Simultaneous determination of 16 mycotoxins in cereals using an Agilent Triple Quadrupole LC/MS system and e-Method

Application Note

Food Testing and Agriculture

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Abstract

A method for the simultaneous determination of 16 mycotoxins in major cereal species has been established using an Agilent Triple Quadrupole LC/MS system. Crushed samples of wheat and maize were extracted with an acetonitrile-water-acetic acid solution (70:29:1, v/v/v). The resulting sample solutions were then separated using an Agilent Eclipse Plus C18 column (2.1 × 100 mm, 1.8 µm), which was monitored by an Agilent Triple Quadrupole LC/MS system equipped with an Agilent Jet Stream electrospray ionization source. Fourteen ^{13}C-labeled mycotoxins were employed as stable isotope-labeled internal standards to improve method accuracy. The resulting method is rapid, simple, accurate, and cost effective, and exhibited good linear correlation, with regression coefficients (R^2) greater than 0.996. The recoveries of 16 mycotoxins in wheat and maize matrices at 3 levels were basically within 85–120%, and RSDs of the replicate sample assay fell within 0.7–8.2%. An FAPAS-positive sample was detected using this method, and the measured values agreed well with the specified values of FAPAS, demonstrating the accuracy of this method. Furthermore, a UHPLC-MS/MS e-Method for the simultaneous determination of 16 mycotoxins was established, greatly simplifying the process for method establishment and optimization. Inter-laboratory validation using the e-Method on different models of Agilent LC/MS systems in a number of laboratories worldwide verified the accuracy of the method and the utility of the e-Method.

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Introduction

Mycotoxins are a range of toxic or harmful substances emerging from the fungal growth process. Currently, more than 400 types of mycotoxins have been discovered in nature[1,2] that have carcinogenic, teratogenic, and mutagenic effects on humans and animals.[3,4] A variety of mycotoxins can be detected in grain; commonly found mycotoxins include aflatoxins (AFT), ochratoxins (OTA), zearalenone (ZEN), deoxynivalenols (DON), fumonisins (FB), and T-2 toxin (T-2). In order to provide safe grain for humans and animals, timely and rapid monitoring, detection, and control of mycotoxin contaminants in grain has become an important topic to countries all over the world.

At present, the primary assay methods for mycotoxins include thin-layer chromatography, fluorospectrometry, ELISA, liquid chromatography (LC), and LC/MS. For multi-residue and multi-contaminant analysis, liquid chromatography-tandem mass spectrometry has been proved to be a robust tool for enabling simultaneous detection of multiple mycotoxins in different cereal species with high sensitivity and selectivity.[5] A reliable quantitative method for the rapid and simultaneous determination of 16 mycotoxins commonly found in major cereal species has been established using an Agilent Triple Quadrupole LC/MS system. This method can meet the requirements for high-throughput and rapid monitoring of multiple mycotoxins commonly found in cereals.

Experimental

Reagents and Samples

All reagents and solvents were chromatographic or analytical grade. Methanol and acetonitrile were purchased from Merck, Germany. Formic acid, acetic acid, and ammonium acetate were purchased from Sigma-Aldrich, Inc. The following 16 mycotoxins and 14 isotope-labeled internal standards were purchased from Romer Labs in Austria: nivalenol (NIV), deoxynivalenol (DON), deoxynivalenol-3-glucoside (DON-3G), 3-acetyldeoxynivalenol (3-AcDON), 15-acetyldeoxynivalenol (15-AcDON), aflatoxin B_1 (AFB_1), aflatoxin B_2 (AFB_2), aflatoxin G_1 (AFG_1), aflatoxin G_2 (AFG_2), ochratoxin A (OTA), T-2 toxin (T-2), HT-2 toxin (HT-2), zearalenone (ZEN), fumonisin B_1 (FB_1), fumonisin B_2 (FB_2), sterigmatocystin (ST), [$^{13}C_{15}$]-NIV, [$^{13}C_{15}$]-DON, [$^{13}C_{17}$]-3-AcDON, [$^{13}C_{17}$]-AFB_1, [$^{13}C_{17}$]-AFB_2, [$^{13}C_{17}$]-AFG_1, [$^{13}C_{17}$]-AFG_2, [$^{13}C_{20}$]-OTA, [$^{13}C_{24}$]-T-2, [$^{13}C_{22}$]-HT-2, [$^{13}C_{18}$]-ZEN, [$^{13}C_{34}$]-FB_1, [$^{13}C_{34}$]-FB_2, and [$^{13}C_{18}$]-ST.

