

7200 Series Q-TOF for GC/MS



A new analytical tool for solving complex analytical problems

June 2011



**ASMS Conference on
Mass Spectrometry and Allied Topics**

June 5-9, 2011

Colorado Convention Center, Denver, CO

**7200 GC/Q-TOF Breakfast
Seminar**

Hospitality Suite

“There’s Something Brewing at Agilent” BrewPub Theme



**Heavy
Matrix
Hefeweizen**



**Super
Sensitive
Stout**



**Clearly
Better
Bitter**



5975E SQ



5975C SQ



5975T LTM SQ

Agilent GC/MS & GC/MS/MS **More Choices – Better Solutions**



220 IT



240 IT



7000 TQ



7200 Q-TOF 

What is it?

7890 + 7000 + 6500 = 7200 GC/Q-TOF



Triple Quadrupole MS

+ =

Time of Flight MS




Quadrupole Time of Flight MS

What Will The 7200 Q-TOF Do For You?

- TOF mode
 - High resolution full scan spectra
 - Accurate mass measurements
 - Fast full spectrum acquisition
- MS/MS mode
 - Product ion spectra – high resolution, accurate mass
 - Sensitivity > TQ product ion methods
- Ideal tool for solving complex analytical problems
- New tools for structural elucidation of unknowns and confirmation of non-targets



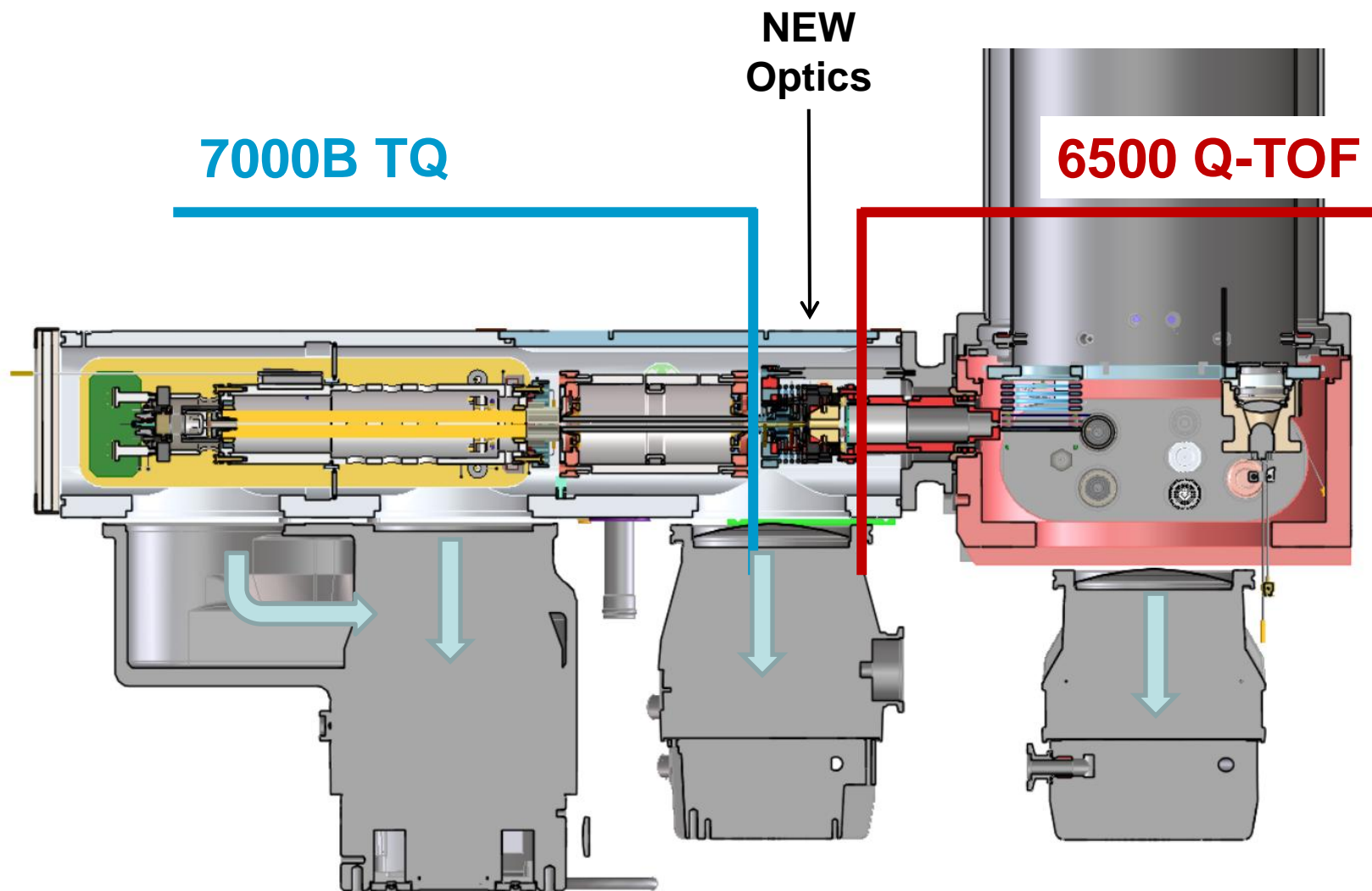
7890 + 7000 + 6500 = 7200 GC/Q-TOF

The image shows various components of an Agilent GC/Q-TOF system. On the left is a GC system with a sample tray. In the center is a large white box with a black panel. On the right is a TOF/Q-TOF mass spectrometer with a control panel. At the bottom center is a GC system with a large cylindrical component. The background is white.

**It's our newest GC/MS . . .
built upon many well proven parts:**

Almost one thousand 7000 TQs
Over one thousand TOFs and Q-TOFs
Many thousand 7890 GCs

7200 Analyzer



New . . . Yet Totally Proven

Dual-stage ion mirror improves second-order time focusing for high mass resolution.

4GHz ADC electronics enable a high sampling rate (32 Gbit/s) which improves the resolution, mass accuracy, and sensitivity for low-abundance samples. Dual gain amplifiers simultaneously process detector signals through both low-gain and high gain channels, extending the dynamic range to 10⁵.

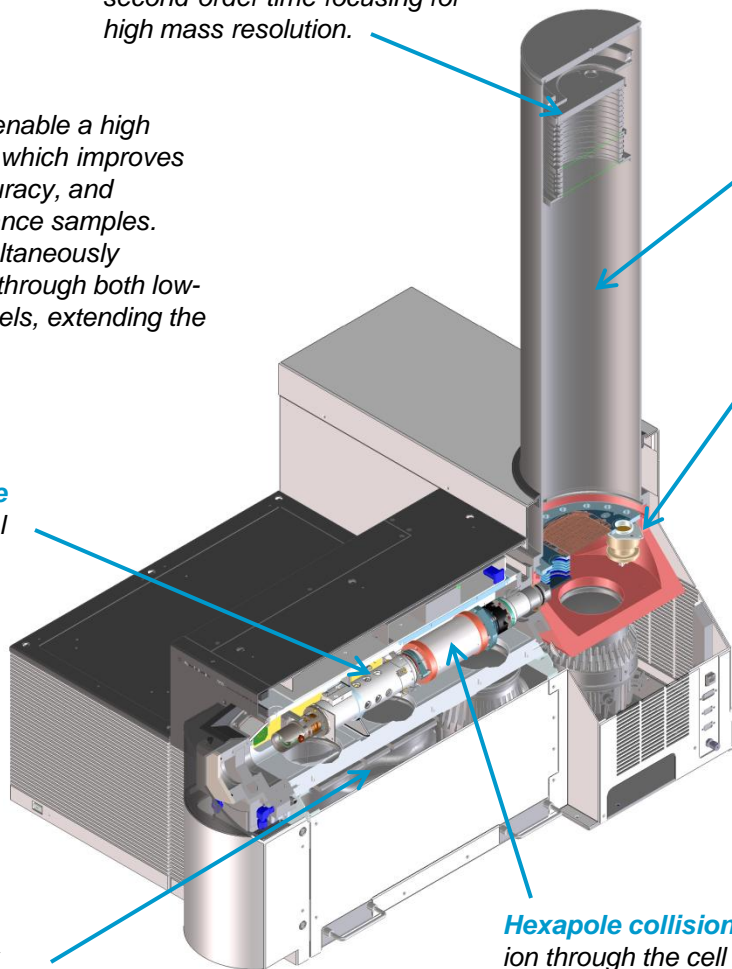
Proprietary INVAR flight tube sealed in a vacuum-insulated shell eliminates thermal mass drift due to temperature changes to maintain excellent mass accuracy, 24/7. Added length improves mass resolution.

Analog-to-digital (ADC) Detector: Unlike time-to-digital (TDC) detectors which record single ion events, ADC detection records multiple ion events, allowing very accurate mass assignments over a wide mass range and dynamic range of concentrations.

Hot, quartz monolithic quadrupole analyzer and collision cell identical to the 7000 Quadrupole MS/MS

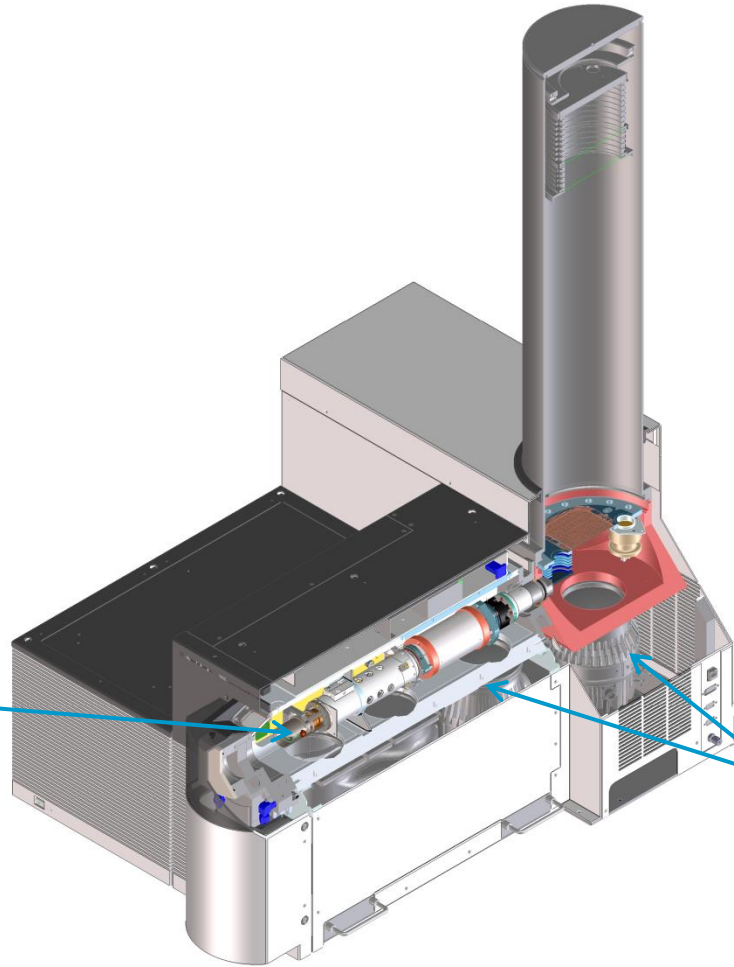
Split-flow turbo differentially pumps the ion source and quadrupole analyzer compartments

Hexapole collision cell accelerates ion through the cell to enable faster generation of high-quality MS/MS spectra without cross-talk



Other New . . . And Improved

New Removable Ion Source
includes repeller, ion volume,
extraction lens and dual filaments

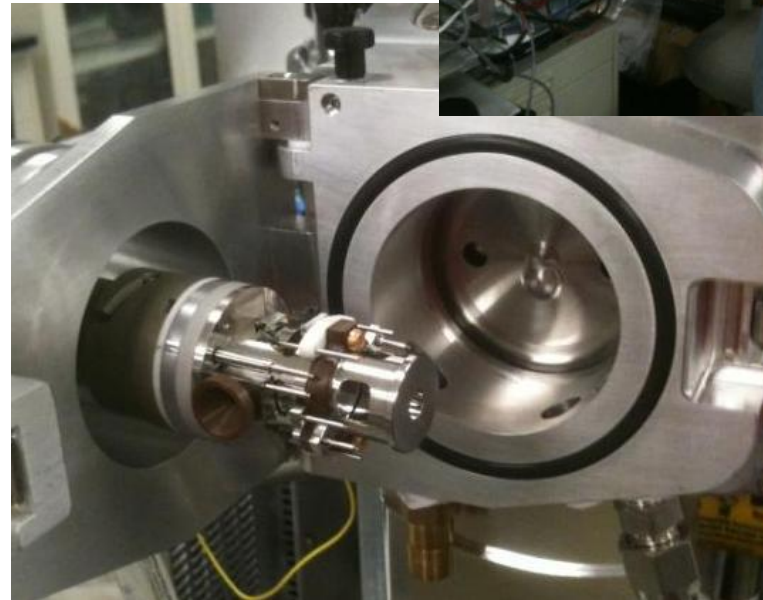


New Internal Reference Mass
can be delivered to the source at
a low and high concentration

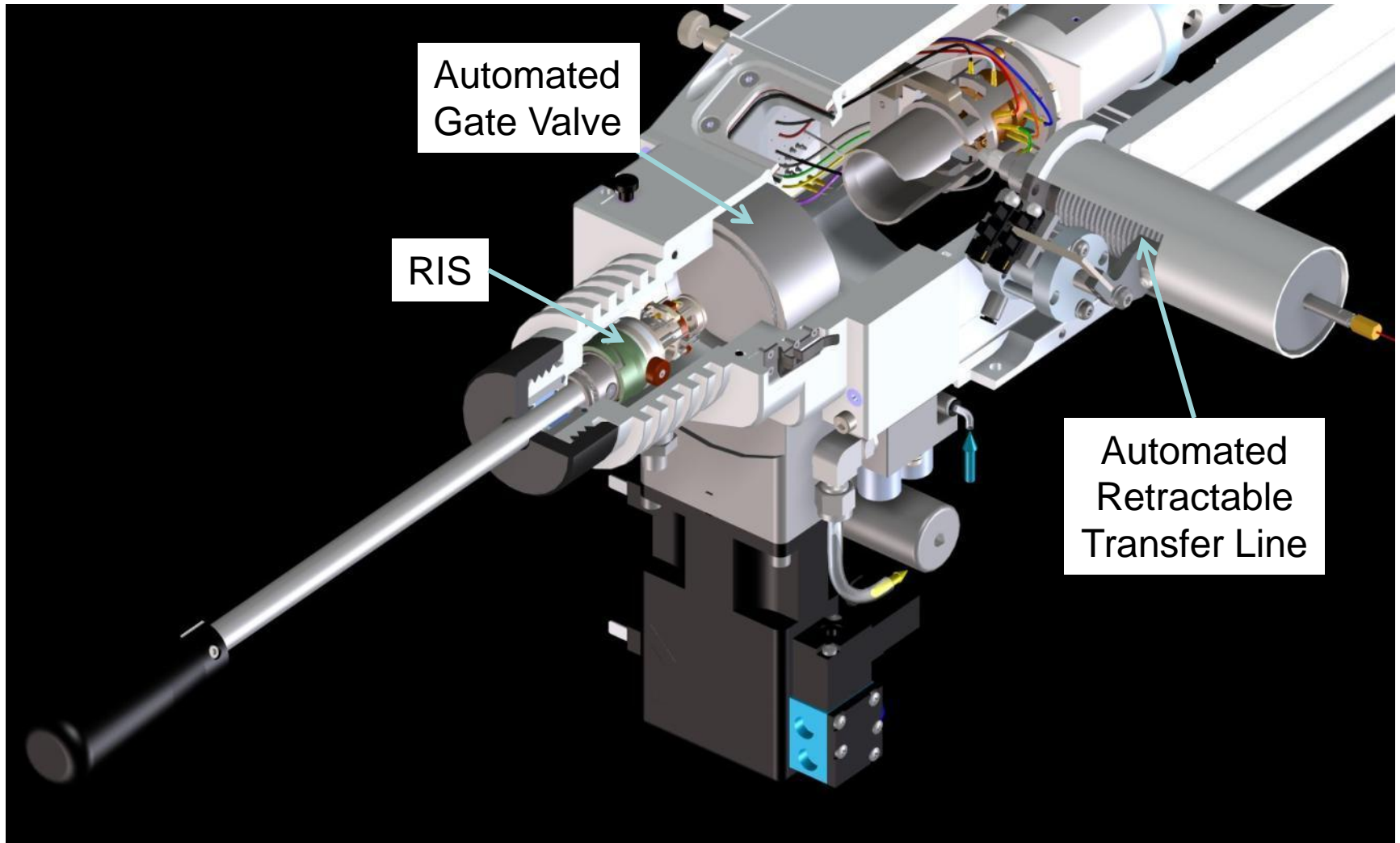
Two 300L/s turbos pump the focusing
optics and flight tube

Removable Ion Source (RIS)

- Allows swap of complete ion source, including filaments, in ~30 minutes without venting
- Allows fast EI/CI source swapping without venting

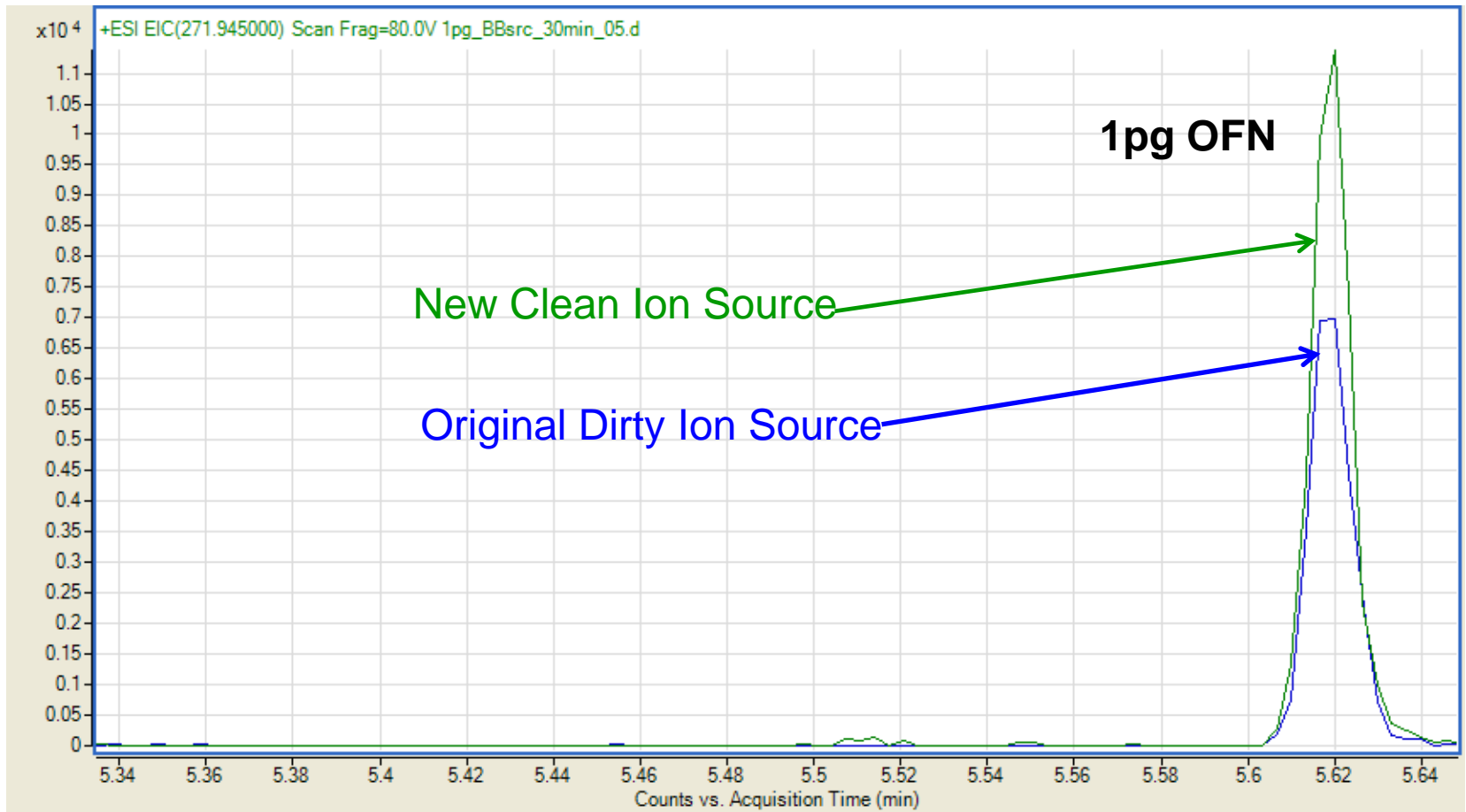


Removable Ion Source (RIS)



