axes.

Table 1 Sets of parameters used in the original and re-optimized method. The laser power was adjusted to get the lower power possible when the TIC signal was reaching 5×10⁸ cps. Values

152 in brackets show a working range.

		sola	riX XR	scimaX 2XR 1 or 2u		
Parameters	(Unit)	Original	Re- optimized	Original	Re- optimized	
Laser focus ^a	%	98	80	93	85	
Laser shots	(#shots)	600	[2 ; 10]	400	6	
Laser frequency	(Hz)	1000	#shots×10	1000	60	
Sweep excitation power	(%)	22	[16 ; 18]	20	18	
Front & back trap plate	(V)	1.5	1.35	3	3.06	
Analyzer entrance	(V)	-10	-10	-10	-10	
Side Kick	(V)	5	[6 ; 10]	0.2	3	
Side Kick Offset	(V)	-1.0	-1.5	-1.5	-1.5	
Time of flight	(ms)	1.2	1.2	1.0	0.7 ^b	

153

^a small and medium laser focus for solariX XR and the scimaX 2XR, respectively

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^b time of flight set at 0,7ms for the 2ω acquisition for 16M data point only

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156 2.6. Data processing

All datasets were visualized with SCiLS Lab 2016b (SCiLS, Bremen, Germany) after conversion into 157 scilslab format using the SQlite file generated by the instrument. MALDI-MSI were generated after total 158 159 ion count normalization (unless specified otherwise) and automatic hot spot removal (at 99% quantile). 160 Database bulk structure searches were performed using the LIPID MAPS Structure Database (LMSD) tool offered by LIPID MAPS® Lipidomics Gateway (lipidmaps.org)^{32,33}. Queries were submitted on the 161 162 full database with a 5mDa mass tolerance for [M+H]⁺, [M+H-H₂O]⁺, [M+Na]⁺, [M+K]⁺, and [M+2Na-H]⁺ 163 ions. The nomenclature of lipids used in this work is based on the recommended lipids classification by 164 Fahy and coworkers³⁴. An in-house script written in R language has been used to calculate the standard 165 deviation for MMA and R.P. for a given m/z window within an MSI dataset converted to imzML format 166 by FlexImaging 5.0.

167 3. <u>Results and discussion</u>

Most of the published work reporting the optimization of MALDI FT-ICR MSI methods was performed on instruments fitted with superconducting magnets of 12T and 15T or above. We propose here to visit or revisit the influence of the instrument parameters to produce MALDI images with the highest possible mass R.P. and MMA that such instruments can offer on most readily available commercial FT-ICR instruments equipped with a 7 or 9.4T magnet.

173 A higher magnetic field limits the space-charge effects inside the ICR cell and provides improved 174 tolerance in regards to the number of injected ions. During MALDI MSI experiments, the amount of 175 injected ion significantly varies due to the intrinsic heterogeneity of the biological material in terms of 176 molecular composition and dynamic range of the acquisition method. Consequently, instruments using 177 lower magnetic fields could be substantially affected by impaired performance. The analytical workflow, 178 from matrix deposition to ion optics parameters, was investigated and applied to MALDI FT-ICR 179 instruments using 7T (scimaX 2XR) or 9.4T (solariX XR) superconducting magnets and the 1 ω or 2 ω 180 detection mode, when available. Additionally, ion source parameters, only poorly explored in the 181 literature, were explored at optimal settings to improve the quality of MALDI images at very high mass 182 R.P.

3.1. Magnetic field and charge-space effects. The determination of the *m*/*z* ratios by FT-ICR is
obtained by converting the rotational frequencies of the ions by Fourier Transformation, which depends

185 on the masses and carried charges under the influence of the applied magnetic fields. The space-186 charge effect limits the performance of an FT-ICR due to the influence of the charge repulsion between 187 ion packets if the ICR cell is loaded with more ions than the magnetic field can constrain. Using a superconductive magnet with higher magnetic fields would limit this influence as explained by in ω_{obs} = 188 qB $2\alpha V$ $q\rho G_i$ Equation 1, where the unperturbed ion frequency ω_{obs} is the observed 189 т a^2B $\epsilon_0 B$ 190 frequency (which is then converted into a signal in the mass spectrum) equaling the unperturbed 191 cyclotron frequency minus the magnetron frequency for an ion in a perfectly quadrupolar static field 192 minus the space-charge component of the mass shift^{35,36}. In Equation 1, q represents the ion charge, 193 B the magnetic field strength, m the ion mass, α the separation between the trapping plates, V the 194 voltage difference between upper and side plates, a the separation between upper and lower plates, p 195 the ion density, G the ion cloud geometry and ε_0 the void permittivity constant.

196
$$\omega_{obs} = \frac{qB}{m} - \frac{2\alpha V}{\alpha^2 B} - \frac{q\rho G_i}{\epsilon_0 B}$$

197 In the third term, the importance of ion density and cloud geometry describes the impact of the 198 number of injected ions on the angular velocity ω and consequently, the mass shift observed in the mass spectra. The influence of the magnetic field also restrains the mass shift to some extent (only in 199 200 the denominator). In this paper, the main focus is on limiting the ion current fluctuation during the MSI 201 acquisition and restricting the observed mass shift to the extent possible. This corresponds to limiting 202 the fluctuations of the space-charge effect components at a constant magnetic field. Nonetheless, the 203 requirement for the magnetic field to produce MALDI images at extreme mass R.P. was evaluated by 204 comparing experimental results from 9.4T to a 7T operated in 1ω and/or 2ω detection modes.

Equation 1

205 Considering theory, the best chance to restrain the experimental mass shift in the average MS 206 images under the specification of the FT-ICR is to prevent space-charge effects. This was investigated 207 by experimental work and a literature survey for the different steps of the production of MALDI images, 208 from sample preparation (matrix deposition protocols) to instrumental parameters (ion optics 209 transmission, ICR ion optics). Furthermore, optimization works for laser adjustments are still scarce in 210 the literature and were also investigated.

The monitored outputs of experimental parameters during measurement at very high mass R.P. (500,000 and above in the lipid mass range) were mainly the stability of the total ion current (TIC) fluctuation, the mass shift (i.e. pixel-to-pixel variation of the *m/z* peak apexes) and the mass R.P. (R.P. expressed as full width at half maximum, FWHM) for the individual pixel and in the profile average mass spectrum of the image. The apparent intra-scan dynamic range between major and minor peaks of lipids was also monitored and reported during the laser parameter optimization.

