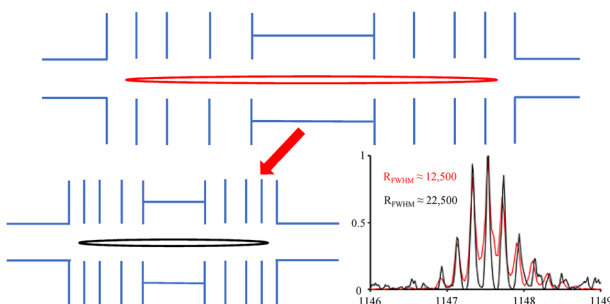


RESEARCH ARTICLE

A Miniaturized Fourier Transform Electrostatic Linear Ion Trap Mass Spectrometer: Mass Range and Resolution

Joshua T. Johnson, Kenneth W. Lee, Jay S. Bhanot, Scott A. McLuckey

Department of Chemistry, Purdue University, 560 Oval Drive, West Lafayette, IN 47907-2084, USA



Abstract. Mass resolution ($M/\Delta M_{FWHM}$) was increased by reducing the axial length of a Fourier transform electrostatic linear ion trap (FT-ELIT) mass spectrometer. The increase in mass resolution corresponds directly to increased axial ion frequencies in the FT-ELIT. Increased mass resolution was demonstrated for equivalent transient lengths in a 5.25" versus 2.625" ELIT using the isotopes of [bradykinin+2H]²⁺ and [insulin+5H]⁵⁺ as test ions. Both bradykinin and insulin show

mass resolution increases of ~90% allowing baseline resolution of the [insulin+5H]⁵⁺ isotopes after only 300 ms of data acquisition. Relative changes in mass/charge range were explored using mirror switching to trap ions injected axially into the ELIT. When trapping ions using mirror switching, the mass/charge range in a FT-ELIT mass spectrometer for a given switch time is determined by the time required for fast ions to enter and exit the trap after one reflection versus the time it takes for slow ions to enter the trap. By reducing the length of the FT-ELIT mass spectrometer while maintaining a constant distance from the point from which ions are initially accelerated to the entrance mirror, only the low m/z limit is affected for a given mirror switching time. For the two ELIT lengths examined here, the effective mass/charge range at any given switch time is reduced from $m/z_{low}-8.9*m/z_{low}$ for the 5.25" ELIT to $m/z_{low}-5.2*m/z_{low}$ for the 2.625" ELIT.

Keywords: Fourier transform mass spectrometry, Electrostatic linear ion trap, Miniaturization

Received: 30 September 2018/Revised: 18 December 2018/Accepted: 19 December 2018/Published Online: 12 February 2019

Introduction

In Fourier transform mass spectrometry (FT-MS), mass resolution ($M/\Delta M_{FWHM}$) is directly related to the frequencies of detected ions. Increased mass resolution results in increased spectral peak capacity and potentially higher mass measurement accuracy making high resolution mass spectrometers particularly useful for complex mixture analysis [1–4]. Existing methods to increase mass resolution relative to magnitude mode FT-based mass analysis include: data processing techniques that consider phase information [5–8], extending data acquisition times [9, 10], and increasing the detection frequencies [11–13]. Increasing detection frequencies can be achieved

by increasing the number of detection events [11, 12, 14], increasing the magnetic field strength in Fourier transform ion cyclotron resonance mass spectrometers (FT-ICR) [15], or by increasing the number of axial oscillations per unit time in electrostatic traps such as the OrbitrapTM [13] and electrostatic linear ion traps (ELIT) [16, 17]. Alternatively, detection at higher harmonics using multiple detection electrodes, which was first demonstrated in the FT-ICR community [11, 18–21], can lead to resolution increases in proportion to the number of detection electrodes. Use of frequency multiplying traps has been limited, however, largely due to the complex nature of the frequency spectra (fractional harmonics) that can arise from imperfectly positioned electrodes. Harmonic overtones naturally exist in many FTMS devices due to signal deviation from an ideal sine-wave. Naturally occurring harmonics are often regarded as spectral artifacts and are widely considered a nuisance as they complicate spectral interpretation [22]. Under conditions in which transient length is pressure-limited, however, resolution increases linearly with harmonic order [23, 24].

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s13361-018-02126-x>) contains supplementary material, which is available to authorized users.

Correspondence to: Scott McLuckey; e-mail: mcluckey@purdue.edu

Multiple detectors have been used in charge detection mass spectrometry (CDMS) to measure the mass of large ion species. CDMS using multiple detectors was initially done using array detection systems such as those developed by Jarrold et al. [25], Austin et al. [26], and Gamero-Castaño [27]. In addition to array detection, measuring induced ion signal multiple times, using an ELIT or Conetrap, has also been used to increase the accuracy of m/z and charge measurements in CDMS [28]. Furthermore, the Williams group has implemented a trapping device that also utilizes an array detection scheme [29]. Whereas CDMS analyzes single ion species and focuses primarily on multiply-charged megadalton ions, electrostatic linear ion traps are also used as conventional mass spectrometers by injecting ion bunches [30]. Introducing multiple detectors in ensemble measurements using an FT-ELIT necessitates precise alignment else fractional harmonic are manifested [12].

