

Accurately Identify and Quantify One Hundred Pesticides in a Single GC Run

Application Note

Author

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Abstract

A selected target compound list of 195 various pesticides was chosen for the evaluation of both the traditional time segment (TS) acquisition and the dMRM acquisition structures. Not only were the MRM acquisition setup procedures examined, but the acquired data were also evaluated. As sample complexity increases, the ability to use dMRM will provide laboratories with the capability to better tackle their large multi-analyte analysis, and to accurately quantify trace quantities of pesticides from high-throughput methods. The use of dynamic MRM (dMRM) acquisition method development provides users the ability to achieve equivalent or better quality data and results by:

- Monitoring the MRM transitions based on the compounds' retention times as they elute from GC
- Reducing the number of MRM transitions active at any given time, allowing for longer dwell times
- Optimizing the dwell times to maintain a constant MS cycle time and constant sampling rate across all peaks



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Introduction

The global agriculture industry uses over a thousand different pesticides for the production of food and foodstuffs. Producers require pesticides to meet the increasing demand for reasonably priced food. Analytical laboratories are then strained to evaluate and quantitate hundreds of pesticides in a single run. Currently, GC/MS/MS MRM analyses use time segment (TS) acquisition methods. TS methods focus on specified MRM transitions within a fixed retention time (RT) window. The more transitions in a time segment, the lower the dwell time and thus the sensitivity of the data acquired. Adding new compounds to the method usually results in redoing the time segments manually, and can be very time-consuming. Using the automated process of dynamic MRM (dMRM) acquisition saves a large amount of method development time. dMRM uses retention time locking (RLT) of the GC/MS system to set the RT of concurrent MRM transitions in a RT window. This automated procedure determines the number of these transitions to group in a RT window based on dwell criteria entered by the user to determine optimal sensitivity for the instrument.

Experimental

Sample preparation

Many laboratories focused on pesticide residue analysis in food commodities routinely use the Quick, Easy, Cheap, Effective, Rugged, and Safe (QuEChERS) method [1,2]. This straightforward sample preparation allows for the analysis of hundreds of pesticides at low concentrations with a single extraction.

A selection of eight different matrices were analyzed. These commodities included yellow onion, navel orange, organic honey, basic cucumber, jasmine rice, fresh leaf baby spinach, black loose leaf tea, and extra virgin olive oil [3]. Each matrix was extracted with a specified QuEChERS methodology, in which various dispersive SPE (dSPE) were used for matrix cleanup (Table 1).

Instrumentation

All analyses were run on an Agilent 7890B GC equipped with an Agilent 7693B Autosampler and an Agilent 7010A Triple Quadrupole GC/MS. Table 2 displays the GC and backflush parameters, and Tables 3 and 4 show the MS/MS method parameters for TS and dMRM, respectively. The GC was configured with a multimode inlet (MMI) equipped with a 4 mm ultra inert, splitless, single taper, glass wool liner (p/n 5190-2293). From the inlet, two Agilent J&W HP-5ms Ultra Inert columns (15 m × 0.25 mm, 0.25 μm; p/n 19091S-431 UI) were coupled to each other through a purged ultimate union (PUU) for the use of midcolumn/post run backflushing (Figure 1).

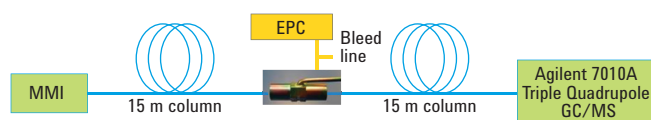


Figure 1. Column configuration for an optimal MRM application.

Table 1. Matrix Selection and Sample Preparation Used for Optimal MRM Application.

Category	Matrix	Sample Prep
High oil	Extra virgin olive oil	3 g oil/7 mL water, EN salts (5982-5650), EMR—L (5982-1010), Polish Pouch (5982-0102), Dry step
Difficult	Black loose leaf tea	3 g tea/7 mL water, EN salts, EN dSPE pigment (5982-5256)
High pigment	Fresh leaf baby spinach	10 g, EN salts, EN dSPE pigment (5982-5356)
High starch	Jasmine rice	3 g rice/7 mL water, EN salts, EN dSPE Fatty (5982-5156)
High water	Basic cucumber	10 g, EN salts, EN dSPE General (5982-5056)
High sugar	Organic honey	5 g honey/5 mL water, EN salts, EN dSPE General (5982-5056)
High acid	Navel orange	10 g, EN salts, EN dSPE Fatty (5982-5156)
Clean 15	Yellow onion (not sweet)	10 g, EN salts, EN dSPE Fatty (5982-5156)

MS Acquisition Method Development

The Agilent MassHunter Pesticide & Environmental Pollutant MRM Database (Rev. A.04.00) and Matrix Optimized Transitions [3] were used to develop the MRM acquisition methods for the evaluation of 195 target pesticides in each matrix (Figure 2). Both the 40 minute and 20 minute constant flow methods referenced in the MRM Database were followed. The top three (highest responding) MRMs for each compound were selected for analysis.

Compound Name	CAS #	Target
1 Phenol	108-95-2	Target
2 Dimefox	115-26-4	Target
3 Dichlorobenzene, 1,2-	95-50-1	Target
4 DBCP (Dibromo-3-chloropropane, 1,2-)	96-12-8	Target
5 Ethiolate	2941-55-1	Target
6 Methamidophos	10265-92-6	Target
7 Dichlorvos	62-73-7	Target
8 Trichlorfon	52-68-6	Target
9 Disulfoton-sulfoxide	2497-07-6	Target
10 Phthalide	87-41-2	Target
11 EPTC	759-94-4	Target
12 Mevinphos, Z-	338-45-4	Target
13 Mevinphos, E-	7786-34-7	Target
14 Butylate	2008-41-5	Target
15 Acephate	30560-19-1	Target
16 Acenaphthene-d10	15067-26-2	Target
17 Heptenophos	23560-59-0	Target
18 Omethoate	1113-02-6	Target
19 Thionazin	297-97-2	Target
20 Propoxur	114-26-1	Target
21 Demeton-S-methyl	919-86-8	Target
22 Cycloate	1134-23-2	Target
23 Ethoprophos	13194-48-4	Target
24 Naled	300-76-5	Target
25 Bendiocarb	22781-23-3	Target
26 Trifluralin	1582-09-8	Target
27 Benfluralin	1851-40-1	Target
28 Monocrotophos	6923-22-4	Target
29 Cadusafos	95465-99-9	Target
30 Phorate	298-02-2	Target
31 BHC-alpha (benzene hexachloride)	319-84-6	Target
32 Hexachlorobenzene	118-74-1	Target

Figure 2. Screen capture of the top portion of the Target Compound List from the P&EP MRM Database (A.04.00).

Table 2. Agilent 7890B GC method conditions.

Parameter	Value
MMI Injection mode	Hot-splitless
Injection volume	1 µL
Inlet temperature	280 °C
Carrier gas	He, constant flow 1.00 mL/min (column 2 = 1.20 mL/min)
MS transfer line temperature	280 °C
Oven program (40 minute method)	60 °C for 1 min 40 °C/min to 120 °C, 0 min 5 °C/min to 310 °C, 0 min
Oven program (20 minute method)	60 °C for 1 min 40 °C/min to 170 °C, 0 min 10 °C/min to 310 °C, 3 min
PUU Backflush settings*	
Timing	1.5 min duration during post run
Oven temperature	310 °C
Aux EPC pressure	~50 psi
Inlet pressure	~2 psi

* Backflush conditions are optimized for an application method in an Agilent Laboratory. A 1.5 minute backflush duration may be too short for other methods; recommendations can be made for a 5 minute backflush duration.

Table 3. Agilent 7010A Triple Quadrupole GC/MS time segment (TS) MRM parameters.

Parameter	Value
Electron energy	70 eV
Tune	atunes.eihs.tune.xml
EM gain	10
MS1 and MS2 resolution	Wide
Collision cell	1.5 mL/min N ₂ and 2.25 mL/min He
Quant/Qual transitions	Matrix Optimized
Dwell times	Time Segment (TS) specific*
Source temperature	300 °C**
Quad temperatures	150 °C

* All dwells in each TS were given the same value (no value under 10 was set) to attain a scan rate of ~5 scans/sec for the TS.

** The recommended source temperature is 280 °C. The source temperature here was run hotter due to internal lab settings.

Table 4. Agilent 7010A Triple Quadrupole GC/MS dynamic MRM (dMRM) parameters.

Parameter	Value
Electron energy	70 eV
Tune	atunes.eihs.tune.xml
EM gain	10
MS1 and MS2 resolution	dMRM unit
Collision cell	1.5 mL/min N ₂ and 2.25 mL/min He
Quant/Qual transitions	Matrix optimized
Dwell times	Optimized by dMRM*
Source temperature	300 °C
Quad temperatures	150 °C

* All dwells in each dMRM RT window were given the same value (no value under 10 was set) to attain a scan rate of ~5 scans/sec for the TS.