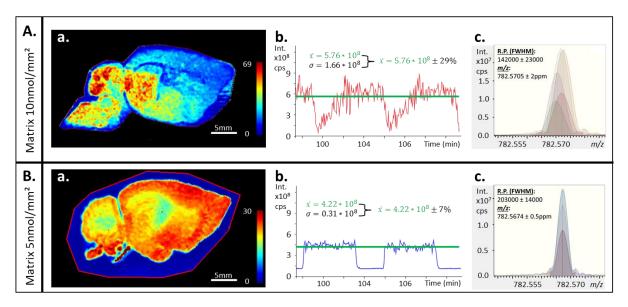
217 The effect of significant TIC fluctuations on the m/z shift was evaluated by monitoring the signal 218 produced by a standard Splash LipidomiX solution of deuterated lipids spotted with α-HCCA matrix on 219 an ITO glass slide. After the acquisition of a single MALDI-MS scan involving 10 laser shots, the 220 instrument was post-calibrated using the signals from [PC (15:0/18:1(d7))+H]+ m/z 753.613, [LysoPC 221 (18:1(d7))+H]⁺ m/z 529.399 and [SM (d18:1/18:1(d9))+H]⁺ m/z 738.647. The acquired signal was 222 observed with an R.P. above 200,000 (FWHM) at their respective m/z and MMA better than 0.5ppm 223 (MMA after post-calibration). When the number of injected ions was increased (i.e. using 400 laser 224 shots), it resulted in a 10x higher total ion count injected into the ICR cell and a mass shift for all 225 experimentally observed m/z values resulting in an MMA between 2 and 8 ppm. The larger amount of 226 ions introduced into the cell in regards to the calibration procedure severely impaired the MMA. An 227 abrupt modification of the TIC intentionally generated by suddenly increasing the number of laser shots 228 was correlated with the observed mass shift. An example is provided in Figure S1 for illustration based 229 on the signal obtained for [PC (15:0/18:1(d7))+H]+.

From an MSI perspective, such TIC variations commonly appear when inhomogeneous matrix deposition creates hot spots, and/or when samples, such as tissue sections, have intrinsically heterogeneous regions in terms of molecular compositions and/or desorbed/ionized efficiencies.

233 3.2. Influence of sample preparation and the amount of sprayed matrix on the total ion 234 current stabilization. Avoiding the formation of hot spots due to inhomogeneous deposition of matrix 235 is important to produce MS images of high quality. The KPMP Consortium (Veličković et al.), and Tressler et al. improved MALDI MSI data after factorial design optimization of the deposited matrix using 236 an automatic sprayer on mice's kidney tissue sections^{24,37}. In the presented work, the amount of 237 238 deposited MALDI matrix was investigated in terms of signal suppression for the analytes of interest 239 when varying the number of laser shots per pixel (see Figure S2). For this purpose, serial sagittal mouse 240 brain slices were prepared with varying amounts of sprayed α -HCCA matrix of 10 and 5 nmol per mm² 241 respectively. MS images were acquired either using several hundreds of laser shots at 1000Hz (Figure 242 1A) or using 6 laser shots at 60Hz (Figure 1B). In the latter, the laser focus of the solariX XR 9.4T 243 Smartbeam II laser was adjusted from 98% to 80% to ablate and desorb an equivalent amount of

244 material per pixel. This allowed the generation of similar TIC values between the MALDI MSI methods. 245 Figure 1A shows an unstable TIC for the method employing sub-optimal parameters while the new set 246 of optimized settings showed a drastically improved TIC stability through the entire acquisition (Figure 247 1B). This resulted in improved alignment of the m/z peaks keeping the mass shifts below 0.5 ppm while 248 improving effective mass R.P. in the mean spectrum to around 400,000 at m/z 400 for all detected ions 249 while keeping the same spatial resolution (Figure 1 A and B panel c). An in-house script has been used 250 to monitor the m/z channels for every pixel and compute the distribution of their measured values (apex 251 of the *m*/*z* peaks) and the R.P. using FWHM. Figure S3 provides a graphical representation of the mass 252 and R.P. distribution for m/z 782.5674 ([PE 39:4+H]+ or [PC 36:4+H]+ (according to the LIPID MAPS 253 database) for both methods which were drastically improved when the TIC fluctuation was restrained.





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256 Figure 1. Comparison of dynamically harmonized MALDI FT-ICR MSI acquired on a solariX XR 9.4T with a manufacturer recommendation-based method (A) and a 6 laser shots-based method 257 (B), see section 3.2 for details. Reconstructed heat maps of the non-normalized Total Ion Count 258 of MS images (a). Portions of the TIC over time of the MSI acquisition and the computed mean 259 intensities with standard deviation (b). Observable gaps on the TIC are values from pixels 260 261 outside of the tissue section and were excluded to compute the standard deviation. The TIC 262 presented in the upper panel was obtained when 10nmol.mm⁻² α -HCCA matrix was deposited using 98% laser focus and from 5nmol.mm⁻² α -HCCA matrix with 80% laser focus (lower panel). 263 Multi-pixel mass spectra overlay of m/z 782.5674 shows the notable improvement in terms of 264 265 mass R.P. and mass accuracy measurements during the MALDI images between the unstable 266 (upper panel) and stable (lower panel) Total Ion Count (c).

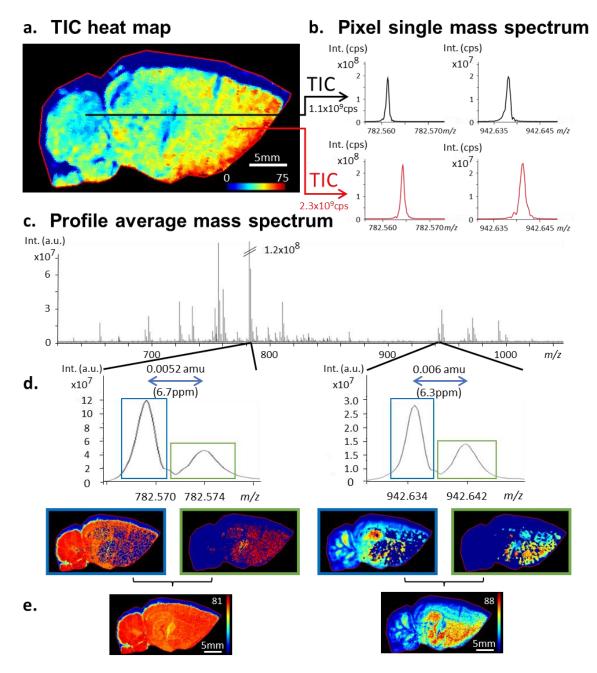
267 3.3. ICR mass analyzer optimization and the influence of ion optic voltages on TIC stability. At

268 first, the method employed was based on values recommended by the manufacturer for MALDI-MSI.