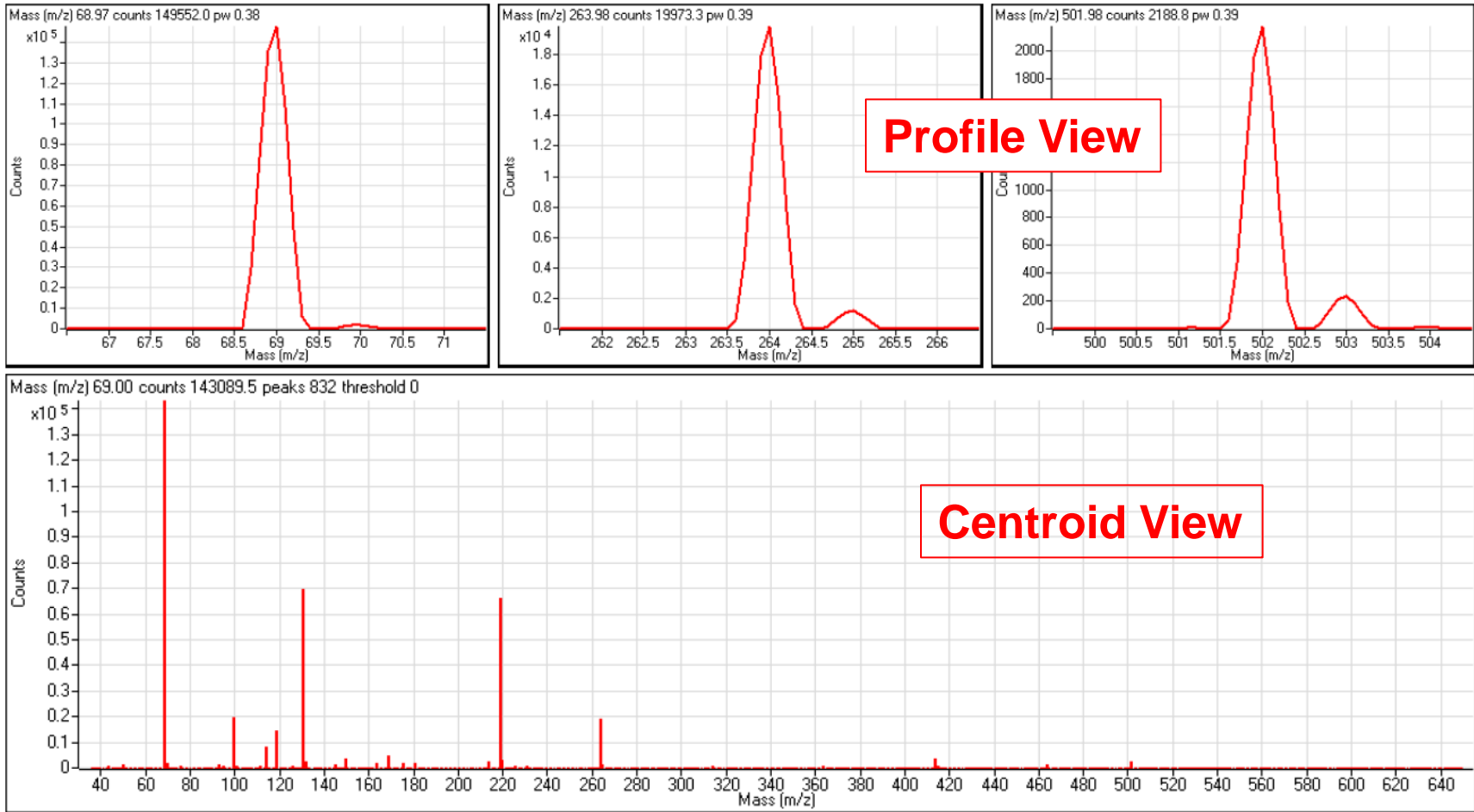
30 minute source swap with RIS

Vent → cool ion source → open chamber and replace/maintain source components → close chamber → pump out → heat source → stabilize vacuum and source temperature



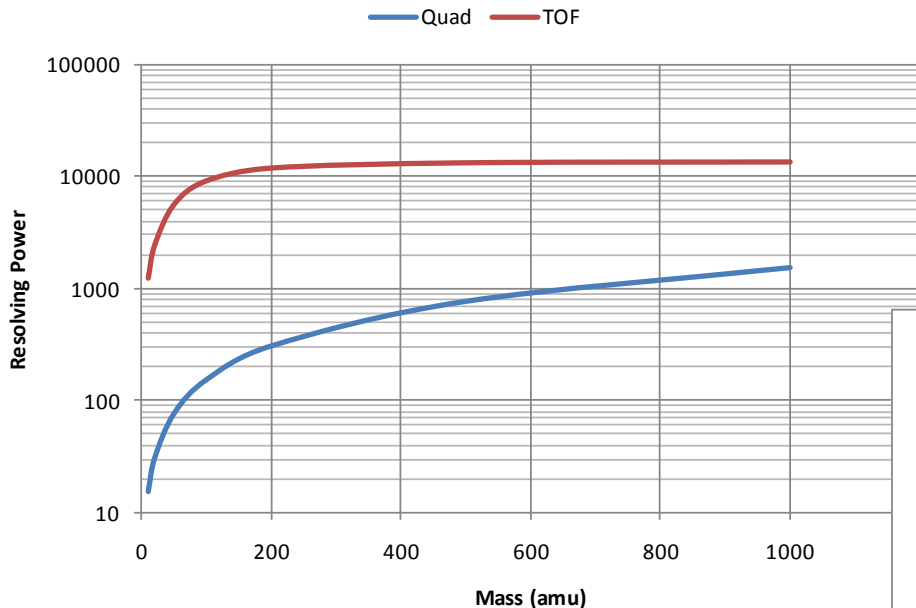
Spectral presentation (Tune File)

Most users think in “centroid”, but the MS operates in “profile”



Comparing Quad & TOF

Resolving Power



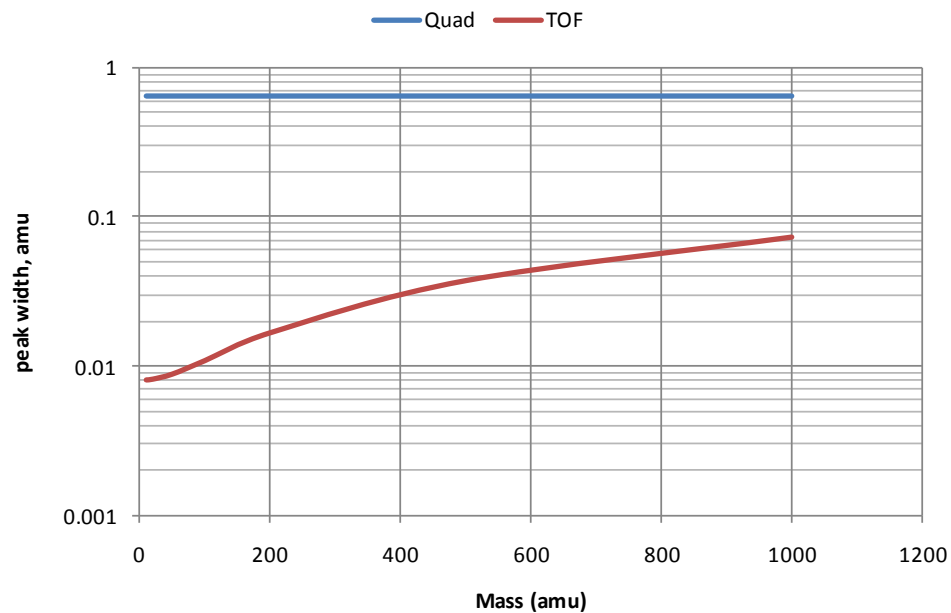
TOF has constant Resolving Power (peak-width changes with mass)



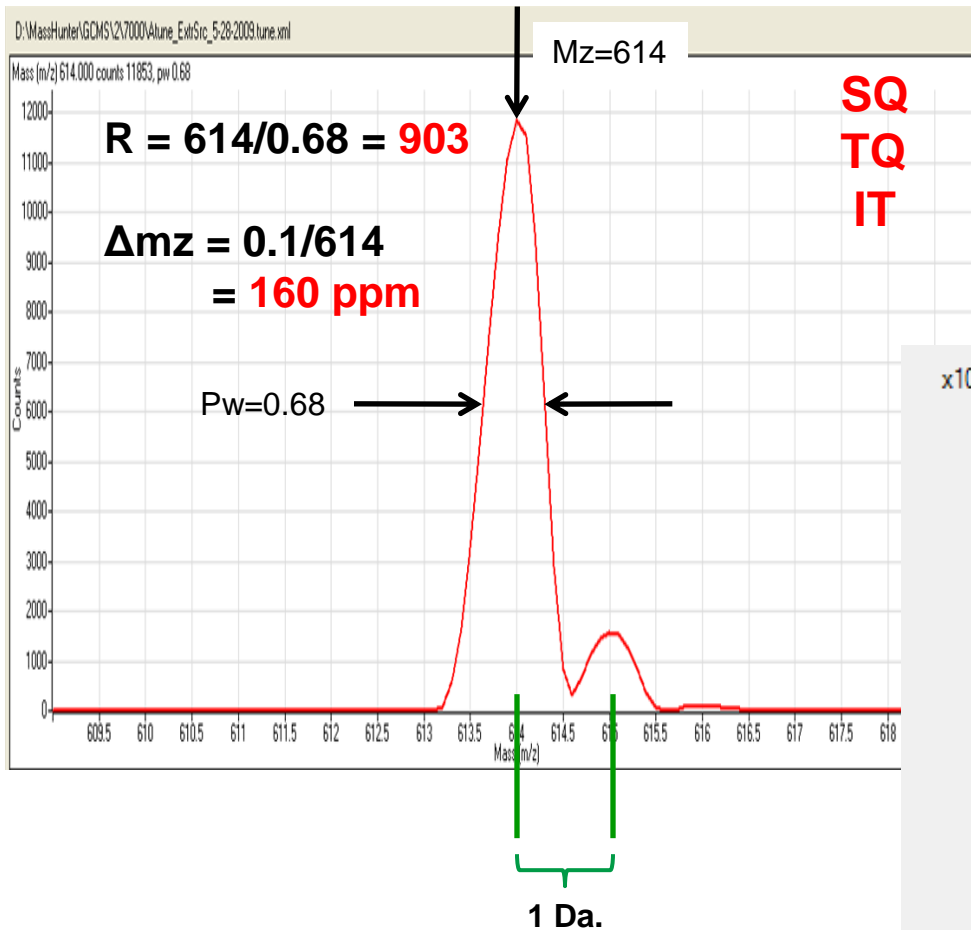
Quads operate with constant peak-width (Resolving Power changes with mass)



Peak Width



Resolving power & mass accuracy



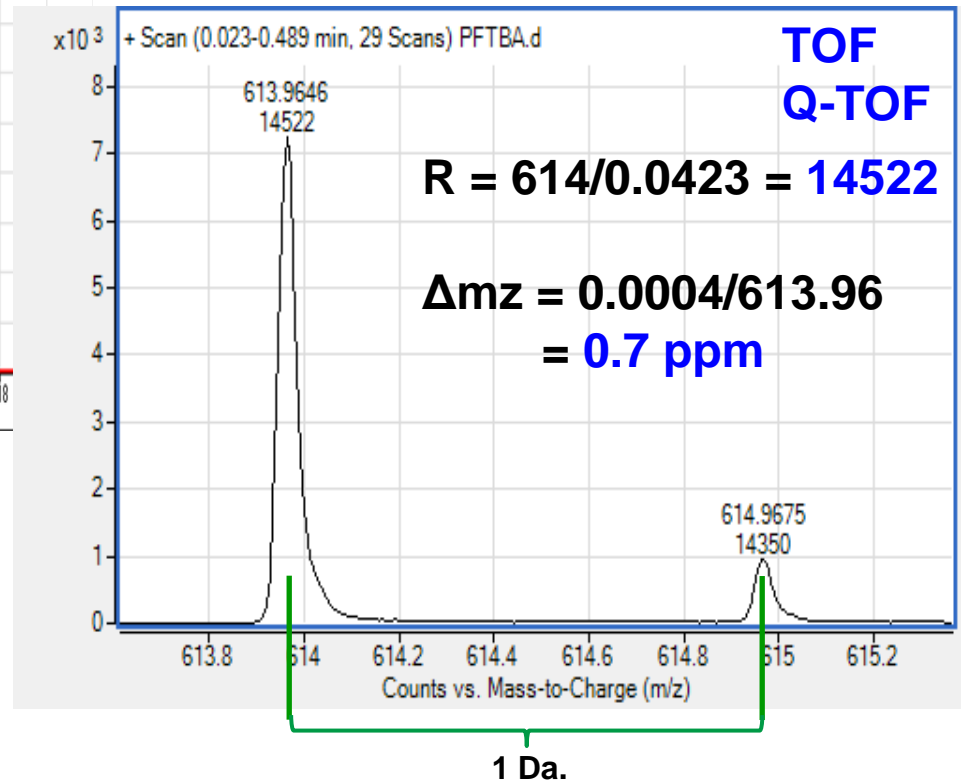
Resolving Power:

$$R = m/z / \text{FWHM}$$

Mass Accuracy: $\Delta m z = dm/mz * 10^6$,
parts per million (ppm)