By reducing the axial length of an ELIT, frequencies and thus resolution are increased at equivalent transient lengths. The introduction of the high-field Orbitrap™ allowed for higher detected frequencies by reducing the dimensions of the mass analyzer and thereby increasing the electric field strength between the inner spindle and outer electrode [13]. Reducing the size of the Orbitrap™ resulted in a frequency increase of ~ 1.8 -fold when compared to the standard Orbitrap™. In much the same way, detected ion frequencies in a FT-ELIT can be increased by simply reducing the spaces between opposing ion mirrors. Herein, the performance of a “miniaturized” ELIT is described to demonstrate the influence of reducing the trap axial dimension on mass resolution and mass/charge range. Comparisons to a previously used ELIT are drawn to demonstrate the relative performance differences between each device. The miniaturized ELIT has been modified by reducing the spacing between the electrodes making up the ion mirrors and by reducing the space separating the ion mirrors. The properties and operation of the previous ELIT have been discussed at length elsewhere [3] and are mentioned here only as means of comparison with the smaller ELIT discussed here.

Experimental

Materials

Bradykinin acetate salt and insulin (from bovine pancreas) were purchased from Sigma-Aldrich (St. Louis, MO, USA). Methanol (MeOH) was purchased from Thermo Fisher Scientific (Waltham, MA, USA). Glacial acetic acid (AcOH) was purchased from Mallinckrodt (Phillipsburg, NJ, USA). HPLC-grade water (H_2O) was purchased from Fisher Scientific (Pittsburgh, PA, USA). LC/MS tuning mix for ESI (G2421A) was purchased from Agilent Technologies (Santa Clara, CA, USA). Insulin was prepared to a final concentration of 100 μM in 49.5/49.5/1 v/v/v MeOH/ H_2O /AcOH. Bradykinin was prepared to a final concentration of 20 μM in 49.5/49.5/1 v/v/v MeOH/ H_2O /AcOH.

Mass Spectrometry

All experiments were carried out on a home-built mass spectrometer. The ELIT described previously has been replaced with a shorter trap in which the spacings between electrodes have been reduced by a factor of 2 (plates 1 to 3 = 3.81 mm, plate 3 to central housing = 5.715 mm). Spacings are maintained using alumina spacers (Kimball Physics). In addition, the length of the central housing was reduced from 50.8 to 25.4 mm. The nano-electrospray ionization (nESI) source and the method by which ions are concentrated and injected into the electrostatic linear ion trap (ELIT) have been described [30]. The electrostatic linear ion traps described in this work are 2.625” and 5.25” in length measured from the beginning of the first trapping electrode to the end of the last trapping electrode.

The charge-sensitive detection electronics have been described previously [31, 32]. The output of the charge sensitive preamplifier (A250, Amptek) was filtered (band-pass, Krohn-Hite Model 3945, Brockton, MA) and amplified (gain = 5) prior to digitization by a PCI-based digitizer (CS1621, 16-bit, Gage Applied Technologies, Lachine, Quebec, Canada) at a rate of 10 MS/s