269 Minimal modifications were the use of the broadband mode in the 300 to 1200 amu mass range working

270 at an estimated R.P. above 400.000 at m/z 800 with 4M data point. The solariX XR 9.4T instrument

was operated following a method optimized by Ferey et al.¹⁵. They optimized the MALDI FT-ICR MSI 271 272 parameters using experimental designs from a 12T magnet instrument fitted with the Paracell. However, 273 our MSI acquisitions performed on our 9.4T magnet suffered from severe mass shifts as shown in 274 Figure 2. For individual pixels of the image, the experimental R.P. was slightly above the one estimated 275 by the FT-ICR control software (FTMS control). Nevertheless, the centroids of the m/z peaks shifted 276 from pixel-to-pixel resulting in an MMA below the specification of the instrument as observed in the 277 profile average mass spectrum of the image. The MSI profile average spectrum showed peak 278 broadening due to the combination of pixels mass spectra where a significant pixel-to-pixel mass shift 279 of the measured m/z occurred. Extreme cases were observed where the m/z peaks were splitting by a 280 few milli amus (i.e. several ppm) as shown in Figure 2d. The reconstructed MS images of m/z 782.57 281 (assumed to be [PC 34:1 + Na]⁺) and 942.64 (assumed to be [CL 36:4 + NH4]⁺), both selected with a 282 mass tolerance of ±0.004, result in biased and incomplete ion distributions unless the targeted ions 283 and their shifted counterparts m/z peak were selected together by extending the mass tolerance to 284 ±0.01 for image reconstruction (Figure 2e). Comparison of the extracted spectra on a per-pixel basis 285 (Figure 2a) showed that peak splitting could again be linked to the regions of interest submitted to large 286 TIC variation despite the ion optics optimization adapted from Ferey et al. for our 9.4T instrument.



287

288 Figure 2. Heat map of the non-normalized TIC of a mouse brain section analyzed by highresolution MALDI FT-ICR MSI on a solariX XR 9.4T using non-optimized MSI method (a). 289 290 Extracted mass spectra from single pixels located in regions with significant differences in Total Ion Current (b). Average mass spectrum (mean spectrum) of the whole MALDI image (c). Zoomed 291 profile average spectrum focused on m/z 782.57 and 942.64 showing artifacts of split peaks and 292 their complementary distributions due to inconsistent mass measurement accuracy during 293 294 acquisition (d). Obtained localizations with a window selection encompassing both m/z peaks 295 shown in the vicinity of m/z 782.57 and 942.64, respectively (e).

296 Ion optic voltages of the ICR mass analyzer were investigated as options to stabilize the TIC signal

297 (i.e. charge-space effects) in our 9.4T FT-ICR. Thus, investigations were focused on ICR parameters,

298 especially analyzer entrance, front and back trapping, sidekick, and excitation sweep voltages. Out of

those parameters, the sidekick was the only parameter that had a slight influence on the TIC stability.

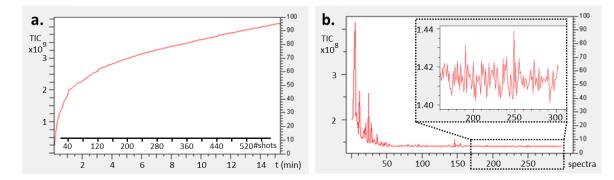
The sidekick offset optimization also showed a limited effect on the mass shift, while the front and back trapping, as well as the excitation sweep, affected the peak shapes (as expected) but not the TIC stability. In contrast, the voltage applied to the analyzer entrance had an effect. An increased analyzer entrance voltage was followed by a gradual decrease of the MS signal. We anticipate that it could potentially be used to limit the introduction of ions inside the ICR cell and act as a real-time ion injection control device. In the end, optimizing the ion optics does not significantly improve the TIC stability during MSI experiments.

308 3.4. Monitoring MALDI processes and the influence of the number of laser shots. Considering 309 a scan being the event of acquiring a mass spectrum from the firing of one or more laser shots, the 310 relationship between the TIC value and the number of laser shots per scan was investigated manually 311 on mice brain tissue sections. Acquisitions ranging from the minimum number of laser shots per scan 312 up to 600 laser shots on a fixed (x,y) position of the sample were performed. Because acquisitions with 313 a single laser shot resulted in the absence of signals from both, the matrix and the tissue, 2 laser shots 314 per scan were employed for the minimum number of laser shots per scan. Under this experimental 315 condition, the laser frequency had to be lowered below 300Hz once again due to an absence of signal 316 above this threshold. Below the laser frequency of 300Hz, no significant variations of the MS signal 317 were observed (data not shown). To investigate the influence of the number of laser shots to produce 318 adequate mass spectra for MSI, the laser shots to laser frequency ratio was kept at 1:10 resulting in a 319 constant laser shots step duration. This 1:10 ratio ranges from 2 to 200 laser shots at a constant ratio 320 because 2000 Hz is the operational limit of the SmartBeam II laser of the solariX XR and the scimaX 321 2XR MALDI sources. By fixing the shooting duration, we should avoid most of the kinetic relaxation 322 influences and balance the potential biases due to the ion extraction from the MALDI plume by the ion 323 optics. Beyond 200 laser shots, the maximal laser frequency would be used at the cost of the constant 324 shooting step duration.

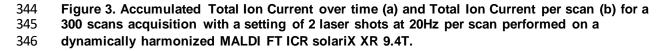
Figure 3a shows the TIC accumulation (summed TIC) for 2 laser shots at 20Hz and Figure 3b shows the TIC value for each scan. Figure 3a indicates that most of the accumulated TIC signal (more than one-half) was obtained from the first 100 laser shots and that initial laser shots produced a rather linear increase in TIC, followed by a smaller amount of ions produced by subsequent laser shots. Then, a further linear increase is observed after about 120 laser shots due to the accumulation of mainly noise

³⁰⁷

330 peaks. Figure 3b points out a noticeable instability of the TIC during the 50 first laser shots. The very 331 first shots showed the highest signal abundance in the mass spectrum with a relatively high relative 332 abundance (> 10% relative intensity) which aligns with the so-called "first-shot phenomenon" first 333 described by the team of Hillenkamp³⁸. The following laser shots, still ablating the same (x,y) position, 334 only poorly contributed to good signal-to-noise ratios for interesting m/z values and the less abundant 335 m/z peaks vanished first. These results suggest that a smaller amount of laser shots is beneficial for the detection of ions with an appropriate signal-to-noise ratio unless the targeted ions require a 336 337 significantly larger amount of laser energy to be detected. Thus, by using fewer laser shots TIC 338 fluctuations will be minimized to only a small percentage ensuring a more controlled number of ions to 339 be injected into the ICR cell. This leads to constant space-charge effects resulting in the production of 340 ultra-high mass R.P. MALDI images. The contribution of the laser shots and the desorption/ionization 341 steps of each pixel being imaged in terms of duration is typically less than 1 second from 2 to 10 laser 342 shots when operating the laser shots to laser frequency at a 1:10 constant ratio.