Apparatus and Equipment

Separation was carried out using an Agilent 1290 Infinity LC system equipped with Agilent components in two configurations as follows:

- G4220A binary pump, G4226A sampler, and G1316C TCC
- G7120A high-speed pump, G7167B Multi-sampler, and G7116B MCT

Agilent 6460/6470/6490/6495 Triple Quadrupole LC/MS systems with AJS electrospray ionization source were used for the analysis. Agilent MassHunter workstation software was used for data acquisition and qualitative and quantitative analysis.

Standards preparation

A single-standard stock solution for 16 mycotoxins was prepared. AFB_1, AFB_2, AFG_1, and AFG_2 were dissolved in methanol; FB_1 and FB_2 were dissolved in acetonitrile:water (50:50, v/v); the remaining compounds were dissolved in acetonitrile. All stock solutions were kept at -20°C. A portion of this mycotoxin single-standard stock solution was pipetted into a 10 mL volumetric flask and diluted with water with the total volume reaching to 10 mL to make a mixed mycotoxin standard working solution, which was kept at -20°C. The concentrations are shown in Table 1. A portion of the mycotoxin stable isotope-labeled single-standard solution was pipetted into a 10 mL volumetric flask and diluted with water with the total volume reaching to 10 mL to make a mixed stable isotope-labeled internal standard working solution, which was kept at -20 °C in the dark. The concentrations are shown in Table 2.

Table 1. Concentrations of constituents in the mixed standard working solution for 16 mycotoxins.

Name	Concentration (µg/mL)	Name	Concentration (µg/mL)
AFB_1	0.1	NIV	20
AFB_2	0.03	DON	15
AFG_1	0.1	DON-3G	2.5
AFG_2	0.03	3-AcDON	4
15-AcDON	2	HT-2	1
ZEN	2	ST	0.1
OTA	0.2	FB_1	2
T-2	0.2	FB_2	1

Table 2. Concentrations of constituents in the mixed standard working solution for 14 stable isotope-labeled internal standards.

Name	Concentration (µg/mL)	Name	Concentration (µg/mL)
[$^{13}C_{17}$]-AFB_1	0.01	[$^{13}C_{15}$]-NIV	2.5
[$^{13}C_{17}$]-AFB_2	0.01	[$^{13}C_{15}$]-DON	2
[$^{13}C_{17}$]-AFG_1	0.01	[$^{13}C_{17}$]-3-AcDON	1
[$^{13}C_{17}$]-AFG_2	0.01	[$^{13}C_{18}$]-ZEN	0.2
[$^{13}C_{20}$]-OTA	0.04	[$^{13}C_{34}$]-FB_1	0.5
[$^{13}C_{24}$]-T-2	0.05	[$^{13}C_{34}$]-FB_2	0.3
[$^{13}C_{22}$]-HT-2	0.125		
[$^{13}C_{18}$]-ST	0.025		

Sample preparation

Wheat and maize samples were crushed with a pulverizer, passed through a test sieve with a 1 mm pore size, then mixed well. A 5 g sample was put into a 50 mL centrifuge tube, into which 20 mL of acetonitrile-water-acetic acid mixed solution (70:29:1, v/v/v) as extration solvent was added, then the mixture was vortexed for 1 min and placed on a rotary shaker for 30 minutes. The solution was centrifuged at 6,000 r/min for 10 minutes; 0.5 mL of supernatant was pipetted into a 1.5 mL centrifuge tube, into which 0.5 mL water was added and mixed well by vortex mixing. The sample was then centrifuged at 12,000 r/min for 10 minutes at 4°C, and the supernatant was passed through a PTFE filter membrane with a 0.2 µm pore size. 180 µL of filtrate was pipetted into a 400 µL insertion tube, into which 20 µL mixed stable isotope-labeled internal standard working solution was added and then mixed well by vortex mixing for analysis.