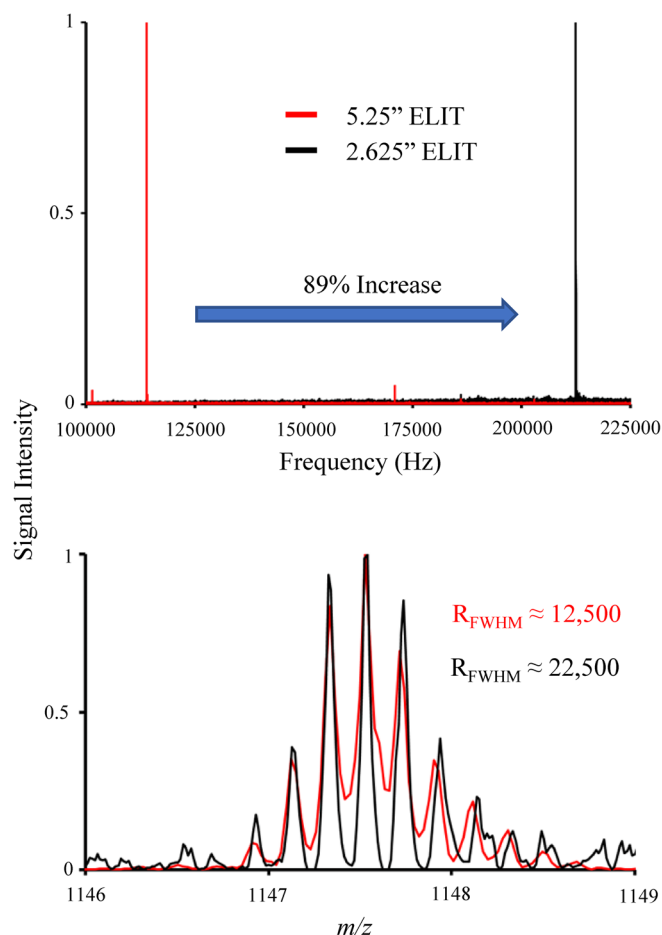


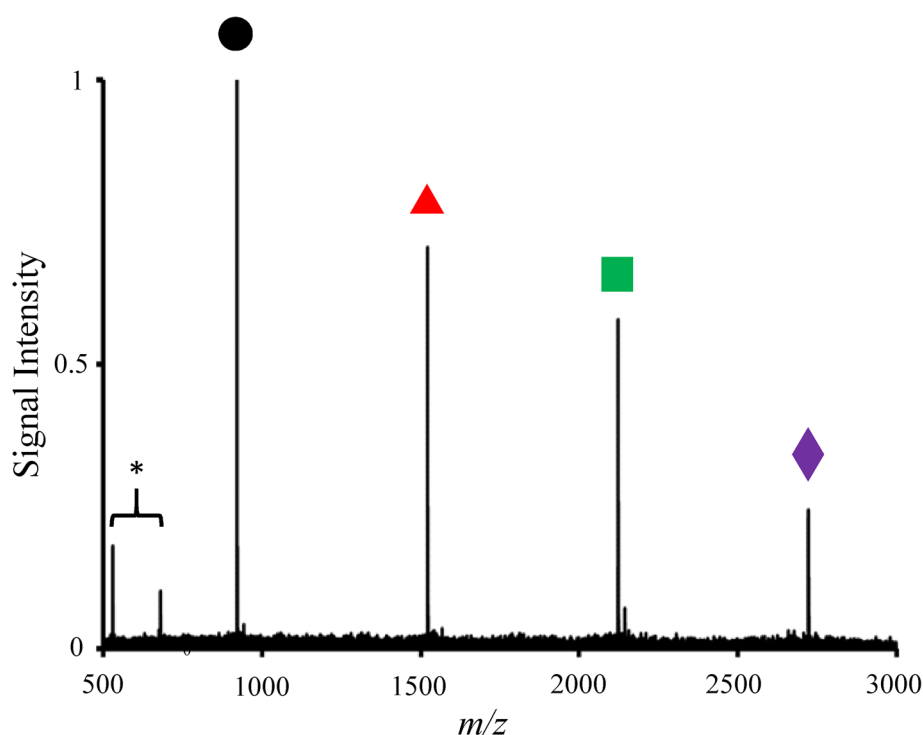
Figure 1. (top) Detected ion frequencies for $[\text{insulin}+5H]^{5+}$ ions in the 5.25” (red) and 2.625” (black) ELITs. eFT mass spectra of $[\text{insulin}+5H]^{5+}$ ions for a 250 ms transient using the 5.25” (red) and 2.625” (black) ELITs. Theoretical fits for the insulin data are provided in Supplemental Figure 1.

(AC coupled, 1 M Ω input impedance, 25 MHz low-pass filter enabled). A program written in LabVIEW 13.0 (National Instruments, Austin, TX) was used to acquire each transient for FT analysis. A custom program, written in MATLAB 2017a, was used to process the transients using the enhanced Fourier transform (eFT) [8].

Ion Optical Simulations

A model of the trapping quadrupole, intermediate lenses, differential pumping region, and 2.625" ELIT was constructed in SIMION v8.1. An additional model using the 5.25" ELIT was also constructed for theoretical frequency and mass range

comparisons. For mass range simulations, ions were initialized within a cylindrical distribution (radius = 0.1 mm, length = 1 mm) located near the end exit of our trapping quadrupole with kinetic energies uniformly distributed between of 0.01 and 0.02 eV. Collisional cooling using nitrogen gas was simulated via a hard-sphere collision model that was included in the SIMION software. The trapping quadrupole was operated at 816 kHz with the RF amplitude set such that the m/z being trapped had a q value of 0.4 on the Mathieu stability diagram. The LINACII electrodes, rod offset, and exit lens were held at 700 V, 1990 V, and 1978 V during the 2-ms ion thermalization step. Ions were ejected from the trapping quadrupole by pulsing the exit lens from 1978 to 1500 V at a zero crossing of the RF. After ion injection,



m/z		R_{FWHM} (150ms Transient)	C-Value
922.01	●	15,300	3.10×10^6
1521.97	▲	11,500	2.99×10^6
2121.93	■	9,800	3.01×10^6
2721.89	◆	8,550	2.97×10^6

Figure 2. eFT mass spectrum of Agilent ESI Tuning Mix (G2421A) from 500 to 3000 m/z (150 ms transient, 100 averages) with corresponding m/z values, resolutions (FWHM), and calculated instrument proportionality constants. The * indicates higher harmonics.

the background pressure was set to zero to avoid unstable trajectories caused by ion/neutral collisions. Mass/charge range simulations for Figures 4 and 5 were done by injecting 100 ions of each mass-to-charge ratio from 100 to 8000 m/z in 50 m/z increments. Low m/z limit simulations were done with 100 ions of each mass-to-charge ratio from 100 to 1500 m/z in 10 m/z increments in order to better approximate the low m/z limits of the 2.625" and 5.25" ELIT.