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3.5. Influence of the number of laser shots for the apparent dynamic range of imaged lipids. New 347 348 sets of mice brain images were produced by MALDIMSI. The number ranged from 10 to 600 at a fixed 349 laser-shooting time duration (i.e. laser shots to laser frequency ratio). As expected, lowering the number 350 of laser shots (from 600 to 10) reduced the overall signal intensities in the mass spectra (TIC) although 351 the detected ions for both methods were comparable. The loss of m/z signals in the method using the 352 lower amount of laser shots was mainly concerning the isotope contributions and peaks that were 353 already close to the 3xS/N (signal over noise) as computed by the software. Interestingly, the absolute 354 intensities of the minor ions were almost not affected compared to the most abundant ones when using 355 fewer laser shots and 5nmol.mm⁻² of deposited matrix on mice's brain tissue sections. Table 2 reports 356 the absolutes intensity, mass accuracy, and intensity ratio between high and low abundant lipids 357 detected in the MS images of mice's brain tissue section when using 10 or 100 laser shots. The lipids 358 were identified according to LIPID MAPS database peak annotation. Ions at m/z 772.53 and 798.54

were the most intense signals observed while m/z 770.51 and 848.56 are among the least intense ions. When comparing 10 to 100 laser shots, the intensities of minor ions were roughly halved while major ions intensities decrease by an order of magnitude. By reducing the number of laser shots per scan the relative intensities of the most intense ions tend to decrease to a larger extent in regards to the less intense ions. Any combination of intense/less intense ion ratios leads to the same observations. Besides, the intensity ratio between ions of comparable intensities (e.g. m/z 772.53 vs 798.54) was almost unaffected by the number of laser shots per scan.

Table 2. Intensities and ratios of detected and identified lipids in a mouse brain tissue section acquired with the MALDI FT-ICR MS (solariX XR 9.4T) instrument for 10 and 100 laser shots

		10 shots				100 shots			
Target m/z Identification					Ratio			Ratio	Ratio
	Identification	Intensity (c.p.s)	Mass	m/z	m/z	Intensity (c.p.s)	Mass	m/z	m/z
	identification		accuracy	772.53	798.54		accuracy	772.53	798.54
			(ppm)	over m/z	over m/z		(ppm)	over m/z	over m/z
				target	target			target	target
770.50975	[PA 36:2+K] ⁺	4.8E+05	-0.09	10.6	11.3	1.3E+06	-0.12	33.1	40.0
848.55643	[PC 38:4+K] ⁺	8.9E+05	-0.25	5.73	6.07	6.5E+06	-0.24	6.61	8.00
772.52519	[PC 32:0+K] ⁺	5.1E+06	-0.13		1.06	4.3E+07	-0.17		1.21
798.54079	[PC 34:1+K]+	5.4E+06	-0.26	0.94		5.2E+07	-0.26	0.83	

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369 The cause of the disparity in the ion intensity ratio when varying the number of laser shots was 370 further investigated. It could indeed be related to either, the ionization process itself or the efficiency of 371 ion transmission by the ion optics and/or the MS analyzer (ICR cell). Similar experiments to determine 372 the influence of the ionization process were conducted on a MALDI-ToF instrument (rapifleX, Bruker, 373 Germany) despite its differences in terms of ion extraction mechanism, source vacuum, and laser 374 compared to the solariX XR and the scmiaX 2XR. To be somehow comparable with the Smartbeam II, 375 the beamscan option of the Smartbeam 3D was not used which avoids the laser energy being swept at 376 the surface of the sample (i.e. matrix blaster). No variation of the ion intensity ratio was observed with 377 the MALDI-ToF as shown in Table 3, despite we used a maximum of 1000 laser shots accumulation 378 instead of 100, regardless of the major or minor ions considered. The ablated surface of the sample of 379 only 25µm² with only 10 laser shots allowed the less abundant ions to still be detected and only matrix 380 signal intensities were strongly affected. The variation of the ion ratio observed with the MALDI FT-ICR 381 was then related to the ion optics and/or the ICR mass analyzer. It is worth reminding that higher 382 magnetic fields improve the dynamic range of the number of trapped ions inside the ICR in the absence 383 of noticeable space charge effects.

Table 3. Intensities and ratio of detected and identified lipids in a mouse brain tissue section acquired with the MALDI ToF MS (rapifleX) instrument (external calibration, enhanced cubic regression) for 10 and 1000 laser shots with the single focus option and without beamscan

Target m/z Identifica		10 shots				1000 shots			
			Ratio		Ratio			Ratio	Ratio
			Mass	m/z	m/z		Mass	m/z	m/z
	Identification	Intensity	accuracy	782.57	798.54	Intensity (c.p.s)	accuracy	782.57	798.54
		(c.p.s)	(ppm)	over m/z	over m/z		(ppm)	over m/z	over m/z
				target	target			target	target
782.567	[PC 36:4+H]+	6.8E+03	+9.7		0.79	1.8E+04	+7.1		0.81
798.541	[PC 34:1+K]+	5.3E+03	+11.2	1.27		1.5E+04	+10.0	1.23	
806.567	[PS 37:0+K]+	4.0E+03	-12.3	1.68	1.33	9.7E+03	-11.1	1.90	1.54
844.546	[PC 36:3+Na]+	4.6E+03	+3.8	1.47	1.16	1.5E+04	6.2	1.22	0.99

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389 3.6. Robustness of the MALDI MSI at ultra-high mass R.P. using the MALDI FT-ICR solariX XR 390 9.4T. When applying the optimized method for extreme resolution MSI with an estimated R.P. over 391 500,000 at m/z 800 (>1.000.000 at m/z 400), a much less pronounced mass shift was observed and 392 most importantly is fully within the instrument specifications (±0.5ppm) even for profile and centroided 393 average MALDI image spectra. FWHM resolutions for the individual spectra are now similar to the ones 394 observed in the profile average spectrum. The acquisition of such mass spectra qualities during an MSI 395 experiment of rat brain samples was previously achieved using a custom prototype of a hybrid linear 396 ion trap coupled to a 21T supra conducting magnet fitted with the Paracell by the NHMFL group at 397 Tallahassee in Florida³⁹. In this work, comparable results were obtained in terms of MSI mass R.P. and 398 MMA with a superconducting magnet of 9.4T using the same ICR cell (see Table S1). By comparing 399 the average spectrum of centroided MSI data performed on seriated brain (Figure 4a) and whole-body 400 zebrafish sections (Figure 4b), the difference in image quality is clearly evident. The new method with 401 a controlled ion injection in the cell (TIC stabilized) resulted in narrow m/z peaks due to a significantly 402 reduced mass shift. The image of the ion distribution in the tissue section is also less noisy whether or 403 not TIC or RMS normalized (RMS not shown). To demonstrate the robustness of the controlled TIC 404 method, replicates of serial brain sections (roughly 12,000 pixels) and zebrafish whole body sections 405 (roughly 20,000 pixels) were acquired using our optimized method (see Figure S5). In all cases, the 406 experimental mass R.P. expected by the acquisition software was surpassed. The imaging method was 407 tested for images with R.P.FWHM beyond 1,000,000 at m/z 800 for the brain region of the zebrafish 408 sample (roughly 1500 pixels). Figure S6 shows observable isotopic fine structures for abundant ions

