Quantitative and Qualitative Confirmation of Pesticides in Beet Extract Using a Hybrid Quadrupole-Orbitrap Mass Spectrometer

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Application Note 617

Key Words
Q Exactive Focus, Orbitrap, pesticides, high resolution, accurate mass, quantitation, target screening, unknown screening, retrospective data analysis

Goal

To describe a method for the analysis of pesticides, showing the utility of a full-scan data-dependent MS/MS workflow to achieve regulatory levels while providing a complete targeted and screening analysis using a high-resolution, accurate mass (HRAM) spectral library for identification and confirmation.

Introduction

As world agricultural trade has expanded and concerns over food safety have grown, the enforcement of stricter pesticide regulations has become of utmost importance. In 2006, Japan introduced the Positive List System that established maximum residue levels (MRLs) for hundreds of agricultural chemicals in food, including approximately 400 pesticides, and set a uniform limit of 10 µg/kg (ppb) for chemicals for which MRLs have not been determined.[1] In 2008, the European Parliament implemented Regulation (EC) No. 396/2005, which harmonized all pesticide MRLs for European Union (EU) member states and set default limits of 10 µg/kg for all pesticide/commodity combinations for which no MRLs have been set.[2] A pesticide safety review of about 1,000 active substances on the market was mandated by EU Directive 91/414/EEC and, upon its completion in 2009, led to the approval of only about 250 substances and effectively set the permissible levels of over 700 de-listed pesticides to the default limit.[3] The EU and Japanese regulations are among the most stringent in the world and have fueled the need for faster and more sensitive analytical methods for cost-efficient, high-throughput screening and quantitation of multi-class pesticide residues.

Here, a method utilizing the Thermo Scientific™ Q Exactive™ Focus hybrid quadrupole-Orbitrap™ mass spectrometer is described. It consists of a generic chromatographic method and a full-scan data-dependent MS/MS (FS-ddMS^2) mass spectrometric method with library searching and fragment confirmation. The FS-ddMS^2 approach was used to generate calibration curves and analyze samples for targeted known compounds. In the typical acquisition setup demonstrated here, a simple full-scan data-dependent MS/MS experiment was associated with new preset confirmation settings for easier and faster method development (Figures 1 and 2).

For evaluation of the method, spiked matrix samples were analyzed by high-resolution, accurate-mass LC-MS/MS.

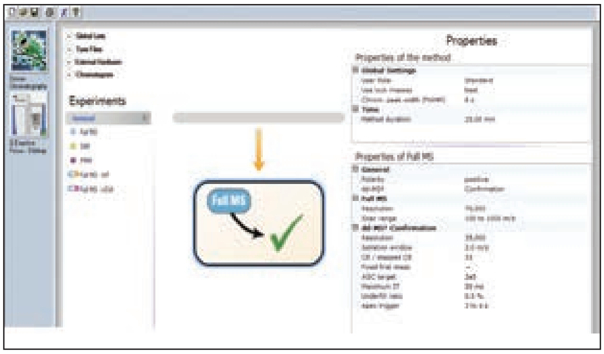


Figure 1. Instrument Setup page, showing full-scan data-dependent MS/MS.

Always whats next.

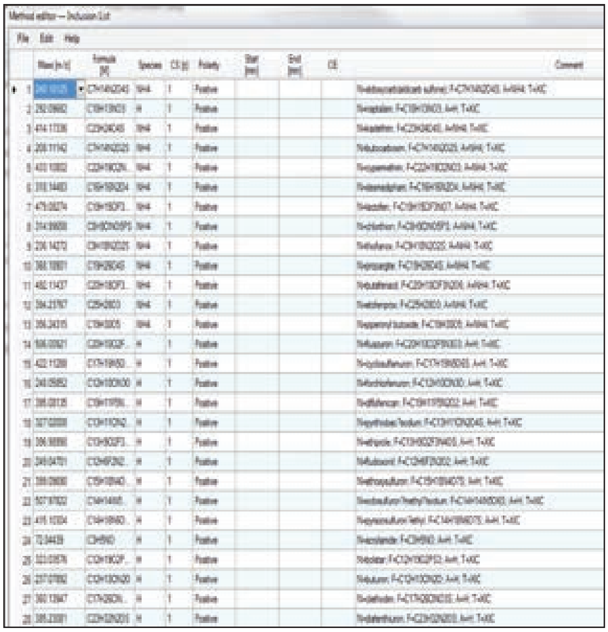


Figure 2. An example of an inclusion list that was added for targeted confirmation of known pesticides in the sample.

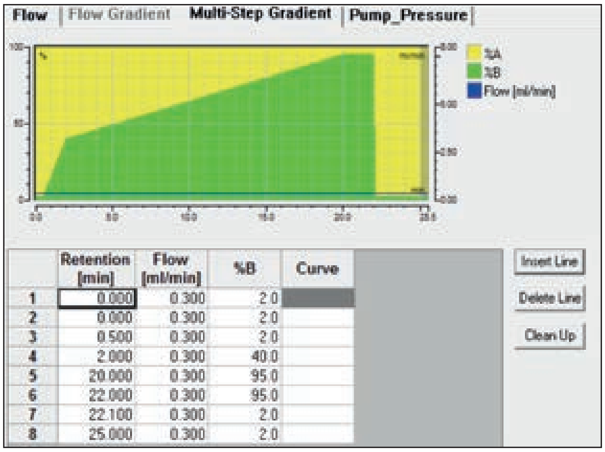
Sample Preparation

Beet samples, provided by the California Department of Food and Agriculture, were extracted using a modified QuEChERS method. Pesticide stock standards (ULTRA Scientific, N. Kingston, RI) were spiked into the QuEChERS extract. Then, the appropriate amount of acetonitrile was added to adjust the organic composition of the final standard solution to 50:25:25 water/matrix/acetonitrile. The concentration of the standards ranged from 0.05 to 200 µg/kg.