Time Segment Method Development

Time segment acquisition development was completed using the graphical user interface (GUI) in the MRM Database and the MassHunter Compound List Assistant (CLA). The Organic Honey Matrix Optimized MRM Database was used as an example for the TS method development (Figure 3). After the Target List was created, the **Build MRM Table** option was selected (Figure 4). Two selections are needed for the development of the MRM Table:

- Method selection (the 40 minute constant flow method was selected in this example)
- Quantifier and qualifier ion selections (Figure 5)

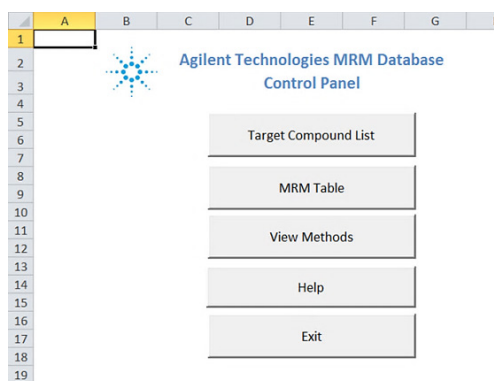


Figure 3. The GUI Homepage of the Organic Honey Matrix Optimized MRM Database, used for TS method development.

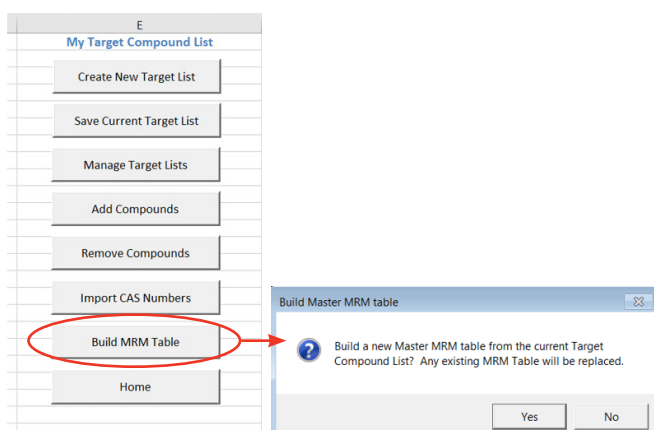


Figure 4. Selecting **Build MRM Table** from the generated Target Compound List.

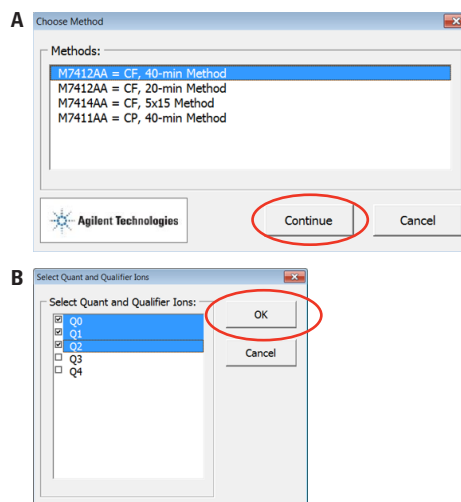


Figure 5. Two selections for MRM Table development: A) Method Selection (the 40 minute M7412AA method option was selected here); B) Quant and Qual Ion selections.

Once the MRM Table was completed, the **Export for CLA Optimizer** option was selected, and the CLA program was launched. The Database saved this export file as a .csv file, and was then imported into the CLA (Figure 6). The optimization parameters were set to use a constant cycle time of 5 msec throughout each TS (Figure 7). The RT deltas can also be edited within the CLA. The method was saved and loaded into MassHunter GC/MS Data Acquisition (DA) B.07.05 (Figure 8).

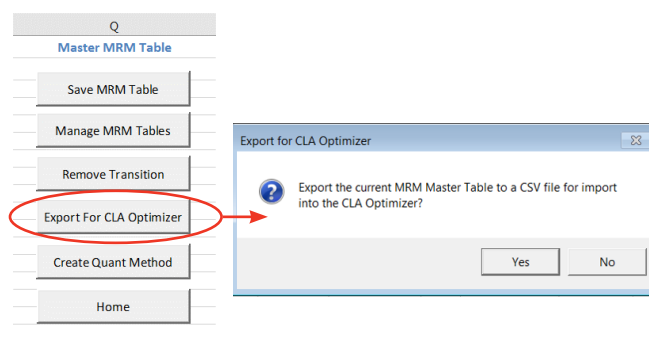


Figure 6. Exporting the MRM Table to a .csv file for the CLA.

dMRM Method Development

dMRM acquisition development was completed using the MS Method Editor within MassHunter Workstation GC/MS Acquisition Software. From within the MS Parameters of MassHunter GC/MS Data Acquisition (B.07.05), the Organic Honey Matrix Optimized MRM Database was imported, and the 40 minute M7412AA constant flow method was selected (Figure 9). The MRM Acquisition Method page is where all of the target compounds for the method are shown (Figure 10). The Compound Browser was used to locate target

compounds and their respective MRMs (the same target list and ions were used as the TS method development). Once chosen, the MRMs are applied to the Import List (Figure 11). The Import List maintains all of the target compounds that are to be used in the method, and their respective MRMs. Once the target list is finalized, they are imported to the Method (Figure 12). The Method Acquisition page is where the RT deltas can be edited, the cycles/sec can be defined, and the dwell times are optimized (Figure 13). Figure 14 displays a view of the 20 minute dMRM acquisition method for the same Target List and respective MRMs.

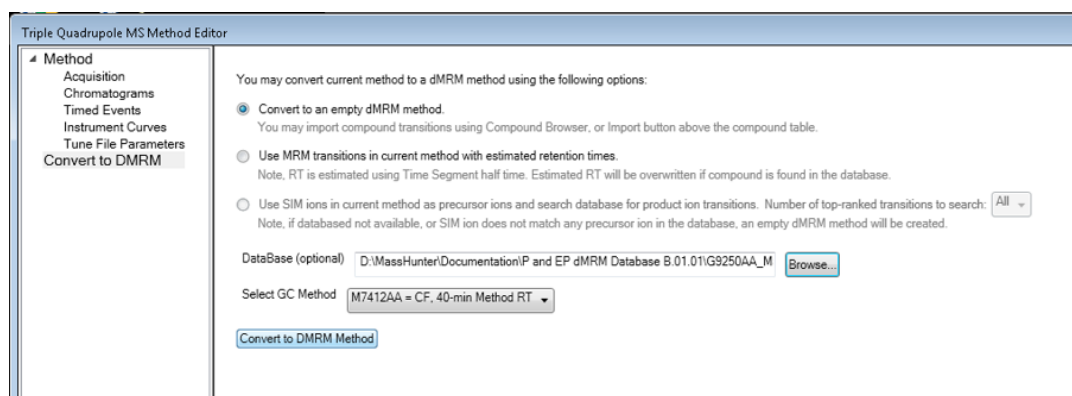


Figure 9. The Organic Honey Matrix Optimized MRM Database was imported into the MS Parameters of Agilent MassHunter GC/MS Data Acquisition B.07.05.

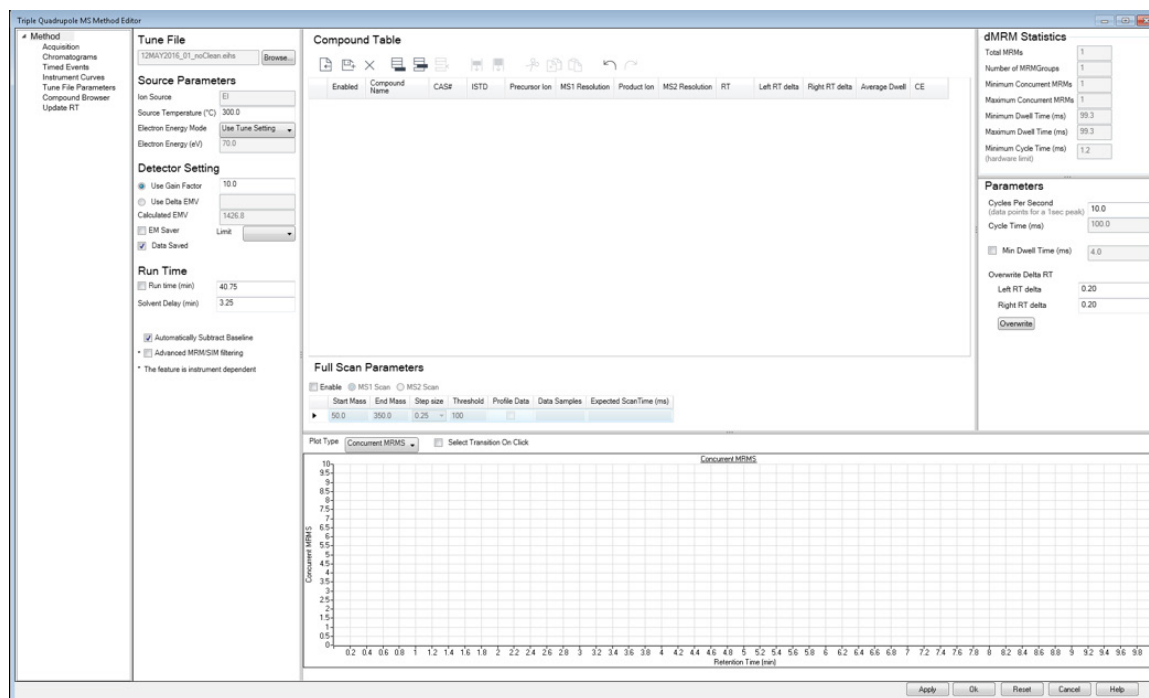


Figure 10. A blank Agilent MRM Acquisition Method page.

