Determination of Aflatoxins in Food by LC/MS/MS

Abstract

A sensitive and selective analytical method for the determination of aflatoxin G1, G2, B1, and B2 residues in cereals using the Agilent G6410AA LC/MS Triple Quadrupole Mass Spectrometer was developed. This method uses simple sample preparation methods followed by LC/MS/MS. The limits of detection for all aflatoxins were less than 1 ng/mL in cereals.

Introduction

Aflatoxins (AFs) belong to a closely related group of secondary fungal metabolites. These mycotoxins are severely toxic metabolites produced mainly by Aspergillus flavus and A. parasiticus, and exposure to them can cause cancer in humans and livestock [1]. Based on epidemiological evidence, AFs have been classified as human liver carcinogens by the World Health Organization and by the U.S. Environmental Protection Agency. Thus, accurate determination of AFs is required to avoid human disease from AF exposure and to advance worldwide surveillance of food. Analysis of AFs in food products is routinely performed by thin-layer chromatography (TLC) and liquid chromatography (LC) with fluorescence detection (FD) in combination with both precolumn derivatization and post-column derivatization. The LC/FD technology is often used due to the high selectivity and sensitivity of these methods. Furthermore, hyphenated techniques such as LC coupled to mass spectrometric (MS) detection have been developed and applied in residual analysis of foods. The high selectivity and sensitivity of MS detection methods associated with the resolution of LC provide decisive advantages to perform qualitative as well as quantitative analysis of a wide range of molecules at trace levels. Several papers describing different kinds of MS methods for the analysis of AFs have been published [2-4.]

Experimental

Sample Preparation

The samples analyzed (peanuts, corn, nutmeg, and red pepper) were obtained from a local market and did not include any AFs. The extraction and cleanup steps for AFs were carried out according to validated methods reported by Tanaka [5]. Briefly, 20 g fine ground sample was poured into a 200-mL Erlenmeyer flask, followed by adding 40 mL acetonitrile-water (9:1, v/v) for corn and cereals. After shaking for 30 min, the mixed solution was centrifuged for 5 min at 1,650 g. The supernatant obtained was filtered through a glass microfiber GF/B grade filter (Whatman Interna-
tional Ltd, Maidstone, UK). A 5-mL portion of the filtrate was applied to a MultiSep number 228 cartridge column for the cleanup. After passing through at a flow rate of 1 mL/min, 2 mL of the first eluate was collected. The eluate was evaporated to dryness at 40 °C under a gentle stream of nitrogen. The residue was reconstituted in 1 mL methanol-water (4:6 v/v) containing 10 mM ammonium acetate.

**Standard Preparation**

Each of the standard reagents, aflatoxin G₂ (AFG₂), aflatoxin G₁ (AFG₁), aflatoxin B₂ (AFB₂) and aflatoxin B₁ (AFB₁), was dissolved in acetonitrile at 1 mg/mL and was stored at 4 °C in the dark until use. To prepare the working standard for LC/MS analysis, each AF stock solution was equally pipetted and transferred to a vial, and it was then diluted with the mobile phase. The final concentration of each AF was 1 ng/mL.

**Chemicals**

The standards AFG₂, AFG₁, AFB₂, and AFB₁ were obtained from Sigma Aldrich Japan (Tokyo, Japan). The purity of these compounds was greater than 99%. Ammonium acetate, toluene, HPLC-grade acetonitrile, and HPLC-grade methanol were obtained from Wako Chemical (Osaka, Japan). Water was purified in-house with a Milli-Q system (Millipore, Tokyo, Japan). The cartridge column of MultiSep number 228 was purchased from Showa Denko (Kanagawa, Japan).

**LC/MS Instrument**

The LC/MS/MS system used in this work consists of an Agilent 1200 Series vacuum degasser, binary pump, well-plate autosampler, thermostatted column compartment, the Agilent G6410 Triple Quadrupole Mass Spectrometer with an electrospray ionization (ESI) source. The objective of the method development was to obtain a fast and sensitive analysis for quantifying AFs in foods. For chromatographic resolution and sensitivity, different solvents and columns were optimized. It was found that a simple solvent system using water, methanol, ammonium acetate, and a 1.8-µm particle size C18 column worked very well.

**LC Conditions**

- **Instrument:** Agilent 1200 HPLC
- **Column:** ZORBAX Extend C18, 100 mm × 2.1 mm, 1.8 µm (p/n 728700-902)
- **Column temp:** 40 °C
- **Mobile phase:** A = 10 mM ammonium acetate in water B = Methanol 40% A/60% B
- **Flow rate:** 0.2 mL/min
- **Injection volume:** 5 µL

**MS Conditions**

- **Instrument:** Agilent 6410 LC/MS Triple Quadrupole
- **Source:** Positive ESI
- **Drying gas flow:** 10 L/min
- **Nebulizer:** 50 psig
- **Drying gas temp:** 350 °C
- **Vcap:** 4000 V
- **Scan:** m/z 100 – 550
- **Fragmentor:** Variable 100 V
- **MRM ions:** Shown in Table 1
- **Collision energy:** Shown in Table 1

**LC/MS/MS Method**

Quantitative analysis was carried out using MRM mode. The parameters for MRM transitions are shown in Table 1.