409 also observable in the profile average spectrum further increasing the confidence of the identification 410 process of these ions. Note that a slight loss in R.P. is still observed in the profile average spectrum 411 compared to individual pixels spectra even with a contained mass shift below 0.5ppm (i.e. in agreement 412 with the instrument specification). At such high R.P. the contribution of a mass shift of 0.5ppm at m/z413 800 (i.e. 0.4 mamu) is still impacting negatively the R.P. In complement, a peak realignment strategy 414 by software post-processing coupled with our proposed MSI method was developed in our group to 415 restore the isotopic fine structure also in the average mass spectrum of MS images having lower mass R.P.^{40,41}. 416

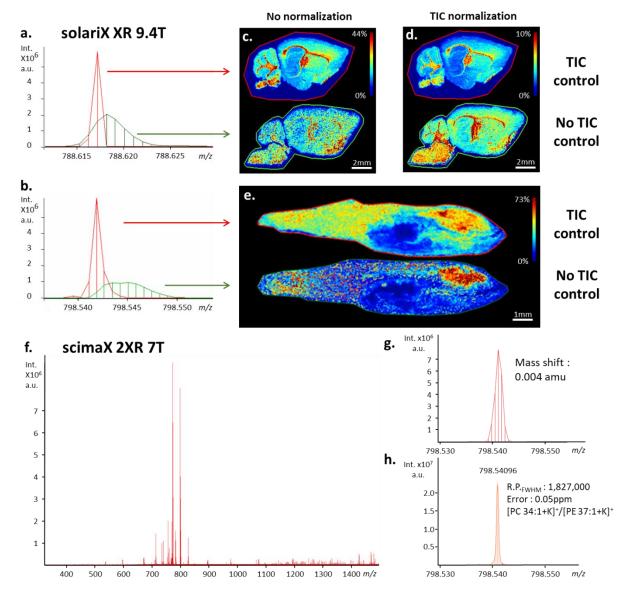


Figure 4. Centroided average MSI mass spectra of mouse brain (a) and zebrafish (b) using a MALDI FT-ICR (solariX XR 9.4T, fitted with ParaCell) instrument, zoomed in on *m/z* 788,62 and 798.54 respectively, showing peak width differences due to MMA obtained with (red) and without (green) TIC stabilization by optimization of the laser shot number (6 laser shots at 60 Hz).

422 Reconstructed MS images without (c) and with (d) TIC normalization, applying or not applying 423 TIC stabilization. Centroided average MSI mass spectrum of a mouse brain tissue section 424 acquired on the scimaX 2XR using the 2ω detection mode with TIC stabilization (f). Zoom in to 425 *m*/z 798.54 showing peak width difference due to MMA (h). Zoom on *m*/z 798.54 in an extracted 426 pixel spectrum showing the obtained R.P. FWHM and MMA. See text for details.

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428 **3.7. Influence of the magnetic field strength**. FT-ICR operating at a high magnetic field (≥ 12T) are 429 typically used for petroleomics analysis by direct infusion electrospray ionization analysis of diluted raw 430 crude oils. Direct infusion allows for a stable TIC signal and fills the ICR cell with a constant number of 431 ions at each scan. Higher magnetic fields allow the storage of a larger number of ions but also a stable 432 ion motion during long transient signal acquisition enabling very high mass R.P. (\geq 1,000,000 at m/z 400). Recently Ge et al⁴² demonstrated for oil samples introduced by direct infusion the capability of 433 434 FT-ICR mass analyzers operating at 7T and 2ω detection to closely match the performance of a 15T instrument. MSI also takes advantage of greater magnetic fields to produce higher quality images^{15,39}. 435 436 In this work, the influence of TIC variation was investigated for an FT-ICR instrument equipped with a ParaCell but using lower magnetic field strength, i.e. 7T. The scimaX 2XR 7T instrument also provides 437 438 the 2w detection mode which recycles the excitation plates into detection plates to improve the duty 439 cycle (transient signal) by a factor of 2 compared to the 1w detection mode. Mice brain images were 440 compared for both 1 ω and 2 ω detection. Also, for this instrument, TIC control improved the MMA and 441 spectral resolutions (See Figure 4f, g, h, and Figure S7). Interestingly, while no direct influence on ion 442 current stability was observed when the 2w detection mode was activated (Figure S8a), the mass shift 443 was easier to constrain compared to 1ω mode datasets (Figure S8b). We assumed that the drastic diminution of the transient signal duration prevented peak coalescence as well as the decoherence of 444 the ion packets inside the ICR cell^{8,43}. It is worth mentioning that the comparison of MS images 445 446 performed on serial tissue sections using 1w and 2w detection mode showed no tangible differences in terms of co-localization of the observed ions (Figure S8b). As an illustration, an MS image acquired 447 448 with the solariX 9.4T and the scimaX 2XR 7T using the 2ω detection mode at 16M data points of 1000 449 pixels of mouse brain tissue section showed an R.P.FWHM above 1,500,000 at m/z 800 and an MMA of 0.15ppm (Figure 4 f, g, and h). The typical time to produce an image of 1000 pixels was 195 minutes 450 using our solariX XR 9.4T (i.e. 1w at 8M data point) and 205 minutes using the scimaX 2XR 7T operating 451 452 at 2ω and 16M data point.

453 Table 4 shows the dynamic range obtained for high and low abundant lipid signals detected during 454 the MSI experiment of 2 consecutive brain sections with the scimaX 2XR using 1 or 2ω detection mode. Note that the 7T instrument still required the ICR cell to be loaded with fewer ions than the 9.4T 455 456 instrument using 1w or 2w detection to restrict the experimental mass shift in average mass spectra. 457 Therefore, fewer laser shots were used to produce the data in Table 4 compared to Table 2 and Table 458 3. The ratios obtained for the scimaX 2XR using 1 ω detection are somewhat similar to what was 459 obtained with the 9.4T solariX XR. The 2w detection mode seems to be also beneficial because the 460 dynamic range of the lipids detected in the MALDI images was less affected than the 1w detection 461 mode. The higher power of the magnet is still beneficial for reaching a wider intra-scan dynamic range, or if the TIC cannot be efficiently stabilized, even after optimizing the laser parameters. Nevertheless, 462 463 MSI acquisition at extreme mass R.P. is possible using the 7T superconducting magnet and 2ω 464 detection.