Triple Quadrupole MS Method Editor

Method
Acquisition
Chromatograms
Tuned Events
Instrument Curves
Tune File Parameters
Compound Browser
Update RT

Search/Filter | Import List

Select GC Method: [M74122AA - CF_40-min Method RT] Show All Records

Filter: Target List Name: [Molecular Formula] Group Name: [Algaecide; Fungicide; Nematocide]

Compound List: 2,4,5-T methyl ester, 2,4-D butyl ester, Acenaphthene-d10, Acetate, Aldrin, Ametryn, Aminoacids, Atrazine, Azinphos-ethyl, Azinphos-methyl, Berberin, Berflurin

Search Text: [] Search Compounds

Columns: Compound Name, Formula, Molecular Weight, CAS#, Group Name, Precursor Ion, Product Ion

Number of top-ranked transitions to select: [3]

Ranked By: Abundance, Response Factor

<input type="checkbox"/>	Formula	Molecular Weight	Compound Name	CAS#	ISTD	Precursor Ion	Product Ion	RT	Left RT delta	Right RT delta	RT Window	Dwell	CE	Abundance	Response
<input checked="" type="checkbox"/>	C6H6O	94.1112	Phenol	108-95-2	<input type="checkbox"/>	94	66.1	3.61	1	1	0.2	10	15	1.00	8.001464E+07
<input checked="" type="checkbox"/>	C6H6O	94.1112	Phenol	108-95-2	<input type="checkbox"/>	94	65.1	3.61	1	1	0.2	10	20	0.78	62242636
<input checked="" type="checkbox"/>	C6H6O	94.1112	Phenol	108-95-2	<input type="checkbox"/>	66	65	3.61	1	1	0.2	10	5	0.33	26318358
<input checked="" type="checkbox"/>	C6H6O	94.1112	Phenol	108-95-2	<input type="checkbox"/>	95	67.1	3.61	1	1	0.2	10	15	0.08	6266749
<input checked="" type="checkbox"/>	C6H6O	94.1112	Phenol	108-95-2	<input type="checkbox"/>	66	51	3.61	1	1	0.2	10	20	0.06	4997724
<input checked="" type="checkbox"/>	C4H12FN2OP	154.1	Dimetox	115-26-4	<input type="checkbox"/>	153	110	4	1	1	0.2	10	10	1.00	5431075
<input checked="" type="checkbox"/>	C4H12FN2OP	154.1	Dimetox	115-26-4	<input type="checkbox"/>	110	47	4	1	1	0.2	10	35	0.89	4814943
<input checked="" type="checkbox"/>	C4H12FN2OP	154.1	Dimetox	115-26-4	<input type="checkbox"/>	110	67	4	1	1	0.2	10	20	0.61	3320161
<input checked="" type="checkbox"/>	C4H12FN2OP	154.1	Dimetox	115-26-4	<input type="checkbox"/>	111	109.9	4	1	1	0.2	10	0	0.56	3177175
<input checked="" type="checkbox"/>	C4H12FN2OP	154.1	Dimetox	115-26-4	<input type="checkbox"/>	154	58	4	1	1	0.2	10	5	0.39	2120272
<input checked="" type="checkbox"/>	C6H4Cl2	147	Dichlorobenzene, 1,2-	95-50-1	<input type="checkbox"/>	146	111.1	4.12	1	1	0.2	10	15	1.00	7.490633E+07
<input checked="" type="checkbox"/>	C6H4Cl2	147	Dichlorobenzene, 1,2-	95-50-1	<input type="checkbox"/>	146	75.1	4.12	1	1	0.2	10	25	0.91	6.850126E+07
<input checked="" type="checkbox"/>	C6H4Cl2	147	Dichlorobenzene, 1,2-	95-50-1	<input type="checkbox"/>	111	75.1	4.12	1	1	0.2	10	10	0.63	46951176
<input checked="" type="checkbox"/>	C6H4Cl2	147	Dichlorobenzene, 1,2-	95-50-1	<input type="checkbox"/>	148	75.1	4.12	1	1	0.2	10	25	0.62	46952972
<input checked="" type="checkbox"/>	C6H4Cl2	147	Dichlorobenzene, 1,2-	95-50-1	<input type="checkbox"/>	148	111.1	4.12	1	1	0.2	10	15	0.38	2.834839E+07
<input checked="" type="checkbox"/>	C3H5Br2Cl	236.3	DBCP	96-12-8	<input type="checkbox"/>	155	75	4.49	1	1	0.2	10	5	1.00	5.02397E+07
<input checked="" type="checkbox"/>	C3H5Br2Cl	236.3	DBCP	96-12-8	<input type="checkbox"/>	157	75	4.49	1	1	0.2	10	5	0.99	4986444
<input checked="" type="checkbox"/>	C3H5Br2Cl	236.3	DBCP	96-12-8	<input type="checkbox"/>	157	77	4.49	1	1	0.2	10	5	0.35	1.739746E+07
<input checked="" type="checkbox"/>	C3H5Br2Cl	236.3	DBCP	96-12-8	<input type="checkbox"/>	159	77	4.49	1	1	0.2	10	5	0.34	17152336
<input checked="" type="checkbox"/>	C3H5Br2Cl	236.3	DBCP	96-12-8	<input type="checkbox"/>	155	49	4.49	1	1	0.2	10	30	0.26	1.296919E+07
<input checked="" type="checkbox"/>	C7H19NO5	161.3	Etholate	2941-55-1	<input type="checkbox"/>	100	72	5.58	1	1	0.2	10	5	1.00	7.155342E+07
<input checked="" type="checkbox"/>	C7H19NO5	161.3	Etholate	2941-55-1	<input type="checkbox"/>	161	100	5.58	1	1	0.2	10	0	0.21	15121155
<input checked="" type="checkbox"/>	C7H19NO5	161.3	Etholate	2941-55-1	<input type="checkbox"/>	161	72	5.58	1	1	0.2	10	15	0.11	7940788
<input checked="" type="checkbox"/>	C7H19NO5	161.3	Etholate	2941-55-1	<input type="checkbox"/>	118	90	5.58	1	1	0.2	10	5	0.02	1435439
<input checked="" type="checkbox"/>	C7H19NO5	161.3	Etholate	2941-55-1	<input type="checkbox"/>	118	58	5.58	1	1	0.2	10	5	0.01	690654
<input checked="" type="checkbox"/>	C2H8O2P2S	141	Methamidophos	10265-92-6	<input type="checkbox"/>	141	95	5.87	1	1	0.2	10	5	1.00	11401272
<input checked="" type="checkbox"/>	C2H8O2P2S	141	Methamidophos	10265-92-6	<input type="checkbox"/>	95	79	5.87	1	1	0.2	10	10	0.02	9312170

Current Path: D:\MassHunter\Documentation\IP and IP-IRM Database B.01.01\Q3250AA_Matrix Optimized_Organic Honey Matrix.xlsm Total Records: 977 Displayed: 977 Selected: 588 Number of Compounds: 196

Apply Ok Reset Cancel Help

Figure 11. The compound browser displays all of the compounds and respective MRMs that are within the loaded Database.