### Table 1. Data Acquisition Parameters of MRM Transitions for Each Aflatoxin

<table>
<thead>
<tr>
<th>No</th>
<th>Mycotoxins</th>
<th>RT (min)</th>
<th>Molecular weight</th>
<th>Precursor ion (m/z)</th>
<th>Product ion (m/z)</th>
<th>Collision energy (V)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Aflatoxin G₂</td>
<td>5.21</td>
<td>330</td>
<td>331</td>
<td>245</td>
<td>30</td>
</tr>
<tr>
<td>2</td>
<td>Aflatoxin G₁</td>
<td>6.61</td>
<td>328</td>
<td>329</td>
<td>243</td>
<td>30</td>
</tr>
<tr>
<td>3</td>
<td>Aflatoxin B₂</td>
<td>8.44</td>
<td>314</td>
<td>315</td>
<td>259</td>
<td>30</td>
</tr>
<tr>
<td>4</td>
<td>Aflatoxin B₁</td>
<td>10.89</td>
<td>312</td>
<td>313</td>
<td>241</td>
<td>30</td>
</tr>
</tbody>
</table>
Results and Discussion

Optimization of MRM Transitions

Determination of the optimal MRM transitions for each aflatoxin was carried out using single-MS full-scan mode followed by product ion scan mode using taflatoxin standard mixtures at 1 µg/mL. Mass spectra of these standard mixtures in full scan mode and product ion scan mode are shown in Figures 1 and 2. The mass spectrum of each aflatoxin by full-scan mode exhibited the protonated molecule [M+H]⁺ as the base peak ion. These ions were selected as precursor ions for MRM mode. The optimum collision voltage is compound dependent. To establish the optimum collision voltage, this parameter was varied from 5 to 40 V using a step size of 5 V. As shown in Figure 2, a distinct optimum in the intensity of the product ion of each AF was observed at 30 V. The product ions that indicated the highest intensity were m/z 245 (AFG₂), 243 (AFG₁), 259 (AFB₂), and 241 (AFB₁), respectively. On the basis of the above results, the collision voltage was set to 30 V.

Table 1 shows the parameters of MRM mode of each aflatoxin.

![Figure 1. Mass spectra of four aflatoxins standard in single-MS full-scan mode at 1 µg/mL (A): aflatoxin G₂, (B): aflatoxin G₁, (C): aflatoxin B₂, and (D): aflatoxin B₁.](image-url)
The MRM chromatogram of each aflatoxin at 0.1 ng/mL is shown in Figure 3. These show excellent signal-to-noise (S/N) ratios for all aflatoxins. The limit of detection (LOD) for each aflatoxin was determined using an S/N ratio of 3 with this MRM chromatogram and is shown in Table 2. To evaluate the linearity of the calibration curves, various concentrations of aflatoxin standard solutions ranging from 0.1 ng/mL to 100 ng/mL were analyzed. As shown in Figure 4 and Table 2, the linearity was very good for all aflatoxins with correlation coefficients ($r^2$) greater than 0.999.

Figure 2. Mass spectra of four aflatoxins standard in product ion scan mode at 1µg/mL (A): aflatoxin G2, (B): aflatoxin G1, (C): aflatoxin B2, and (D): aflatoxin B1.
Figure 3. MRM chromatograms of four aflatoxin standards at 0.1 ng/mL in MRM mode.

Figure 4. Calibration curves of four aflatoxins ranged from 0.1 ng/mL to 100 ng/mL.
Table 2. Linearity and LODs of Four Aflatoxins

<table>
<thead>
<tr>
<th>No</th>
<th>Mycotoxins</th>
<th>$r^2$</th>
<th>LOD (ng/mL)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Aflatoxin G$_2$</td>
<td>0.9999</td>
<td>0.025</td>
</tr>
<tr>
<td>2</td>
<td>Aflatoxin G$_1$</td>
<td>0.9992</td>
<td>0.020</td>
</tr>
<tr>
<td>3</td>
<td>Aflatoxin B$_2$</td>
<td>0.9999</td>
<td>0.025</td>
</tr>
<tr>
<td>4</td>
<td>Aflatoxin B$_1$</td>
<td>0.9993</td>
<td>0.020</td>
</tr>
</tbody>
</table>

The matrix effect of this method was investigated by using cereal and corn extracts spiked with mycotoxin standards at 0.2 ng/mL. Typical MRM chromatograms of cereal and corn extract are shown in Figures 5 and 6, respectively. There were no additional peaks from sample matrix in either food when compared with the mycotoxin standard mixture. These results indicate that MRM mode has very high selectivity.

Figure 5. MRM of four aflatoxins in cereal extract spiked at 0.2 ng/g.
Furthermore, the change on the peak intensity of each aflatoxin by the sample matrix was investigated by comparison with the peak intensity of aflatoxin standards. As these results show in Table 3, the relative intensity of each pesticide ranged from 88 to 96%. Thus, matrix effects such as ion suppression may be insignificant and it is possible to use external standards instead of matrix-matched standards.

Table 3. Relative Intensity of Each Aflatoxin in Sample Extracts

<table>
<thead>
<tr>
<th>No</th>
<th>Mycotoxins</th>
<th>Relative intensity (%)</th>
<th>Cereal</th>
<th>Corn</th>
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<tbody>
<tr>
<td>1</td>
<td>Aflatoxin G2</td>
<td>88</td>
<td>91</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Aflatoxin G1</td>
<td>92</td>
<td>94</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Aflatoxin B2</td>
<td>93</td>
<td>96</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Aflatoxin B1</td>
<td>97</td>
<td>95</td>
<td></td>
</tr>
</tbody>
</table>

Conclusions

The multi-aflatoxin method by LC/MS/MS described here was suitable for the determination of four aflatoxins in cereal and corn extract due to its high sensitivity and high selectivity. Another advantage of this method is that ion suppression was not observed for all food samples studied. Thus, it may eliminate the need for matrix-matched standards, which makes analysis more tedious for samples from different origins.

References