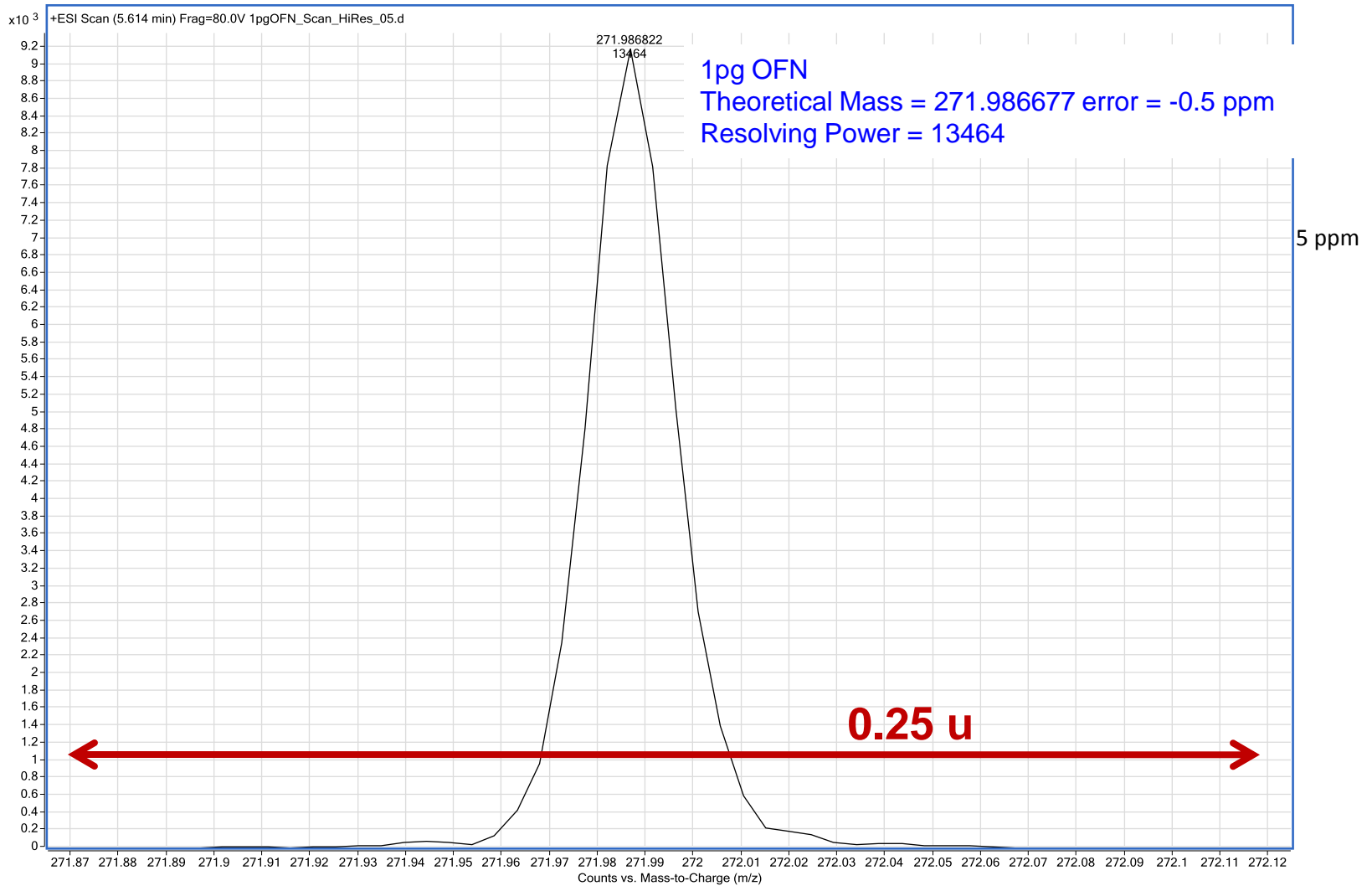
PFTBA mass 614

C12F24N=613.964203

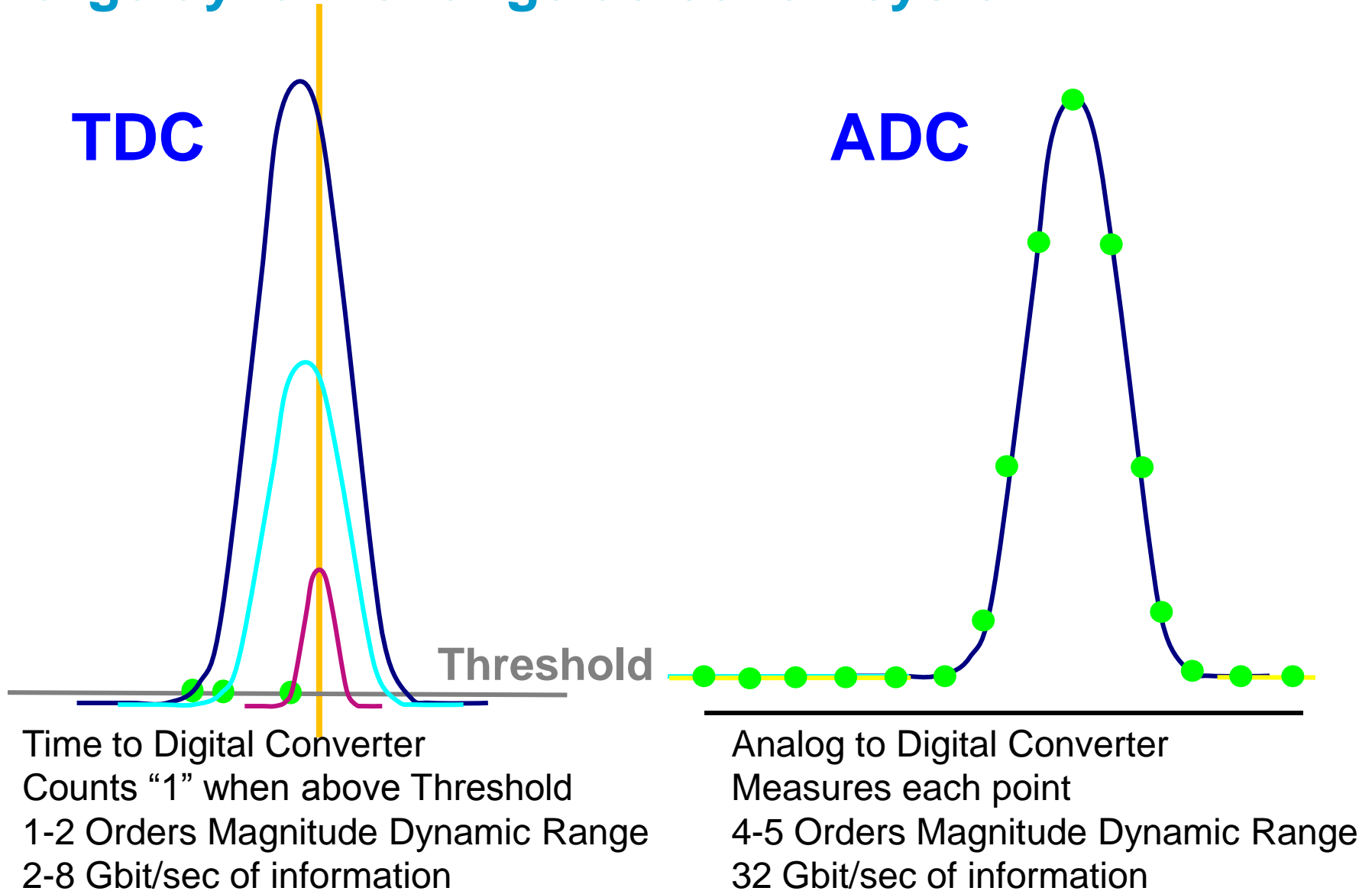


OFN Results

Later Prototype Q-TOF

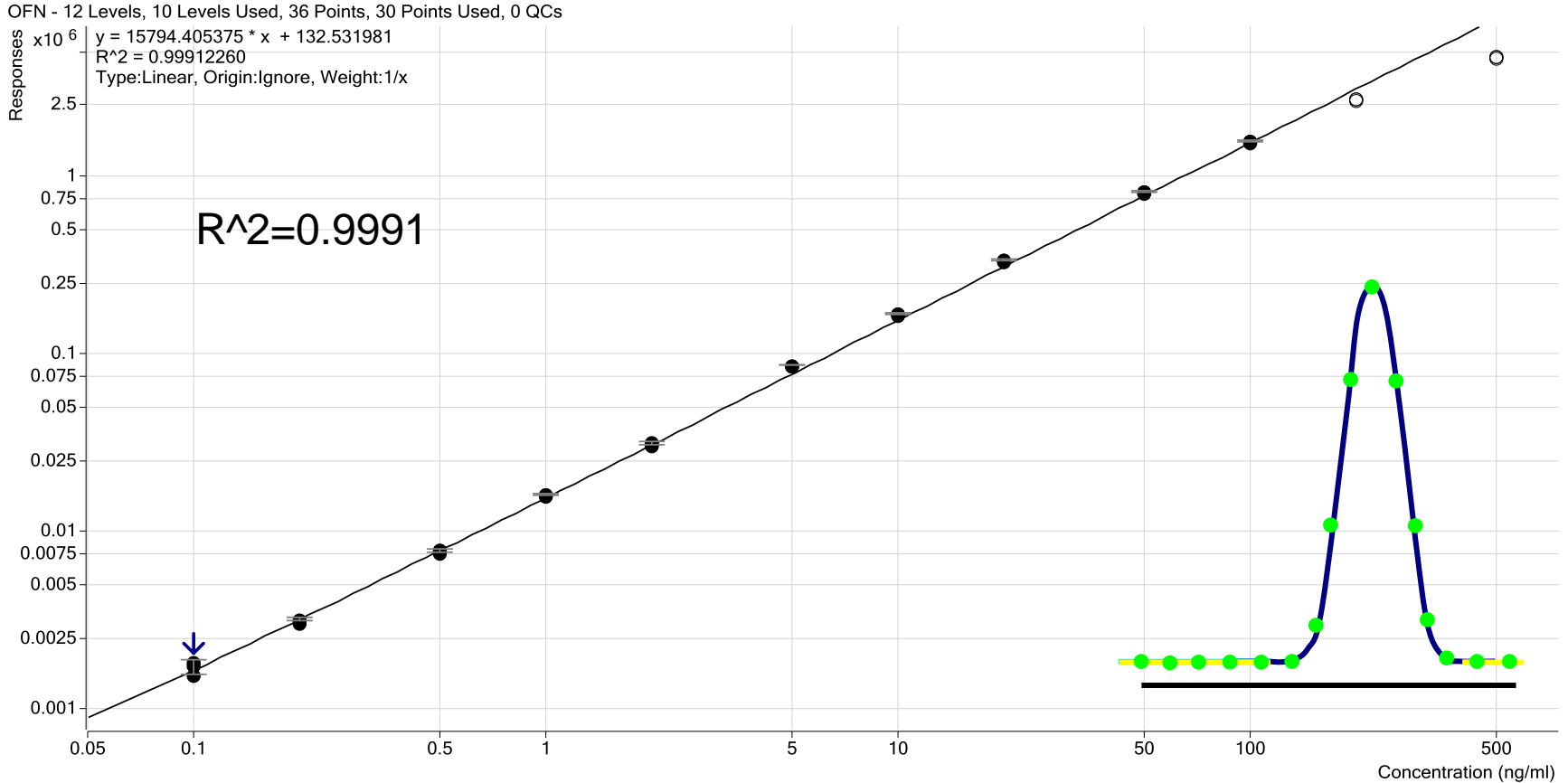


Large dynamic range detection system



Response linearity and mass accuracy

ADC advantages



5 Hz acquisition, RIS

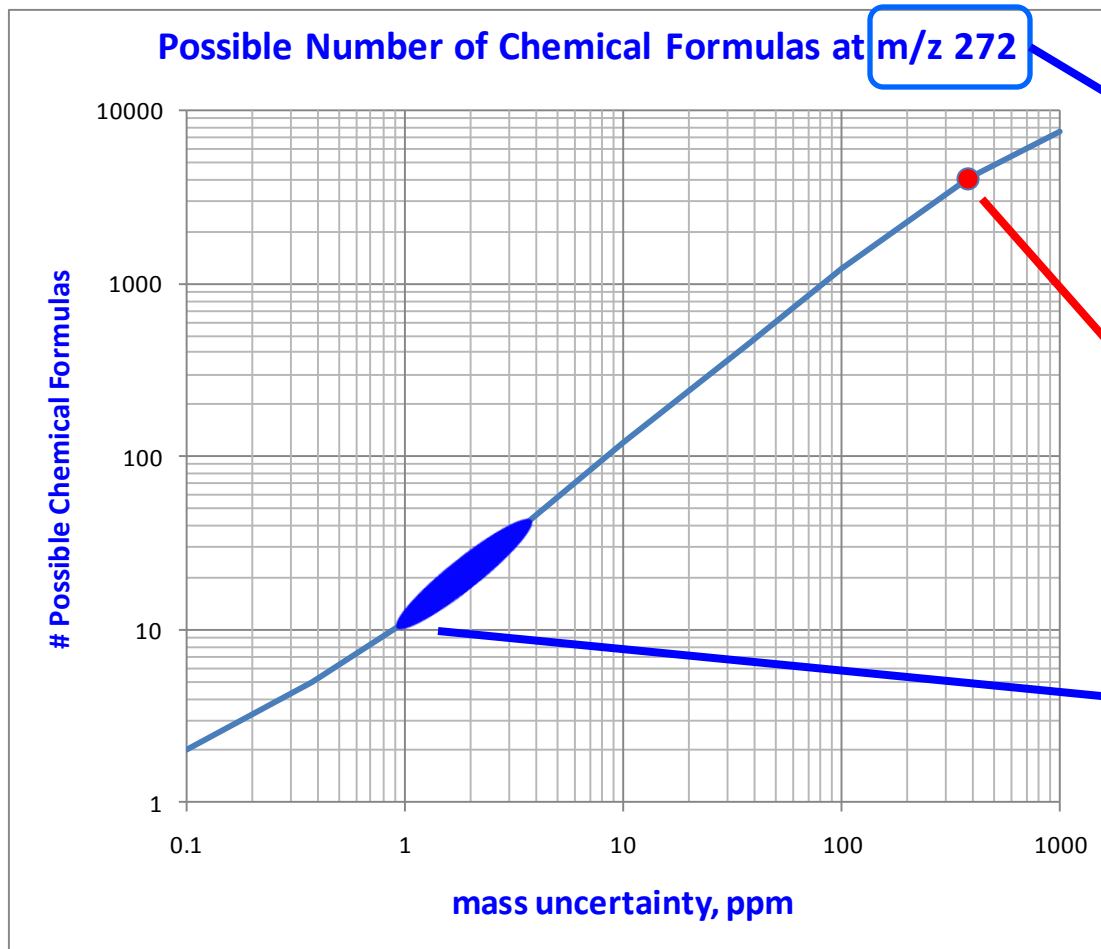
LOD about 0.01 pg

Accurate mass makes mass defect important

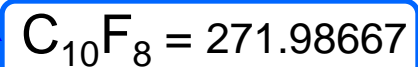
Type	Element	Symbol	Integer Mass	Exact Mass	Abundance	X+1 Factor	X+2 Factor	Mass Defect
X	Hydrogen	H	1	1.0078	99.99			0.0078
		D or ² H	2	2.0141	0.01			0.0141
X+1	Carbon	¹² C	12	12	98.91			0
		¹³ C	13	13.0034	1.1	1.1n _C	0.0060n _C ²	0.0034
X+1	Nitrogen	¹⁴ N	14	14.0031	99.6			0.0031
		¹⁵ N	15	15.0001	0.4	0.37n _N		0.0001
X+2	Oxygen	¹⁶ O	16	15.9949	99.76			-0.0051
		¹⁷ O	17	16.9991	0.04	0.04n _O		-0.0009
		¹⁸ O	18	17.9992	0.2		0.20n _O	-0.0008
X	Fluorine	F	19	18.9984	100			-0.0016
X+2	Silicon	²⁸ Si	28	27.9769	92.2			-0.0231
		²⁹ Si	29	28.9765	4.7	5.1n _{Si}		-0.0235
		³⁰ Si	30	29.9738	3.1		3.4n _{Si}	-0.0262
X	Phosphorus	P	31	30.9738	100			-0.0262
X+2	Sulfur	³² S	32	31.9721	95.02			-0.0279
		³³ S	33	32.9715	0.76	0.8n _S		-0.0285
		³⁴ S	34	33.9679	4.22		4.4n _S	-0.0321
X+2	Chlorine	³⁵ Cl	35	34.9689	75.77			-0.0311
		³⁷ Cl	37	36.9659	24.23	32.5n _{Cl}		-0.0341
X+2	Bromine	⁷⁹ Br	79	78.9183	50.5			-0.0817
		⁸¹ Br	81	80.9163	49.5		98.0n _{Br}	-0.0837
X	Iodine	I	127	126.9045	100			-0.0955

Many possible formulas with an MSD or IT

But only a few with TOF



Octafluoronaphthalene (CAS 313-72-4)



mass uncertainty		# of Possible Formulas
ppm	amu	
1000	0.3	7657
368	0.1	4050
100	0.03	1223
37	0.01	466
10	0.003	120
4	0.001	43
1	0.0003	11
0.4	0.0001	5
0.1	0.00003	2

Formulas made of:
C, H, N, O, F, & Cl

Accurate mass reduces risk of investing effort on the wrong molecule

Internal Reference Mass (IRM)

- The goal for the 7200 is for easy and reliable ~2-5ppm mass accuracy under all conditions
 - Agilent has developed a proprietary Internal Reference Mass (IRM) delivery system for “on the fly” mass axis correction
 - IRM is the use of known background ions to “lock” the mass axis for each scan
 - Requires reliable IRM calibration signals with and without matrix



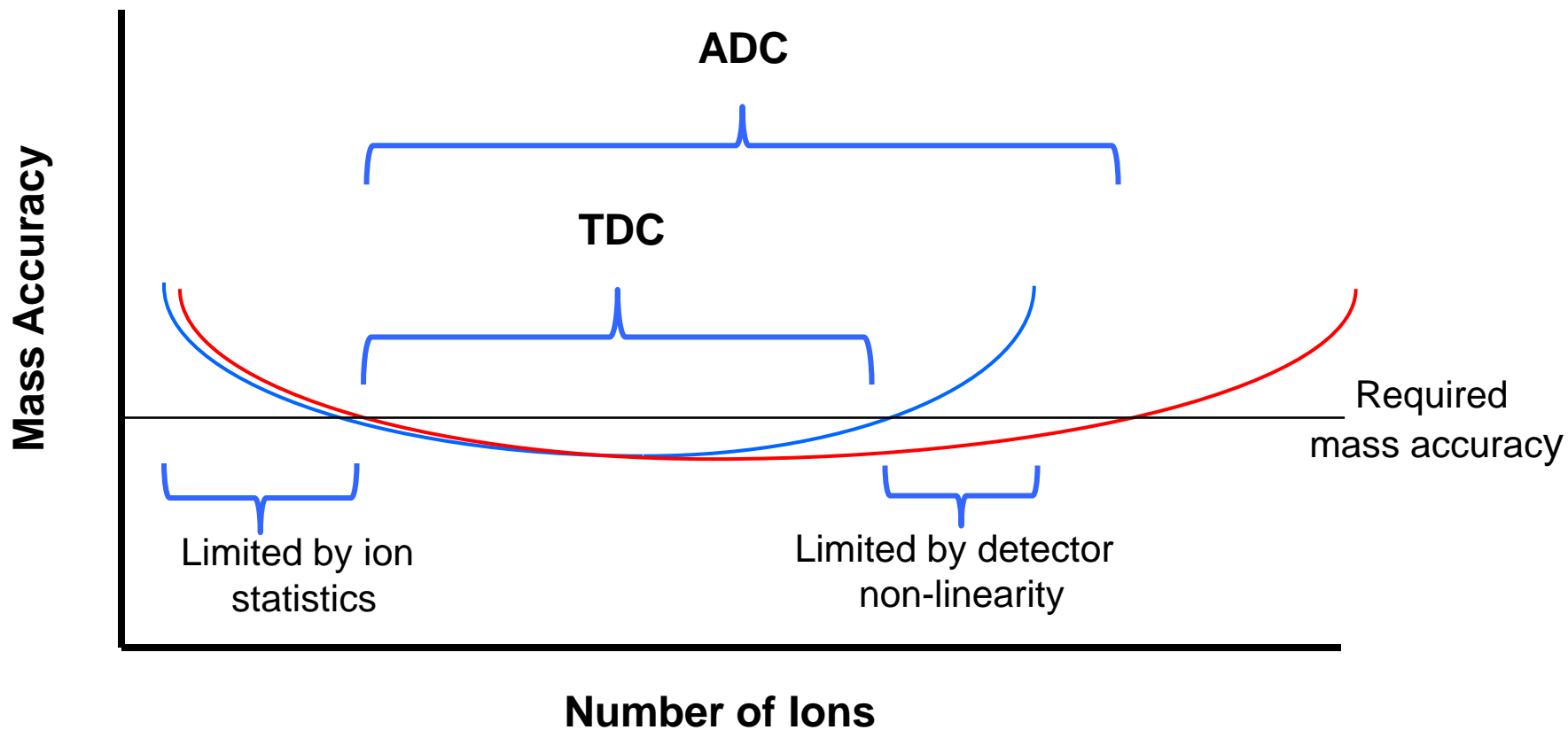
7200 provisional instrument performance

Specifications...

- Resolving Power: >10K at m/z 272 (>13K typical)
- Mass Accuracy: <5 ppm at m/z 272 (<2ppm typical)
- MS Sensitivity: 1 pg OFN S/N > 400:1
- Dynamic Range: > 3 orders of magnitude
- Quad Mass range: 20-1050 Da (0.7-4.0 Da FWHM)
- TOF Mass range: 20-1700 Da
- Spectral Rate: 1-50 spectra/sec

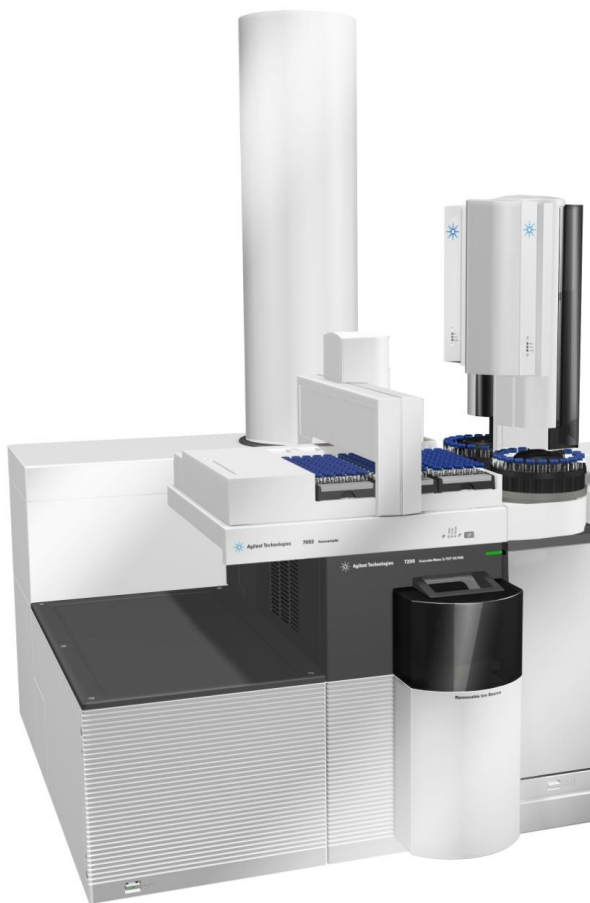
All specifications subject to change

Mass accuracy



7200 Series Q-TOF for GC/MS

How is this new capability used - application results



Pesticides in Food

Tom Doherty, Phil Wylie, Chris Sandy, Bill Russ

Fluorotelomer Alcohols in Biosolids (PCI)

Anthony Macherone

Volatile Sulfur-containing Compounds in Beverages

Nobuo Ochiai, Kikuo Sasamoto – Gerstel KK, Japan
Ryo Ogasawara, Hajime Kawakami – Agilent

Volatile Photodegradation Products in Beer

Stephan Baumann

Metabolomics

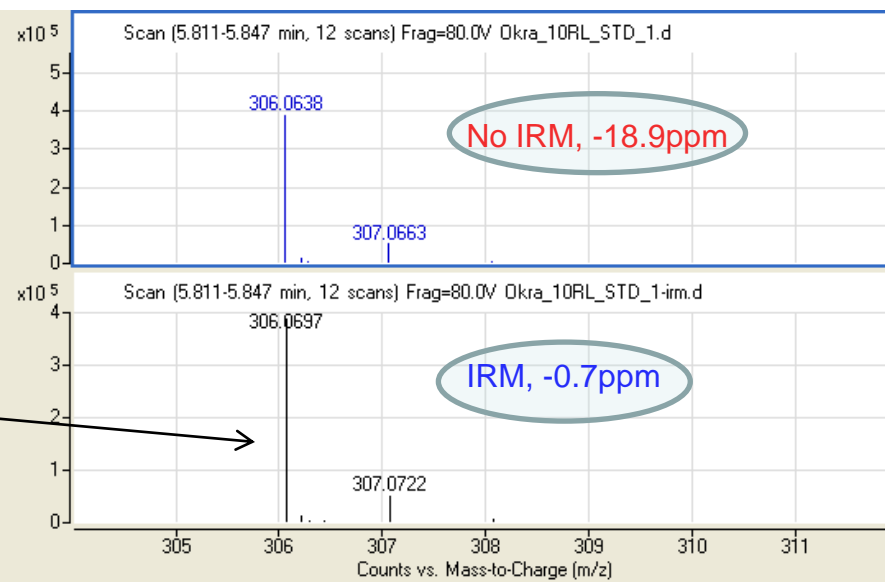
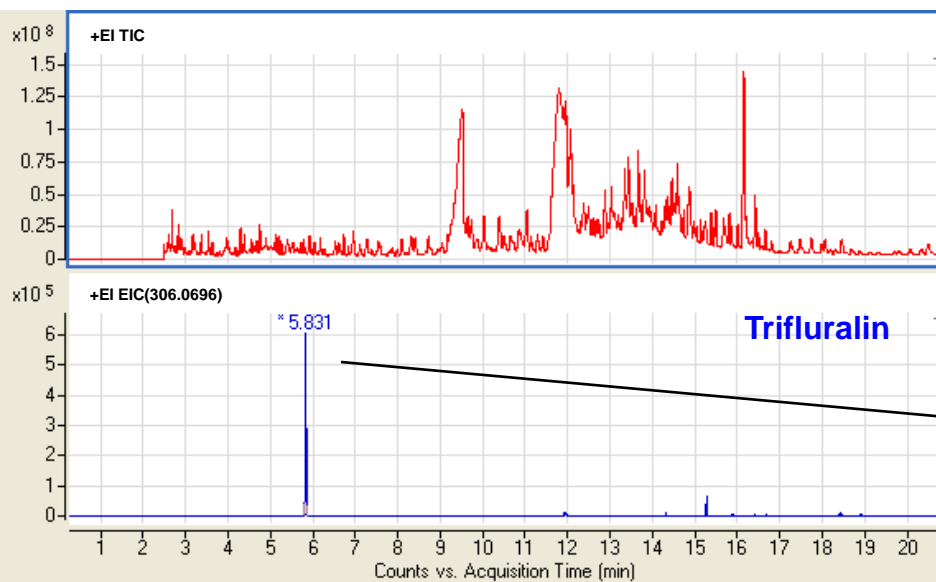
Oscar Yanes, Maria Vinaixa, Jesus Breznes –
Tarragona University, Spain