Liquid Chromatography Method

A generic LC method was used for all samples:

Instrumentation	Thermo Scientific™ Dionex™ UltiMate™ 3000 LC system, consisting of: · Pump: HPG-3200RS · Autosampler: WPS3000TRS · Column Warmer: TCC3000RS · Degasser: SRD3400
Column	Thermo Scientific™ Accucore™ aQ 100 x 2.1 mm, 2.6 µm particle size (p/n 17326-102130)
Column temperature	30 °C
Mobile phase A	0.1% formic acid, 5 mM ammonium formate in water
Mobile phase B	0.1% formic acid, 5 mM ammonium formate in methanol
Gradient	Refer to Figure 3
Sample injection	10 µL
Instrument run time	25 min



	Retention [min]	Flow [ml/min]	%B	Curve
1	0.000	0.300	2.0	
2	0.000	0.300	2.0	
3	0.500	0.300	2.0	
4	2.000	0.300	40.0	
5	20.000	0.300	95.0	
6	22.000	0.300	95.0	
7	22.100	0.300	2.0	
8	25.000	0.300	2.0	

Figure 3. Flow gradient.

Mass Spectrometry Method

A generic FS-ddMS^2 method on a Q Exactive Focus MS system was used for all samples as described below:

Full Scan	
Resolution setting	70,000 (FWHM) at m/z 200
Mass range	100–1000 m/z
ddMS^2	
Resolution setting	35,000 (FWHM) at m/z 200
Isolation windows	2.0 m/z
Spray voltage	3500 V
Sheath gas	35 arb
Aux gas	10 arb
Sweep gas	1 arb
Capillary temperature	325 °C
Heater temperature	350 °C
RF-lens level	50
HCD collision energy	33 eV

Data Processing

Data processing was performed using Thermo Scientific™ TraceFinder™ software version 3.2. For generation of extracted ion chromatograms, an extraction window of 5 ppm was used. For targeted screening, a built-in compound database (>1500 compounds), consisting of compound name, precursor and fragment m/z values, and retention time, was used together with a spectral library (>7500 spectra) for confirmation of targeted residues.

Results and Discussion

Data analysis was performed within TraceFinder software with the help of green, yellow, and red flags that can quickly be sorted for review. Figure 4 demonstrates the capability of the flagging feature within TraceFinder software, which can identify issues with compounds and help the analyst make quick decisions if the sample contains that compound.

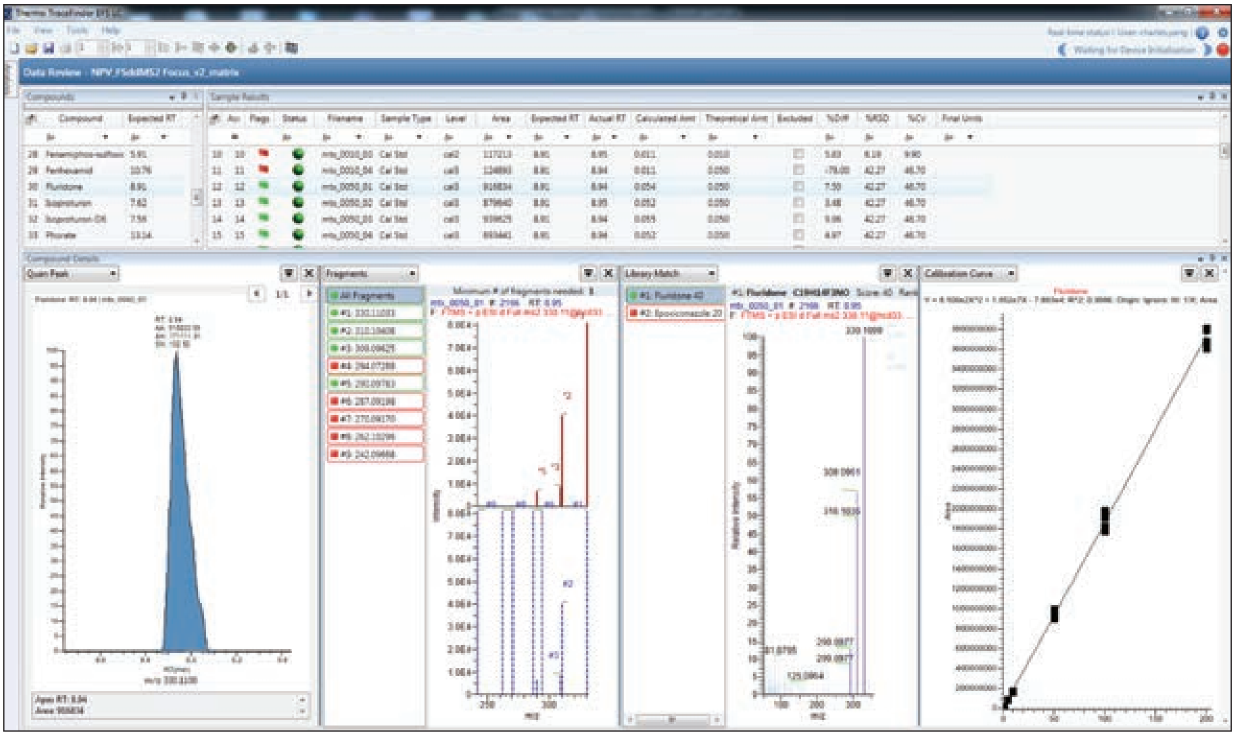


Figure 4. Flagging feature, showing that one fluridone sample has a green flag while the other sample has a red flag. A green flag indicates that all of the parameters were met and there was no issue with the calibration curve. A red flag indicates that there was a problem with the sample from the library search, fragment ion confirmation, or the calculated amount was out of range. The flagging details describe the issues with the sample.

Figure 5 demonstrates the compound details in the Quan Peak, Fragment Matching, Spectra Matching, and Calibration Curve views of TraceFinder software, which can assist the analyst in quickly looking through the data set for confirmation.