Results and Discussion

Mass Resolution

Reduction in the axial dimension of an ELIT at constant trapping voltages can be used to increase the detected frequencies of ions in the device thereby increasing mass resolution per unit acquisition time. Reducing the length of our ELIT by a factor of 2 resulted in a $\sim 90\%$ increase in oscillation frequencies. The frequency increase and the resulting resolution increase are demonstrated using ions of the +5 charge state of bovine insulin in Figure 1. After a 250-ms data acquisition time, the isotopes of $[\text{insulin}+5\text{H}]^{5+}$ are not fully resolved in the 5.25" ELIT; however, in the 2.625" ELIT, the +5 charge state is baseline resolved with a resolution increase equal to the observed frequency increase. Peak shifting on the right side of the red spectra in Figure 1 is a result of space charge due to high ion densities. We have demonstrated previously that at lower ion densities (i.e., shorter accumulation times), peaks remain uncoalesced [23].

In an FT-ELIT, resolution, R , increases linearly with acquisition time, T_{acq} , and decreases with the square root of m/z . In the absence of dephasing, resolution follows the equation below:

$$R = CT_{\text{acq}}/(m/z)^{1/2}$$

where C is a proportionality constant that depends on the device. This proportionality constant is directly related to mass resolution and should be independent of mass/charge value provided detected ion signals persist over the duration of the acquisition time. In Figure 2, measured proportionality constants are reported over a range of m/z values (~ 1800 m/z) produced using Agilent LC/MS tuning mix for ESI (G2421A). The consistency of the proportionality constants over a wide m/z range demonstrates that the increased mass resolution in the miniaturized device applies for a wide range of masses under a single fixed set of trapping conditions, which demonstrates the ability of the FT-ELIT to operate as a broadband mass spectrometer.

A mass resolution of $\sim 37,400$ FWHM was achieved for the +2 charge state of bradykinin at m/z 530.8 using a 300 ms acquisition time in the 2.625" ELIT. For comparison, an equivalent acquisition time on the 5.25" FT-ELIT yielded a resolution of roughly 20,050 FWHM for the same m/z value (see Figure 3). Alternatively, in the 2.625" ELIT, a resolution of approximately 20,050 FWHM can be reached after only 154 ms of data acquisition. Using the proportionality constants calculated for $[\text{bradykinin}+2\text{H}]^{2+}$ ion in the 5.25" and 2.625" ELITs,