Triple Quadrupole MS Method Editor

Method

- Acquisition
- Chromatograms
- Timed Events
- Instrument Curves
- Tune File Parameters
- Compound Browser
- Update RT

Search/Filter Import List

Compound Name	CAS#	ISTD	Precursor Ion	Product Ion	RT	Left RT delta	Right RT delta	Dwell	CE	Abundance
2,4,5-T methyl ester	1928-37-6	<input type="checkbox"/>	109	74	16.01	.1	.1	10	25	0.61
2,4,5-T methyl ester	1928-37-6	<input type="checkbox"/>	233	190	16.01	.1	.1	10	15	0.77
2,4,5-T methyl ester	1928-37-6	<input type="checkbox"/>	268	233.1	16.01	.1	.1	10	10	1.00
2,4-D butyl ester	94-80-4	<input type="checkbox"/>	174.9	111	17.93	.1	.1	10	10	0.61
2,4-D butyl ester	94-80-4	<input type="checkbox"/>	185	155	17.93	.1	.1	10	20	0.67
2,4-D butyl ester	94-80-4	<input type="checkbox"/>	162	63	17.93	.1	.1	10	35	1.00
Acenaphthene-d10	15067-26-2	<input checked="" type="checkbox"/>	160.1	158.1	10.05	.1	.1	10	20	0.18
Acenaphthene-d10	15067-26-2	<input checked="" type="checkbox"/>	162.1	160.1	10.05	.1	.1	10	20	0.94
Acenaphthene-d10	15067-26-2	<input checked="" type="checkbox"/>	164.1	162.1	10.05	.1	.1	10	15	1.00
Acephate	30560-19-1	<input type="checkbox"/>	78.9	47	9.08	.1	.1	10	10	0.22
Acephate	30560-19-1	<input type="checkbox"/>	142	96	9.08	.1	.1	10	5	0.24
Acephate	30560-19-1	<input type="checkbox"/>	136	94	9.08	.1	.1	10	15	1.00
Alachlor	15972-60-8	<input type="checkbox"/>	160.1	132.1	18.41	.1	.1	10	15	0.41
Alachlor	15972-60-8	<input type="checkbox"/>	188.1	132.1	18.41	.1	.1	10	20	0.42
Alachlor	15972-60-8	<input type="checkbox"/>	188.1	160.1	18.41	.1	.1	10	10	1.00
Aldrin	309-00-2	<input type="checkbox"/>	264.9	192.9	19.57	.1	.1	10	35	0.64
Aldrin	309-00-2	<input type="checkbox"/>	262.9	190.9	19.57	.1	.1	10	35	0.66
Aldrin	309-00-2	<input type="checkbox"/>	262.9	192.9	19.57	.1	.1	10	35	1.00
Ametryn	834-12-8	<input type="checkbox"/>	185	170	18.46	.1	.1	10	5	0.68
Ametryn	834-12-8	<input type="checkbox"/>	227	170.1	18.46	.1	.1	10	10	0.70
Ametryn	834-12-8	<input type="checkbox"/>	227	58.1	18.46	.1	.1	10	10	1.00
Aminocarb	2032-59-9	<input type="checkbox"/>	136	77	15.67	.1	.1	10	25	0.68
Aminocarb	2032-59-9	<input type="checkbox"/>	150	134	15.67	.1	.1	10	20	0.96
Aminocarb	2032-59-9	<input type="checkbox"/>	151	136.1	15.67	.1	.1	10	15	1.00
Altrazine	1912-24-9	<input type="checkbox"/>	200	94	15.29	.1	.1	10	20	0.80
Altrazine	1912-24-9	<input type="checkbox"/>	214.9	200.2	15.29	.1	.1	10	5	0.86
Altrazine	1912-24-9	<input type="checkbox"/>	214.9	58.1	15.29	.1	.1	10	10	1.00
Azinphos-ethyl	2642-71-9	<input type="checkbox"/>	160	77.1	30.6	.1	.1	10	20	0.79
Azinphos-ethyl	2642-71-9	<input type="checkbox"/>	160	132.1	30.6	.1	.1	10	0	0.82
Azinphos-ethyl	2642-71-9	<input type="checkbox"/>	132	77.1	30.6	.1	.1	10	15	1.00
Azinphos-methyl	86-50-0	<input type="checkbox"/>	132.1	77	29.34	.1	.1	10	15	0.79
Azinphos-methyl	86-50-0	<input type="checkbox"/>	160	77	29.34	.1	.1	10	20	0.81
Azinphos-methyl	86-50-0	<input type="checkbox"/>	77	51	29.34	.1	.1	10	15	1.00
Bendiocarb	22781-23-3	<input type="checkbox"/>	126	108	13.8	.1	.1	10	5	0.34
Bendiocarb	22781-23-3	<input type="checkbox"/>	126	52.1	13.8	.1	.1	10	15	0.65
Bendiocarb	22781-23-3	<input type="checkbox"/>	166	151.1	13.8	.1	.1	10	10	1.00
Berfluralin	1861-40-1	<input type="checkbox"/>	275.9	202.1	14.01	.1	.1	10	15	0.23
Berfluralin	1861-40-1	<input type="checkbox"/>	292	206	14.01	.1	.1	10	10	0.52
Berfluralin	1861-40-1	<input type="checkbox"/>	292	264	14.01	.1	.1	10	5	1.00
Berthiavalicarb-isopropyl	177406-68-7	<input type="checkbox"/>	180	127	29.69	.1	.1	10	20	0.68
Berthiavalicarb-isopropyl	177406-68-7	<input type="checkbox"/>	72	55	29.69	.1	.1	10	10	0.89
Berthiavalicarb-isopropyl	177406-68-7	<input type="checkbox"/>	180	83	29.69	.1	.1	10	35	1.00
BHC-alpha	319-84-6	<input type="checkbox"/>	218.9	183	14.29	.1	.1	10	5	0.93

Number of Compounds: 196 Number of Transitions: 588

Figure 12. The Import List maintains all of the target compounds and their respective MRMs that are intended for the acquisition method.

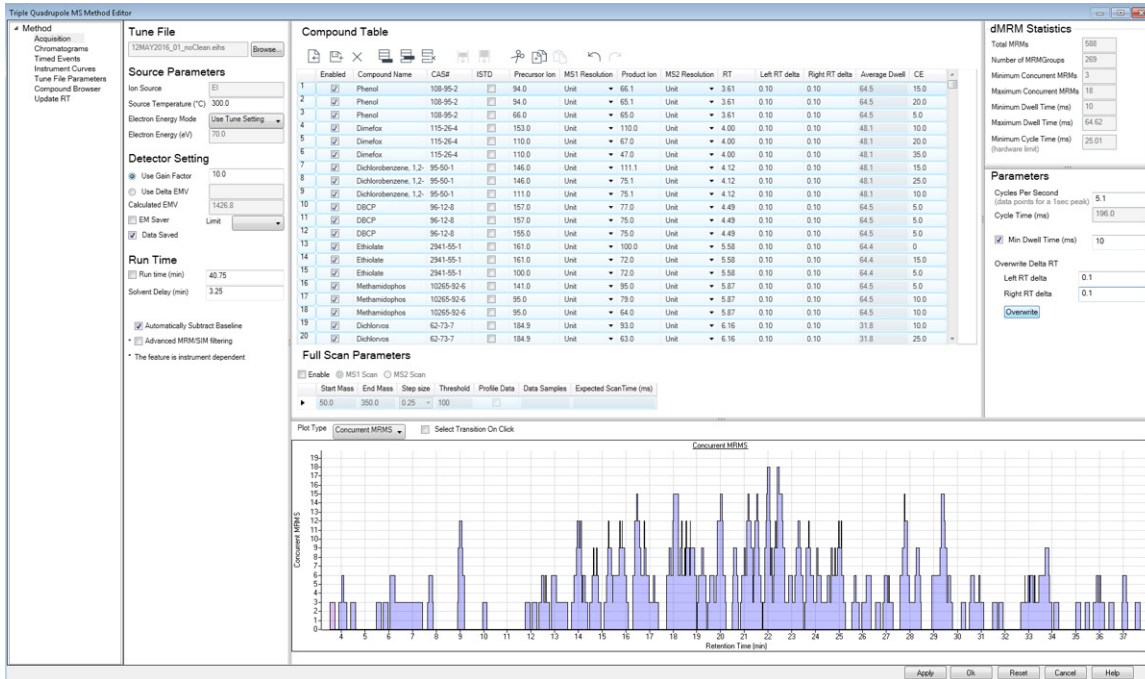


Figure 13. The Method Acquisition page shows the Target List and respective MRMMS for the 40 minute peak method.