LC conditions

Column:	Agilent Eclipse Plus C18, 2.1 × 100 mm, 1.8 µm, p/n 959764-902	
Flow rate:	0.3 mL/min	
Temperature:	35°C	
Injection volume:	2 µL	
Mobile phase:	A) Aqueous solution containing 1% acetic acid and 5 mmol/L ammonium acetate	
	B) Methanol	
Gradient elution procedure:	Time (min)	B%
	0.0	10.0
	2.0	10.0
	3.0	20.0
	7.0	24.0
	10.5	30.0
	13.5	60.0
	15.0	70.0
	18.0	75.0
	18.1	95.0
	21.9	95.0
	22.0	10.0

Mass spectrometric conditions

Agilent Triple Quadrupole LC/MS systems used in this study were equipped with an AJS electrospray ionization source; specific ionization source parameters are shown in Table 3. For Agilent 6490/6495 Triple Quadrupole LC/MS systems utilizing iFunnel ion transmission and focusing technique, the high pressure RF was 150(+)/90(-) and the low pressure RF was 60(+)/60(-).

Based on compound retention times, time segments were set for MS data acquisition (Table 4). Delta EMV was set depending on the model of each instrument in use separately to meet the requirements for sensitivity. To minimize the amount of matrix going into the spray chamber, the HPLC flow was diverted to waste for the first 1.8 minutes of the analysis, then again from 18 minutes until the end of the analysis.

MRM parameters of 16 mycotoxins and 14 isotope-labeled internal standards are shown in Table 5.

Table 3. Ionizaiton source parameters.

Parameter	Agilent 6460/6470 MS/MS	Agilent 6490/6495 MS/MS
Dry gas temperature	300°C	150°C
Dry gas flow rate	7 L/min	15 L/min
Nebulizer pressure	35 psi	35 psi
Sheath gas temperature	350°C	370°C
Sheath gas flow rate	11 L/min	12 L/min

Table 4. Time segments.

No.	Start time (min)	Valve	Capillary voltage (V)	Nozzle voltage (V)
1	0	To waste	3500(+/-)	0(+)/1000(-)
2	1.8	To MS	3500(+/-)	0(+)/1000(-)
3	3.6	To MS	3500(+/-)	0(+)/1000(-)
4	8.0	To MS	3500(+/-)	0(+)/1000(-)
5	12.4	To MS	3500(+/-)	0(+)/1000(-)
6	14.9	To MS	3500(+/-)	500(+)/1000(-)
7	16.5	To MS	2500(+/-)	500(+)/1000(-)
8	18.0	To waste	3500(+/-)	0(+)/1000(-)

Table 5. MRM parameters of 16 mycotoxins and 14 isotope-labeled internal standards.

Time segment	Compound name	Precursor ion (m/z)	Product ion (m/z)	Fragmentor (V)	Collision energy (V)	Polarity
2	[^{13}C]-NIV	386	295.1	90	10	Negative
	NIV	371	281.1*/59.1	90	10/30	Negative
3	[^{13}C]-DON	370.1	279.0	90	10	Negative
	DON	355.1	265.0*/247.0	90	10/10	Negative
	DON-3G	517.1	427.0*/247.0	120	20/20	Negative
4	15-AcDON	356.1	261.0/137.0*	90	15/15	Positive
	[^{13}C]-3-AcDON	356.2	245.1	110	10	Positive
	3-AcDON	339.2	231.1*/213.1	110	10/20	Positive
5	[^{13}C]-AFB_1	330.1	301.1	160	21	Positive
	AFB1	313.2	285.1*/241.1	160	22/38	Positive
	[^{13}C]-AFB_2	332.2	303.0	160	21	Positive
	AFB_2	315.2	287.1*/259.1	160	24/30	Positive
	[^{13}C]-AFG_1	346.1	257.1	150	25	Positive
	AFG_1	329.2	311.1*/243.1	150	20/25	Positive
	[^{13}C]-AFG_2	348.1	330.1	160	23	Positive
	AFG_2	331.2	313.1*/245.1	160	23/30	Positive
6	[^{13}C]-FB_1	756.5	356.4	180	45	Positive
	FB_1	722.4	352.3/334.3*	180	45/45	Positive
	[^{13}C]-T-2	508.3	322.1	110	10	Positive
	T-2	484.3	305.1*/185.1	110	10/20	Positive
	[^{13}C]-HT-2	464.1	278.1	100	10	Positive
	HT-2	442.2	263.1/215.1*	100	10/10	Positive
7	[^{13}C]-FB_2	740.5	358.3	180	45	Positive
	FB_2	706.5	336.3*/318.3	180	45/45	Positive
	[^{13}C]-OTA	424.2	250.1	120	25	Positive
	OTA	404.1	358.0/239.0*	120	10/25	Positive
	[^{13}C]-ST	343.1	327.1	150	20	Positive
	ST	325	310.0/281.0*	150	20/36	Positive
	[^{13}C]-ZEN	335.2	185.0	190	25	Negative
	ZEN	317.1	175.0*/130.8	190	25/33	Negative