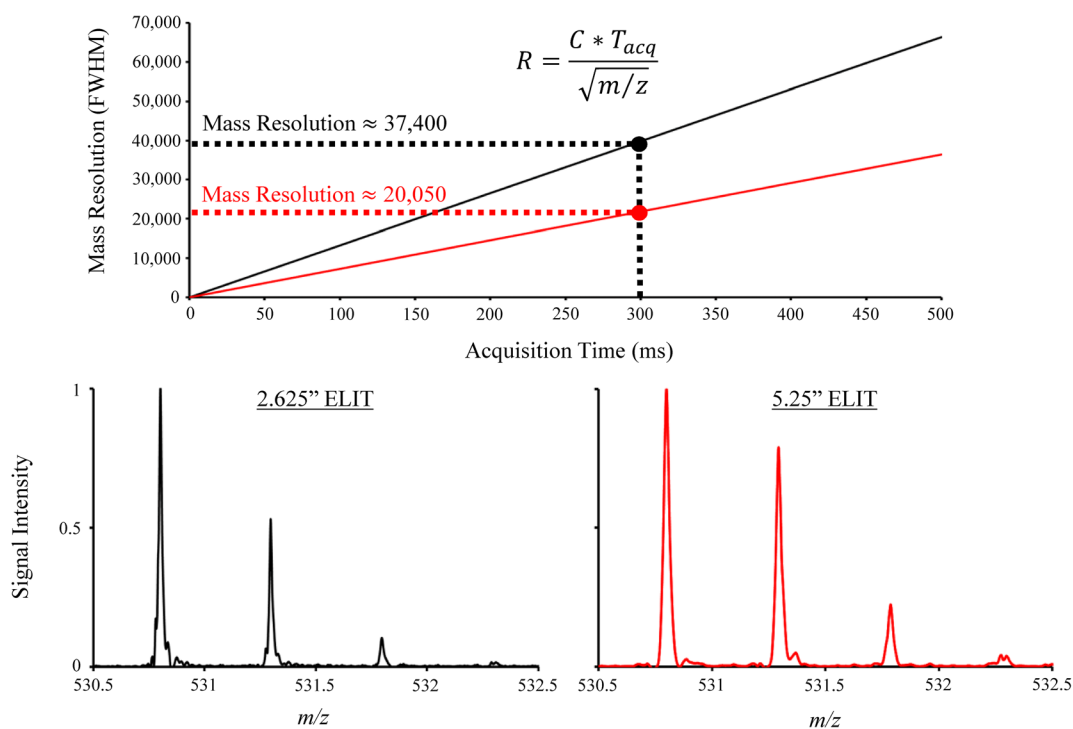


Figure 3. Theoretical resolution trends for the 2.625" (black) and 5.25" (red) FT-ELIT mass analyzers at m/z 530.8 based on the average proportionality constant calculated using eFT mass spectra of bradykinin $^{2+}$ from 100, 150, 200, 250, and 300 ms transients in either device

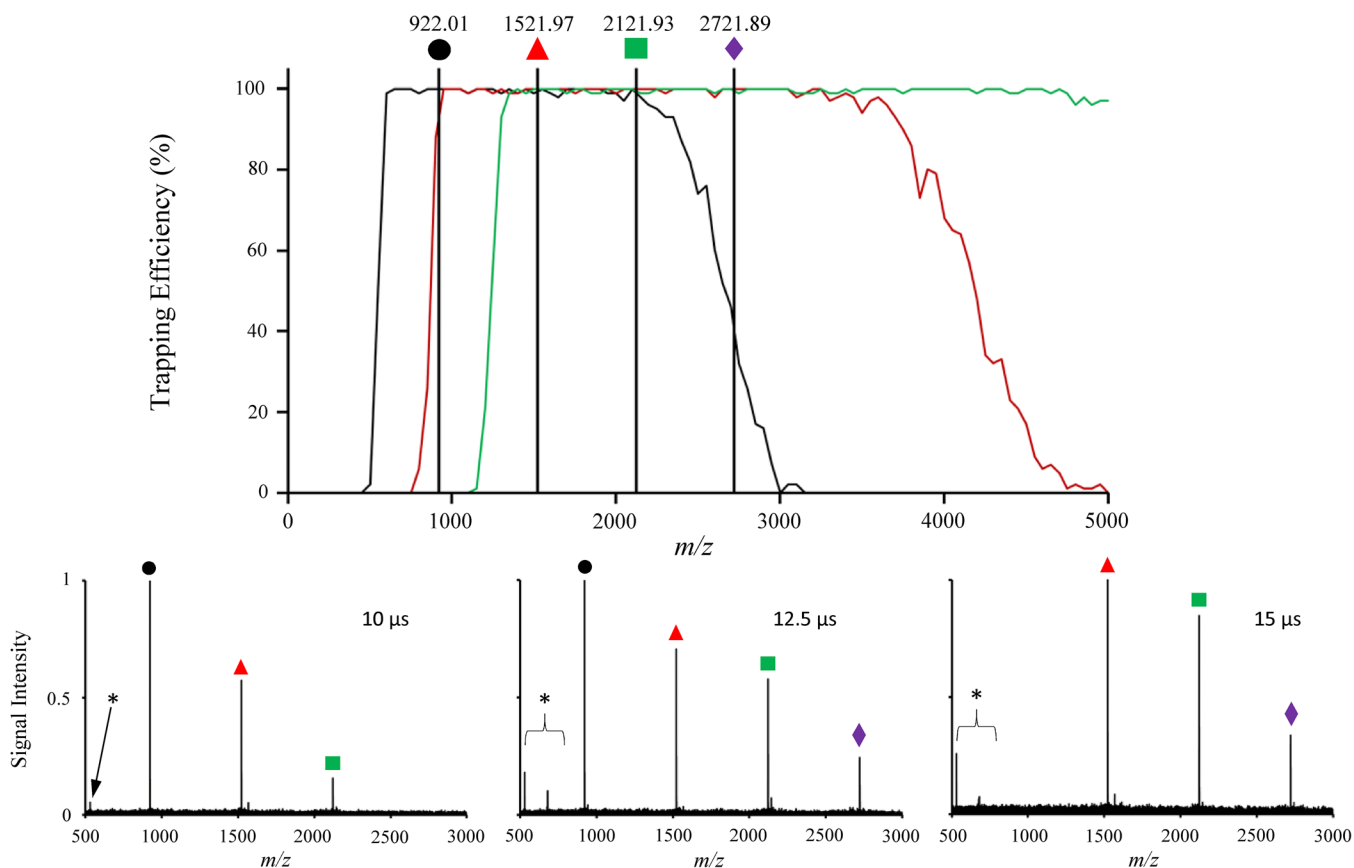


Figure 4. Mass/charge range simulated as a function of mirror switching time (μs). Agilent ESI tuning mix (G2421A) from m/z 500 to 3000 (150 ms transient, 100 averages). The * indicates higher harmonics

theoretical resolutions for different acquisition times were calculated and plotted in Figure 3. Such plots illustrate the relative

resolution performance of the two analyzers and can be used to predict resolution for different acquisition times.