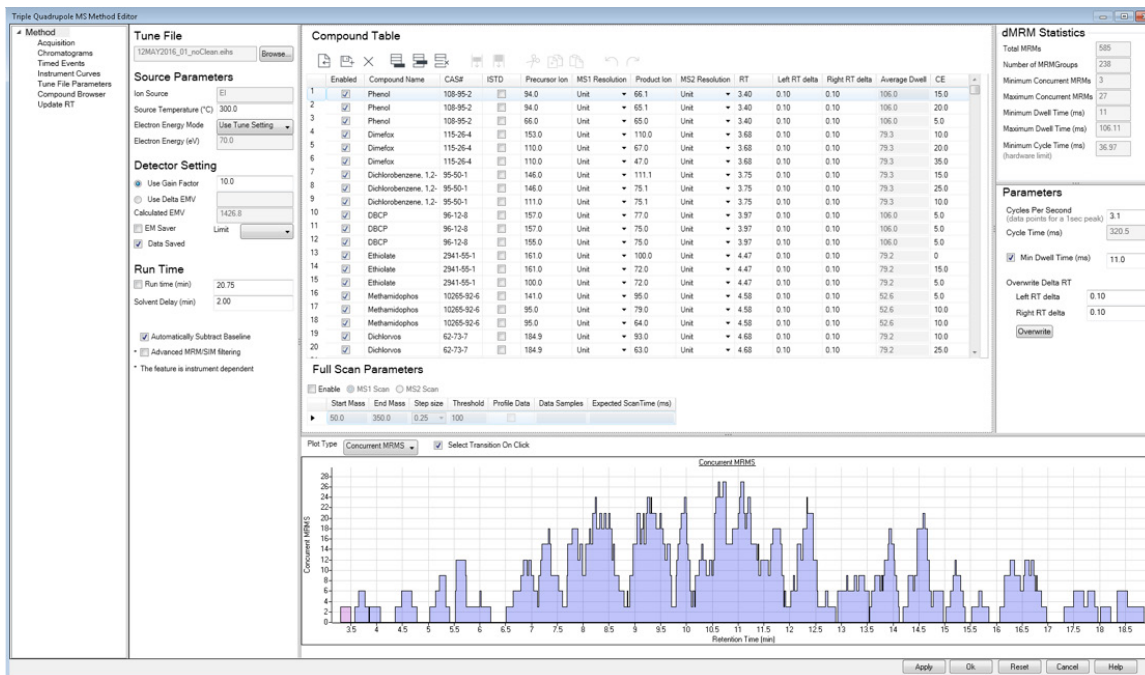


Figure 14. The Method Acquisition page shows the same Target List and respective MRMMS for the 20 minute peak method.

Key elements of dMRM method development

- **Typical method development time:** ~5-10 minutes depending on how detailed the MS method is
- **Adding target compounds:** One-by-one selection, group selection, or searching a CAS# list
- **Removing target compounds:** One-by-one or multiple selection
- **Adding MRM transitions:** One-by-one or multiple selection
- **Removing MRM transitions:** One-by-one or multiple selection removal
- **Quant and qualifier selection:** Same selection for all or choice for each target compound
- **Use of MassHunter DA for method optimization:** RT deltas can be set one-by-one or filled down within columns; dwell optimization by algorithm or user-defined settings

Evaluation

The dMRM acquisition method provides users with another way to set up their MS acquisition method parameters. Whether the user chooses to use TSs or the dMRM functionalities, they both aid in achieving optimal analysis. Figures 15-20 are various selected chromatograms that were observed and analyzed in both TS and dMRM acquisition methods.

Results and Discussion

There are two ways to view the difference in the chromatographic displays:

- MassHunter Qualitative Analysis Software (B.07.00 SP1, or later)
- MassHunter Quantitative Analysis Software (B.07.01, or later)

Figures 19-26 show a selected representation of the 195 target compounds in various matrices. The concentration shown for the various target analytes ranged between 180-380 ppb. A higher concentration was used for viewing ability; further analysis was done showing that 90% of all target compounds achieved a calibration curve with $R^2 \geq 0.990$. All analyzed pesticides obtained a %RSD of repeated measurements of $\leq 30\%$, and 90% of the analyzed pesticides were found to have a limit of quantitation (LOQ) $\leq 1.5 \text{ pg}/\mu\text{L}$ [3].

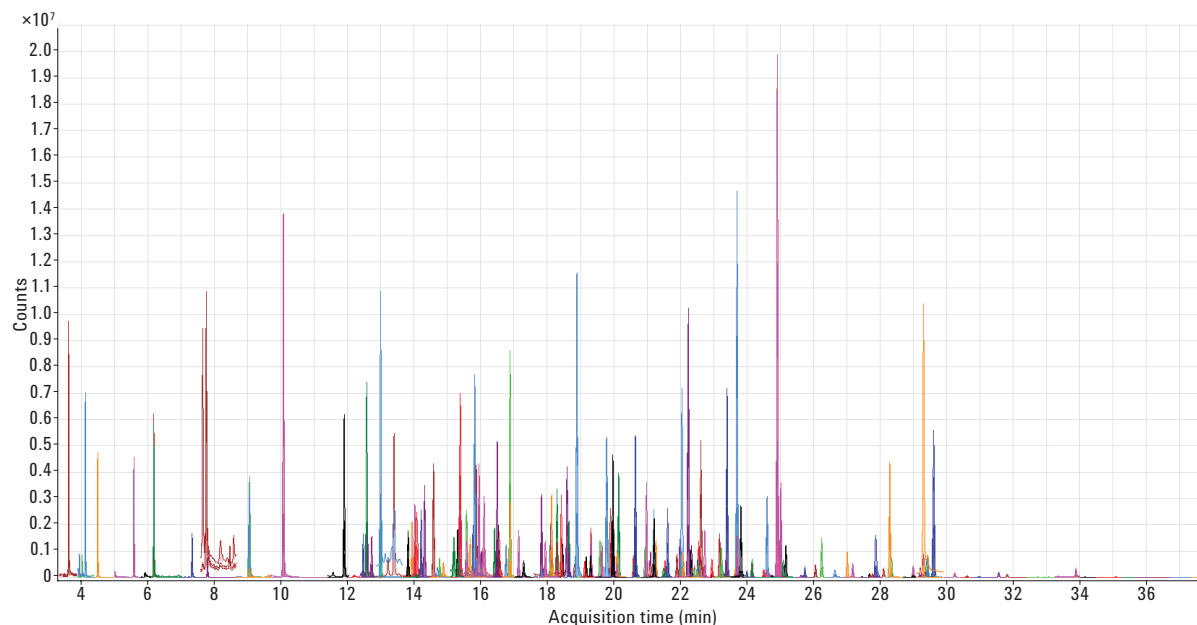


Figure 15. Organic honey 40 minute analysis chromatogram of 195 target compounds with three MRM transitions per compound using the TS MS parameters.

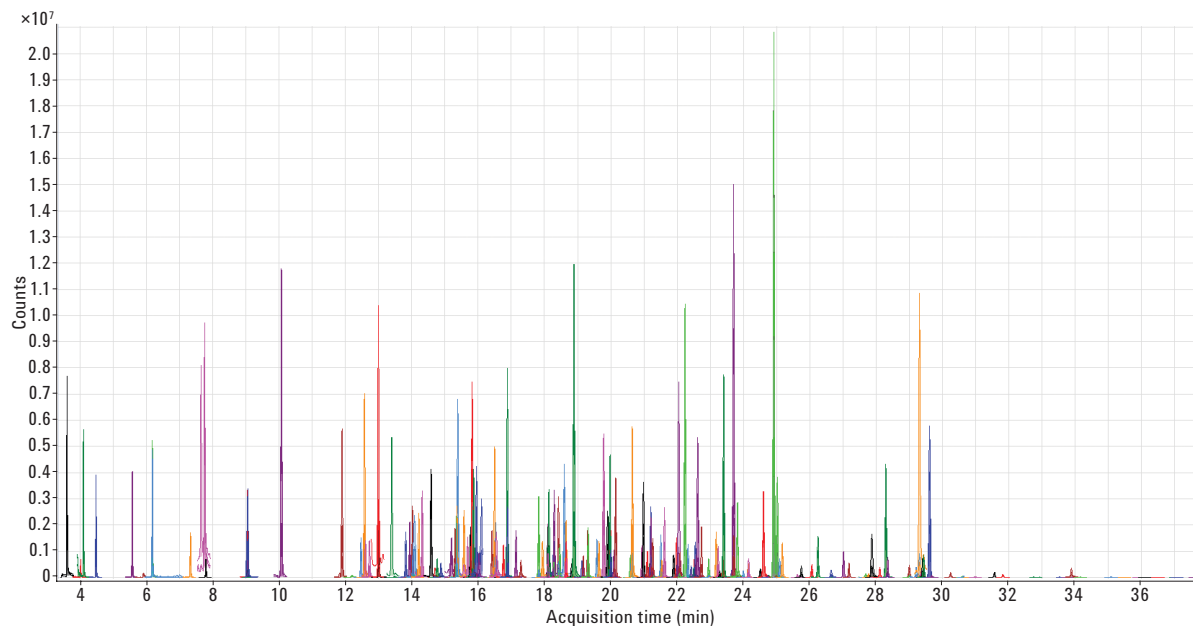


Figure 16. Organic honey 40 minute analysis chromatogram of 195 target compounds with three MRM transitions per compound using the dMRM MS parameters.