Results and Discussion

Optimization of UHPLC-MS/MS conditions

Due to differences in the sensitivity of each compound, a single-standard solution with a concentration of 0.5-2.0 µg/mL was chosen to optimize MS parameters. Mycotoxin compounds are likely to form adduct ions such as $[M+H]^+$, $[M+NH_4]^+$, $[M+Na]^+$, $[M-H]^-$, $[M+HCOO]^-$ and $[M+CH_3COO]^-$, and the response intensity of each adduct ion depends on the nature of the compound and the composition of the mobile phase used. Both $[M+H]^+$ and $[M-H]^-$ for NIV showed weak response, and in the mobile phase containing acetic acid, the response of $[M+CH_3COO]^-$ increased significantly. DON-3G showed the same trend. Consequently, NIV, DON, and DON-3G were chosen for analysis in negative mode using $[M+CH_3COO]^-$ as the precursor ion. ZEN was also detected in negative mode, with $[M-H]^-$ as the precursor ion. Among mycotoxins detected in positive mode, $[M+NH_4]^+$ was selected as the precursor ion for 15-AcDON, T-2, and HT-2, while $[M+H]^+$ was chosen as the precursor ion for the remaining mycotoxins. For most compounds, the highest sensitivity was achieved when the nozzle voltage was set to 0 V under positive mode. However, for FB_1 and FB_2, setting an appropriate nozzle voltage led to a higher response. In this method, the nozzle voltage was set to 500 V during the time segment when FB_1 and FB_2 eluted. Although the sensitivity was lost to some extent for the other compounds during the same acquisition time segment, the response of FB_1 and FB_2 increased by over 50% compared to that obtained with the nozzle voltage of zero, enhancing the overall performance of this method.

To ensure formation of different adduct ions such as $[M+H]^+$, $[M+NH_4]^+$, $[M-H]^-$ and $[M+CH_3COO]^-$, sufficient concentrations of acetic acid and ammonium acetate were required in the mobile phase. Since 3-AcDON and 15-AcDON are isomers, the possibility of ion pair interference still remained, even though different ion pairs had been targeted. To minimize misjudgment in the case of a complex matrix, it was essential to optimize chromatographic conditions to separate both isomers by baseline. With the Eclipse Plus C18 column, an optimized gradient elution profile was applied to realize the baseline separation for the isomer pair, i.e., 3-AcDON and 15-AcDON. Consequently, 16 mycotoxins were well separated within 18 minutes (Figure 1). Among the 16 mycotoxins, 12 were detected under positive mode and 4 were detected under negative mode. According to the retention time, time segments were set for data acquisition. Since ZEN and OTA were coeluted in the same time segment but detected under different polarity, rapid polarity switching mode was selected in the corresponding time segment.

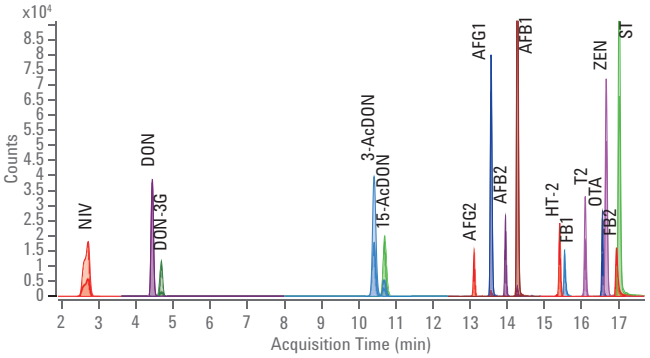

Figure 1. Overlaid MRM chromatograms of the mixed standard working solution for 16 mycotoxins.