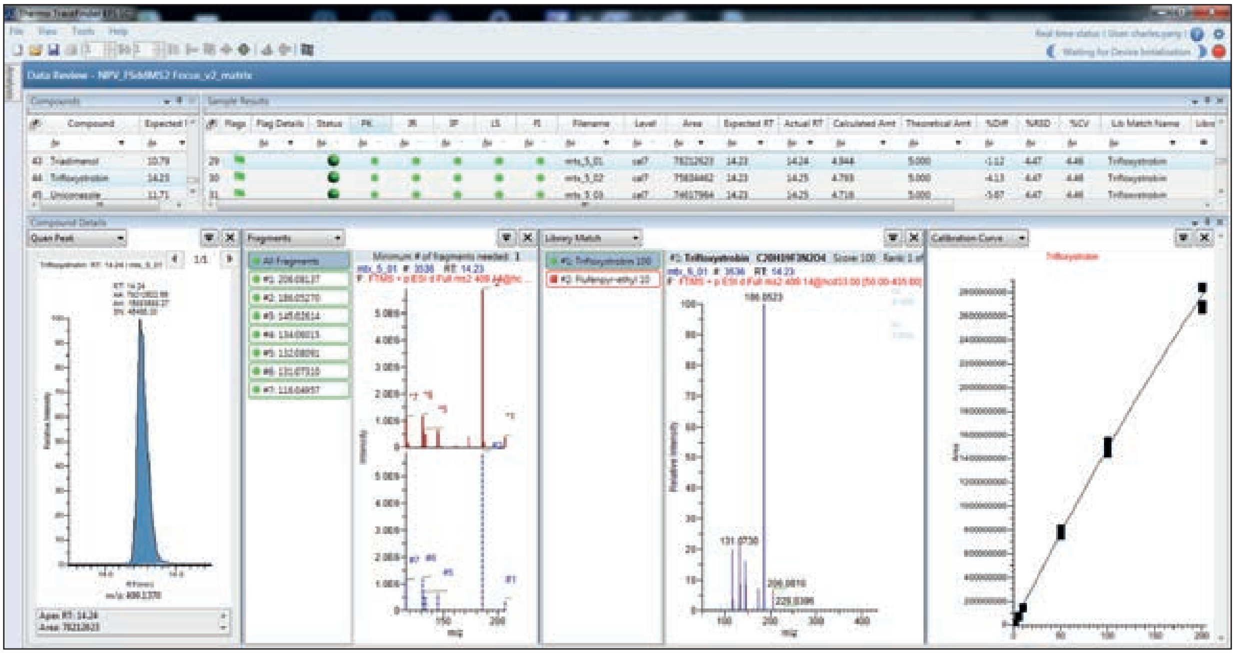


Figure 5. Tryfloxystrobin at 5 ppb, showing compound details in lower portion to highlight quick data review.

The detection results of the pesticides analyzed in the beet matrix are shown in Table 1. Detection limits varied depending on the compound. The determination of the limit of quantitation (LOQ) was based on the presence of a minimum of one fragment ion as well as reproducibility at each level as stated by the EU SANCO regulations.[4] Table 1 also shows the %RSD of n=4 at each level and available EU regulation limits for listed pesticides.[4] All RSDs were found to be well below the guidelines which require RSDs of less than 15% in order to be accepted as the LOQ.

All compounds showed good calibration curves with R^2 better than 0.99 as shown in Table 2.

Table 1. LOD/LOQ based on fragment confirmation and %RSD values compared to available EU regulation limits for pesticides.

Compound	LOD (µg/kg)	%RSD	LOQ (µg/kg)	%RSD	EU Regulation Limits (µg/kg)
Allethrin	0.91	6.25	5.13	3.27	
Atrazine	0.10	6.09	0.58	10.34	50
Azoxystrobin	0.10	3.99	0.55	11.77	15,000
Bendiocarb	0.73	6.88	0.73	6.88	
Benoxacor	0.09	6.99	0.53	8.99	
Bioresmethrin	0.77	4.44	5.24	4.98	
Boscalid	0.10	4.37	0.55	12.19	30,000
Bupirimate	0.10	3.83	0.10	3.83	50
Cadusafos	0.44	11.63	0.88	6.11	10
Carbendazim	0.53	12.39	1.04	5.58	100
Chloropyrifos	0.44	11.79	0.91	5.41	50
Coumaphos	0.10	6.00	0.60	13.19	
Cyazofamid	0.44	11.26	0.86	4.66	10
Cyproconazole	0.44	11.98	0.90	5.65	50
DEF	0.09	5.67	0.59	8.80	
Dimethenamid	0.10	2.23	0.57	11.82	10
DMST	0.09	3.46	0.58	10.71	
Fenamiphos-sulfone	0.09	5.97	0.57	12.16	20
Fluoridone	0.09	5.00	0.53	12.34	
Isoproturon	0.10	7.37	0.63	12.76	10
Phorate	0.91	5.23	4.92	2.46	10
Propetamphos	0.73	7.66	4.92	3.19	
Rotenone	0.05	42.34	0.10	4.72	10
Sulprofos	0.45	9.10	0.86	2.88	
Spirodiclofen	0.44	9.98	0.86	5.59	20
Thiobencarb	0.47	8.55	0.91	3.61	10
Triadimenol	5.12	2.93	5.12	2.93	100
Trifloxystrobin	0.10	2.91	0.10	2.91	20
Uniconcazole	0.45	13.48	0.87	4.54	

Table 2. R^2 results of 29 pesticides in beet matrix.

Compound	R^2
Allethrin	0.9989
Atrazine	0.9988
Azoxystrobin	0.9983
Bendiocarb	0.992
Benoxacor	0.9987
Bioresmethrin	0.9989
Boscalid	0.9988
Bupirimate	0.9984
Carbendazim	0.9982
Chlorpyrifos	0.9987
Coumaphos	0.9989
Cyazofamid	0.9985
Cyproconazole	0.9987
DEF	0.9988
Dimethenamid	0.9987
DMST	0.9989
Fenamiphos-sulfone	0.9988
Fluridone	0.9986
Isoproturon	0.9985
Phorate	0.9984
Propetamphos	0.9985
Rotenone	0.9986
Spirodiclofen	0.9983
Sulprofos	0.9989
Thiobencarb	0.9989
Thiodicarb	0.9986
Triadimenol	0.9977
Trifloxystrobin	0.9987
Uniconazole	0.9988

Figure 6 shows the capability of the Q Exactive Focus MS to scan quickly with polarity switching at 10 ppb. Due to the many pesticides that were spiked into the matrix, it was necessary to include internal standards to check and correct for shifts in retention times, as shown in Figures 7, 8, and 9.