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Table 4. Intensities and ratio of detected and identified lipids in a mouse brain tissue section acquired with the MALDI FT-ICR-MS (scimaX 2XR 7T) instrument for 6 and 400 laser shots

		6 laser shots				400 laser shots			
Target m/z	Identification	Intensity (c.p.s)	Mass Accuracy (ppm)	Ratio <i>m/z</i> (a) over m/z target	Ratio <i>m/z</i> (b) over m/z target	Intensity (c.p.s)	Mass Accuracy (ppm)	Ratio <i>m/z</i> (a) over m/z target	Ratio <i>m/z</i> (b) over m/z target
				scimaX 2	2XR 7T, 1	ω detectio	on mode		
713.45181 [[PA 34:1+K]+	8.0E+5	+0.40	6.63	30.0	2.7E+6	+0.61	7.04	18.5
844.52531 [PC 38:6+K]+	2.4E+5	+0.53	22.1	100	Not detected	+0.58	N.C.	N.C.
772.52519 [PC 32:0+K]+	5.3E+6	+0,37		4.53	1.9E+7	+0.56		2.63
798.54079 [l	PC 34:1+K]+	2.4E+7	+0.26	0.22		5.0E+7	+0.44	0.38	
	scimaX 2XR 7T, 2ω detection mode								
713.45181 [[PA 34:1+K]+	4.3E+6	+0.23	3.72	4.88	4.9E+6	+0.40	4.29	10.4
844.52531 [PC 38:6+K]+	3.9E+6	+0.17	4.10	5.38	4.3E+6	+0.33	3.13	7.61
772.52519 [PC 32:0+K]+	1.6E+7	+0,22		1.31	2.1E+7	+0.37		2.43
798.54079 [l	[PC 34:1+K]+	2.1E+7	+0.26	0.76		6.7E+7	+0.31	0.41	

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m/z (a) corresponds to 772,53 and m/z (b) correspond to 798,54

469 N.C. Not Computed

470 **3.8. Improvement of peak annotation.** Lastly, database queries for mass lists obtained with the 471 optimized method showed an improvement in terms of peak annotations: fewer false positives and 472 negatives were observed due to the improved R.P., and MMA. Figure S9 shows some examples of 473 database results as histograms of the matching counts at a given mass accuracy (in ppm) to detect 474 readily any oddities in the dataset. When the TIC was not stabilized (not optimized method), most of 475 the identifications had mass accuracy around -1.5 ppm. These values were not consistent with the 476 specification of a properly calibrated FT-ICR instrument and they do not fit with the requirement for 477 proper annotation of lipids from the LIPID MAPS database. In contrast, the MALDI image acquired with 478 the optimized method and stabilized TIC led to a larger number of identifications, with scores around 479 +0.4ppm that are well within the nominal performance for the instrument. The number of total matches 480 is drastically improved due to fewer false-negative identifications and similarly, potentially fewer false-481 positive results. Of course, the addition of the isotopic fine structure further improved the confidence 482 level of the identified lipids.

483 4. Conclusion

484 In this work, we successfully limited the space-charge effects and limited the resulting mass shift to 485 improve mass accuracy for MALDI MS images of mouse brains and Zebrafish tissue sections by 486 introducing a controlled TIC injection method in the ICR cell. The method was successfully applied on 487 the solariX XR 9.4T and the scimaX 2XR 7T, two commercially available dual-source ESI/MALDI 488 instruments fitted with the Paracell®. Under optimal instrumental settings, this was achieved primarily 489 by optimizing lasers parameters and the concentration of deposited/sprayed matrix. MSI with a 490 resolving mass power beyond 1,000,000 at m/z 800 was successfully achieved within around 200 491 minutes for 1000 imaged pixels (transient duration of 11.7sec at 8M data points in an operated mass 492 range between m/z 300 and 1200 using the common Amplitude mode for the solariX XR 9.4T, and a 493 transient of 12.3sec for the scimaX 2XR 7T in 2ω detection mode at 16M data points) with no mass 494 shift beyond 1 ppm (typical mass shift < 0.5ppm) which correlates to approximatively 0.5 mamu in the 495 lipid mass range. The resulting images were less noisy, i.e. showing higher contrast and appearing by 496 this to be sharper, at constant lateral resolution and matrix deposition method. Extreme resolution MS 497 images obtained with relatively limited power of magnetic fields (< 12T) require a stabilized TIC 498 throughout the acquisition to retain the instrument specifications. The intra-scan dynamic range 499 obtained during this work using the commercially available 9.4T and 7T instruments seemed to be 500 around 100, while Bowman et al.³⁹ reported a dynamic range of around 500 using a custom 21T MALDI 501 FT-ICR instrument. Using 2w detection on higher magnetic field instruments will speed up the scan time by a factor of 2, allowing more samples to be measured at constant mass R.P. in the same time frame. Peak annotations using the LIPID MAPS database correspond to identification scores better than 0.4ppm, limiting misidentification of lipids, especially for measurement generating isotopic fine structures. Revisiting the laser parameters improved method reproducibility from pixels-to-pixels and also from sample-to-sample, which improved the robustness of our method by successfully performing similar MALDI images of consecutive tissue sections in replicates.

It was found that the entrance voltage to the analyzer affects the number of ions introduced into the ICR cell in an interesting way that could potentially be used to limit the overflow of ions to be injected into the ICR cell, acting as an ion injection control device. The idea would be to limit ion current fluctuations in real-time for samples with high concentration heterogeneity of target compounds. This would require further investigation as it is currently considered a double-edged sword, as the signal can be easily lost if this voltage value is not properly set.

