High Speed Analysis: Combining Fast GC with Time-of-Flight Mass Spectrometry for Complex Sample Analysis in Under One Minute

Jonelle Shiel, Matthew Soyk, Viatcheslav Artaev | LECO Corporation, Saint Joseph, MI USA
Alexander B. Fialkov | School of Chemistry, Tel Aviv University; Aviv Amirav | School of Chemistry, Tel Aviv University and Aviv Analytical

Introduction

The demand for more efficiency and productivity in the laboratory has led to applications using Fast GC-MS methods for routine analysis in a wide range of fields. Many of these applications can involve complex mixtures with some components at trace levels. The fast analysis time requires some unique capabilities, including a GC with fast column heating and cooling for high throughput, a mass spectrometer with high data acquisition speed, and a fast response ion source in order to correctly characterize narrow peaks generated by Fast GC. To make sense of the resulting compressed data, the software needs the capabilities of automatic peak finding and deconvolution of coeluting peaks to perform correct and meaningful identifications and quantitation. The performance of an instrument capable of combining Fast GC and TOFMS is illustrated in this poster.

To demonstrate capabilities, a separation of the entire Mega Mixture (69 of 76 components), can be completed in under one minute using Fast GC and a pre-production prototype benchtop TOFMS, which, with the FAST option, increases the scan speed maximum from 50 to 100 spectra/second. In addition, a sample containing Synthetic Drug Standards was also separated in under one minute. Forensic laboratories typically experience large workloads with little resources, therefore, fast turnaround times for analyses are valuable for this application. The total analysis time, including time between runs, is about 2.5 minutes for these examples.

Instrument Set-Up

- The Fast GC is easily mounted onto a standard GC detector port. The column used is standard. A piece is cut to a much shorter length than typical GC Columns (3 m). It is installed in the typical fashion in the GC inlet, and then fed into the low thermal mass heating tube of the Fast GC.
- The column comes out of the Fast GC, passes again through the GC oven region, and into the transfer line between the GC and the time-of-flight mass spectrometer. The metal tube in the Fast GC is resistively heated by electrical current to obtain the fast heating rates (typically 200-600 °C/min).
- The GC has a pressure program for the inlet, and the oven is held at a constant temperature similar to the transfer line. The Fast GC parameters are controlled with a separate electronics box and stand-alone software.
- The instrument is pictured in Figure 1.

Figure 1. Instrument Configuration: Agilent 7890GC with the Aviv Analytical Fast GC mounted onto the detector port, and the Pegasus® BT GC-TOFMS pre-production prototype with increased maximum scan speed from 50 to 100 spectra/second.

Methods Mega Mixture

- Sample: Mega Mixture (Restek#31850) diluted to 50,000 pg/µl with a 100:1 split resulting in 500 pg on column.

Gas Chromatograph	Agilent 7890
Injection	1µL, Split 100:1, 340 °C
Carrier Gas	He, Ramped Pressure:10 psi (0 min), 24 psi/min to 34 psi (0 min)
Temperature	Isothermal 330 °C
Fast GC	**Aviv Analytical**
Column	Rxi-5SilMS 3 m x 0.15 mm ID x 0.15 µm
Temperature	50 °C to 350 °C in 50 seconds, hold at 350 °C for 10 seconds
Mass Spectrometer	**LECO Pegasus BT Prototype with Increased Scan Speed**
Transferline Temperature	330 °C
Ion Source Temperature	300 °C
Spectra Acquisition Rate	80 spectra/second
Mass Range	30 to 650 m/z

Results Mega Mixture

Figure 2 displays the Analytical Ion Chromatogram for the analysis of the Mega Mixture. 69 of 76 components of the Mega Mixture were separated and identified using a Fast GC Method in under one minute.