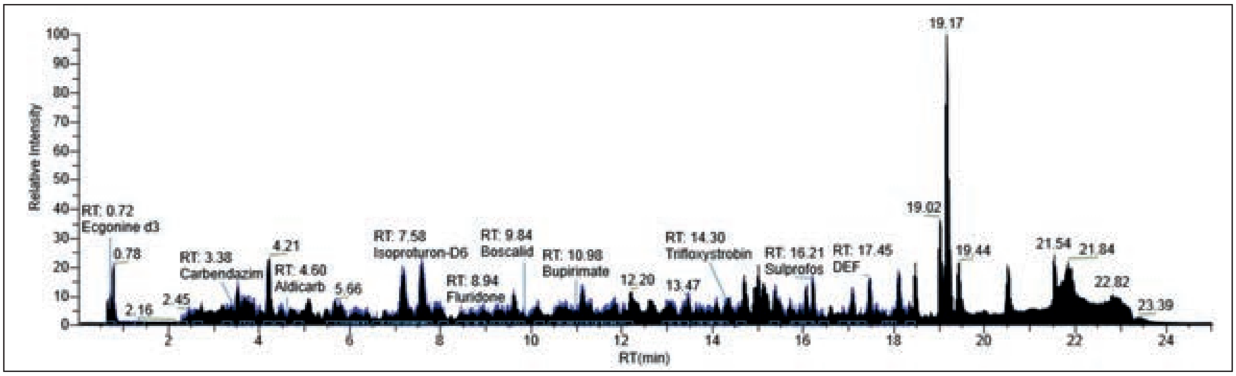


Figure 6. Total ion current (TIC) chromatogram of spiked pesticides in beets at 10 ppb.

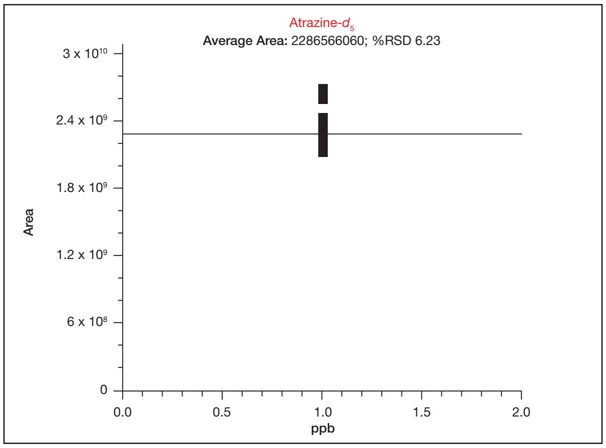


Figure 7. Atrazine-d_5, %RSD = 6.23 (beet matrix).

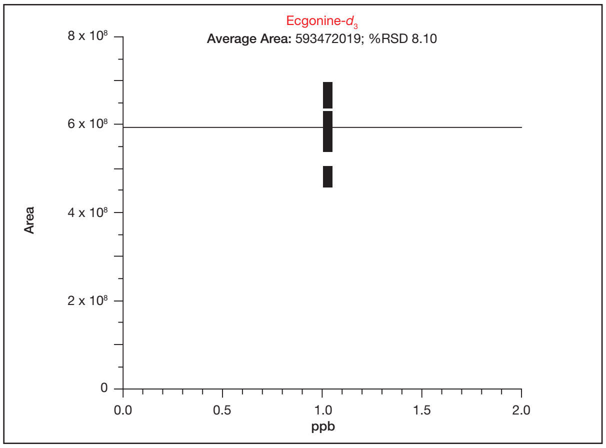


Figure 8. Ecgonine-d_3, – early eluter, %RSD = 8.10 (beet matrix).

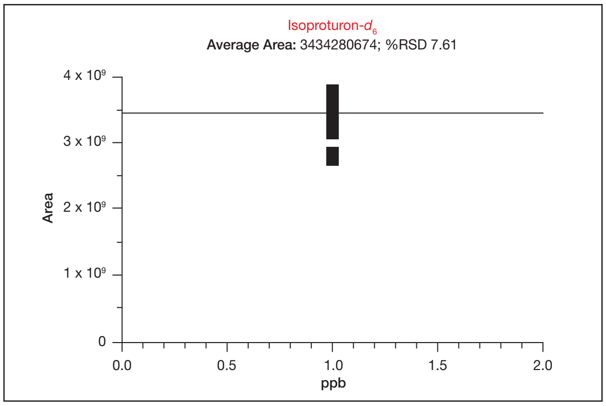
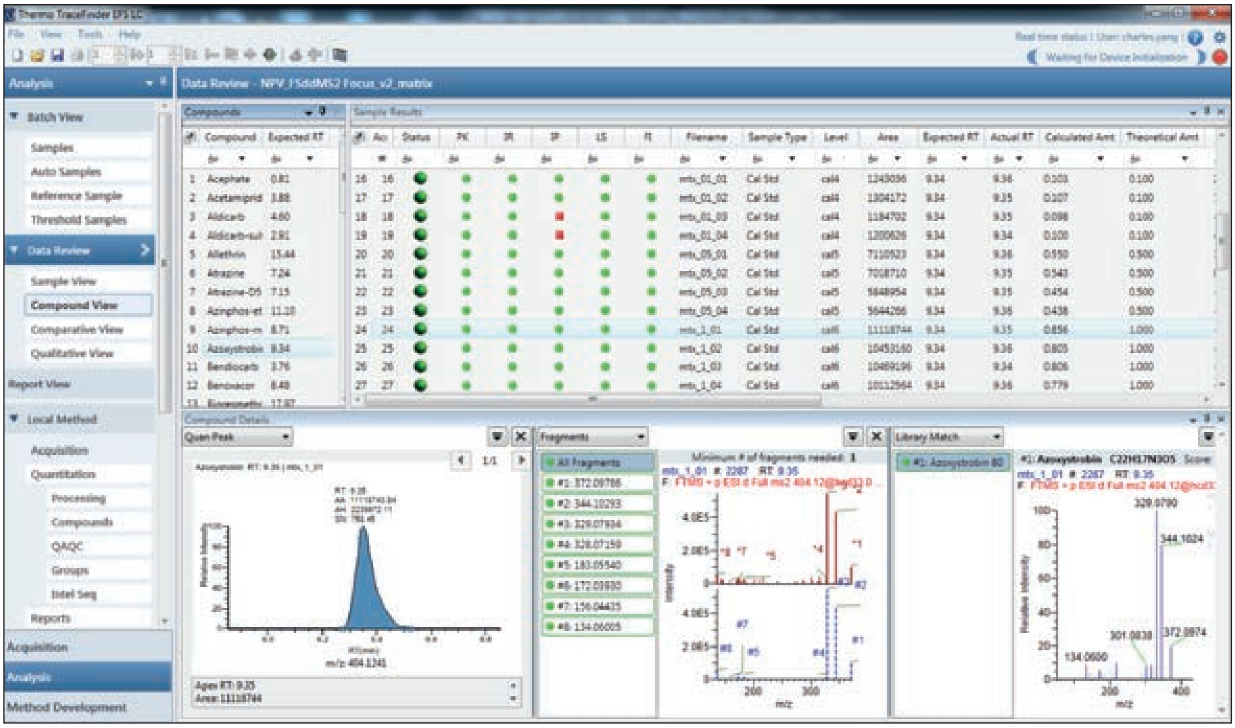


Figure 9. Isoproturon-d_6, %RSD = 7.61 (beet matrix).