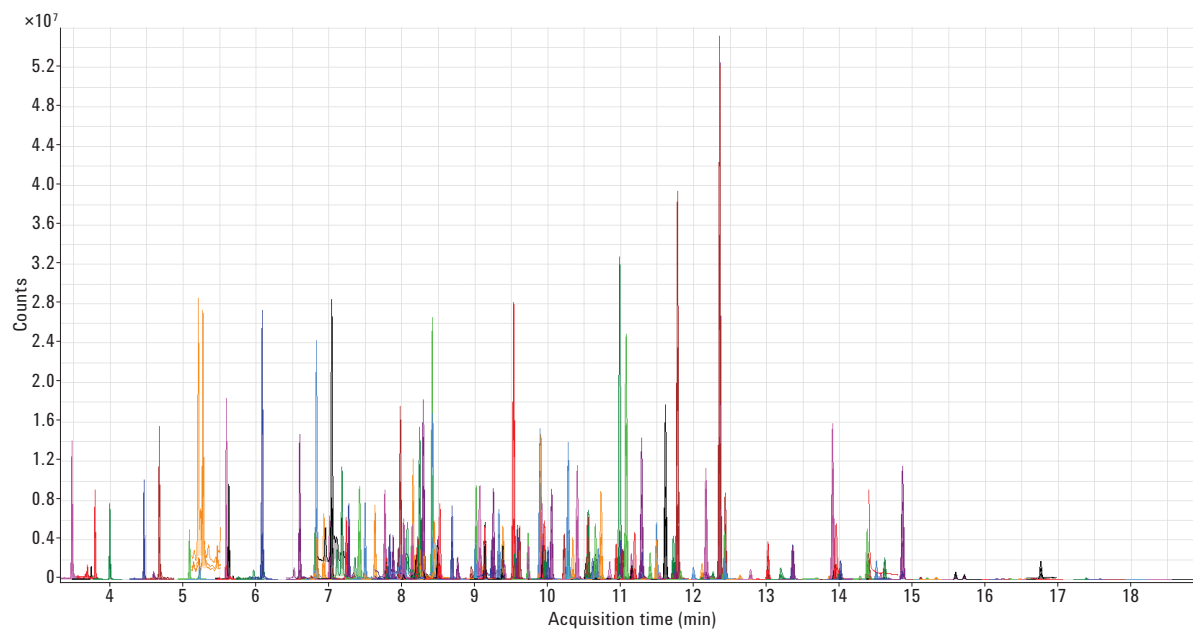


Figure 17. Organic honey 20 minute analysis chromatogram of 195 target compounds with three MRM transitions per compound using the dMRM MS parameters.

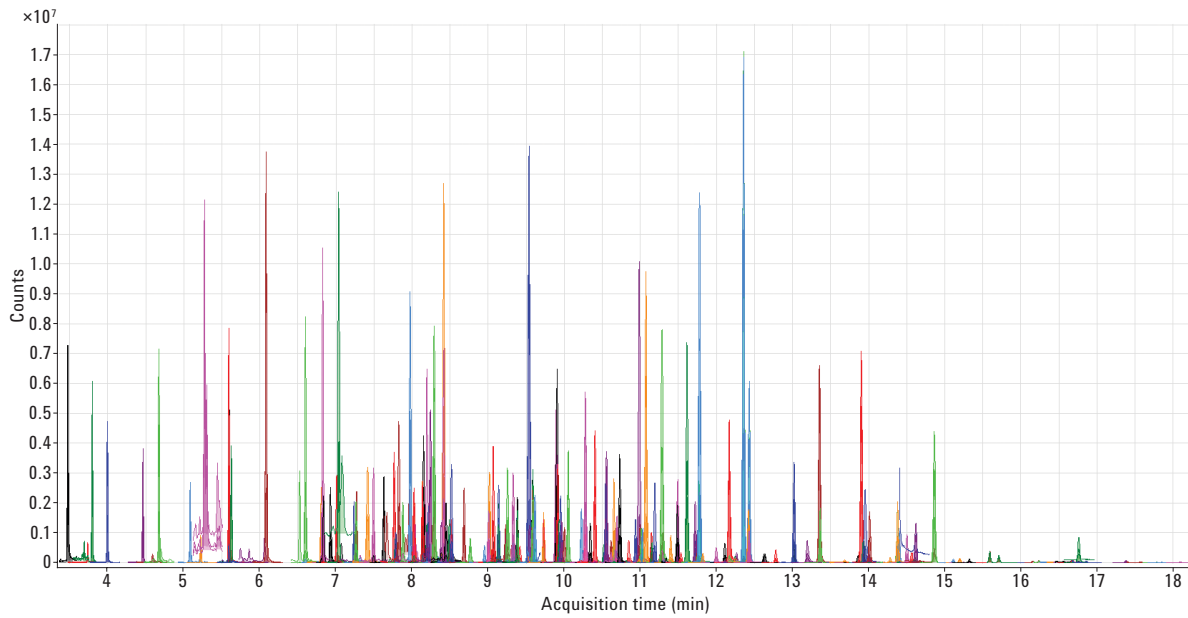


Figure 18. Extra virgin olive oil 20 minute analysis chromatogram of 195 target compounds with three MRM transitions per compound using the dMRM MS parameters.

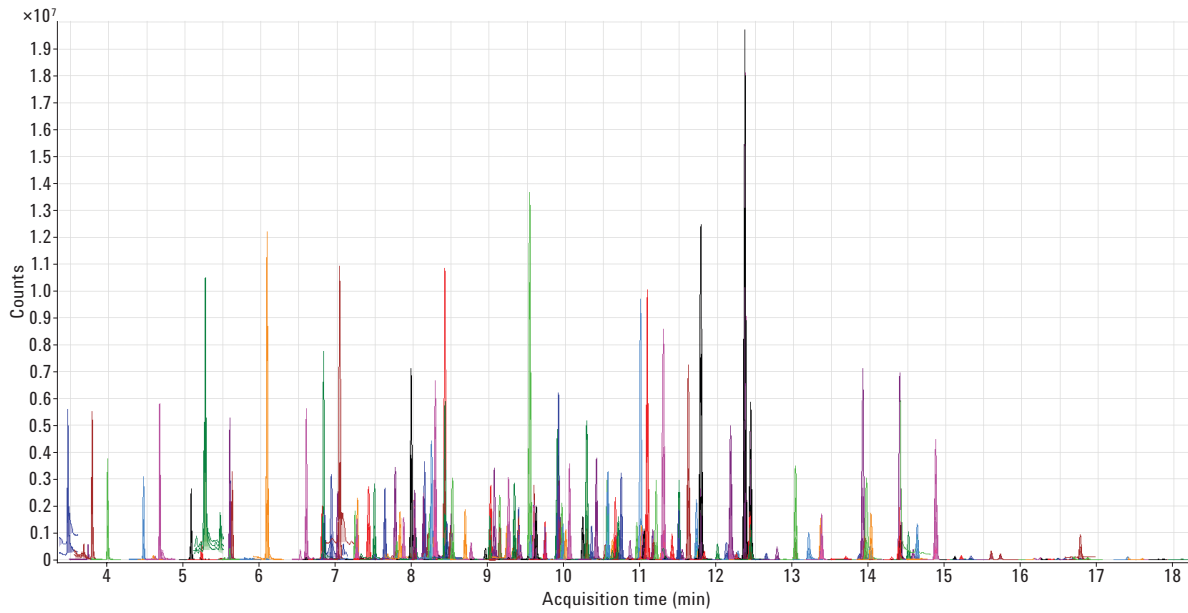


Figure 19. Navel orange 20 minute analysis chromatogram of 195 target compounds with three MRM transitions per compound using the dMRM MS parameters.