Calibration curve

Appropriate volumes of the mixed mycotoxin standard working solution were accurately pipetted and serially diluted with acetonitrile-water-acetic acid solution (35:64.5:0.5, v/v/v) to make a series of mixed standard working solutions with different concentrations. Thereafter, a 20 µL mixed standard working solution for 14 stable isotope-labeled internal standards was added to a 400 µL insertion tube, into which 180 µL of each prepared serial standard working solution was pipetted. After vortex mixing, the mixture was loaded for the generation of internal standard calibration curves (Figure 2). All 16 mycotoxins showed good linearity, with correlation coefficients (R^2) greater than 0.996. Since neither DON-3G nor 15-AcDON have corresponding commercialized stable isotope-labeled internal standards, [$^{13}C_{15}$]-DON and [$^{13}C_{17}$]-3-AcDON, which are analogous to them in structure, were used as their internal standards, respectively.

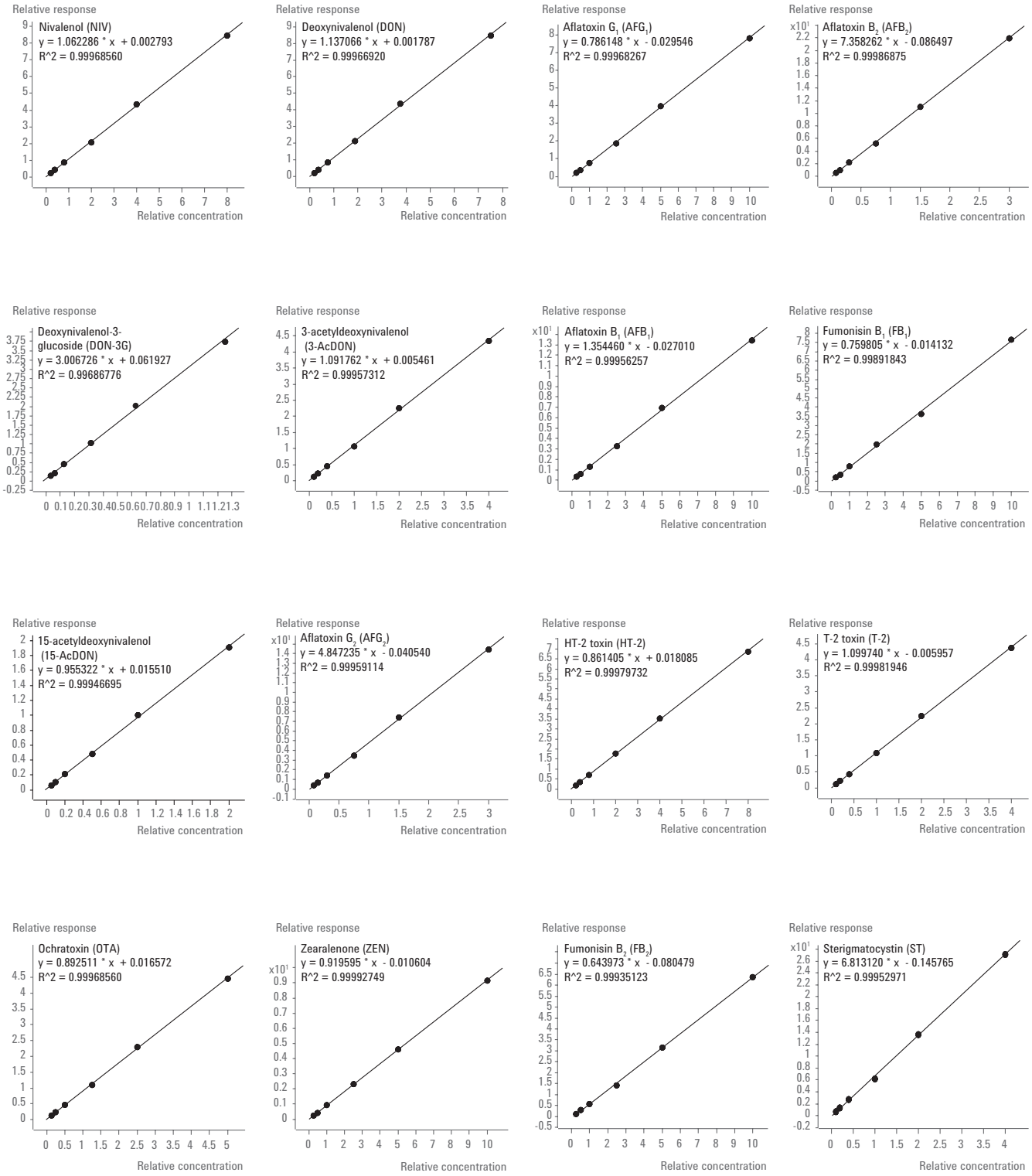

Figure 2. Calibration curves for 16 mycotoxins.

Recovery and positive sample analysis

Mixed mycotoxin standard working solutions with high, medium, and low concentrations were added to the blank samples (wheat and maize), followed by sample preparation and instrumental analysis based on the above optimized method. The spiked concentrations, recovery rates, and relative standard deviations (RSDs) are shown in Table 6. For 16 mycotoxins at three levels in two kinds of cereal matrices, the majority of the spiked recoveries were within 85–120% and the RSDs of the replicate duplicate sample assays were within 0.7–8.2%. Figure 3 shows the overlaid TIC chromatograms of 6 consecutive injections for the spiking recovery test in the maize matrix, demonstrating the method is highly stable.