Pesticides in Food

Internal reference mass correction in matrix

100ppb pesticides in Okra extract

Analyte	RT	Theoretical Mass	Measured Accurate Mass (Da)		Mass Error, ppm	
			No IRM	With IRM	No IRM	With IRM
Trifluralin	5.83	306.0696	306.0638	306.0698	-18.9	0.7
Ethion	13.03	230.9732	230.9689	230.9744	-18.6	5.2
Iprodione	14.26	314.0094	314.0030	314.0101	-20.4	2.2
Indoxacarb	18.06	527.0702	527.0603	527.0730	-18.8	5.3



TOF Accurate Mass to Eliminate Matrix Interferants

Okra QuEChERS Extract

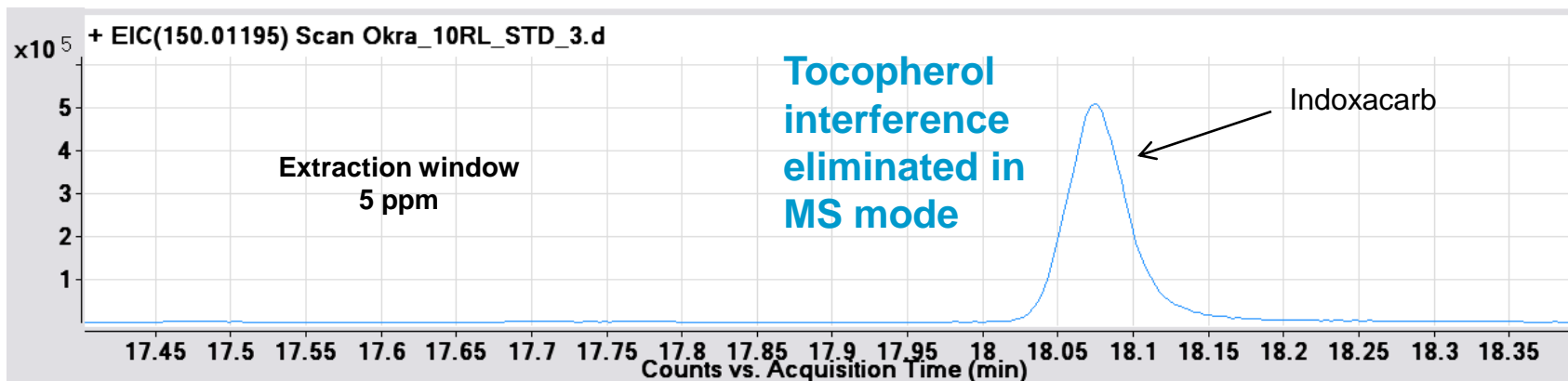
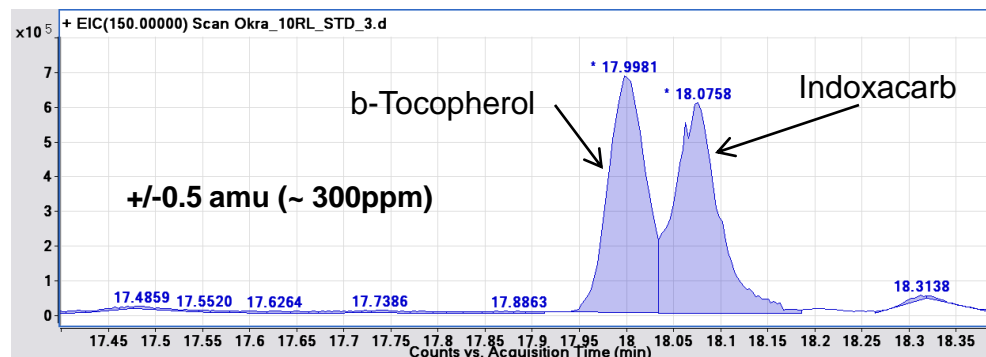
Matrix interferant ion (b-Tocopherol)

150.06839 Da

Analyte Indoxacarb ion (100pg)

150.01195 Da (fragment ion)

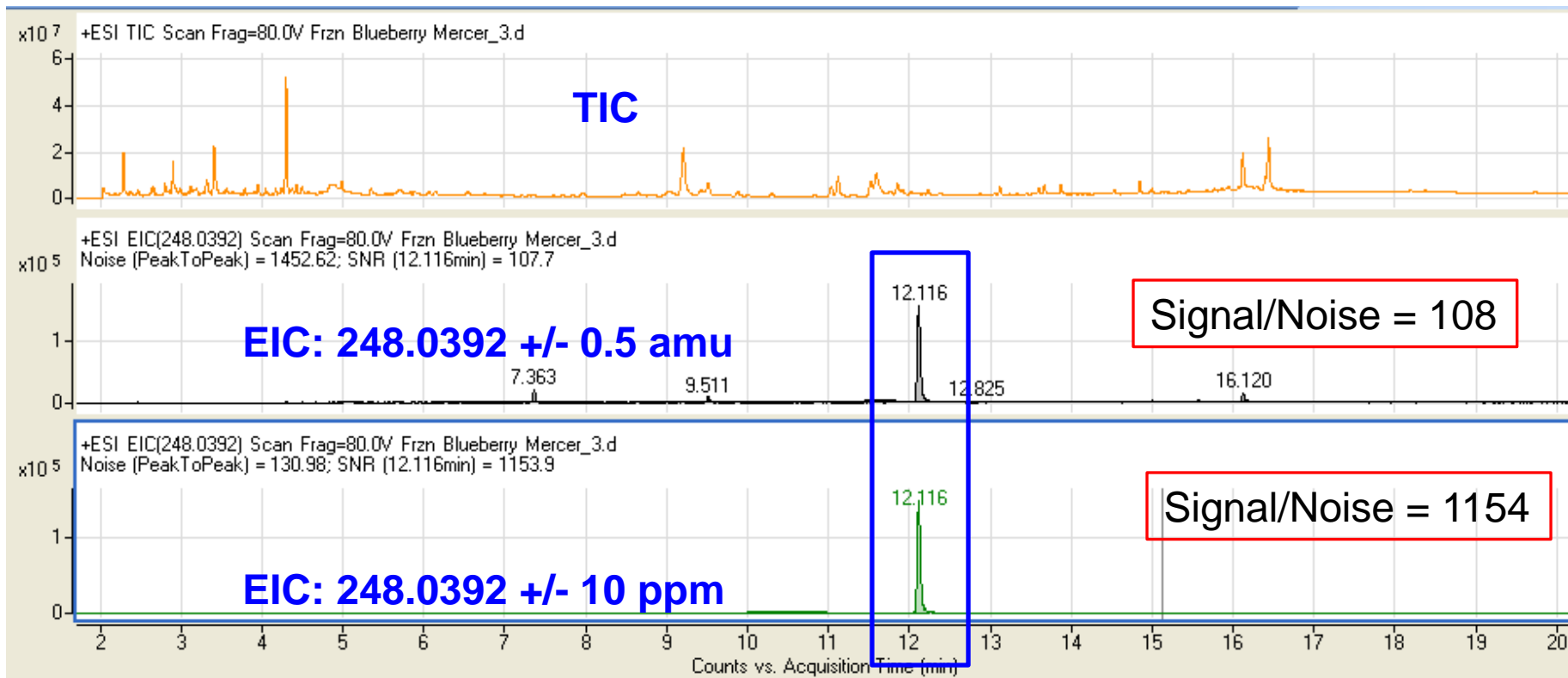
$\Delta m = 0.0564$ Da.



If even more selectivity is needed, option of MS/MS MS/MS with high resolution and accurate mass!

Fludioxonil in Frozen Blueberry Extract

38 ppb in extract



Why add 'Q' to TOF to make Q-TOF?

Add 'Q+CID' to TOF solution

Sometimes the combined power of
GC Resolution (**Agilent**)

+

MS Resolving Power (**Agilent**)

Is not enough based upon:
Small Δ Mass Defect (**Nature**)

+

Intense Matrix Ions (**Sample**)

High resolution MS/MS can solve some of these problems

How is it used?

Structure elucidation

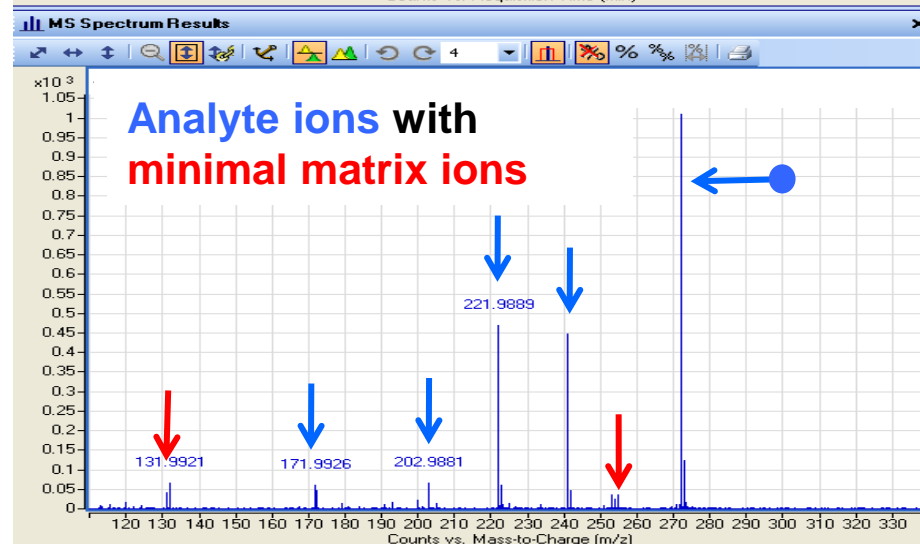
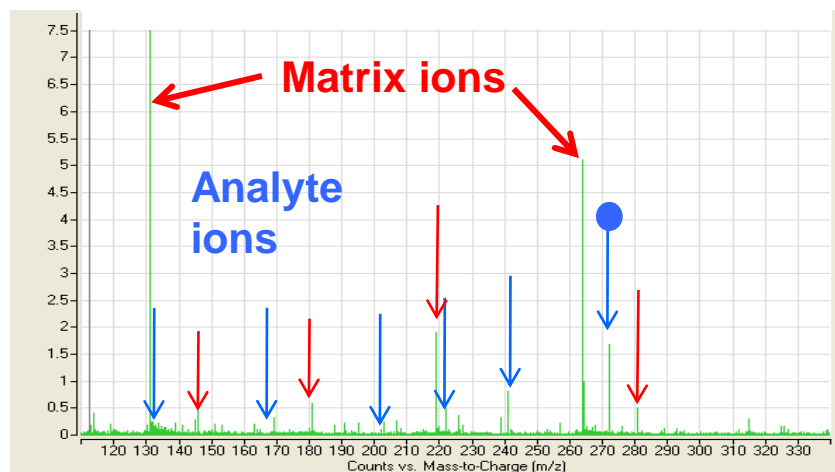
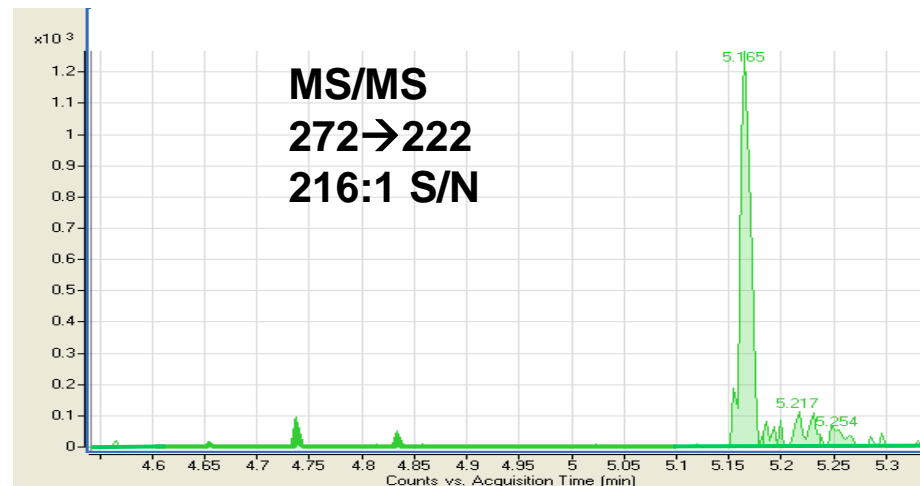
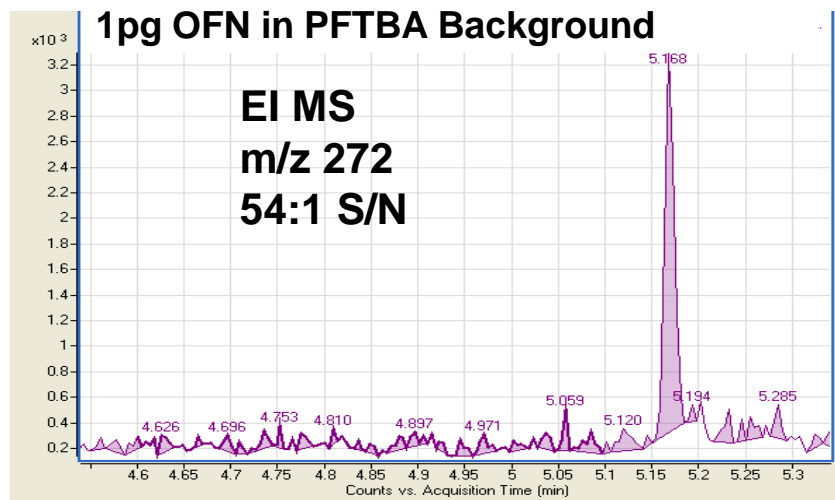
- Structural Elucidation from product Ion spectra using high resolution and accurate mass
- Start with full scan EI spectrum
- Use CID on each fragment mass to confirm structure of fragment
 - Select Fragment 1 to be precursor 1 $\xrightarrow{\text{CID}}$ Product ions
 - Select Fragment 2 to be precursor 2 $\xrightarrow{\text{CID}}$ Product ions

***Precursor-product ion relationship is documented
and ion molecular formula confirmed by accurate mass***

***Requires multiple analyses and much more sensitive than NMR
Will not replace NMR, but will complement nicely***

MS/MS chemical noise reduction

If resolution and accurate mass are not enough



Accurate Mass Library Workflow

Using NIST MS Interpreter and MassHunter Qual Formula Calculator

TIC Chromatogram

MassHunter Formula Calculator

Formula (M)	Ion Formula	Mass (MFG)	m/z (Calc)	Diff (ppm)
C ₉ H ₁₂ O ₃ P	C ₅ H ₁₅ N ₀ P ₃ S	168.0612	168.0612	-2.4
C ₉ H ₁₂ O ₃ S	C ₉ H ₁₂ O ₃ S	168.0609	168.0609	-4.25
C ₇ H ₁₀ N ₃ S	C ₇ H ₁₀ N ₃ S	168.0595	168.0595	-11
C ₈ H ₁₁ N ₀ P	C ₈ H ₁₁ N ₀ P	168.0578	168.0578	-22
C ₁₂ H ₈ O	C ₁₂ H ₈ O	168.0575	168.0575	-24.3
C ₈ H ₁₀ N ₀ D ₃	C ₈ H ₁₀ N ₀ D ₃	168.0661	168.0661	26.59
C ₄ H ₁₂ N ₂ O ₃ S	C ₄ H ₁₂ N ₂ O ₃ S	168.0569	168.0569	-28.19
C ₄ H ₁₃ N ₂ O ₃ P	C ₄ H ₁₃ N ₂ O ₃ P	168.0664	168.0664	28.43
C ₁₀ H ₆ N ₃	C ₁₀ H ₆ N ₃	168.0562	168.0562	-32.3
C ₁₁ H ₈ N ₂	C ₁₁ H ₈ N ₂	168.0687	168.0687	42.53
C ₇ H ₁₁ N ₃ P	C ₇ H ₁₁ N ₃ P	168.0691	168.0691	44.38
C ₃ H ₁₁ N ₃ O ₃ P	C ₃ H ₁₁ N ₃ O ₃ P	168.0538	168.0538	-46.4
C ₅ H ₁₄ N ₀ D ₃ S	C ₅ H ₁₄ N ₀ D ₃ S	168.0694	168.0694	46.64

NIST MS Search

NIST MS Interpreter

Chemical Structure

CCOC(=O)C1=CC=C(C=C1)OC

Formula Calculator

Determine all possible formulas consistent with measured mass

Formula Calculator

Mass and charge
Mass or m/z: 260.8598
Charge: 1

Charge carrier
Positive ions: electron Negative ions: H
MS ion electron state: allow both even and odd

Elements and limits

Element	Minimum	Maximum
C	0	12
H	0	8
O	0	0
N	0	0
S	0	0
Cl	0	6
[13C]	0	0
F	0	0

Formula (M)	Ion Formula	Mass (MFG)	m/z (Calc)	Diff (ppm)
C7 H2 Cl5	C7 H2 Cl5	260.8599	260.8594	-1.67
C10 H Cl4	C10 H Cl4	260.8832	260.8827	87.74
C4 H3 Cl6	C4 H3 Cl6	260.8366	260.836	-91.07

C₇H₂Cl₅

-1.67 ppm diff

The image shows a 3D ball-and-stick model of a heptachloroheptane derivative (C₇H₂Cl₅). The carbon backbone is shown in black, with five chlorine atoms (Cl) in red and two hydrogen atoms (H) in white. The structure is a complex polycyclic system with a central ring and several side chains, all heavily substituted with chlorine atoms.

Fragment ion mass with high mass accuracy

Helps unambiguously identify corresponding formula and hence exact mass of a fragment

Most probable fragment ion

	Molecular Ion		Fragment Ions							
			1		2		3		4	
Pesticide	m/z	Formula	Δ ppm	Formula	Δ ppm	Formula	Δ ppm	Formula	Δ ppm	Formula
Chlorpyrifos-methyl	320.8944	C7H7Cl3NO3PS	-0.7	C7 H7 Cl [³⁷ Cl] N O3 P S	0.0	C7 H7 Cl2 N O3 P S	0.0	C2 H6 O2 P S		
			215.4	C6 H2 Cl3 N O2 P S						
Dichlorvos	219.9454	C4H7Cl2O4P	1.6	C4H7ClO4P	-0.9	C2H6O3P	3.7	C4 H7 [³⁷ Cl] O4 P		
						336.5	C3 H2 Cl2 O3 P			
Endosulfan sulfate	419.8112	C9 H6 Cl6 O4 S	-2.1	C9 H6 Cl4 [³⁷ Cl] O4 S	-0.7	C5 Cl5 [³⁷ Cl]	0.0	C5 Cl4 [³⁷ Cl]2		
						-220.9	C8 H3 Cl5			
Propachlor	211.0758	C11 H14 Cl N O	-1.0	C10 H11 Cl N O	1.1	C11 H14 N O	1.8	C8 H8 Cl N O	-3.9	C6 H5
								771.6	C2 H2 Cl O	
Fluazifop-p-butyl	383.1339	C19 H20 F3 N O4	-2.2	C19 H20 F2 N O4	-1.1	C14 H11 F3 N O2	-1.3	C12 H7 F3 N O	2.1	C6 H3 F3 N
								-494.2	C7 H14 O3	
Triazophos	313.0645	C12 H16 N3 O3 P S	-1.4	C10 H12 N3 O3 P S	-2.7	C8 H8 N3 O3 P S	-0.6	C8 H7 N3 O	-1.9	C8 H8 N3 O
			-47.7	C11 H14 N2 O3 P S	-54.1	C9 H10 N2 O3 P S				

Examples from building accurate mass pesticide library

Fluorotelomer Alcohols in Biosolids

Fluorotelomer Alcohols

- Source unknown, but probably intermediate degradation products of fluorinated polymers
- Oxidize to form fluorinated carboxylic acid, some of which are toxic
- Methods needed for studying their transport and fate in the environment
- Have the form $F_3C(CF_2)_{N-1}(CH_2)_M OH$
- *N:M FTOH* is the shorthand notation
- Positive CI, 20% CH₄