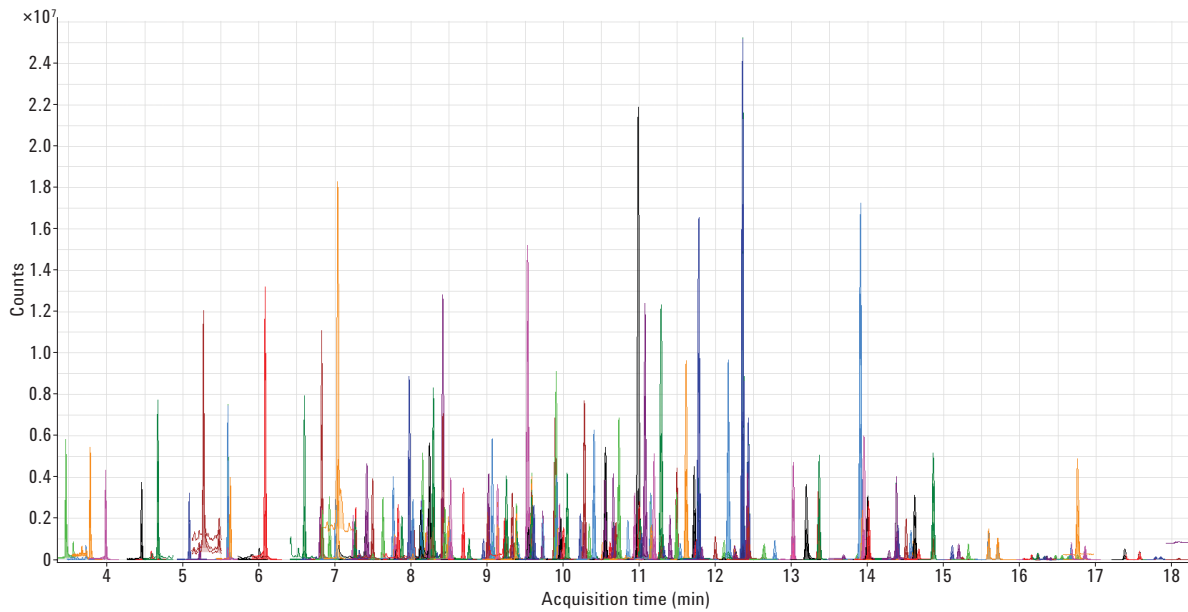


Figure 20. Fresh leaf baby spinach 20 minute analysis chromatogram of 195 target compounds with three MRM transitions per compound using the dMRM MS parameters.

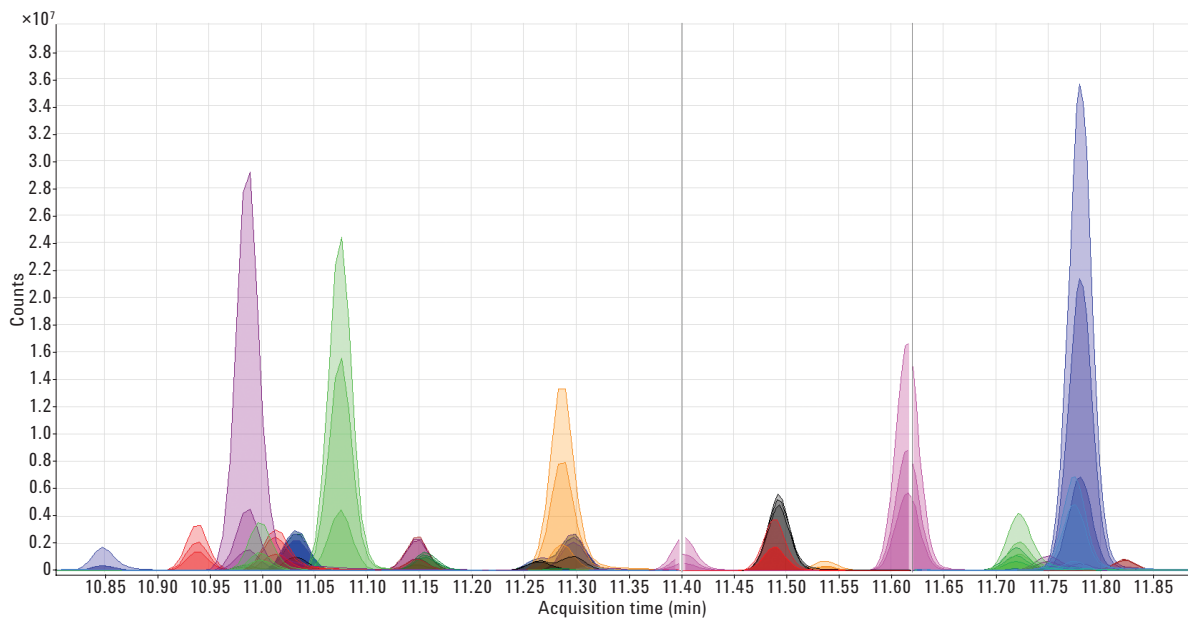


Figure 21. Organic honey TS chromatogram of RT range (40 minute method) in Agilent MassHunter Qualitative Analysis.

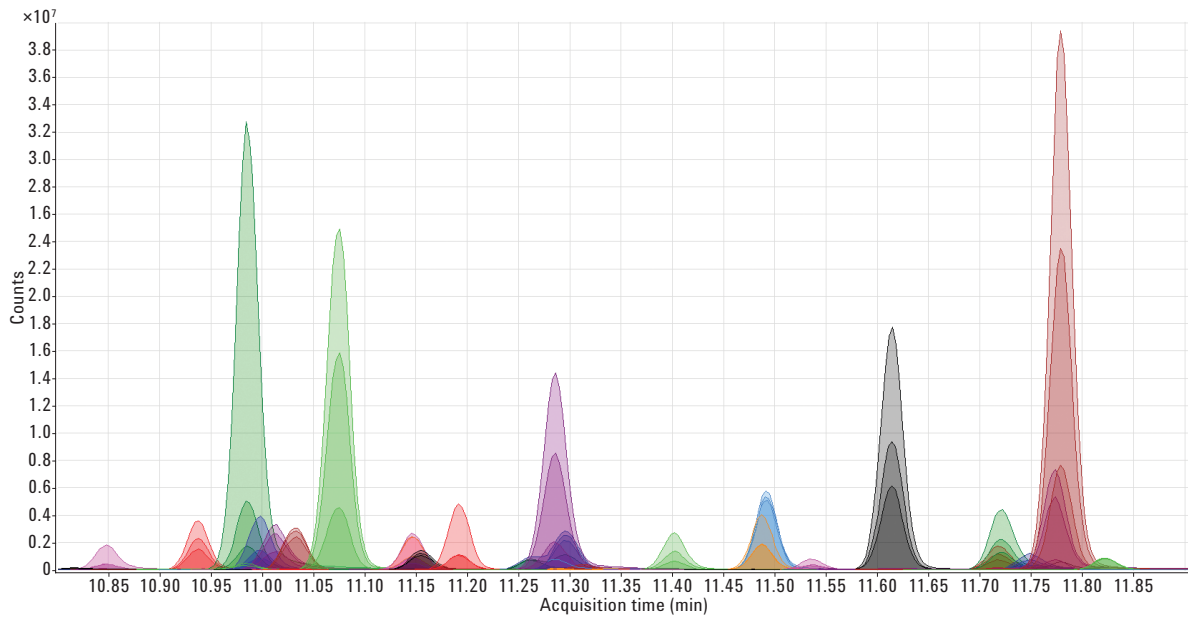


Figure 22. Organic honey dMRM chromatogram of RT range (40 minute method) in Agilent MassHunter Qualitative Analysis.

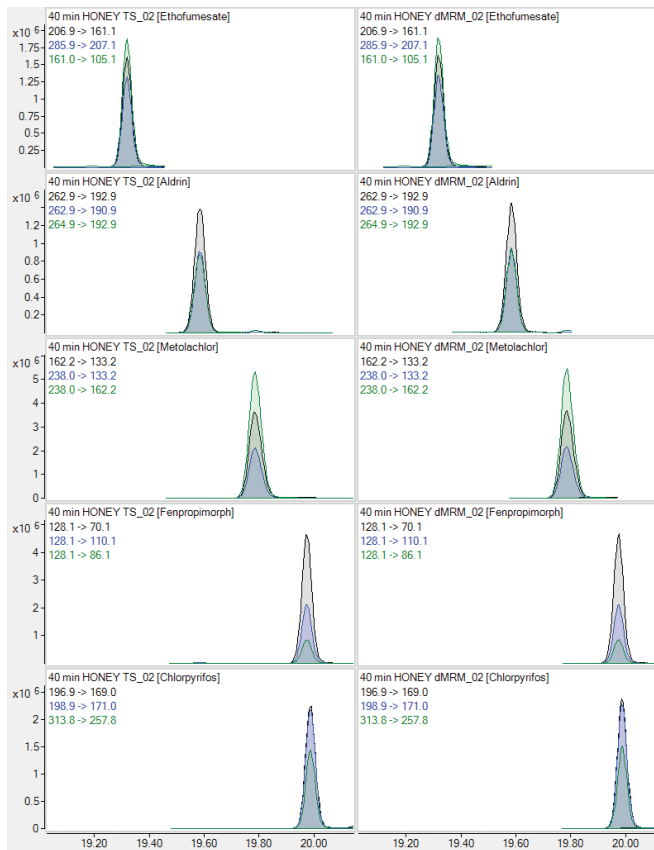


Figure 23. Organic honey TS chromatograms (left) and dMRM chromatograms (right) of selected compounds for RT range (40 minute method) in Agilent MassHunter Quantitative Analysis.