Analysis of the FAPAS test sample showed good agreement between the measured and specified values (Table 7), demonstrating the reliability of this method. The sample preparation procedure in this method is simple, with no need for a cleanup step, and enabled accurate quantitation of 16 mycotoxins in cereals.

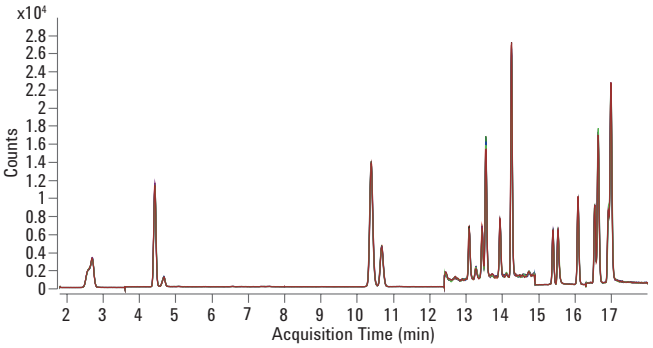

Figure 3. Overlaid TIC spectra of 6 consecutive injections of spiked samples in maize matrix.

Table 6. Spike recovery and precision values of 16 mycotoxins in wheat and maize matrices.

Compound	Spiked concentration (µg/kg)	Wheat		Maize		Compound	Spiked concentration (µg/kg)	Wheat		Maize	
		Recovery (%)	RSD (%)	Recovery (%)	RSD (%)			Recovery (%)	RSD (%)	Recovery (%)	RSD (%)
NIV	100	97.2	1.6	103.1	1.8	AFB_1	0.5	113.3	2.2	123.6	3.1
	200	88.0	2.3	97.5	4.1		1	100.4	3.6	108.1	7.3
	500	92.3	0.9	87.3	1.3		2.5	102.4	2.3	91.1	4.9
DON	75	109.3	1.8	109.7	2.7	HT-2	5	113.8	2.6	113.0	3.8
	150	101.5	1.9	105.0	4.1		10	107.2	3.2	111.7	6.1
	375	100.7	1.8	92.9	1.8		25	101.9	3.8	101.0	4.5
DON-3G	12.5	105.6	4.8	106.1	2.5	FB_1	10	87.7	5.5	94.3	8.2
	25	88.8	2.1	97.2	4.2		20	70.9	6.0	86.0	8.1
	62.5	93.5	6.2	85.7	1.6		50	85.5	5.7	91.4	5.4
3-AcDON	20	110.8	1.9	113.1	2.0	OTA	1	114.4	4.0	113.8	7.3
	40	92.8	1.0	105.4	3.4		2	95.2	1.1	102.8	4.0
	100	100.0	0.9	93.5	1.2		5	95.1	4.0	86.4	2.8
15-AcDON	10	115.9	2.7	115.9	3.1	T-2	1	119.5	2.4	114.9	2.3
	20	102.1	1.4	106.5	3.2		2	108.8	4.0	112.1	4.2
	50	103.4	1.1	97.2	1.9		5	99.6	3.5	97.4	3.3
AFG_2	0.15	102.8	5.3	127.3	4.0	ZEN	10	116.7	1.5	107.6	2.8
	0.3	105.5	6.1	106.2	3.0		20	106.9	1.7	105.3	6.0
	0.75	96.1	4.0	93.5	2.8		50	106.0	1.9	95.2	2.0
AFG_1	0.5	118.7	3.1	128.2	2.8	ST	0.5	111.3	1.5	113.2	2.1
	1	102.1	4.1	109.5	4.9		1	96.4	4.4	102.4	4.2
	2.5	96.1	4.0	94.5	3.4		2.5	100.6	3.0	92.7	2.7
AFB_2	0.15	129.4	5.5	104.9	4.8	FB_2	5	107.5	3.8	109.8	4.7
	0.3	105.6	1.4	105.0	3.4		10	85.1	2.4	93.1	0.7
	0.75	99.9	1.9	94.4	6.7		25	94.1	5.7	89.9	4.0