Increasingly, more and more compounds are being analyzed in a single run, which can cause issues with co-elutors. A new HRAM MS/MS spectral library and compound database has been generated that is fully integrated and searchable using TraceFinder software to identify compounds with high levels of confidence. The spectral library includes more than five individual, high-resolution spectra for every compound it contains. Each compound was analyzed at multiple collision energies. Figures 10–13 showcase the matching significance of having an extensive spectral library with more than five individual spectra per compound.



Data Review - NPV_FSddMS2 Focus_v2_matrix

#	Compound	Expected RT
1	Acephate	0.81
2	Acetamiprid	3.88
3	Aldicarb	4.60
4	Aldicarb-sul	2.91
5	Allethrin	15.44
6	Atrazine	7.24
7	Atrazine-D5	7.15
8	Azinphos-et	11.10
9	Azinphos-m	8.71
10	Azoxystrobi	9.34
11	Bendiocarb	3.76
12	Benoxacor	8.48
13	Bioresmethr	17.97

#	Acc	Status	PK	IR	IP	LS	FI	Filename	Sample Type	Level	Area	Expected RT	Actual RT	Calculated Amt	Theoretical Amt
16	16	●	●	●	●	●	●	mtx_01_01	Cal Std	cal4	1249096	9.34	9.36	0.103	0.100
17	17	●	●	●	●	●	●	mtx_01_02	Cal Std	cal4	1304172	9.34	9.35	0.107	0.100
18	18	●	●	●	■	●	●	mtx_01_03	Cal Std	cal4	1184702	9.34	9.35	0.098	0.100
19	19	●	●	●	■	●	●	mtx_01_04	Cal Std	cal4	1200626	9.34	9.34	0.100	0.100
20	20	●	●	●	●	●	●	mtx_05_01	Cal Std	cal5	7110523	9.34	9.36	0.550	0.500
21	21	●	●	●	●	●	●	mtx_05_02	Cal Std	cal5	7018710	9.34	9.35	0.543	0.500
22	22	●	●	●	●	●	●	mtx_05_03	Cal Std	cal5	5848954	9.34	9.35	0.454	0.500
23	23	●	●	●	●	●	●	mtx_05_04	Cal Std	cal5	5644266	9.34	9.36	0.438	0.500
24	24	●	●	●	●	●	●	mtx_1_01	Cal Std	cal6	11118744	9.34	9.35	0.856	1.000
25	25	●	●	●	●	●	●	mtx_1_02	Cal Std	cal6	10453160	9.34	9.36	0.805	1.000
26	26	●	●	●	●	●	●	mtx_1_03	Cal Std	cal6	10469196	9.34	9.34	0.806	1.000
27	27	●	●	●	●	●	●	mtx_1_04	Cal Std	cal6	10112564	9.34	9.36	0.779	1.000

Azoxystrobin RT: 9.35 | mtx_1_01

RT: 9.35
AA: 11118743.84
AH: 2239872.11
SN: 781.48

m/z: 404.1241

Apex RT: 9.35
Area: 11118744

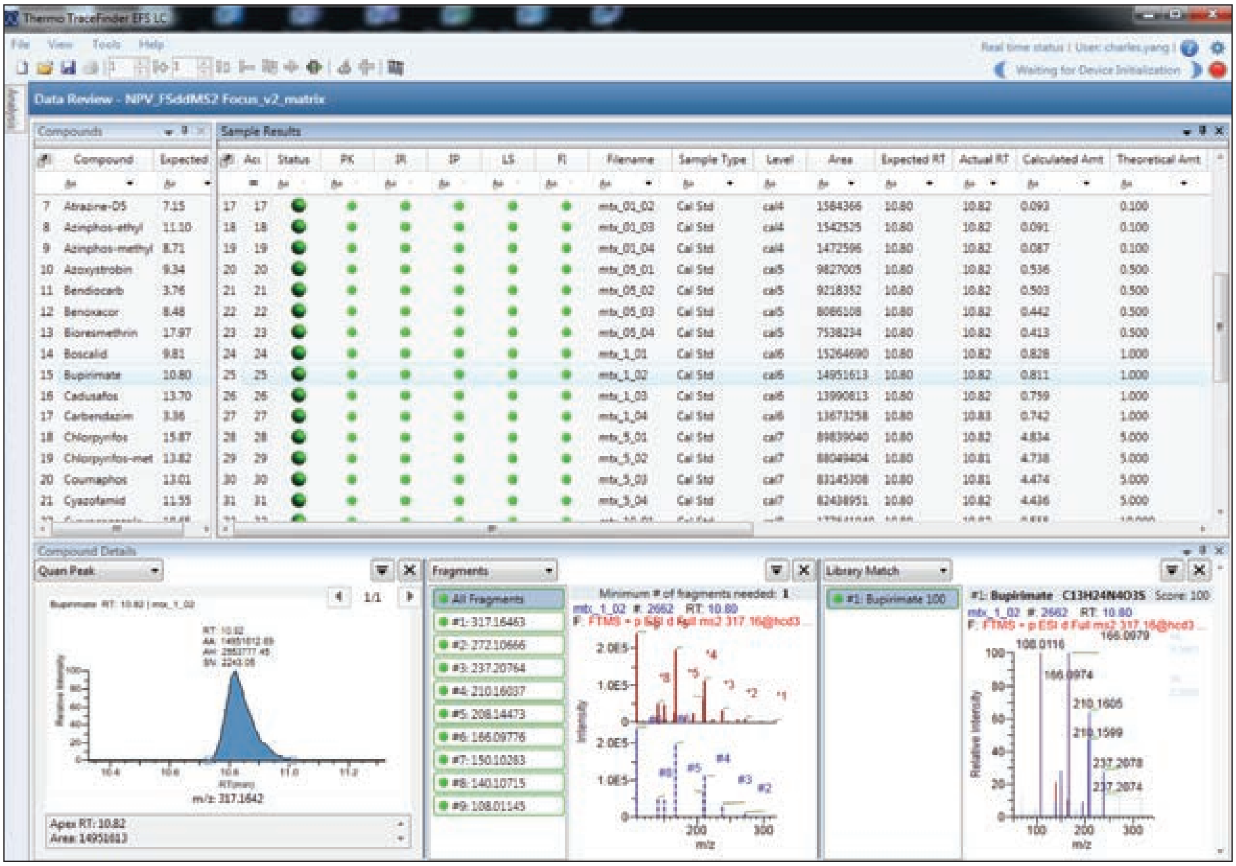
All Fragments
#1: 372.09786
#2: 344.10293
#3: 329.07934
#4: 328.07159
#5: 180.05540
#6: 172.03930
#7: 156.04425
#8: 134.06005