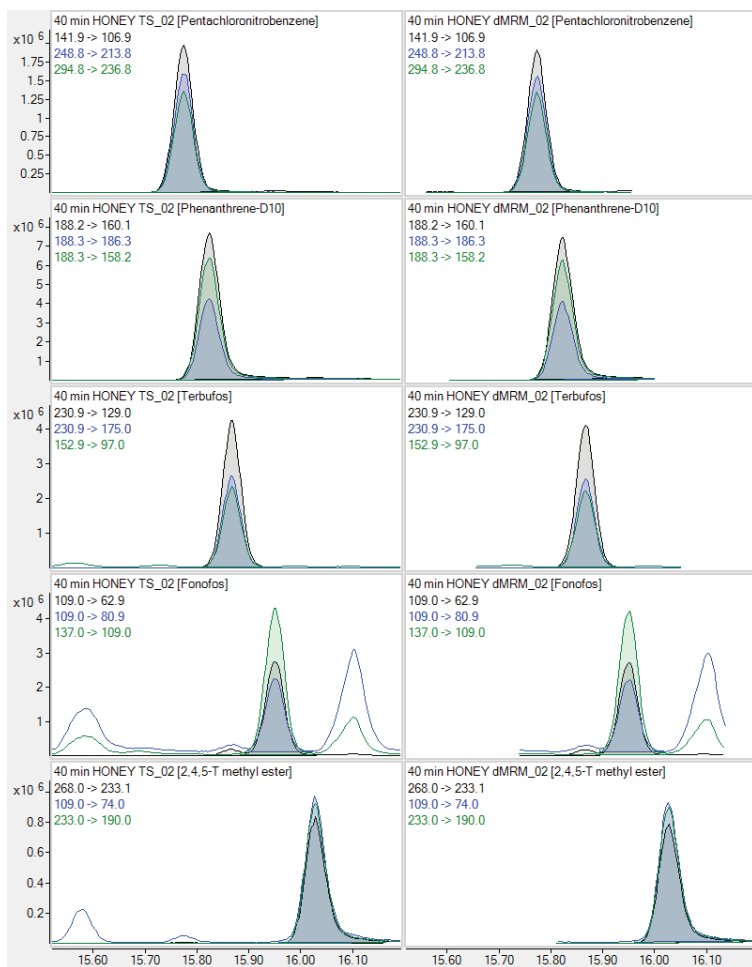


Figure 24. Organic honey TS chromatograms (left) and dMRM chromatograms (right) of selected compounds for RT range (40 minute method) in Agilent MassHunter Quantitative Analysis.

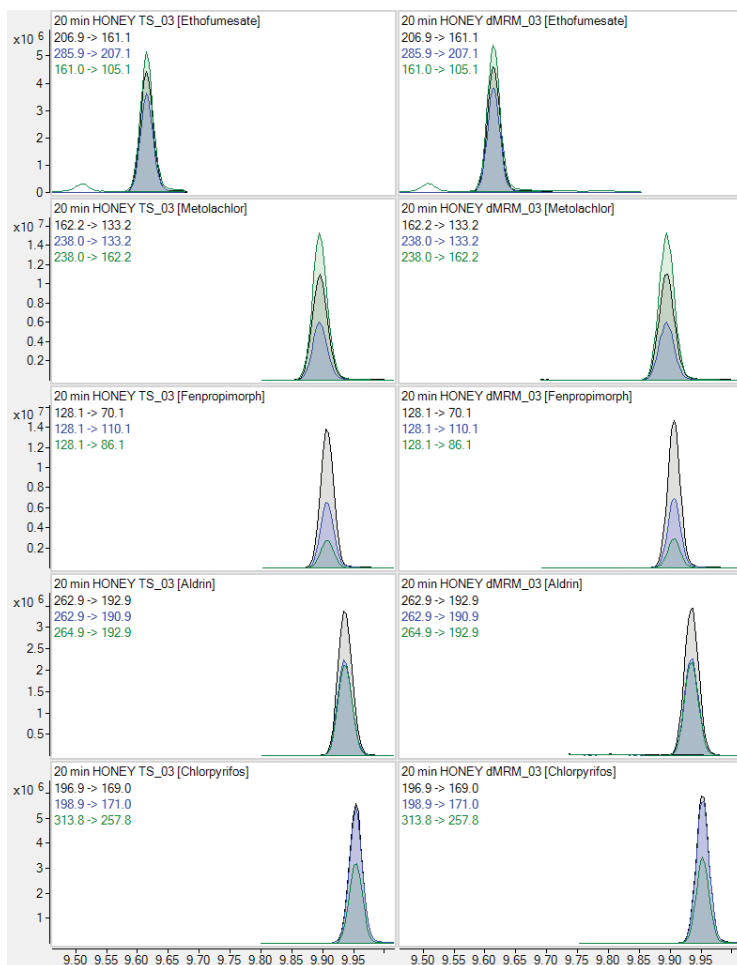


Figure 25. Organic honey TS chromatograms (left) and dMRM chromatograms (right) of selected compounds for RT range (20 minute method) in Agilent MassHunter Quantitative Analysis

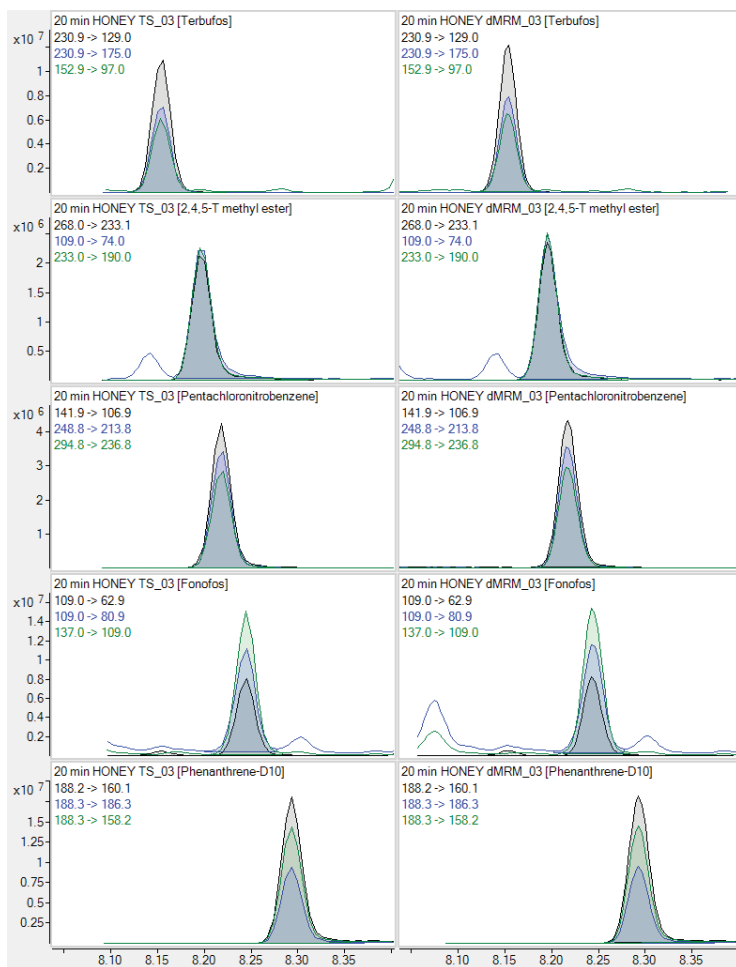


Figure 26. Organic honey TS chromatograms (left) and dMRM chromatograms (right) of selected compounds for RT range (20 minute method) in Agilent MassHunter Quantitative Analysis.

Conclusions

Standard GC/MS/MS Pesticide methods use TS acquisition methods with a gain of 10, dwell times of 10 msec, and 2-3 MRMs/compound. The Agilent MassHunter Data Acquisition's dMRM functionality for MS acquisition method development provides users the ability to achieve equivalent or better quality data and results by:

- Monitoring the MRM transitions based on the compounds' retention times as they elute from the GC
- Reducing the number of MRM transitions active at any given time allowing for longer dwell times
- Optimizing the dwell times to maintain a constant MS cycle time and constant sampling rate across all peaks

As sample complexity increases, the ability to use dMRM will provide laboratories with the capability to better tackle their large multi-analyte analysis, and to accurately quantify trace quantities of pesticides from high-throughput methods.

References

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2. Lehotay, S. J.; Mastovská, K.; Lightfield, A. R. J. *AOAC Int.* **2005**, *88*, 615-629.
3. Westland, J.; Stevens, J. *An Optimal Method for the Analysis of Pesticides in a Variety of Matrices*; Application note, Agilent Technologies, Inc. Publication number 5991-7303EN, **2016**.

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