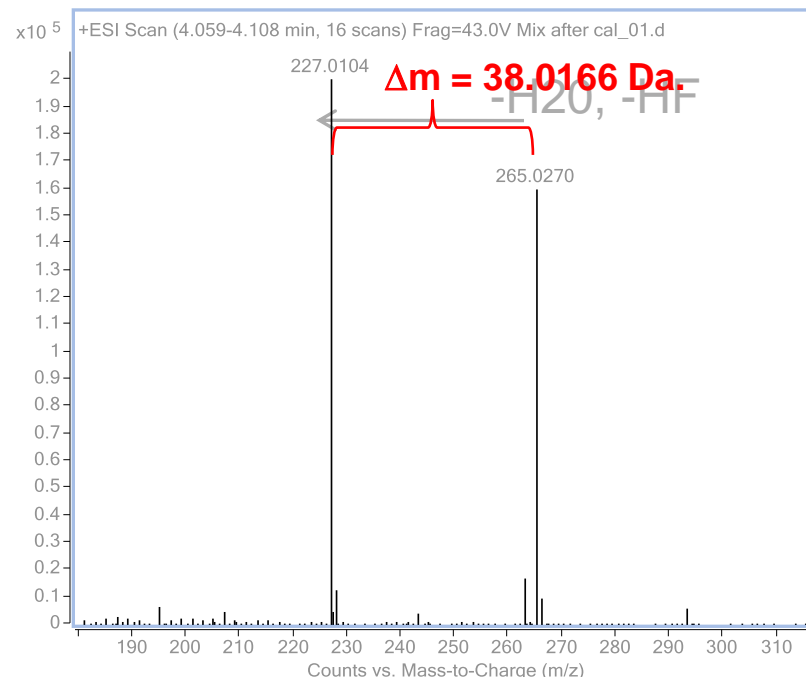
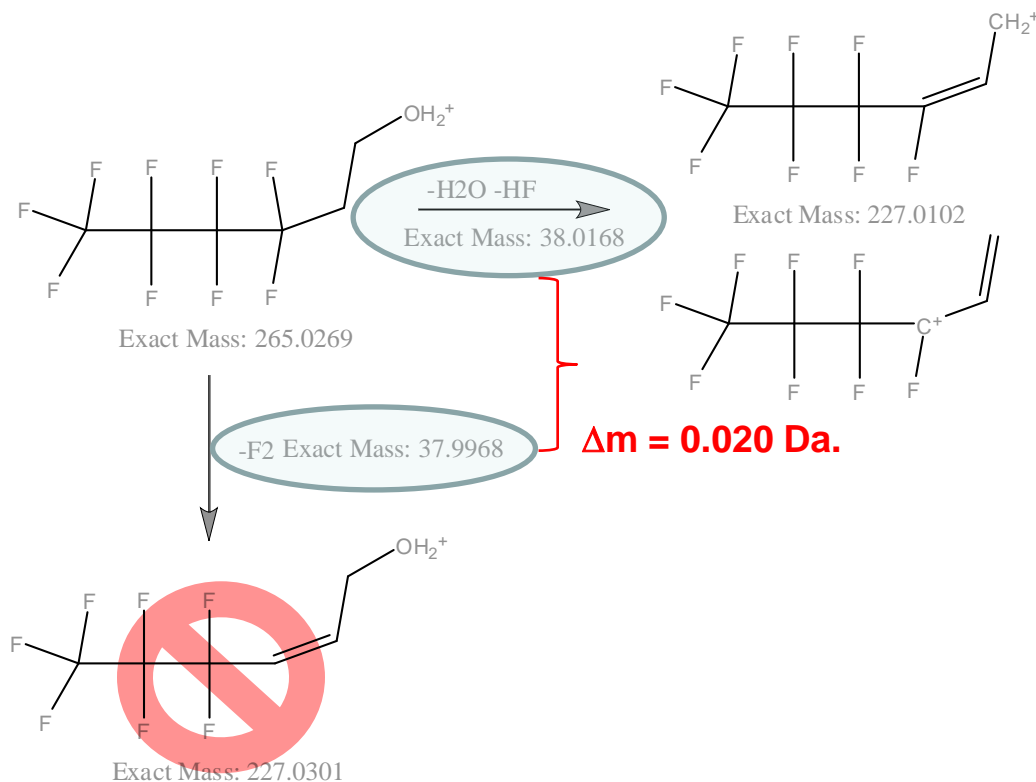
Fluorotelomer Alcohol Mass Accuracy

Protonated Molecular Ion (PCI)

Acronym	Formula	Exact Mass + H	Observed Mass	Δ ppm
4:2 FTOH	$C_6H_5F_9O$	265.0269	265.0270	-0.38
6:2 FTOH	$C_8H_5F_{13}O$	365.0206	365.0206	0
8:2 FTOH	$C_{10}H_5F_{17}O$	465.0142	465.0140	0.43
10:2 FTOH	$C_{12}H_5F_{21}O$	565.0078	565.0078	0
7:2 sFTOH	$C_9H_5F_{15}O$	415.0174	415.0190	-3.85
5:1 FTOH	$C_6H_3F_{11}O$	301.0081	301.0079	0.66
6:1 FTOH	$C_7H_3F_{13}O$	351.0049	351.0050	-0.28
7:1 FTOH	$C_8H_3F_{15}O$	401.0017	401.0016	0.25
8:1 FTOH	$C_9H_3F_{17}O$	450.9985	450.9985	0
9:1 FTOH	$C_{10}H_3F_{19}O$	500.9953	500.9956	-0.60
10:1 FTOH	$C_{11}H_3F_{21}O$	550.9921	550.9922	-0.18
11:1 FTOH	$C_{12}H_3F_{23}O$	600.9889	600.9896	-1.16
MeFOSE	$C_{11}H_8F_{17}NO_3S$	558.0026	558.0042	-2.87
EtFOSE	$C_{12}H_{10}F_{17}NO_3S$	572.0183	572.0167	2.80

Fluorotelomer Neutral Loss Mechanism Inferred

PCI, methane

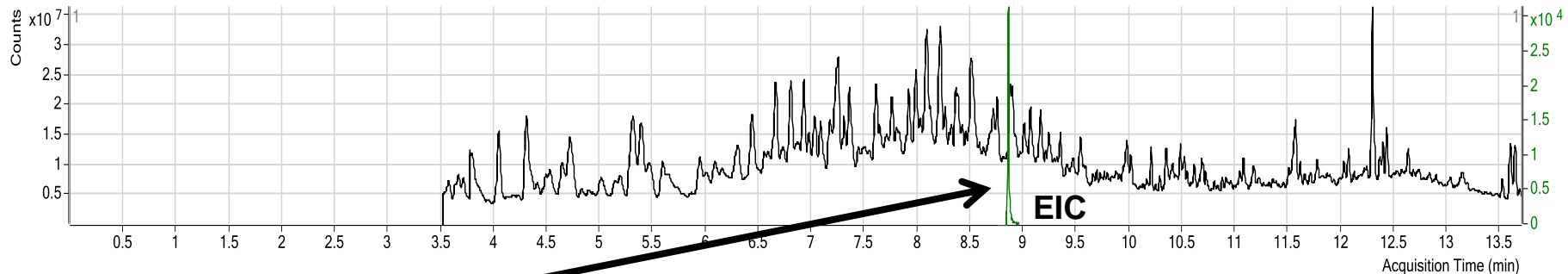


Acronym	Observed Base Peak m/z	Molecular ion $-\text{F}_2$ m/z	Δ ppm	Molecular ion $-\text{H}_2\text{O}, -\text{HF}$ m/z	Δ ppm
4:2 FTOH	227.0104	227.0301	86.77	227.0102	-0.88

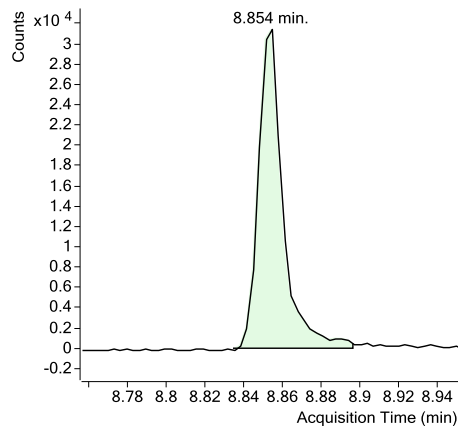
11:1 FTOH Spiked in Biosolid Extract

PCI, methane

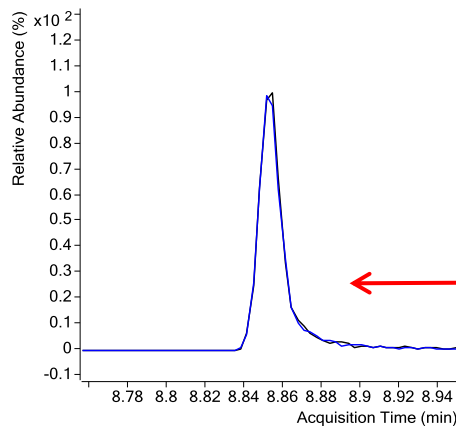
+ TIC Scan Extracted Solvent 3.d



Quant ion
 $m/z = 580.9784$



Qualifier ion
 $m/z = 600.9845$

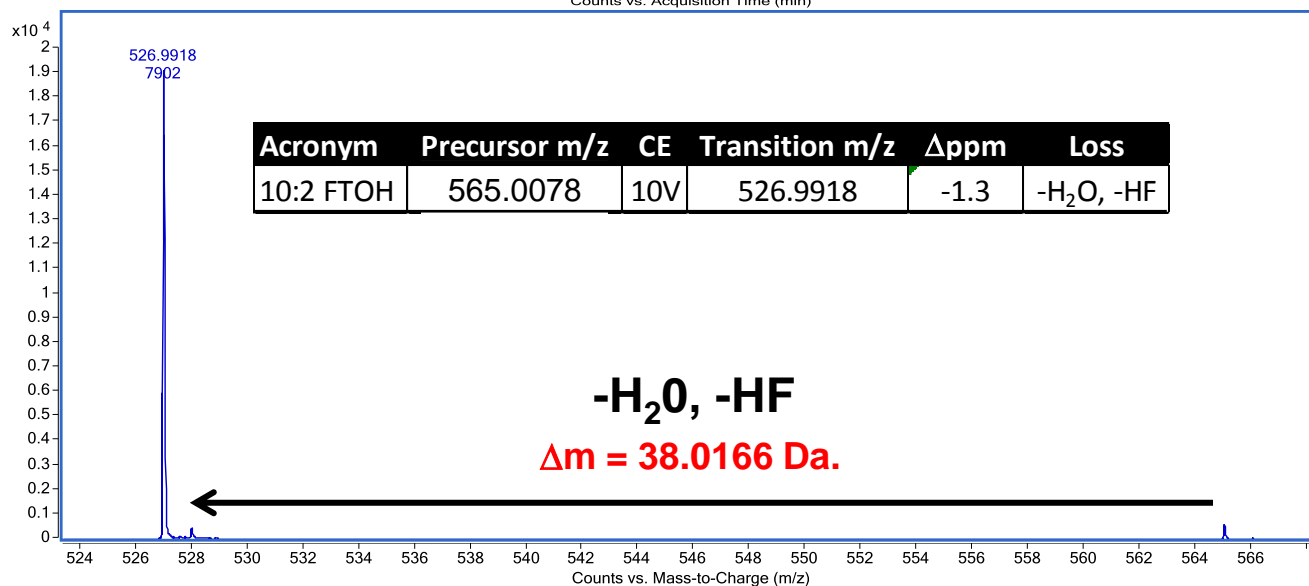
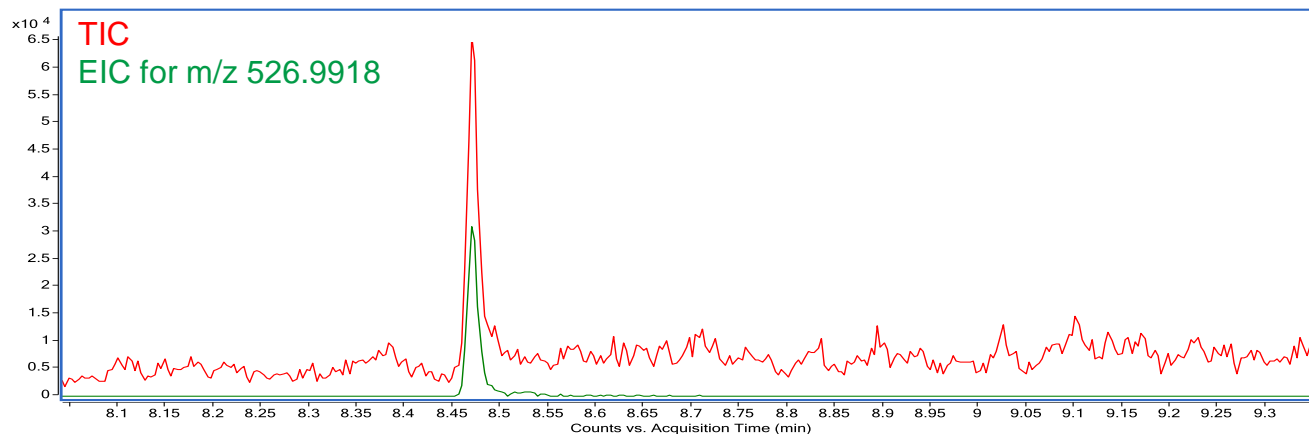


Spiked at 50 pg/ml level

Excellent qualifier ratio in the presence of nearly 10^3 excess of matrix. EIC of $m/z=580.9784$ overlaid on $m/z=600.9845$

10:2 FTOH Fluorotelomer Alcohol MS/MS

PCI, methane



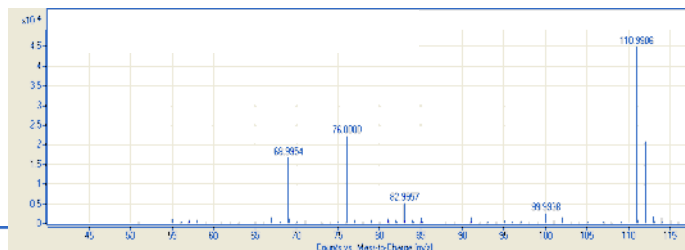
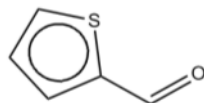
Identification and Quantification of Sulfur-Containing Compounds in Beverages

Compounds affecting taste and flavor

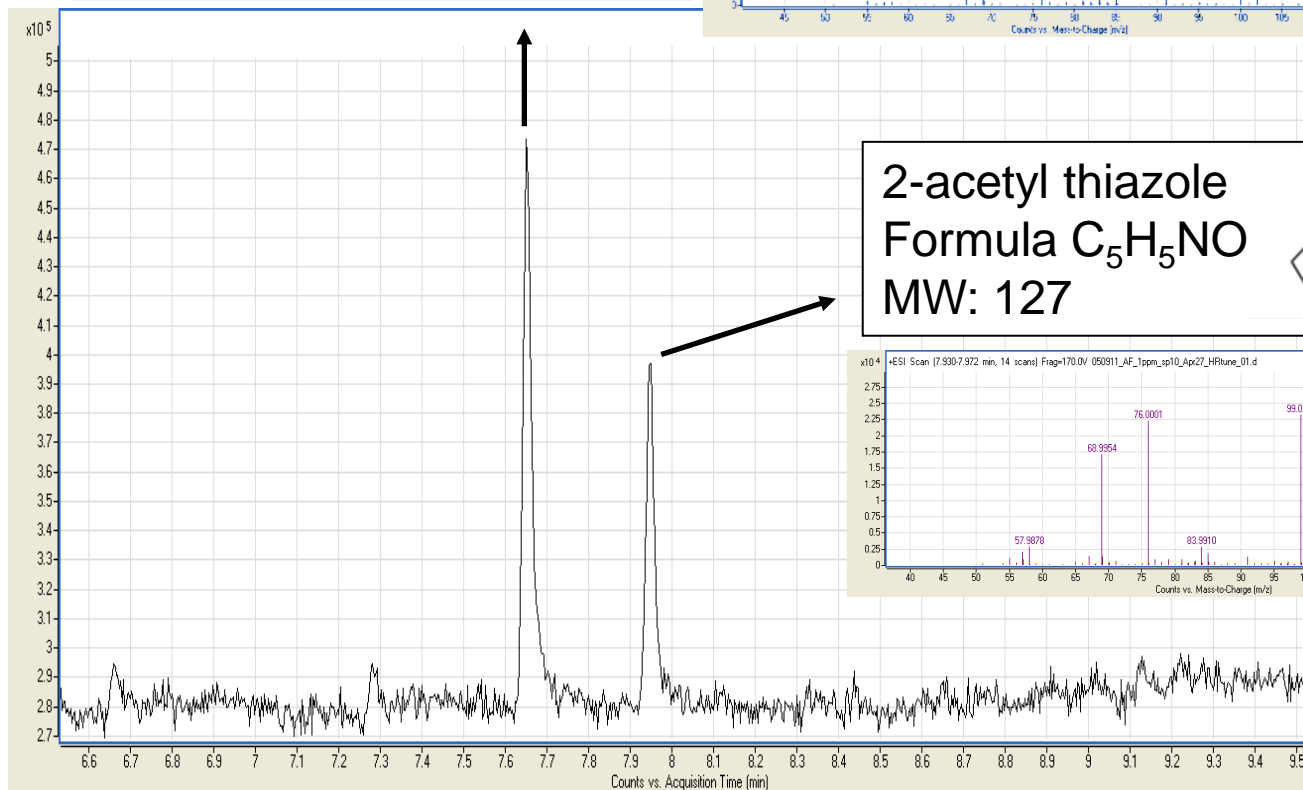
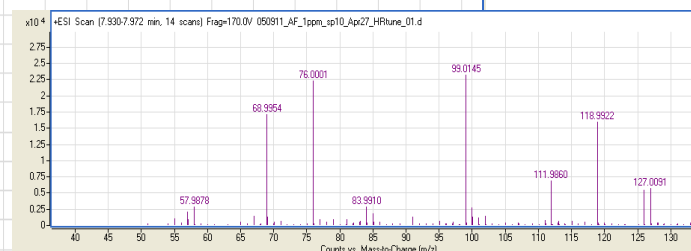
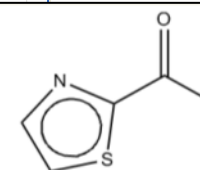
- 2-formyl thiophene and 2-acetyl thiazole are common contaminants
- Low sensory threshold and can have negative effect on product flavor or aroma
- Easy to separate from each other
- Often requires sophisticated extraction/enrichment procedures and/or powerful 2D GC techniques for separation from matrix for quantitation
- Method highlights
 - Simple L/L extraction in dichloromethane (10:1 enrichment)
 - 1:10 split injection with SSL inlet
 - DB-5MS column 30 m x 0.25 mm x 0.25 μ m

Standards at 100 pg On Column

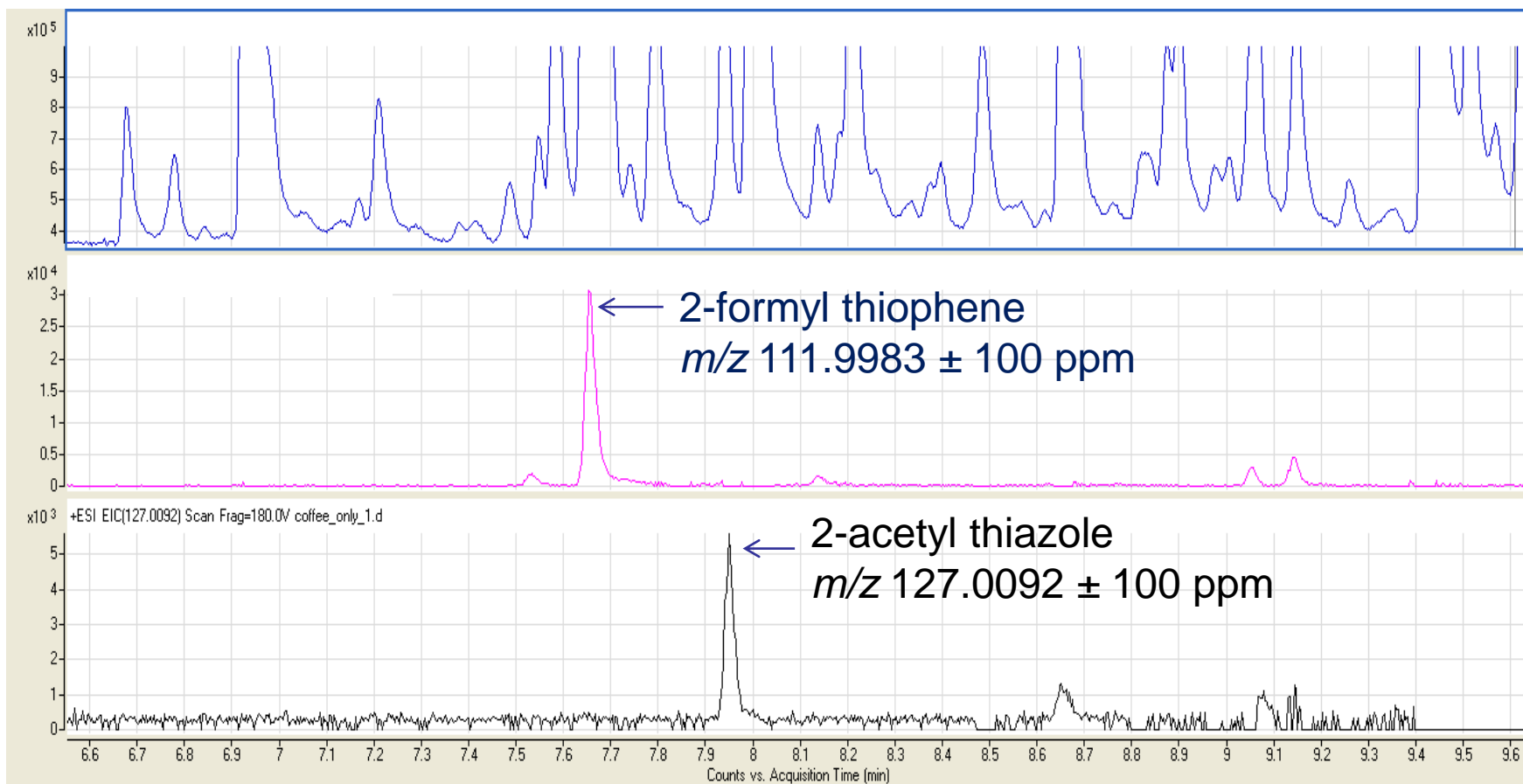
2-formyl thiophene
Formula C_5H_4OS
MW: 112