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531 References

- Le Rhun, E.; Duhamel, M.; Wisztorski, M.; Gimeno, J.-P.; Zairi, F.; Escande, F.; Reyns, N.;
 Kobeissy, F.; Maurage, C.-A.; Salzet, M.; Fournier, I. Evaluation of Non-Supervised MALDI
 Mass Spectrometry Imaging Combined with Microproteomics for Glioma Grade III
 Classification. *Biochimica et Biophysica Acta (BBA) Proteins and Proteomics* 2017, 1865 (7),
 875–890.
- 537 (2) Ellis, S. R.; Cappell, J.; Potočnik, N. O.; Balluff, B.; Hamaide, J.; Van der Linden, A.; Heeren,
 538 R. M. A. More from Less: High-Throughput Dual Polarity Lipid Imaging of Biological Tissues.
 539 Analyst 2016, 141 (12), 3832–3841.
- Lamont, L.; Eijkel, G. B.; Jones, E. A.; Flinders, B.; Ellis, S. R.; Porta Siegel, T.; Heeren, R. M.
 A.; Vreeken, R. J. Targeted Drug and Metabolite Imaging: Desorption Electrospray Ionization
 Combined with Triple Quadrupole Mass Spectrometry. *Anal. Chem.* 2018, *90* (22), 13229–
 13235.
- 544 (4) Wang, J.; Wang, C.; Han, X. Tutorial on Lipidomics. *Analytica Chimica Acta* 2019, *1061*, 28–
 545 41. https://doi.org/10.1016/j.aca.2019.01.043.
- 546 (5) Marshall, A. G.; Hendrickson, C. L. High-Resolution Mass Spectrometers. *Annual Rev. Anal.* 547 *Chem.* 2008, 1 (1), 579–599.
- Kostyukevich, Y. I.; Vladimirov, G. N.; Nikolaev, E. N. Dynamically Harmonized FT-ICR Cell
 with Specially Shaped Electrodes for Compensation of Inhomogeneity of the Magnetic Field.
 Computer Simulations of the Electric Field and Ion Motion Dynamics. *J. Am. Soc. Mass Spectrom.* 2012, *23* (12), 2198–2207.
- 552 (7) Nikolaev, E. N.; Kostyukevich, Y. I.; Vladimirov, G. N. Fourier Transform Ion Cyclotron
 553 Resonance (FT ICR) Mass Spectrometry: Theory and Simulations: FT ICR MS. *Mass Spec Rev* 554 2016, 35 (2), 219–258.
- 8) Boldin, I. A.; Nikolaev, E. N. Fourier Transform Ion Cyclotron Resonance Cell with Dynamic
 Harmonization of the Electric Field in the Whole Volume by Shaping of the Excitation and
 Detection Electrode Assembly: New Principle of Ion Detection in a FTICR Penning Trap. *Rapid Commun. Mass Spectrom.* 2011, 25 (1), 122–126.
- Jertz, R.; Friedrich, J.; Kriete, C.; Nikolaev, E. N.; Baykut, G. Tracking the Magnetron Motion in
 FT-ICR Mass Spectrometry. *J. Am. Soc. Mass Spectrom.* **2015**, *26* (8), 1349–1366.
- (10) Popov, I. A.; Nagornov, K.; N.Vladimirov, G.; Kostyukevich, Y. I.; Nikolaev, E. N. Twelve Million
 Resolving Power on 4.7 T Fourier Transform Ion Cyclotron Resonance Instrument with
 Dynamically Harmonized Cell—Observation of Fine Structure in Peptide Mass Spectra. J. Am.
 Soc. Mass Spectrom. 2014, 25 (5), 790–799.
- 565 (11) Nikolaev, E. N.; Gorshkov, M. V.; Mordehai, A. V.; Talrose, V. L. Ion Cyclotron Resonance
 566 Signal-Detection at Multiples of the Cyclotron Frequency. *Rapid Commun. Mass Spectrom.*567 **1990**, *4* (5), 144–146.
- Fan, Y.; Ridge, D. P.; Rockwood, A. L. Harmonic Signal Enhancement in Ion Cyclotron
 Resonance Mass Spectrometry Using Multiple Electrode Detection. *International Journal of Mass Spectrometry and Ion Processes* 1988, *84* (3), 293–304.
- 571 (13) Schweikhard, L. Theory of Quadrupole Detection Fourier Transform-Ion Cyclotron Resonance.
 572 International Journal of Mass Spectrometry and Ion Processes 1991, 107 (2), 281–292.
- 573 (14) Pan, Y.; Ridge, D. P.; Wronka, J.; Rockwood, A. L.; Marshall, A. G. Resolution Improvement by
 574 Using Harmonic Detection in an Ion Cyclotron Resonance Mass Spectrometer. *Rapid Commun.*575 *Mass Spectrom.* 1987, 1 (7–8), 120–121.
- 576 (15) Ferey, J.; Marguet, F.; Laquerrière, A.; Marret, S.; Schmitz-Afonso, I.; Bekri, S.; Afonso, C.;
 577 Tebani, A. A New Optimization Strategy for MALDI FTICR MS Tissue Analysis for Untargeted
 578 Metabolomics Using Experimental Design and Data Modeling. *Anal Bioanal Chem* 2019, *411*579 (17), 3891–3903.
- Longuespée, R.; Kriegsmann, K.; Cremer, M.; Zgorzelski, C.; Casadonte, R.; Kazdal, D.;
 Kriegsmann, J.; Weichert, W.; Schwamborn, K.; Fresnais, M.; Schirmacher, P.; Kriegsmann,
 M. In MALDI–Mass Spectrometry Imaging on Formalin-Fixed Paraffin-Embedded Tissue

- 583 Specimen Section Thickness Significantly Influences *m/z* Peak Intensity. *Prot. Clin. Appl.* **2019**, 584 13 (1), 1800074.
- 585 (17) Goodwin, R. J. A. Sample Preparation for Mass Spectrometry Imaging: Small Mistakes Can
 586 Lead to Big Consequences. *Journal of Proteomics* 2012, 75 (16), 4893–4911.
- 587 (18) Shimma, S.; Sugiura, Y. Effective Sample Preparations in Imaging Mass Spectrometry. *Mass Spectrometry* 2014, 3 (Special_Issue), S0029–S0029.
- Morikawa-Ichinose, T.; Fujimura, Y.; Murayama, F.; Yamazaki, Y.; Yamamoto, T.; Wariishi, H.;
 Miura, D. Improvement of Sensitivity and Reproducibility for Imaging of Endogenous
 Metabolites by Matrix-Assisted Laser Desorption/Ionization-Mass Spectrometry. *J. Am. Soc. Mass Spectrom.* 2019, *30* (8), 1512–1520.
- Kaletaş, B. K.; van der Wiel, I. M.; Stauber, J.; Lennard J. Dekker; Güzel, C.; Kros, J. M.; Luider,
 T. M.; Heeren, R. M. A. Sample Preparation Issues for Tissue Imaging by Imaging MS: Sample
 Preparation Issues for Tissue Imaging. *Proteomics* 2009, *9* (10), 2622–2633.
- 596 (21) Grassl, J.; Taylor, N. L.; Millar, Ah. Matrix-Assisted Laser Desorption/Ionisation Mass
 597 Spectrometry Imaging and Its Development for Plant Protein Imaging. *Plant Methods* 2011, 7
 598 (1), 21.
- (22) Nishidate, M.; Hayashi, M.; Aikawa, H.; Tanaka, K.; Nakada, N.; Miura, S.; Ryu, S.; Higashi, T.;
 (30) Ikarashi, Y.; Fujiwara, Y.; Hamada, A. Applications of MALDI Mass Spectrometry Imaging for
 (31) Pharmacokinetic Studies during Drug Development. *Drug Metabolism and Pharmacokinetics*(4), 209–216.
- (23) Prideaux, B.; Stoeckli, M. Mass Spectrometry Imaging for Drug Distribution Studies. *Journal of Proteomics* 2012, 75 (16), 4999–5013.
- (24) Tressler, C.; Tilley, S.; Yang, E.; Donohue, C.; Barton, E.; Creissen, A.; Glunde, K. Factorial
 Design to Optimize Matrix Spraying Parameters for MALDI Mass Spectrometry Imaging. *J. Am.*607 Soc. Mass Spectrom. 2021, 32 (12), 2728–2737.
- 608 (25) Römpp, A.; Guenther, S.; Schober, Y.; Schulz, O.; Takats, Z.; Kummer, W.; Spengler, B.
 609 Histology by Mass Spectrometry: Label-Free Tissue Characterization Obtained from High610 Accuracy Bioanalytical Imaging. *Angewandte Chemie International Edition* 2010, *49* (22),
 611 3834–3838.
- 612 (26) Barry, J. A.; Robichaud, G.; Muddiman, D. C. Mass Recalibration of FT-ICR Mass Spectrometry
 613 Imaging Data Using the Average Frequency Shift of Ambient Ions. J. Am. Soc. Mass Spectrom.
 614 2013, 24 (7), 1137–1145.
- 615 (27) Smith, D. F.; Kharchenko, A.; Konijnenburg, M.; Klinkert, I.; Paša-Tolić, L.; Heeren, R. M. A.
 616 Advanced Mass Calibration and Visualization for FT-ICR Mass Spectrometry Imaging. *J. Am.*617 Soc. Mass Spectrom. 2012, 23 (11), 1865–1872.
- (28) Youmans, K. L.; Tai, L. M.; Nwabuisi-Heath, E.; Jungbauer, L.; Kanekiyo, T.; Gan, M.; Kim, J.;
 619 Eimer, W. A.; Estus, S.; Rebeck, G. W.; Weeber, E. J.; Bu, G.; Yu, C.; LaDu, M. J. APOE4620 Specific Changes in Aβ Accumulation in a New Transgenic Mouse Model of Alzheimer Disease.
 621 Journal of Biological Chemistry 2012, 287 (50), 41774–41786.
- (29) Oakley, H.; Cole, S. L.; Logan, S.; Maus, E.; Shao, P.; Craft, J.; Guillozet-Bongaarts, A.; Ohno,
 M.; Disterhoft, J.; Van Eldik, L.; Berry, R.; Vassar, R. Intraneuronal Beta-Amyloid Aggregates,
 Neurodegeneration, and Neuron Loss in Transgenic Mice with Five Familial Alzheimer's
 Disease Mutations: Potential Factors in Amyloid Plaque Formation. *Journal of Neuroscience*2006, *26* (40), 10129–10140.
- 627 (30) Goodwin, R. J. A.; Pennington, S. R.; Pitt, A. R. Protein and Peptides in Pictures: Imaging with
 628 MALDI Mass Spectrometry. *Proteomics* 2008, *8* (18), 3785–3800.
- 629 (31) Sládková, K.; Houška, J.; Havel, J. Laser Desorption Ionization of Red Phosphorus Clusters
 630 and Their Use for Mass Calibration in Time-of-Flight Mass Spectrometry. *Rapid Commun. Mass*631 Spectrom. 2009, 23 (19), 3114–3118.
- (32) (32) Fahy, E.; Sud, M.; Cotter, D.; Subramaniam, S. LIPID MAPS Online Tools for Lipid Research.
 Nucleic Acids Research 2007, *35* (Web Server), W606–W612.
- 634 (33) Sud, M.; Fahy, E.; Cotter, D.; Brown, A.; Dennis, E. A.; Glass, C. K.; Merrill, A. H.; Murphy, R.