Minimum # of fragments needed: 1
mtx_1_01 # 2287 RT 9.36
F: FTMS + p ESI d Full ms2 404.12@hcd30.0 ...

#1: Azoxystrobin 80

#1: Azoxystrobin C22H17N3O5 Score
mtx_1_01 # 2287 RT 9.36
F: FTMS + p ESI d Full ms2 404.12@hcd3...

Figure 10. Azoxystrobin library match confirmation with fragmentation confirmation at 1 ppb, showing a library match score of 80% confidence in the lower right pane.



Data Review - NPV_FSddMS2 Focus_v2_matrix

#	Compound	Expected
7	Atrazine-D5	7.15
8	Azinphos-ethyl	11.10
9	Azinphos-methyl	8.71
10	Azoxystrobin	9.34
11	Bendiocarb	3.76
12	Benoxacor	8.48
13	Bioresmethrin	17.97
14	Boscalid	9.81
15	Bupirimate	10.80
16	Cadusafos	13.70
17	Carbendazim	3.36
18	Chlorpyrifos	15.87
19	Chlorpyrifos-met	13.82
20	Coumaphos	13.01
21	Cyazofamid	11.55

#	Acc	Status	PK	IR	IP	LS	FI	Filename	Sample Type	Level	Area	Expected RT	Actual RT	Calculated Amt	Theoretical Amt
17	17	●	●	●	●	●	●	mtx_01_02	Cal Std	cal4	1584366	10.80	10.82	0.093	0.100
18	18	●	●	●	●	●	●	mtx_01_03	Cal Std	cal4	1542525	10.80	10.82	0.091	0.100
19	19	●	●	●	●	●	●	mtx_01_04	Cal Std	cal4	1472596	10.80	10.82	0.087	0.100
20	20	●	●	●	●	●	●	mtx_05_01	Cal Std	cal5	9827005	10.80	10.82	0.536	0.500
21	21	●	●	●	●	●	●	mtx_05_02	Cal Std	cal5	9218352	10.80	10.82	0.503	0.500
22	22	●	●	●	●	●	●	mtx_05_03	Cal Std	cal5	8086108	10.80	10.82	0.442	0.500
23	23	●	●	●	●	●	●	mtx_05_04	Cal Std	cal5	7538234	10.80	10.82	0.413	0.500
24	24	●	●	●	●	●	●	mtx_1_01	Cal Std	cal6	15264690	10.80	10.82	0.826	1.000
25	25	●	●	●	●	●	●	mtx_1_02	Cal Std	cal6	14951613	10.80	10.82	0.811	1.000
26	26	●	●	●	●	●	●	mtx_1_03	Cal Std	cal6	13990813	10.80	10.82	0.759	1.000
27	27	●	●	●	●	●	●	mtx_1_04	Cal Std	cal6	13673258	10.80	10.83	0.742	1.000
28	28	●	●	●	●	●	●	mtx_5_01	Cal Std	cal7	89839040	10.80	10.82	4.834	5.000
29	29	●	●	●	●	●	●	mtx_5_02	Cal Std	cal7	88049404	10.80	10.81	4.738	5.000
30	30	●	●	●	●	●	●	mtx_5_03	Cal Std	cal7	83145308	10.80	10.81	4.474	5.000
31	31	●	●	●	●	●	●	mtx_5_04	Cal Std	cal7	82438951	10.80	10.82	4.436	5.000