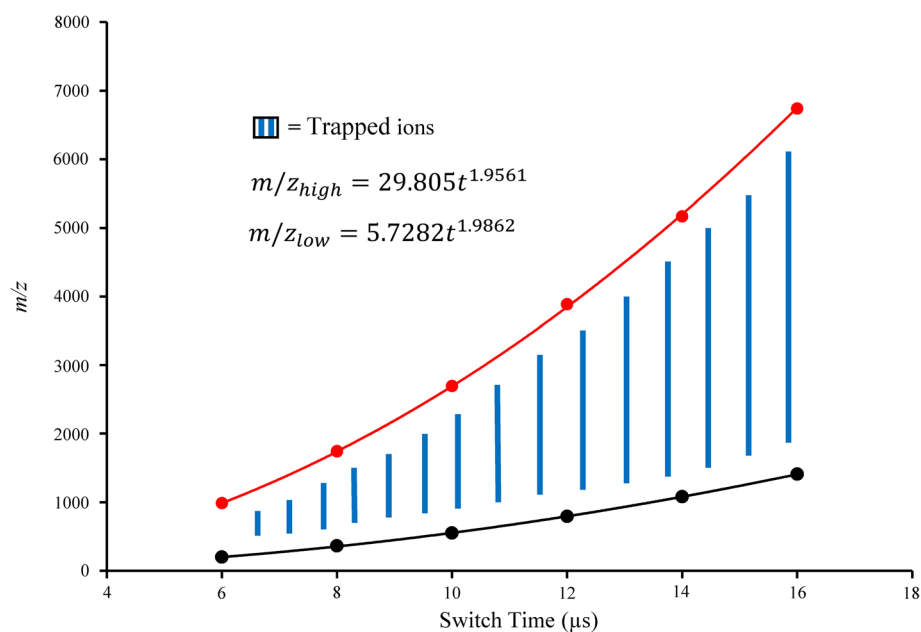


Figure 5. Ions trapped with an efficiency of at least 50% for mirror switching times from 6 to 16 μs in the 2.625'' ELIT. Trapping efficiencies were determined using SIMION v8.1. Ions between the m/z_{high} (red) and the m/z_{low} (black) are stably trapped for a given mirror switching time

Mass/Charge Range

Ion capture in an ELIT can be affected by either “potential lift” or “mirror switching” approaches, both of which have been described previously [33]. Of the two techniques, mirror switching offers larger mass/charge ranges and is used in the current work. Mirror switching involves the release of ions from an accumulation quadrupole while the entrance mirror voltage is low enough to allow ions to enter the ELIT with a subsequent increase in the entrance mirror voltage (i.e., mirror switching) to capture the ions that are in the ELIT. The time between dumping the ions from the accumulation quadrupole and the switching of the entrance mirror voltage to capture ions in the ELIT, referred to herein as the mirror switching time, determines the mass/charge range of the ions captured in the ELIT. Ions with flight times from the accumulation quadrupole to the entrance mirror that are roughly equal to or longer than the mirror switching time are too slow to enter the ELIT, which establishes the upper m/z limit. The lower m/z limit coincides with ions with flight times from the exit of the accumulation quadrupole to the far mirror and back out of the ELIT that are roughly equal to or less than the mirror switching time. Experimental mass/charge ranges are demonstrated in Figure 4 using Agilent LC/MS tuning mix for ESI (G2421A).

Upper and lower m/z limits of the 2.625" ELIT were calculated using various mirror switching times in SIMION v8.1 for the geometries and voltages relevant to the experiments of Figure 4 and the results were consistent with the experimental observations for the tuning mix. In Figure 5, trapped m/z values between 6 and 16 μ s switch times are used to illustrate the relationship between mirror switching time and m/z range for the 2.625" ELIT using a 50% trapping efficiency as an arbitrary working regime to define the upper and lower m/z limits. Fits of the lower (m/z_{low}) and upper (m/z_{high}) m/z limits as functions of the mirror switching time are shown as black and red lines, respectively. The data approximately follow a power-of-2 relationship which is consistent with the relationship between ion velocity and m/z . The ratio of the coefficients in the two fits can be used to estimate the mass range at any mirror switching time (i.e., $m/z_{\text{high}} = 5.2 * m/z_{\text{low}}$). For comparison, in the 5.25" ELIT, an analogous simulation exercise yielded the relationship $m/z_{\text{high}} = 8.9 * m/z_{\text{low}}$. Hence, for a given low m/z limit, the longer ELIT yields a roughly 71% larger upper m/z limit. Alternatively, for a given upper m/z limit, which corresponds to a given mirror switching time, the lower m/z limit for the 2.625" ELIT is $1.71 \times$ greater than that of the 5.25" ELIT.