2-acetyl thiazole
Formula C_5H_5NO
MW: 127

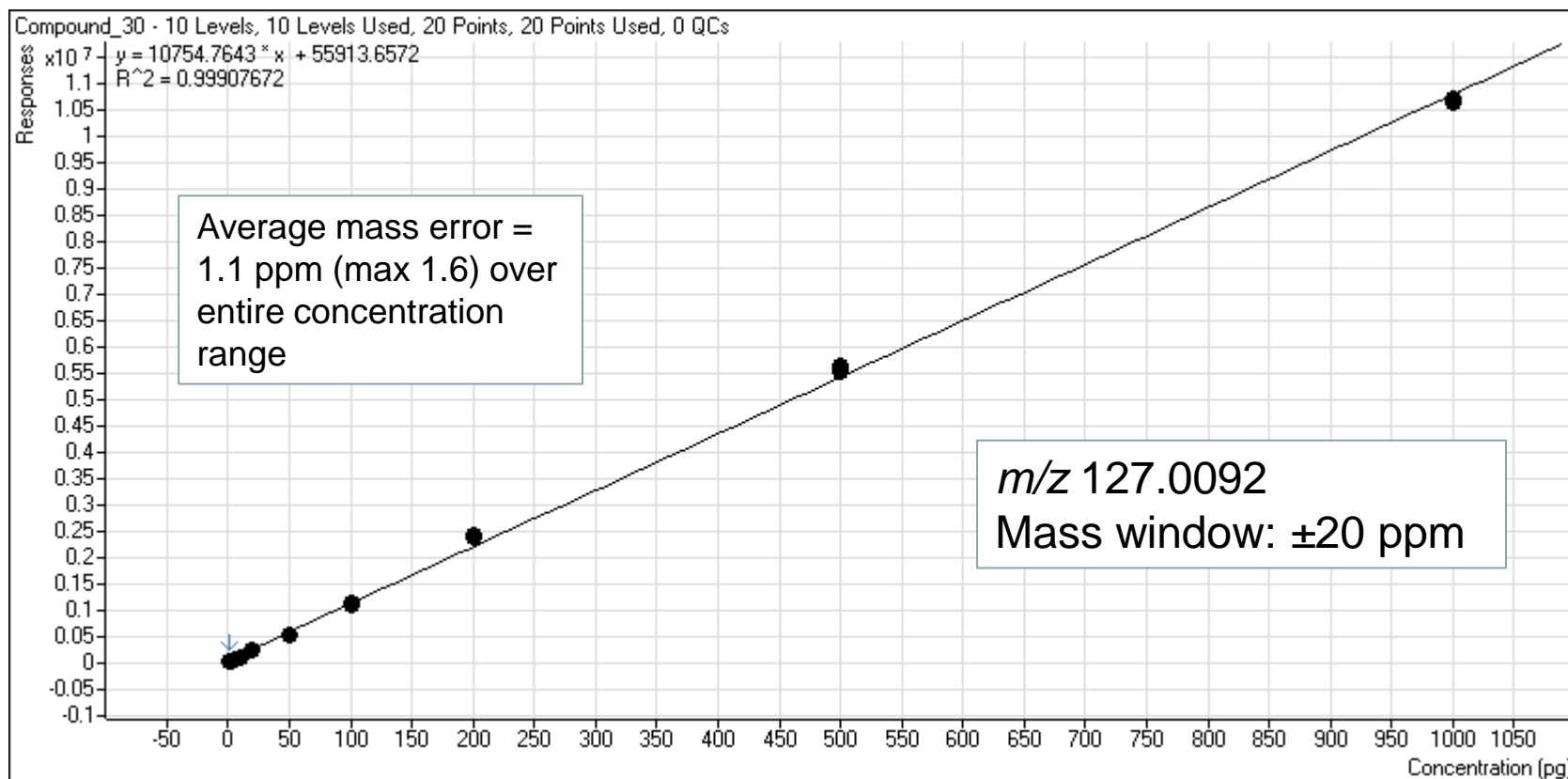


TIC and EICs of Coffee Extract



2-Acetyl Thiazole calibration

STD addition calibration curve for 2-acetyl thiazole in spiked coffee
(STD amount: 1, 2, 5, 10, 20, 50, 100, 200, 500, 1000 pg)



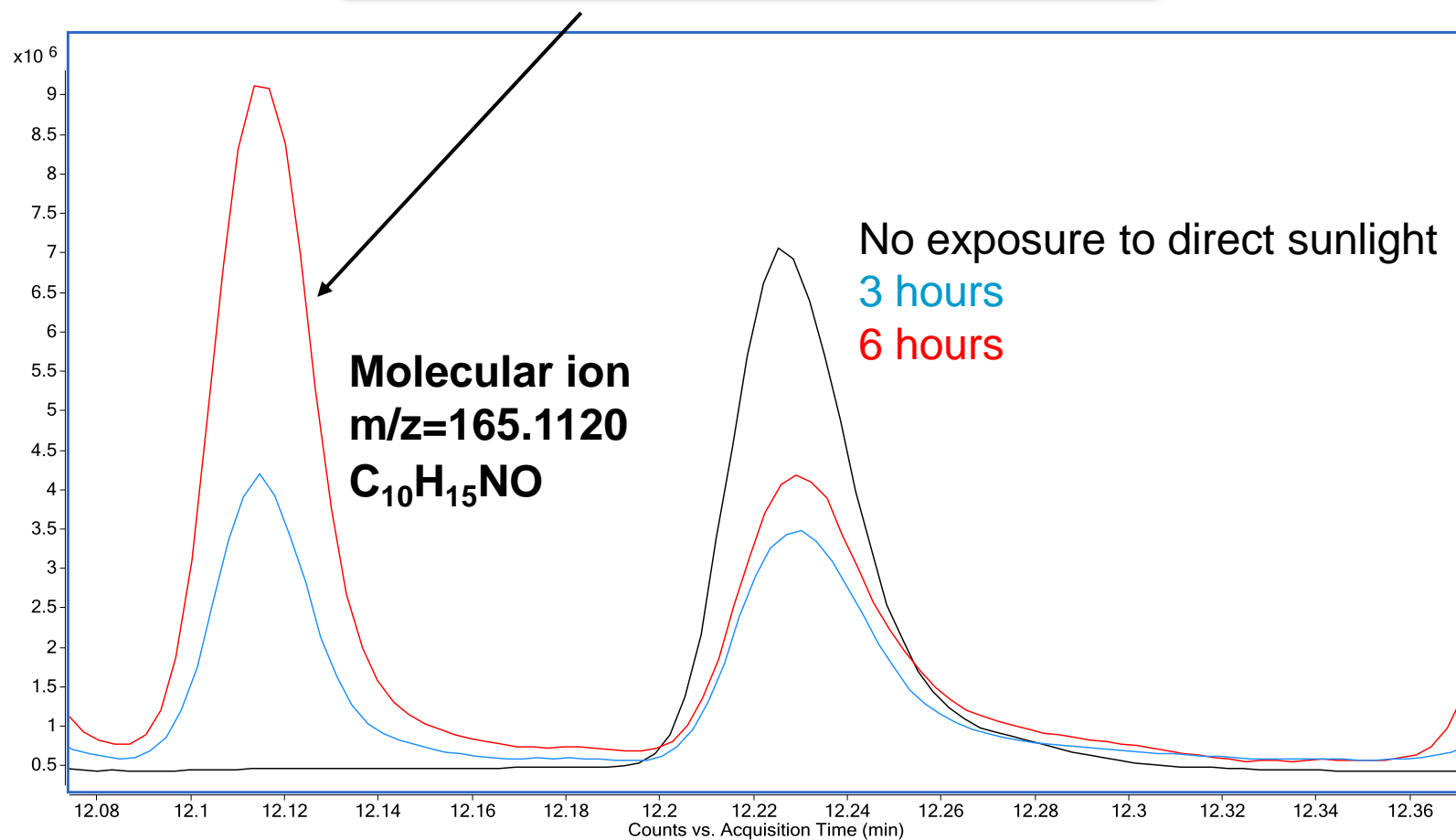
Photodegradation Products in Beer

Photodegradation Products in Beer

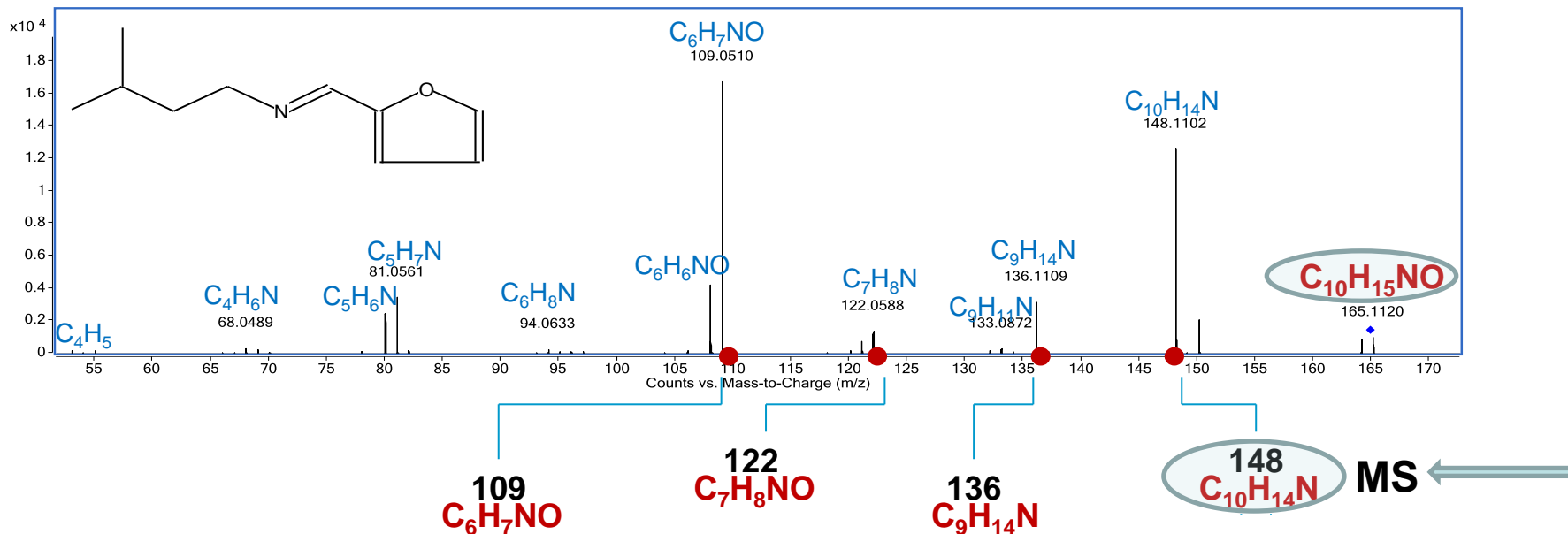
- Completely **untargeted** (initially) study of beer photodegradation
- Method highlights
 - 30 min extraction at 30 °C using manual SPME holder and conditioned 50/30 µm DVB/Carboxen/PDMS StableFlex SPME fiber (Supelco), no agitation
 - Desorption at 300 °C for 2 min in the SSL injector; 1:10 split
 - Agilent J&W column DB-5MS 30 m x 0.25 mm x 0.25 µm

Changes in the Chromatogram

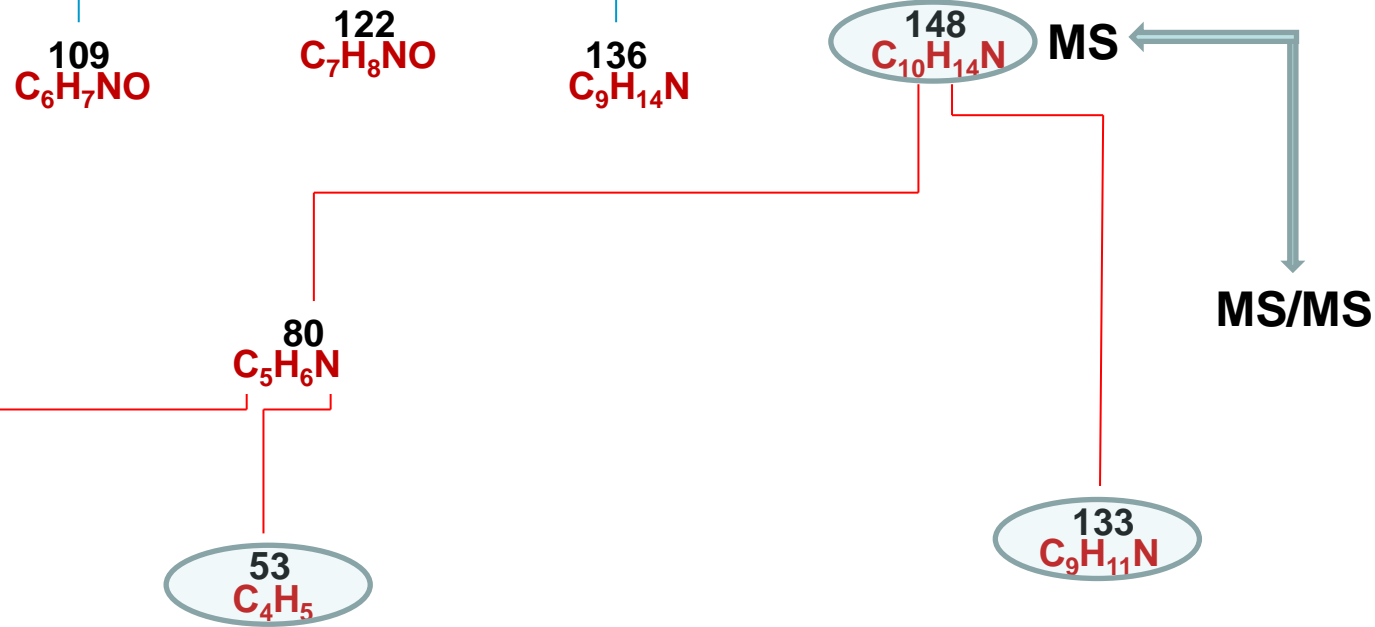
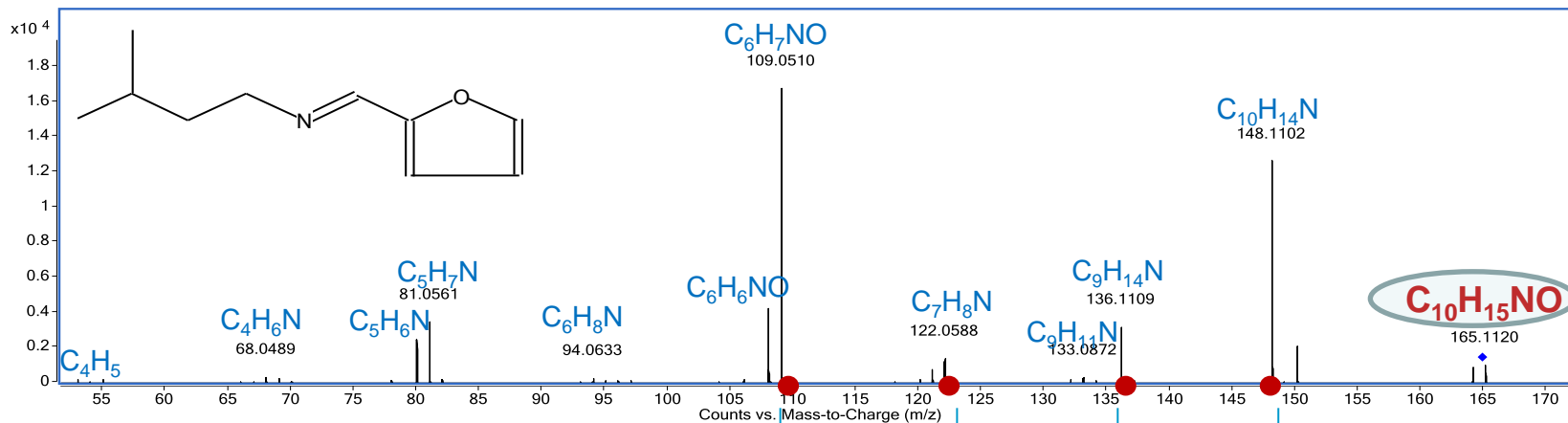
Appears following the exposure of the sample to direct sunlight. Peak height is dependent on the duration of exposure to the sun



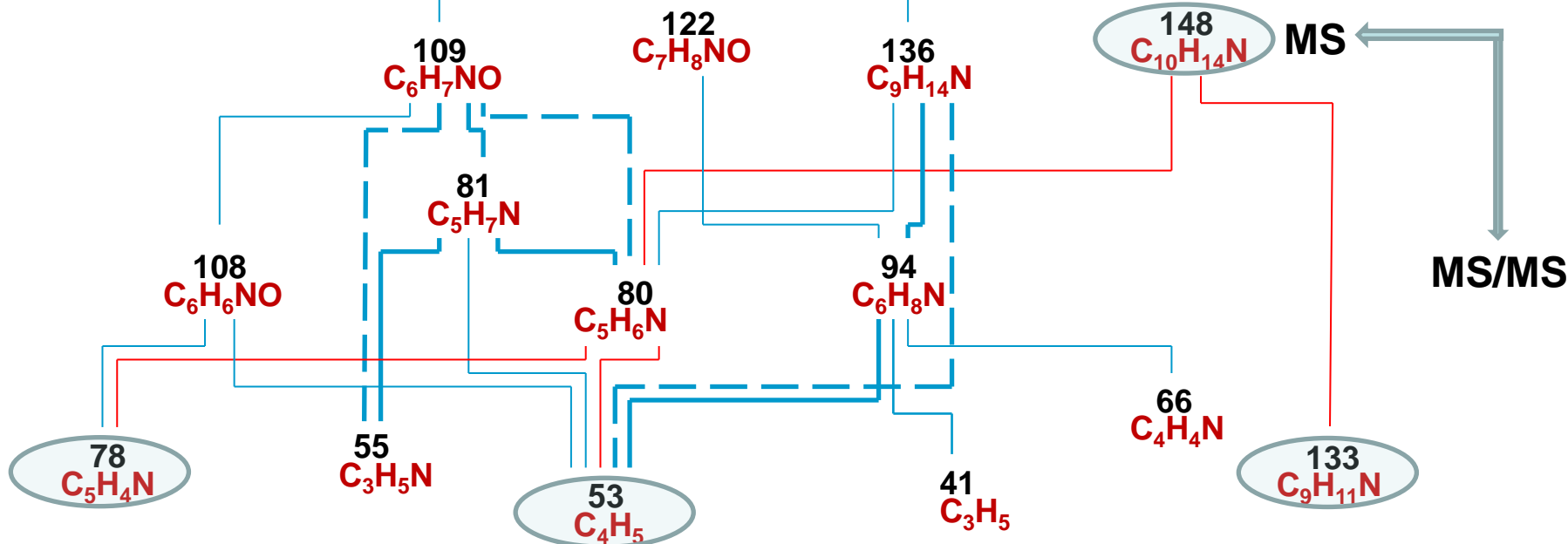
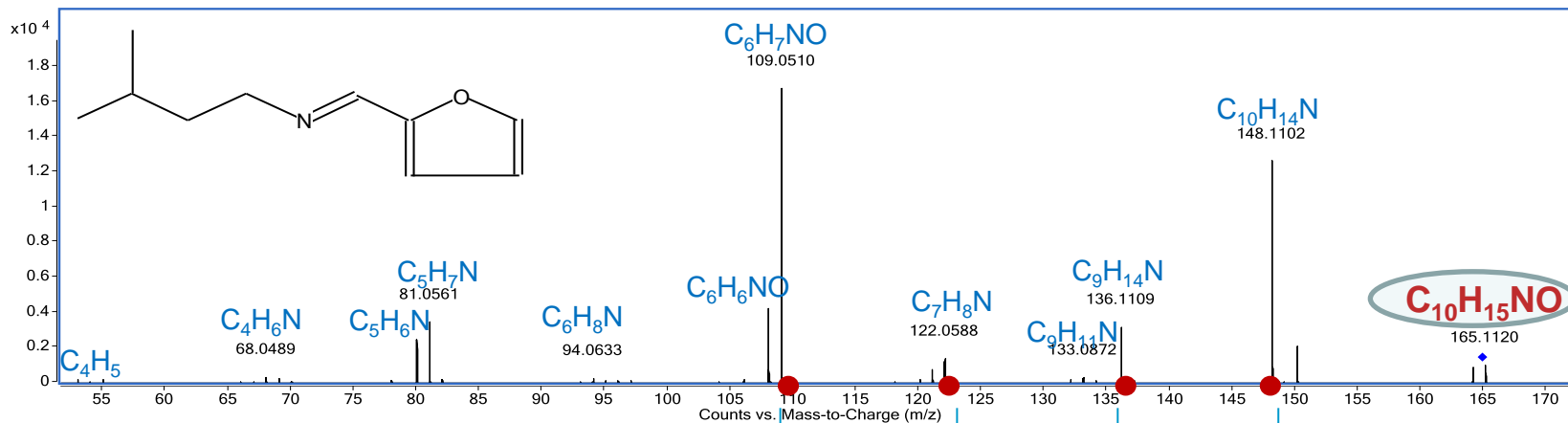
Summary of MS/MS Experiments