Bupirimate RT: 10.82 | mtx_1_02

RT: 10.82
AA: 14951612.69
AH: 2863777.45
SN: 2243.05

m/z: 317.1642

Apex RT: 10.82
Area: 14951613

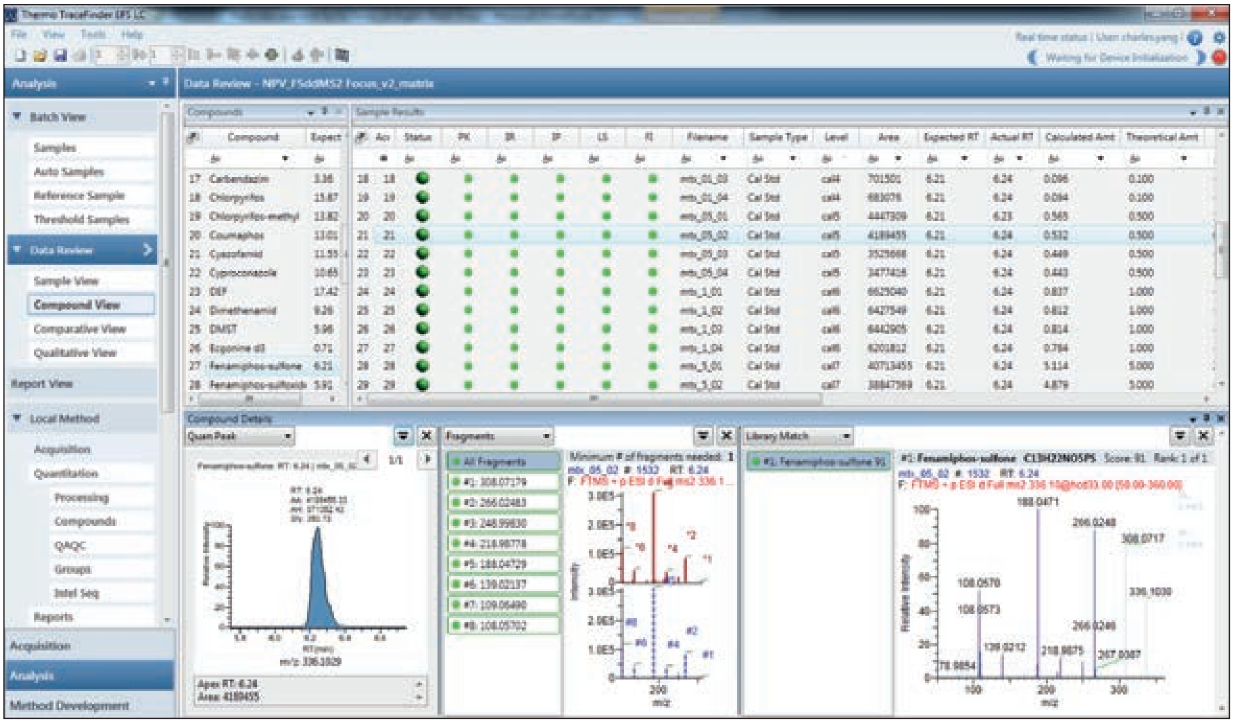
All Fragments
#1: 317.16463
#2: 272.10666
#3: 237.20764
#4: 210.16037
#5: 208.14473
#6: 166.09776
#7: 150.10283
#8: 140.10715
#9: 108.01145

Minimum # of fragments needed: 1
mtx_1_02 # 2662 RT 10.80
F: FTMS + p ESI d Full ms2 317.16@hcd3...

#1: Bupirimate 100

#1: Bupirimate C13H24N4O3S Score: 100
mtx_1_02 # 2662 RT 10.80
F: FTMS + p ESI d Full ms2 317.16@hcd3...

Figure 11. Bupirimate library match confirmation with fragmentation confirmation at 5 ppb, showing a library match score of 100% confidence in the lower right pane.



Data Review - NPV_F5ddMS2 Focus_v2_matrix

	Compound	Expect
17	Carbendazim	3.36
18	Chlorpyrifos	13.87
19	Chlorpyrifos-methyl	13.82
20	Coumaphos	13.01
21	Cyazofamid	11.55
22	Cyproconazole	10.65
23	DEF	17.42
24	Dimethenamid	9.26
25	DMST	5.96
26	Ecgonine d3	0.71
27	Fenamiphos-sulfone	6.21
28	Fenamiphos-sulfoxide	5.91

	Acq	Status	PK	IR	IP	LS	FI	Filename	Sample Type	Level	Area	Expected RT	Actual RT	Calculated Amt	Theoretical Amt
18	18	●	●	●	●	●	●	mtx_01_03	Cal Std	cal4	701501	6.21	6.24	0.096	0.100
19	19	●	●	●	●	●	●	mtx_01_04	Cal Std	cal4	683076	6.21	6.24	0.094	0.100
20	20	●	●	●	●	●	●	mtx_05_01	Cal Std	cal5	4447309	6.21	6.23	0.565	0.500
21	21	●	●	●	●	●	●	mtx_05_02	Cal Std	cal5	4189455	6.21	6.24	0.532	0.500
22	22	●	●	●	●	●	●	mtx_05_03	Cal Std	cal5	3525668	6.21	6.24	0.449	0.500
23	23	●	●	●	●	●	●	mtx_05_04	Cal Std	cal5	3477426	6.21	6.24	0.443	0.500
24	24	●	●	●	●	●	●	mtx_1_01	Cal Std	cal6	6625040	6.21	6.24	0.837	1.000
25	25	●	●	●	●	●	●	mtx_1_02	Cal Std	cal6	6427549	6.21	6.24	0.812	1.000
26	26	●	●	●	●	●	●	mtx_1_03	Cal Std	cal6	6442905	6.21	6.24	0.814	1.000
27	27	●	●	●	●	●	●	mtx_1_04	Cal Std	cal6	6201812	6.21	6.24	0.784	1.000
28	28	●	●	●	●	●	●	mtx_5_01	Cal Std	cal7	40713455	6.21	6.24	5.114	5.000
29	29	●	●	●	●	●	●	mtx_5_02	Cal Std	cal7	38847569	6.21	6.24	4.879	5.000

Apex RT: 6.24
Area: 4189455

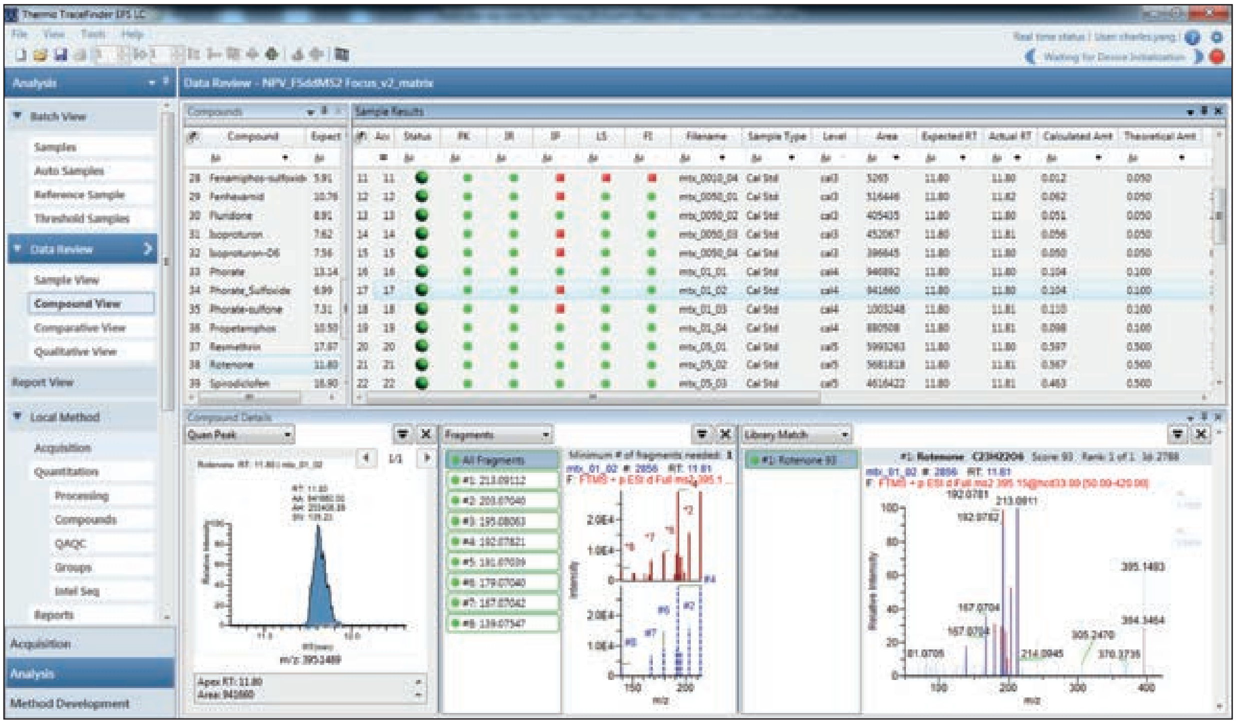
All Fragments
#1: 308.07179
#2: 266.02483
#3: 248.99830
#4: 218.98778
#5: 188.04729
#6: 139.02137
#7: 109.05490
#8: 108.05702