- 635 C.; Raetz, C. R. H.; Russell, D. W.; Subramaniam, S. LMSD: LIPID MAPS Structure Database.
 636 *Nucleic Acids Research* 2007, *35* (Database), D527–D532.
- (34) Fahy, E.; Subramaniam, S.; Brown, H. A.; Glass, C. K.; Merrill, A. H.; Murphy, R. C.; Raetz, C.
 R. H.; Russell, D. W.; Seyama, Y.; Shaw, W.; Shimizu, T.; Spener, F.; van Meer, G.;
 VanNieuwenhze, M. S.; White, S. H.; Witztum, J. L.; Dennis, E. A. A Comprehensive
 Classification System for Lipids. *Journal of Lipid Research* 2005, *46* (5), 839–861.
- (35) Francl, T. J.; Sherman, M. G.; Hunter, R. L.; Locke, M. J.; Bowers, W. D.; McIver, R. T.
 Experimental Determination of the Effects of Space Charge on Ion Cyclotron Resonance
 Frequencies. *International Journal of Mass Spectrometry and Ion Processes* 1983, *54* (1–2),
 189–199.
- (36) Easterling, M. L.; Mize, T. H.; Amster, I. J. Routine Part-per-Million Mass Accuracy for HighMass Ions: Space-Charge Effects in MALDI FT-ICR. *Anal. Chem.* **1999**, *71* (3), 624–632.
- (37) Veličković, D.; Zhang, G.; Bezbradica, D.; Bhattacharjee, A.; Paša-Tolić, L.; Sharma, K.;
 648 Alexandrov, T.; Anderton, C. R.; KPMP Consortium. Response Surface Methodology As a New
 649 Approach for Finding Optimal MALDI Matrix Spraying Parameters for Mass Spectrometry
 650 Imaging. J. Am. Soc. Mass Spectrom. 2020, 31 (3), 508–516.
- (38) Horneffer, V.; Strupat, K.; Hillenkamp, F. Localization of Noncovalent Complexes in MALDIPreparations by CLSM. *J. Am. Soc. Mass Spectrom.* **2006**, *17* (11), 1599–1604.
- (39) Bowman, A. P.; Blakney, G. T.; Hendrickson, C. L.; Ellis, S. R.; Heeren, R. M. A.; Smith, D. F.
 Ultra-High Mass Resolving Power, Mass Accuracy, and Dynamic Range MALDI Mass
 Spectrometry Imaging by 21-T FT-ICR MS. *Anal. Chem.* **2020**, *92* (4), 3133–3142.
- (40) La Rocca, R.; Kune, C.; Tiquet, M.; Stuart, L.; Eppe, G.; Alexandrov, T.; De Pauw, E.; Quinton,
 L. Adaptive Pixel Mass Recalibration for Mass Spectrometry Imaging Based on Locally
 Endogenous Biological Signals. *Anal. Chem.* 2021, *93* (8), 4066–4074.
- McCann, A.; Rappe, S.; La Rocca, R.; Tiquet, M.; Quinton, L.; Eppe, G.; Far, J.; De Pauw, E.;
 Kune, C. Mass Shift in Mass Spectrometry Imaging: Comprehensive Analysis and Practical
 Corrective Workflow. *Anal Bioanal Chem* **2021**, *413* (10), 2831–2844.
- 662 (42) Ge, J.; Ma, C.; Qi, Y.; Wang, X.; Wang, W.; Hu, M.; Hu, Q.; Yi, Y.; Shi, D.; Yue, F.; Li, S.;
 663 Volmer, D. A. Quadrupole Detection FT-ICR Mass Spectrometry Offers Deep Profiling of
 664 Residue Oil: A Systematic Comparison of 2ω 7 Tesla versus 15 Tesla Instruments. *Analytical*665 *Science Advances* 2021, 2 (5–6), 272–278.
- (43) van Agthoven, M. A.; Lam, Y. P. Y.; O'Connor, P. B.; Rolando, C.; Delsuc, M.-A. TwoDimensional Mass Spectrometry: New Perspectives for Tandem Mass Spectrometry. *Eur Biophys J* 2019, *48* (3), 213–229.