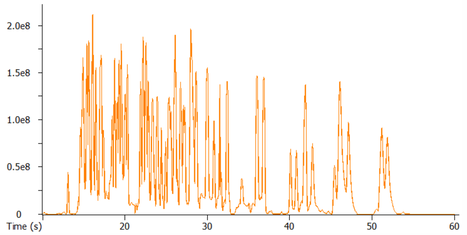

Figure 2. Analytical Ion Chromatogram of the Mega Mixture at 500 pg on column separated in under one minute.

Some compounds in the chromatogram were coeluting. The Pegasus BT ChromaTOF® brand software with NonTarget Deconvolution® and peak finding capabilities can mathematically separate the spectra of overlapping compounds for peak identification. Figure 3 is an example of coelutions occurring in a one second window with peaks identified using deconvolution and automatic peak finding. The inset shows a zoomed-in window of a Restek chromatogram of the same peaks separated on a standard 30 m column. This shows that the peaks are not well separated, even using a longer column and standard conditions.

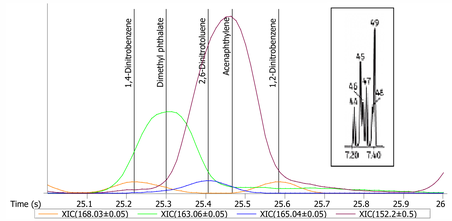

Figure 3. One second zoomed-in window from 25 to 26 seconds. Automatic peak finding utilizing deconvolution found 5 peaks in this area. Deconvoluted peak widths are approximately 150 to 200 ms. Inset is a zoomed-in window of Restek chromatogram of the same peaks 45-49 separated on a standard 30 m column.

Figures 4 through 6 show the automated mass spectral deconvolution for the five components of the Mega Mixture identified in the one second window displayed in Figure 3.

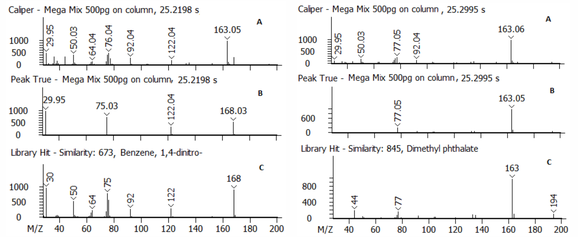

Figure 4. Shown in succession is the (A) Caliper (Raw Mass Spectrum), (B) Peak True (Deconvoluted Mass Spectrum), and (C) Library Hit for the first two peaks found in Figure 3: 1,4-Dinitrobenzene and Dimethyl phthalate.

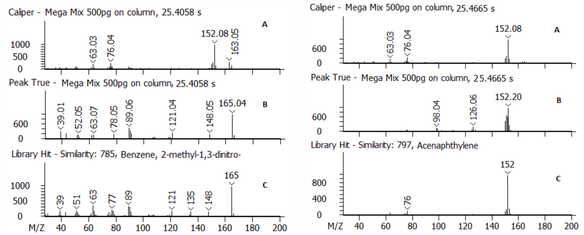

Figure 5. Shown in succession is the (A) Caliper (Raw Mass Spectrum), (B) Peak True (Deconvoluted Mass Spectrum), and (C) Library Hit for the third and fourth peaks found in Figure 3: 2,6-Dinitrotoluene and Acenaphthylene.

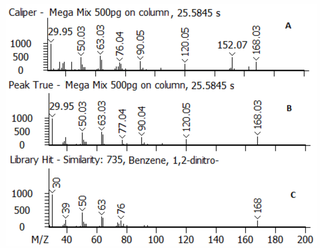

Figure 6. Shown in succession is the (A) Caliper (Raw Mass Spectrum), (B) Peak True (Deconvoluted Mass Spectrum), and (C) Library Hit for the fifth peak found in Figure 3: 1,2-Dinitrobenzene.

Methods Synthetic Drug Sample

Sample: Synthetic Drug sample—Standards were purchased separately from Cayman Chemical Company and prepared into a mixture of 70 pg/µL.