Conclusions

Reducing the length of FT-ELIT mass spectrometers offers a simple way to enhance mass resolution albeit with a proportionally reduced mass range. Mass resolution increases linearly with frequency. For an equivalent transient length, which implies an equivalent path-length, resolution is higher in a shorter

ELIT. Mass resolution in a 2.625" ELIT increased by $\sim 90\%$ when compared to a 5.25" ELIT. Although a shorter trap has higher mass resolution, it has a smaller mass/charge range. For mirror switching at a fixed distance from the ion accumulation quadrupole to the entrance mirror and a fixed mirror switching time, the upper m/z limit is independent of the length of the ELIT. Only the low m/z limit is affected by reducing the length of the ELIT. For the instrument geometry used in this work, the m/z range for the 5.25" ELIT was reduced from $(m/z_{\text{low}} - 8.9 - m/z_{\text{low}})$ to $(m/z_{\text{low}} - 5.2 m/z_{\text{low}})$ when reducing the trap length to 2.625". However, the m/z range is readily adjusted by changing the mirror switching time. Hence, it is possible, in principle, to access a practically unlimited m/z range by stitching together spectra obtained at different mirror switching times.

Acknowledgements

This work was supported by the National Science Foundation NSF CHE-1708338. The instrument was initially constructed with AB Sciex support. We thank Mark Carlsen, Randy Replogle, Phil Wyss, Tim Selby, and Ryan Hilger of the Jonathan Amy Facility for Chemical Instrumentation for helpful discussions and their help with construction of the mass spectrometer. We also acknowledge Mircea Guna, Dr. James W. Hager, and Dr. Eric Dzeikonski of AB Sciex for helpful discussions, data analysis software, and for providing the collision cell with LINAC.

References

1. Kim, S., Rodgers, R.P., Marshall, A.G.: Truly “exact” mass: elemental composition can be determined uniquely from molecular mass measurement at ~ 0.1 mDa accuracy for molecules up to ~ 500 Da. *Int. J. Mass Spectrom.* **251**, 260–265 (2006)
2. Smith, D.F., Podgorski, D.C., Rodgers, R.P., Blakney, G.T., Hendrickson, C.L.: 21 tesla FT-ICR mass spectrometer for ultrahigh-resolution analysis of complex organic mixtures. *Anal. Chem.* **90**, 2041–2047 (2018)
3. Dziekonski, E.T., Johnson, J.T., Lee, K.W., McLuckey, S.A.: Fourier-transform MS and closed-path multireflection time-of-flight MS using an electrostatic linear ion trap. *Anal. Chem.* **89**, 10965–10972 (2017)
4. Marshall, A.G., Hendrickson, C.L., Jackson, G.S.: Fourier transform ion cyclotron resonance mass spectrometry: a primer. *Mass Spectrom. Rev.* **17**, 1–35 (1998)
5. Comisarow, M.B., Marshall, A.G.: Selective-phase ion cyclotron resonance spectroscopy. *Can. J. Chem.* **52**, 1997–1999 (1974)
6. Marshall, A.G., Comisarow, M.B., Parisod, G.: Relaxation and spectral line shape in Fourier transform ion resonance spectroscopy. *J. Chem. Phys.* **71**, 4434–4444 (1979)
7. Hilger, R.T., Wyss, P.J., Santini, R.E., McLuckey, S.A.: Absorption mode Fourier transform electrostatic linear ion trap mass spectrometry. *Anal. Chem.* **85**, 8075–8079 (2013)
8. Lange, O., Damoc, E., Wiegand, A., Makarov, A.: Enhanced Fourier transform for Orbitrap mass spectrometry. *Int. J. Mass Spectrom.* **369**, 16–22 (2014)
9. Comisarow, M.B., Marshall, A.G.: Theory of Fourier transform ion cyclotron resonance mass spectroscopy. I. Fundamental equations and low-pressure line shape. *J. Chem. Phys.* **64**, 110–119 (1976)
10. 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. *Rapid Commun. Mass Spectrom.* **25**, 122–126 (2011)