Minimum # of fragments needed: 1
mtx_05_02 #: 1532 RT: 6.24
F: FTMS + p ESI d Full ms2 336.1...

#1: Fenamiphos-sulfone 91

#1: Fenamiphos-sulfone C13H22NO5PS Score: 91 Rank: 1 of 1
mtx_05_02 #: 1532 RT: 6.24
F: FTMS + p ESI d Full ms2 336.10@hcd33.00 [50.00-360.00]

Figure 12. Fenamiphos-sulfone library match confirmation with fragmentation confirmation at 5 ppb, showing a library match score of 91% confidence in the lower right pane.



Data Review - NPV_F5ddMS2 Focus_v2_matrix

	Compound	Expect
28	Fenamiphos-sulfoxide	5.91
29	Fenhexamid	10.76
30	Fluridone	8.91
31	Isoproturon	7.62
32	Isoproturon-D6	7.56
33	Phorate	13.14
34	Phorate_Sulfoxide	6.99
35	Phorate-sulfone	7.31
36	Propetamphos	10.50
37	Resmethrin	17.07
38	Rotenone	11.80
39	Spirodiclofen	16.90

	Acq	Status	PK	IR	IP	LS	FI	Filename	Sample Type	Level	Area	Expected RT	Actual RT	Calculated Amt	Theoretical Amt
11	11	●	●	●	■	■	■	mtx_0010_04	Cal Std	cal3	5265	11.80	11.80	0.012	0.050
12	12	●	●	●	■	●	●	mtx_0050_01	Cal Std	cal3	516446	11.80	11.82	0.062	0.050
13	13	●	●	●	●	●	●	mtx_0050_02	Cal Std	cal3	405435	11.80	11.80	0.051	0.050
14	14	●	●	●	■	●	●	mtx_0050_03	Cal Std	cal3	452067	11.80	11.81	0.056	0.050
15	15	●	●	●	■	●	●	mtx_0050_04	Cal Std	cal3	396645	11.80	11.80	0.050	0.050
16	16	●	●	●	●	●	●	mtx_01_01	Cal Std	cal4	946892	11.80	11.80	0.104	0.100
17	17	●	●	●	■	●	●	mtx_01_02	Cal Std	cal4	941660	11.80	11.80	0.104	0.100
18	18	●	●	●	■	●	●	mtx_01_03	Cal Std	cal4	1003248	11.80	11.81	0.110	0.100
19	19	●	●	●	●	●	●	mtx_01_04	Cal Std	cal4	880508	11.80	11.81	0.098	0.100
20	20	●	●	●	●	●	●	mtx_05_01	Cal Std	cal5	5993263	11.80	11.80	0.597	0.500
21	21	●	●	●	●	●	●	mtx_05_02	Cal Std	cal5	5681818	11.80	11.81	0.567	0.500
22	22	●	●	●	●	●	●	mtx_05_03	Cal Std	cal5	4616422	11.80	11.81	0.463	0.500

Apex RT: 11.80
Area: 941660

All Fragments
#1: 213.09112
#2: 203.07040
#3: 195.08063
#4: 192.07821
#5: 181.07039
#6: 179.07040
#7: 157.07042
#8: 139.07547

Minimum # of fragments needed: 1
mtx_01_02 #: 2856 RT: 11.81
F: FTMS + p ESI d Full ms2 395.1...

#1: Rotenone 93

#1: Rotenone C23H22O6 Score: 93 Rank: 1 of 1 36.2788
mtx_01_02 #: 2856 RT: 11.81
F: FTMS + p ESI d Full ms2 395.15@hcd33.00 [50.00-420.00]

Figure 13. Rotenone library match confirmation with fragmentation confirmation at 1 ppb, showing a library match score of 93% confidence in the lower right pane.

Conclusion

The benchtop Q Exactive Focus MS provided easy access to full quantitative, confirmation, and screening data in a single injection. The high resolution and mass accuracy enabled quantification of the compounds over a wide dynamic range (0.05–200 ng/mL) with linear fit, correlation better than 0.99, and %RSD below 15%. Confirmation by the precursor-selected MS/MS gave an option to use spectral and library matching and pattern recognition within TraceFinder software. The new environmental and food safety HRAM spectral library provided more confidence in the data with its multiple, high-resolution spectra at numerous collision energies for use in any experiment.

References

1 http://www.mhlw.go.jp/english/topics/foodsafety/positivelist060228/introduction.html

2 http://europa.eu/legislation_summaries/food_safety/plant_health_checks/l21289_en.htm

3 http://ec.europa.eu/food/plant/protection/evaluation/rev_prog_exist_pest_en.htm

4 European Commission Health & Consumer Protection Directorate-General, Safety of the Food Chain - Chemicals, Contaminants, Pesticides. Guidance Document on Analytical Quality Control and Validation Procedures for Pesticide Residues Analysis in Food and Feed. SANCO/12571/2013. http://ec.europa.eu/food/plant/plant_protection_products/guidance_documents/docs/qualcontrol_en.pdf

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