Table 7. Specified and measured values of the FAPAS sample.

Analyte	Specified value (µg/kg)	Measured value (µg/kg)
DON	1247±193	1239.4
AFB_1	5.42±1.19	5.2
FB_1	797±202	760.3
FB_2	360±91.5	330.3
T-2	160±33.7	145.7
HT-2	105±23.1	108.2
ZEN	286±55.2	303.4
OTA	2.4±0.53	2.3

Use of the UHPLC-MS/MS e-Method

Introduction of the e-Method

As many parameters are involved in an LC/MS multi-residue assay, a lot of instrumental parameters have to be optimized when creating a new LC-MS/MS method, requiring much time and effort. To enhance efficiency, we took advantage of state-of-the-art performance of the Agilent LC/MS system in combination with unique features of its MS software to establish an e-Method with "plug-and-play" functionality. Using such an approach, data acquisition and quantitative analysis can be quickly carried out after verifying the instrumental configuration, selecting the corresponding e-Method, and simple testing. Thereby, the developing time can be greatly shortened and the application difficulty can be reduced. Application of an e-Method allows standardization of the analysis process within a laboratory and easy promotion of the method among laboratories.

The e-Method consists of three parts:

1. *.m file – A method file that can be directly invoked by MassHunter acquisition software. The method file in this format contains LC parameters, ionization source parameters for the triple quadrupole LC/MS system, and acquisition parameters of an MRM mode for 16 mycotoxins and 14 stable isotope-labeled internal standards.

2. *.quantmethod.xml file – A target compound quantitative method file that can be directly used by MassHunter quantitative analysis software. 16 mycotoxins are quantitated by an internal standard method, and a concentration series of isotope-labeled internal standard calibration curves is set in accordance with the industrial standard of grain and oils inspection (Inspection of Grain and Oils–Determination of 16 Mycotoxins in Cereals).

3. *.pdf file – Contains user instructions and remarks for the e-Method.

Invoking the e-Method acquisition method

After verifying instrumental configuration and opening acquisition software, the *.m acquisition method file corresponding to the instrument model can be directly invoked. After checking the parameter settings for the LC and MS modules sequentially, sample analysis can be conducted.

The standard solution at the lowest point of the concentration series for calibration curves should be examined first, and the retention time of each compound checked to ensure that the time segment setting in the method under the specific laboratory conditions is appropriate. The starting time point of a time segment can be adjusted according to the elution time window for the compounds when necessary. The peak area of each compound should be checked to see if the ΔEMV setting in the method is appropriate, and the ΔEMV setting in corresponding time segment can be modified according to the actual peak area when necessary.

Invoking and updating the e-Method quantitative method

To perform quantitative analysis, open MassHunter Quantitative Analysis software, select "Create batch" and import data to be quantitatively analyzed into the batch. Select data for a higher concentration standard, invoke quantitative method *.quantmethod.xml in the e-Method as shown in Figure 4, and enter the editing interface of quantitative method.