Summary of MS/MS Experiments



Summary of MS/MS Experiments



Metabolomics: Unknowns Analysis Tool to Identify Components of Bovine Plasma

Unknowns Analysis (MassHunter Quant)

Using deconvolution and spectral library matching to identify unknowns

The image displays three overlapping screenshots of the MassHunter Quant Method dialog box, illustrating the configuration for unknowns analysis. The first screenshot (left) shows the 'Deconvolution' tab with parameters such as Resolution (100), Peak filter (28), and Extraction window (Left m/z delta: 0.3, Right m/z delta: 0.7). The second screenshot (middle) shows the 'Library Search' tab, where the NIST library is selected (C:\Data\MassHunter\NIST08.L) and search criteria like 'Enable screening' and 'Adjust Score' are checked. The third screenshot (right) shows the 'Compound Identification' tab, with parameters like Max hit count (2), Min match factor (65), and Ratio percent uncertainty (40). A callout box on the right contains the following text:

- Using NIST library search
- Not using RT match (in this particular example)

Unknowns Analysis (MassHunter Quant)

Using deconvolution and spectral library matching to identify unknowns

Agilent MassHunter Unknowns Analysis - QC_mix1_HR_unkn_analysis4_Thresh001_MMF65_all2hits.uaf

File Edit View Analyze Method Report Tools Help

Analyze All All Target Non-Target **HR** Non-Hit Primary

Samples

Sample Name	File Name	Components	Hits	Target Ma
QC_mix1_HR_05	QC_mix1_HR_05.d		226	130

Components

Component RT	Is Primary Hit	Compound Name	Match Factor	CAS#	Formula
12.8071	<input checked="" type="checkbox"/>	Phosphoric acid, bis(trimethylsilyl) ...	81.3	55887-73-5	C11H31O5PSi3
13.1237	<input checked="" type="checkbox"/>	1,1,1-trimethyl-N-((2E)-1-methyl-3-(...	95.2	1000333-94-7	C13H31N3OSi3
13.8587	<input checked="" type="checkbox"/>	Hexagol	73.2	2075-73-8	C12H22O2
13.8944	<input checked="" type="checkbox"/>	Glutamic acid, trimethylsilyl ester	94.1	15985-07-6	C14H33NO4Si3
13.9705	<input checked="" type="checkbox"/>	Asparagine, N,N,N'-tris(trimethylsilyl)...	72.5	1000153-03-0	C16H40N2OSi3
14.4280	<input checked="" type="checkbox"/>	N-Acetyl aspartic TMS	77.0	1000141-41-9	C15H33NO5Si3
14.4599	<input checked="" type="checkbox"/>	L-Asparagine, N,N2-bis(trimethylsilyl)...	95.2	55649-62-2	C13H32N2OSi3
15.2475	<input checked="" type="checkbox"/>	1,4-Butanediamine, N,N,N',N'-tetra...	91.7	39772-63-9	C16H44N2Si4
15.5067	<input checked="" type="checkbox"/>	3,6,9,12-Tetraoxa-2,13-disilatetra...	80.5	62185-58-4	C12H30O4Si2
15.8731	<input checked="" type="checkbox"/>	Anthraquinone, 1-(p-fluorophenyl)-	65.5	20760-63-8	C20H11FO2
15.9863	<input checked="" type="checkbox"/>	1-Cyclohexene-1-carboxylic acid, ...	91.8	55520-78-0	C19H42O5Si4
16.0825	<input checked="" type="checkbox"/>	1,2,3-Propanetricarboxylic acid, 2-...	90.3	14330-97-3	C18H40O7Si4
16.4556	<input checked="" type="checkbox"/>	Tetradecanoic acid, trimethylsilyl ...	65.6	18603-17-3	C17H36O2Si
16.8772	<input checked="" type="checkbox"/>	Glucose oxime hexakis(trimethylsilyl)	76.6	120850-89-7	C24H61NO6Si6
17.0779	<input checked="" type="checkbox"/>	Galactose oxime hexakis(trimethylsilyl)	82.0	120850-89-6	C24H61NO6Si6
17.1725	<input checked="" type="checkbox"/>	L-Lysine, N2,N6,N6-tris(trimethylsilyl)...	80.2	55429-07-7	C18H46N2OSi4
18.1158	<input checked="" type="checkbox"/>	Trimethylsilyl ether of glycerol	68.2	6787-10-6	C12H32O3Si3
20.2171	<input checked="" type="checkbox"/>	Octadecanoic acid, trimethylsilyl e...	91.3	18748-91-9	C21H44O2Si
20.3897	<input checked="" type="checkbox"/>	Trimethylsilyl ether of glycerol	67.3	6787-10-6	C12H32O3Si3
20.7871	<input checked="" type="checkbox"/>	D-Mannose, 2,3,4,5-tetrakis-O-(tri...	88.9	55530-76-2	C25H64NO9PSi6
20.9522	<input checked="" type="checkbox"/>	D-Mannose, 2,3,4,5-tetrakis-O-(tri...	79.9	55530-76-2	C25H64NO9PSi6
21.7629	<input checked="" type="checkbox"/>	Octahydroxanthren-1,9-dione, 3,3-...	65.3	71827-88-8	C23H34O3
21.8763	<input checked="" type="checkbox"/>	Eicosanoic acid, trimethylsilyl ester	89.2	55530-70-6	C23H48O2Si
22.0018	<input checked="" type="checkbox"/>	1H-Indole-3-ethanamine, N,N,1-tri...	86.4	55429-74-8	C22H44N2OSi4
22.2105	<input checked="" type="checkbox"/>	Cadaverine, N,N,N',N'-tetrakis(trim...	72.1	65898-76-2	C17H46N2Si4
22.6204	<input checked="" type="checkbox"/>	Phthalic acid, octyl 2-pentyl ester	84.7	1000315-48-0	C21H32O4
22.7495	<input checked="" type="checkbox"/>	2-Thiobarbituric acid, S-trimethylsilyl...	69.0	1000352-46-9	C13H28N2OS...
23.3250	<input checked="" type="checkbox"/>	alpha-D-Glucopyranoside, 1,3,4-...	85.1	19159-25-2	C36H80N11Si8

Chromatogram

+ TIC Scan QC_mix1_HR_05.d

Spectrum

Component RT: 14.4599

L-Asparagine, N,N2-bis(trimethylsilyl), trimethylsilyl ester

Ion Peaks

Component RT: 14.4599

Molecular Structure

Asparagine

Bovine plasma Unknowns Analysis results (partial)

Component RT	Compound Name	CAS#	Formula	Match Factor
9.73	L-Isoleucine, N-(trimethylsilyl)-, trimethylsilyl ester	7483-92-3	C12H29NO2Si2	78.22
9.81	L-Proline, 1-(trimethylsilyl)-, trimethylsilyl ester	7364-47-8	C11H25NO2Si2	75.45
10.03	Butanedioic acid, bis(trimethylsilyl) ester	40309-57-7	C10H22O4Si2	81.68
10.11	2-Phenyl-1-(p-tolyl)benzimidazole	3510-25-6	C20H16N2	58.53
10.21	Methyl 8-methyl-decanoate	1000336-49-1	C12H24O2	61.59
10.43	Phosphoric acid, 2-isothiocyanatoethyl bis(trimethylsilyl) ester	56051-85-5	C9H22NO4PSSi2	51.03
10.63	Serine tritms	64625-17-8	C12H31NO3Si3	85.27
10.68	Nonanoic acid, trimethylsilyl ester	82326-11-2	C12H26O2Si	88.03
10.85	Glycine, N-formyl-N-(trimethylsilyl)-, trimethylsilyl ester	55517-31-2	C9H21NO3Si2	50.55
10.96	N,O,O-Tris(trimethylsilyl)-L-threonine	2--2-7537	C13H33NO3Si3	78.77
11.15	Dodecyl trifluoroacetate	1000351-74-5	C14H25F3O2	64.8
11.29	Decanedioic acid, bis(tert-butyldimethylsilyl) ester	104255-98-3	C22H46O4Si2	71.42
11.48	Glyoxime, bis(trimethylsilyl)-	54731-39-4	C8H20N2O2Si2	51.54
11.7	2,4(1H,3H)-Pyrimidinedione, dihydro-1,3-bis(trimethylsilyl)-	74810-47-2	C10H22N2O2Si2	63.24
11.91	2-Piperidone, 1-(trimethylsilyl)-3-[(trimethylsilyl)amino]-	32565-12-1	C11H26N2OSi2	51.39
11.95	Decanoic acid, trimethylsilyl ester	55494-15-0	C13H28O2Si	73.52
12.05	Cycloheptasiloxane, tetradecamethyl-	107-50-6	C14H42O7Si7	54.25
12.19	(Z,Z)-3-Methyl-3H-cyclonona(def)biphenylene	110823-80-8	C18H14	51.04
12.29	Butanedioic acid, [(trimethylsilyl)oxy]-, bis(trimethylsilyl) ester	38166-11-9	C13H30O5Si3	68.14
12.33	Pyrazine, 3,6-dihydro-3,6-dimethyl-2,5-bis(trimethylsilyloxy)-	1000156-30-2	C12H26N2O2Si2	50.63
12.49	3,6,9,12-Tetraoxa-2,13-disilatetradecane, 2,2,13,13-tetramethyl-	62185-58-4	C12H30O4Si2	68.69
12.59	2-Hydroxymandelic acid, ethyl ester, di-TMS	1000071-88-8	C16H28O4Si2	53.02
12.72	L-Proline, 5-oxo-1-(trimethylsilyl)-, trimethylsilyl ester	30274-77-2	C11H23NO3Si2	70.45

What about TOF *SPEED*?

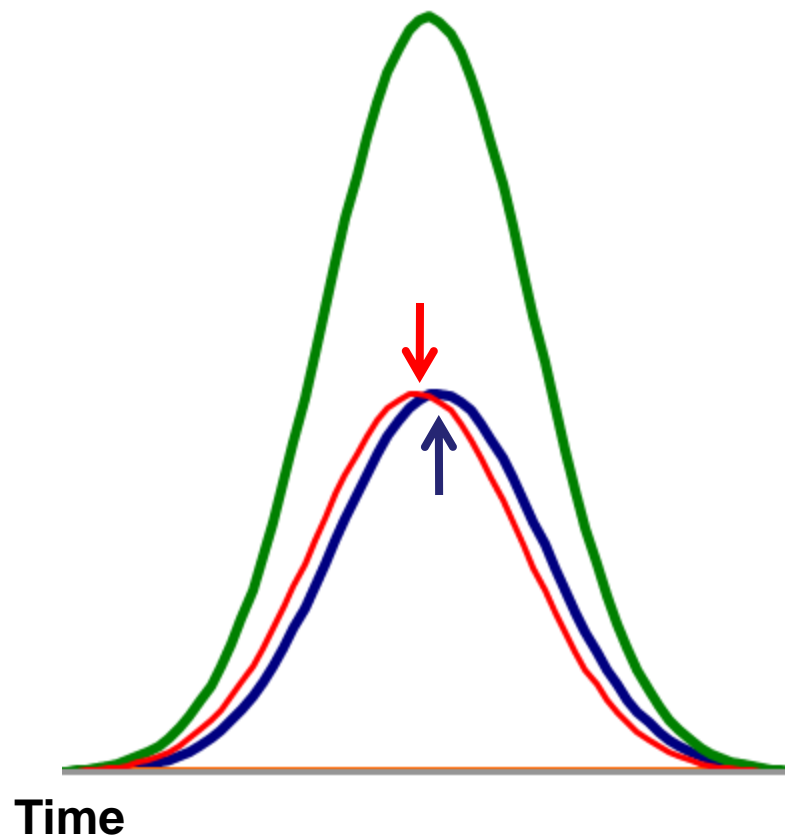
TOF always collects full mass range
Q-TOF always display full product ion spectrum

- **Acquisition Rate:** transients (pulses) /second
 - 10,000 transients/second
- Sum of transients = **Spectral Rate:**
 - Typical max rate: 25-200 spectra/sec (**Hz**) to disk
 - Usable rate is limited by signal level (ion count)
- New analysis opportunities for GC/MS:
 - High Throughput: ~20 Hz
 - Ultra high resolution GC: ~ 40Hz
 - GCxGC: ~50-200 Hz

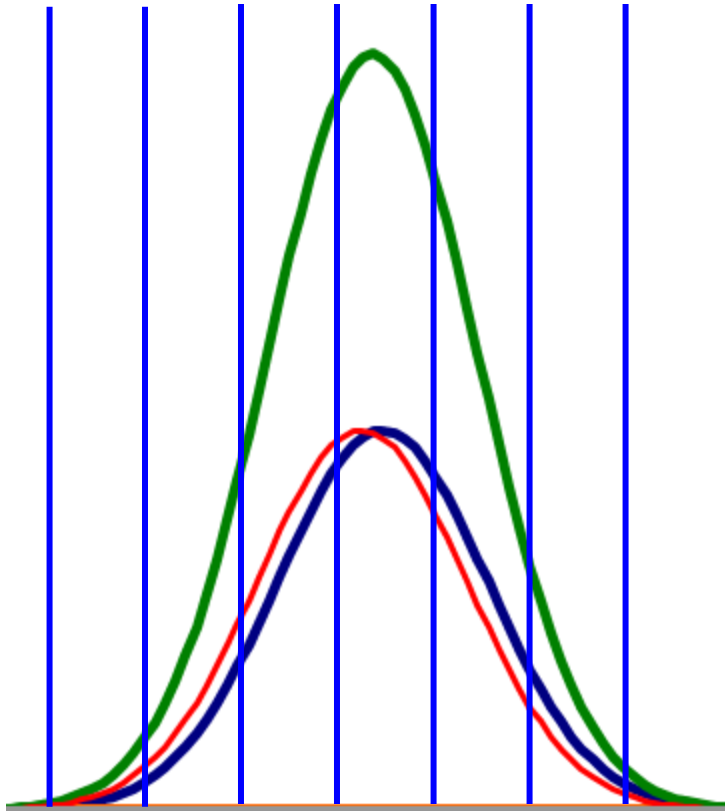


“Speed” enhances deconvolution

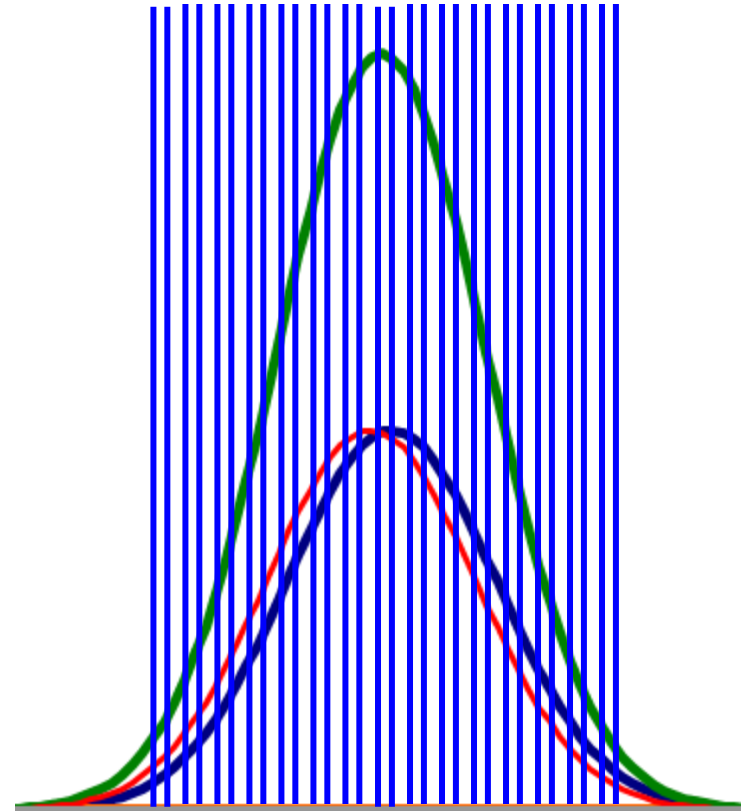
Deconvolution Requires Time Offset



High data rate = better deconvolution

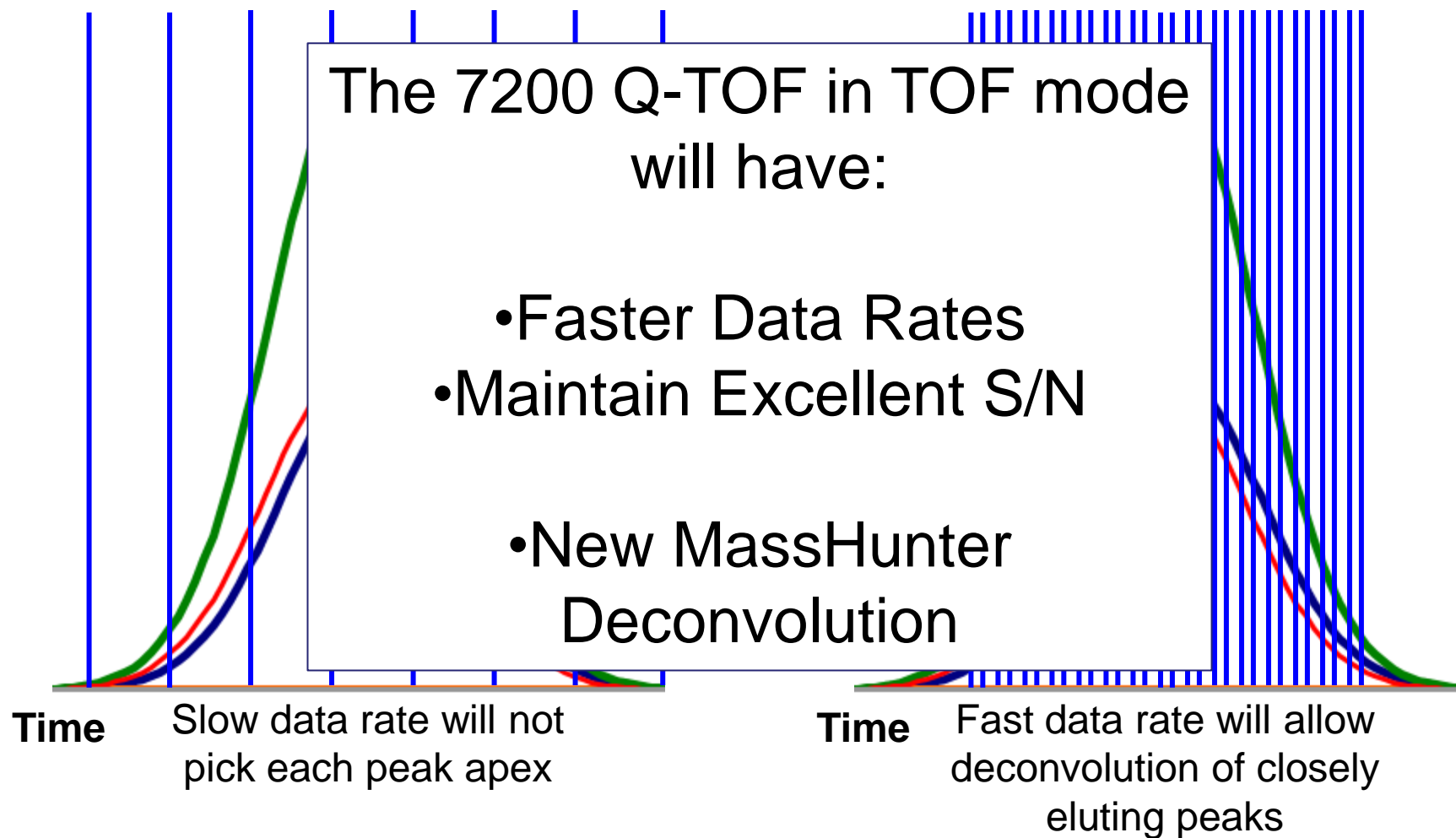


Time Slow data rate will not pick each peak apex



Time Fast data rate will allow deconvolution of closely eluting peaks

High data rate = better deconvolution



And What about Q-TOF File Size?