11. Nikolaev, E.N., Rakov, V., Futrell, J.H.: Analysis of harmonics for an elongated FTMS cell with multiple electrode detection. *Int. J. Mass Spectrom. Ion Process.* **157**, 215–232 (1996)
12. Dziekonski, E.T., Santini, R.E., McLuckey, S.A.: A dual detector Fourier transform electrostatic linear ion trap utilizing in-trap potential lift. *Int. J. Mass Spectrom.* **405**, 1–8 (2016)
13. Denisov, E., Damoc, E., Lange, O., Makarov, A.: Orbitrap mass spectrometry with resolving powers above 1,000,000. *Int. J. Mass Spectrom.* **325**, 80–85 (2012)
14. Shaw, J.B., Gorshkov, M.V., Wu, Q., Paša-Tolić, L.: High speed intact protein characterization using 4X frequency multiplication, ion trap harmonization, and 21 tesla FTICR-MS. *Anal. Chem.* **90**, 5557–5562 (2018)
15. Marshall, A.G., Guan, S.: Advantages of high magnetic field for Fourier transform ion cyclotron resonance mass spectrometry. *Rapid Commun. Mass Spectrom.* **10**, 1819–1823 (1996)
16. Zajfman, D., Rudich, Y., Sagi, I., Strasser, D., Savin, D.W., Goldberg, S., Rappaport, M., Heber, O.: High resolution mass spectrometry using a linear electrostatic ion beam trap. *Int. J. Mass Spectrom.* **229**, 55–60 (2003)
17. Ring, S., Pedersen, H.B., Heber, O., Rappaport, M.L., Witte, P., Bhushan, K.G., Altstein, N., Rudich, Y., Sagi, I., Zajfman, D.: Fourier transform time-of-flight mass spectrometry in an electrostatic ion beam trap. *Anal. Chem.* **72**, 4041–4046 (2000)
18. Pan, Y., Ridge, D., Wronka, J., Rockwood, A.L., Marshall, A.: Resolution improvement by using harmonic detection in an ion cyclotron resonance mass spectrometer. *Rapid Commun. Mass Spectrom.* **1**, 120–121 (1987)
19. Pan, Y., Ridge, D., Rockwood, A.L.: Harmonic signal enhancement in ion cyclotron resonance mass spectrometry using multiple electrode detection. *Int. J. Mass Spectrom. Ion Process.* **84**, 293–304 (1988)
20. Nikolaev, E., Gorshkov, M.: Dynamics of ion motion in an elongated cylindrical cell of an ICR spectrometer and the shape of the signal registered. *Int. J. Mass Spectrom. Ion Process.* **64**, 115–125 (1985)
21. Limbach, P.A., Grosshans, P.B., Marshall, A.G.: Harmonic enhancement of a detected ion cyclotron resonance signal by use of segmented detection electrodes. *Int. J. Mass Spectrom. Ion Process.* **123**, 41–47 (1993)
22. Mathur, R., O'Connor, P.B.: Artifacts in Fourier transform mass spectrometry. *Rapid Commun. Mass Spectrom.* **23**, 523–529 (2009)
23. Dziekonski, E.T., Johnson, J.T., McLuckey, S.A.: On the utility of higher harmonics in electrospray ionization Fourier transform electrostatic linear ion trap mass spectrometry. *Anal. Chem.* **89**, 4392–4397 (2017)
24. Grosshans, P.B., Marshall, A.G.: Can Fourier transform mass spectral resolution be improved by detection at harmonic multiples of the fundamental ion cyclotron orbital frequency? *Int. J. Mass Spectrom. Ion Process.* **107**, 49–81 (1991)
25. Smith, J.W., Siegel, E.E., Maze, J.T., Jarrold, M.F.: Image charge detection mass spectrometry: pushing the envelope with sensitivity and accuracy. *Anal. Chem.* **83**, 950–956 (2011)
26. Barney, B.L., Daly, R.T., Austin, D.E.: A multi-stage image charge detector made from printed circuit boards. *Rev. Sci. Instrum.* **84**, 114101 (2013)
27. Gamero-Castaño, M.: Induction charge detector with multiple sensing stages. *Rev. Sci. Instrum.* **78**, 043301 (2007)
28. Hogan, J.A., Jarrold, M.F.: Optimized electrostatic linear ion trap for charge detection mass spectrometry. *J. Am. Soc. Mass Spectrom.* **29**, 1–10 (2018)
29. Elliott, A.G., Merenbloom, S.I., Chakrabarty, S., Williams, E.R.: Single particle analyzer of mass: a charge detection mass spectrometer with a multi-detector electrostatic ion trap. *Int. J. Mass Spectrom.* **414**, 45–55 (2017)
30. Hilger, R.T., Dziekonski, E.T., Santini, R.E., McLuckey, S.A.: Injecting electrospray ions into a Fourier transform electrostatic linear ion trap. *Int. J. Mass Spectrom.* **378**, 281–287 (2015)
31. Hilger, R.T., Santini, R.E., McLuckey, S.A.: Square wave modulation of a mirror lens for ion isolation in a Fourier transform electrostatic linear ion trap mass spectrometer. *Int. J. Mass Spectrom.* **362**, 1–8 (2014)
32. Hilger, R.T., Santini, R.E., McLuckey, S.A.: Tandem mass spectrometry in an electrostatic linear ion trap modified for surface-induced dissociation. *Anal. Chem.* **86**, 8822–8828 (2014)
33. Dziekonski, E.T., Johnson, J.T., Hilger, R.T., McIntyre, C.L., Santini, R.E., McLuckey, S.A.: Voltage-induced frequency drift correction in Fourier transform electrostatic linear ion trap mass spectrometry using mirror-switching. *Int. J. Mass Spectrom.* **410**, 12–21 (2016)