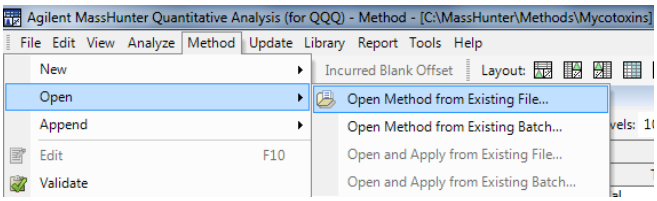

Figure 4. Invoking the quantitative method.

In the editing interface of the quantitative method, choose "Update Retention Times..." as shown in Figure 5, select the compound(s) for which the retention time needs to be updated, and click "Select All"; the software will update the retention time automatically in the quantitative method according to the acquired data. Following a similar procedure, you can update ratios of qualitative ions to quantitative ions by clicking "Update Qualifier Ratios...".

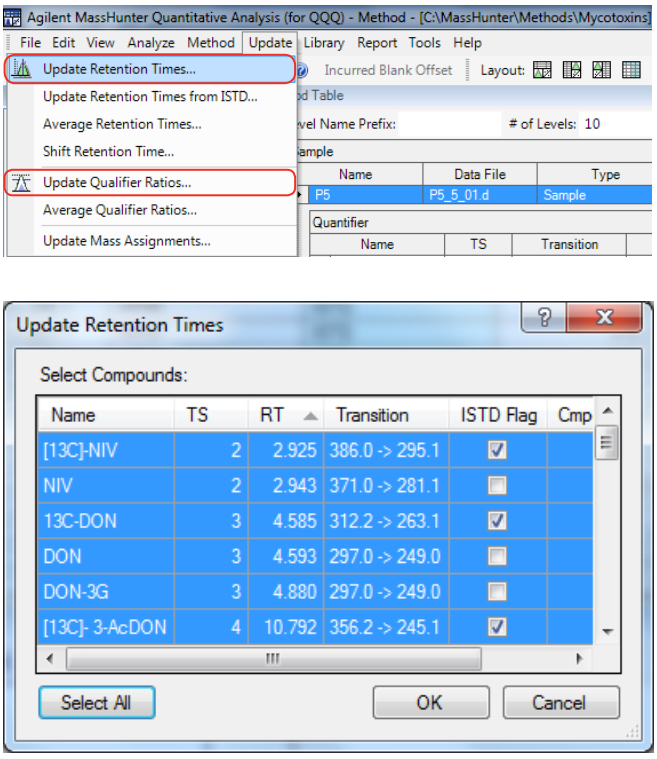

Figure 5. Updating retention times and qualifier ratios.

In the *.quantmethod.xml file, the concentration series for calibration curves of 16 mycotoxins are set in accordance with the industrial standard of grain and oils inspection (Inspection of Grain and Oils–Determination of 16 Mycotoxins in Cereals). Researchers may also modify the concentration series for calibration curves under the "Concentration Setup" section of the editing interface, as needed.

Inter-laboratory validation using the e-Method

Using the e-Method established in this application note, inter-laboratory validation was carried out among a number of laboratories worldwide, involving instruments such as Agilent 6460/6470/6490/6495 Triple Quadrupole LC/MS systems. All results met the required validation standards, demonstrating the accuracy of the method and the feasibility of applying the e-Method among laboratories. The e-Method makes it easier to promote and standardize the LC-MS/MS determination method among laboratories, greatly simplifying method establishment and optimization and making instrument operation easier and faster, thus shortening the analysis cycle and improving efficiency.

Conclusion

In this application note, an analytical method capable of rapid and accurate determination of mycotoxins in major cereal species has been established and successfully applied to the analysis of 16 mycotoxins in wheat and maize. An FAPAS-positive sample was analyzed using the method established in this application note, and the measured values agreed well with the specified values from FAPAS. This method allows simple preparation, requires less time, and yields good linear correlation, with sensitivity, recovery, and precision meeting the requirement for analysis of mycotoxins in cereals. It is therefore promising for application to routine monitoring of mycotoxins in cereals. The establishment and application of the e-Method simplifies its development and enables "plug-and-play" functionality, benefitting both the promotion and standardization of the LC-MS/MS method among laboratories.

The e-Method described in this application note is available at www.agilent.com/zh-cn/promotions/020617-mycotoxin-grain-cn

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