- Typical file sizes for pesticide analysis
 - MSD SIM – 0.8-1 MB/18-min run
 - MSD scan – 3-5 MB/40-min run
 - TQ MRM – 5 MB/20-min run
 - TQ scan – 8 MB/20-min run
 - IT MS/MS – 2.5 MB/45-min run (99 compounds)
- **TOF or Q-TOF Typical run**
 - **800-1200 MB/20-min run at 5 Hz, profile**
 - **Centroid only reduces 5-10X**

Note: File size depends on the threshold, number of target compounds, number of masses/compound, and runtime etc.

- Can accurate mass measurements be made in a real matrix?
- What are the limitations?

Successful Applications Require the Correct Combination of:

GC Resolution (**Agilent**)

+

MS Resolving Power (**Agilent**)

+

Δ Mass Defect (**Mother Nature**)

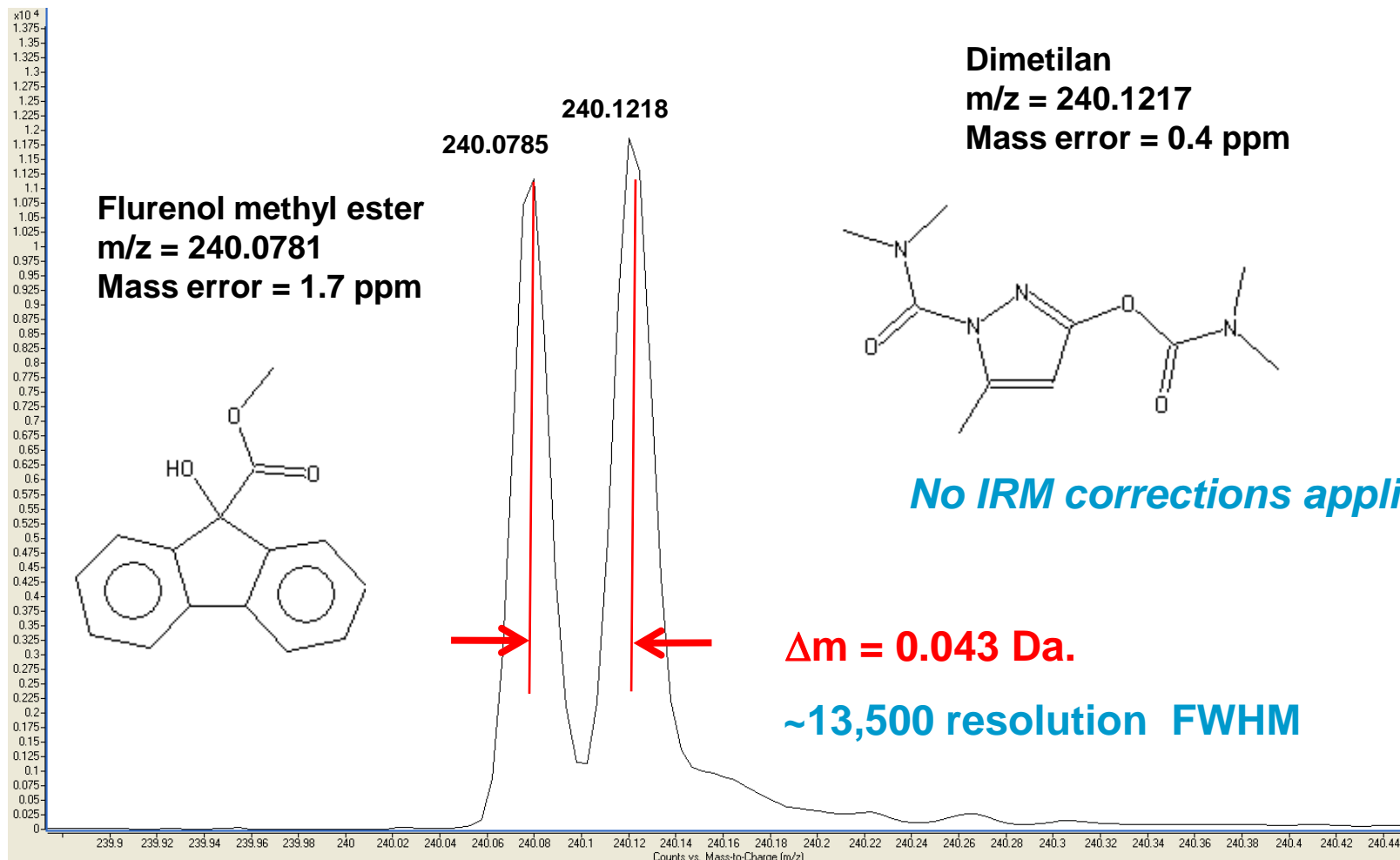
+

Relative Ion Intensities (**Sample**)

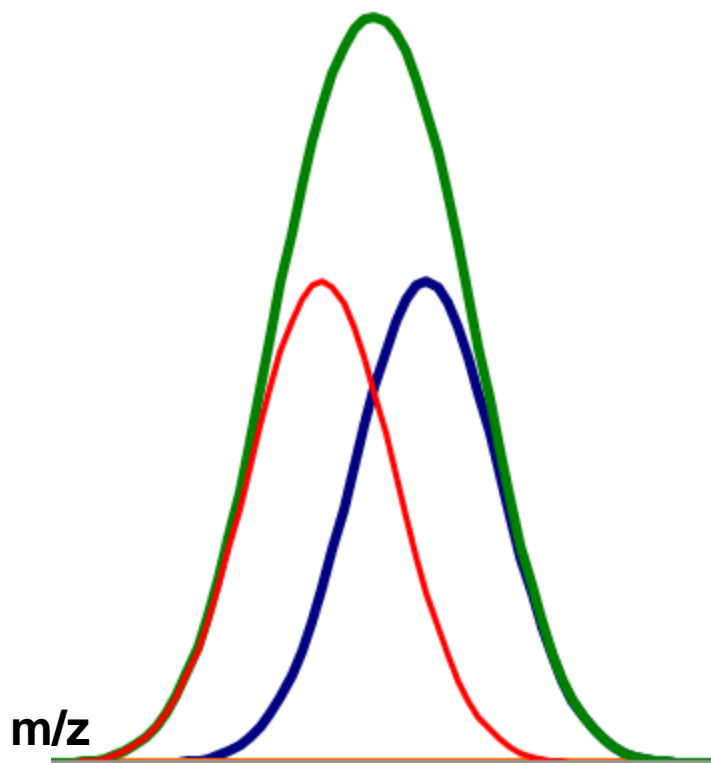
We may have a little to learn about these new apps.

How much "R" and "Defect" is enough?

Intensity Ratio = 1:1



Intensity affects the rResult



Two mass peaks with FWHM
0.7 u with 0.5 u between
centroided m/z value

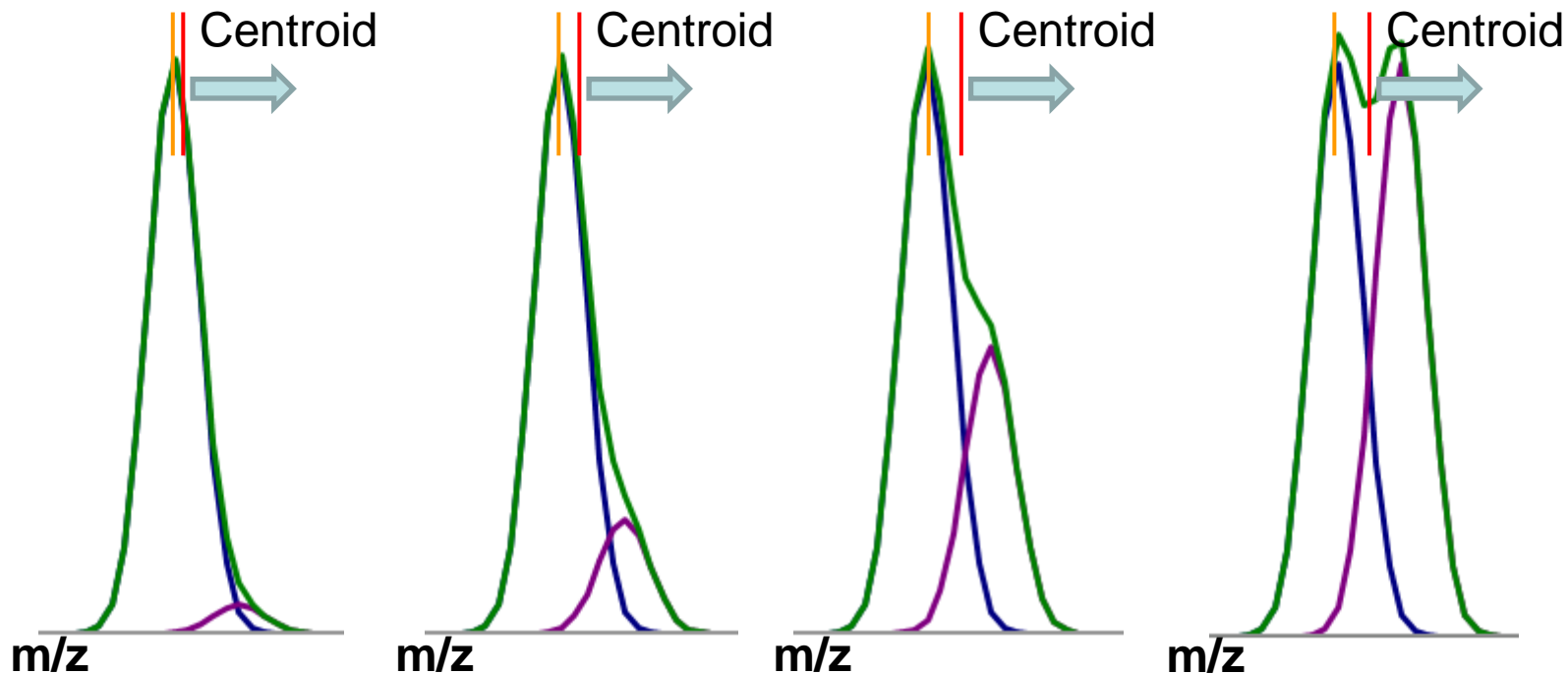


Two mass peaks with FWHM
0.05 u with 0.5 u between
centroided m/z value

GC or MS:

Relative intensity affects the result

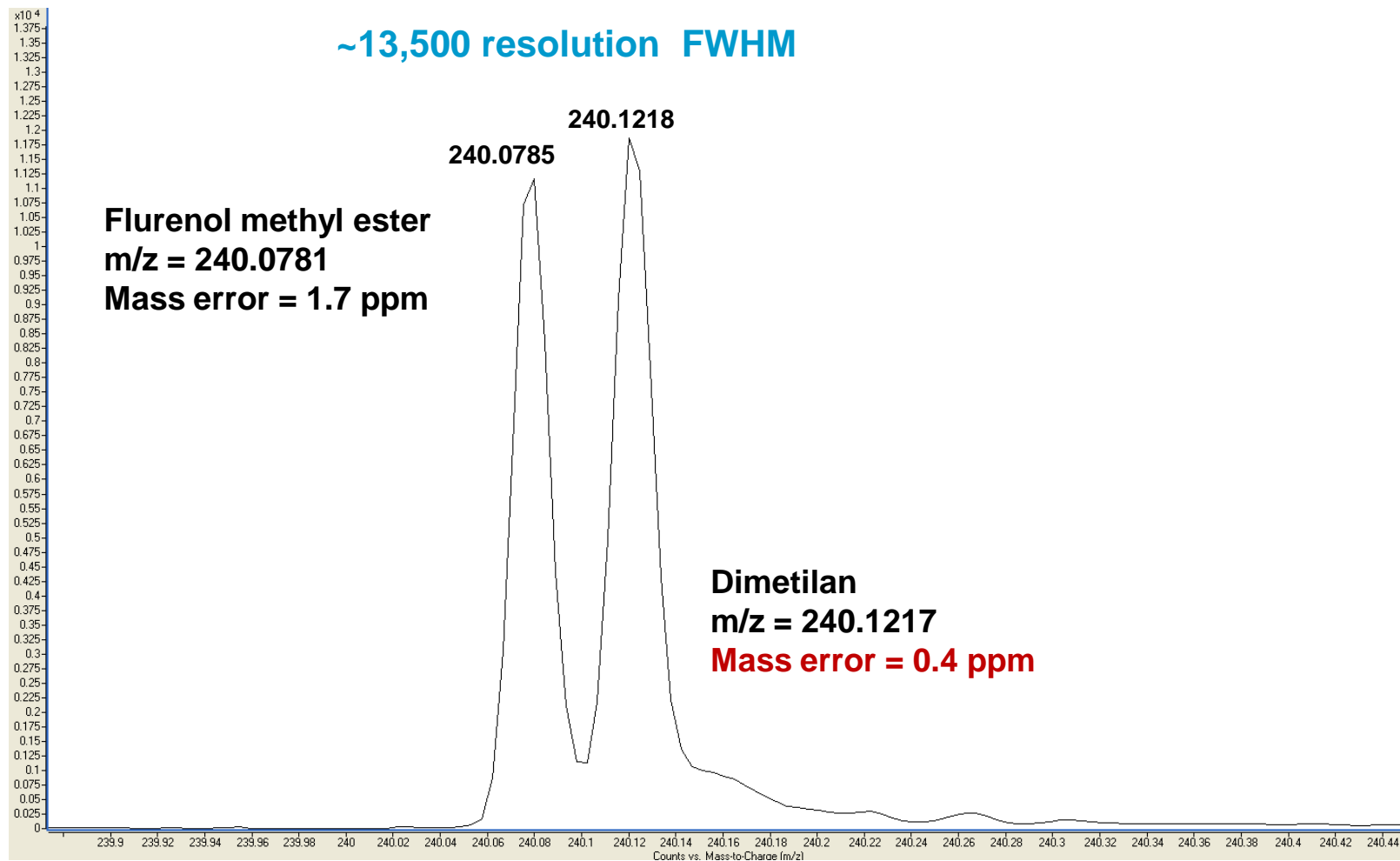
Profile view of mass peaks



Centroid view of mass peaks obscures this fact

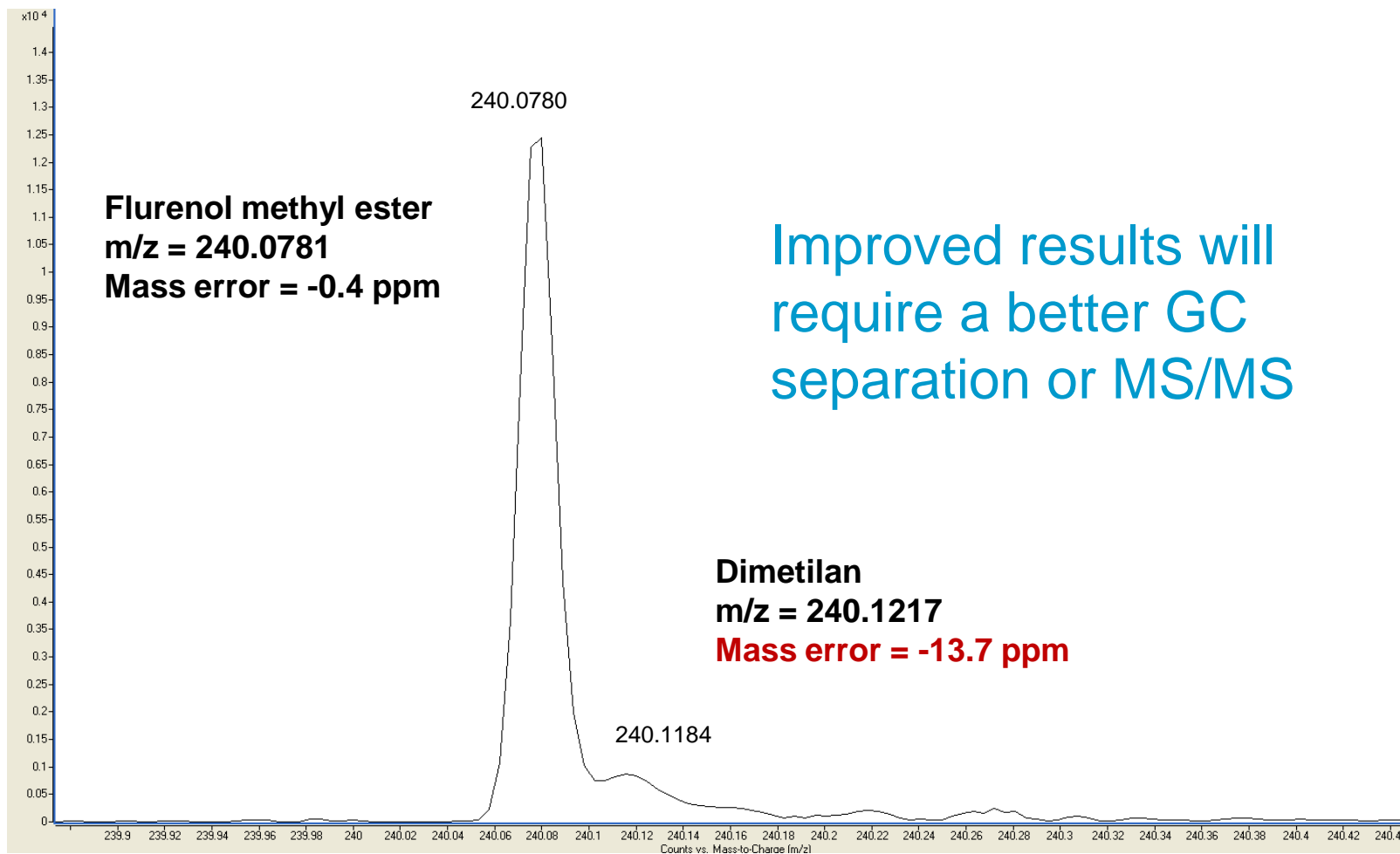
How much “R” and “Defect” is enough?

Intensity Ratio = 1:1



How much “R” and “Defect” is enough?

Intensity Ratio = 1:0.02



Improved results will require a better GC separation or MS/MS

Future Webinars: Balancing Performance Criteria

- Resolving Power: >10K at m/z 272 (>13K typical)
- Mass Accuracy: <5 ppm at m/z 272 (<2ppm typical)
- MS Sensitivity: 1 pg OFN S/N > 400:1
- Dynamic Range: > 3 orders of magnitude
- Quad Mass range: 20-1050 Da (0.7-4.0 Da FWHM)
- TOF Mass range: 20-1700 Da
- Spectral Rate: 1-50 spectra/sec

All specifications subject to change

Key Features of the 7200

1. Internal Reference Mass for routine sub 5ppm mass accuracy even in heavy matrix
2. Removable Ion Source
(including filaments)
3. Q-TOF MS/MS:
 - Chemical noise reduction
 - Selectivity
 - Structural information
 - Method development
4. Removable Ion Source for quick source cleaning and EI/CI swapping without breaking vacuum
5. Software tools – formula calculator



5975E SQ



5975C SQ



5975T LTM SQ

Agilent GC/MS & GC/MS/MS More Choices – Better Solutions



220 IT



240 IT



7000 TQ



7200 Q-TOF 