Gas Chromatograph	Agilent 7890
Injection	1µL, Split 5:1, 300 °C
Carrier Gas	He, Ramped Pressure:10 psi (0 min), 24 psi/min to 34 psi (0 min)
Temperature	Isothermal 300 °C
Fast GC	**Aviv Analytical**
Column	Rxi-5SilMS 3 m x 0.15 mm ID x 0.15 µm
Temperature	50 °C to 350 °C in 50 seconds, hold at 350 °C for 10 seconds
Mass Spectrometer	**LECO Pegasus BT Prototype with Increased Scan Speed**
Transferline Temperature	300 °C
Ion Source Temperature	250 °C
Spectra Acquisition Rate	80 spectra/second
Mass Range	30-645 m/z

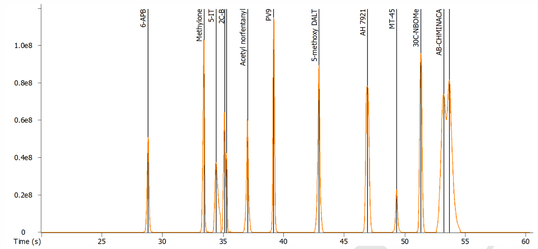

Figure 7. Analytical Ion Chromatogram of a Synthetic Drug sample at 14 pg on column separated in under one minute.

Table 1. Peak Table of 13 components found in a Synthetic Drug sample separated in under one minute.

Name	Formula	R.T. (s)	Similarity	Quant S/N	FWHH (s)	Area	Height
6-APB	$C_{11}H_{13}NO$	28.8161	837	8110	0.148	485009446	20707482
Methylone	$C_{11}H_{13}NO_3$	33.4190	868	9190	0.130	592853609	28422556
5-IT	$C_{11}H_{14}N_2$	34.4217	871	2609	0.281	190016178	10789581
N,N-DMT	$C_{12}H_{16}N_2$	35.1210	674	9531	0.140	694897469	28820159
2C-B	$C_{10}H_{14}BrNO_2$	35.2829	629	2428	0.108	151516588	10549259
Acetyl norfentanyl	$C_{13}H_{18}N_2O$	37.0178	778	6637	0.143	534533003	13356634
PV9	$C_{18}H_{27}NO$	39.1890	835	30831	0.135	982733911	42380372
5-methoxy DALT	$C_{17}H_{22}N_2O$	42.9146	822	18008	0.148	1342907679	34950505
AH 7921	$C_{16}H_{22}Cl_2N_2O$	46.9071	862	11569	0.298	1317484921	35012967
MT-45	$C_{24}H_{32}N_2$	49.3268	730	12879	0.137	1256718279	29844047
30C-NBOMe	$C_{20}H_{26}ClNO_3$	51.3289	866	12191	0.202	3309153317	45207033
AB-CHMINACA	$C_{20}H_{28}N_4O_2$	53.1988	817	14346	0.468	1172999250	19794288
AM2201 benzimidazole analog	$C_{23}H_{21}FN_2O$	53.6880	829	10742	0.432	844937430	16638780

Conclusion

- Data was shown that a separation of the Mega Mixture (69 of 76 components) can be completed in under one minute using Fast GC and a pre-production prototype benchtop TOFMS. Total run time about 2.5 minutes.
- Since the peak widths in this rapid separation are narrower than typical chromatographic peaks (100-200 ms), a high acquisition speed (80 s/s) was used in order to get necessary number of mass spectral points across the peak for appropriate deconvolution and quantitation.
- With such a large number of peaks eluting in a short time there are multiple coelutions. Examples of coelutions where automatic peak find and the *NonTarget Deconvolution* algorithm allowed peak identification were demonstrated.
- Additionally an application was shown of a Synthetic Drug sample being separated in under one minute. This is an example of an application that benefits from fast turnaround time of about 2.5 minutes allowed by this instrument configuration.

LECO®
Delivering the Right Results