

Investigation of Naturally Occurring
Fumonisin B₁ and Glycated Fumonisin
B₁ in Korean FeedstuffsJongsung Ahn^{1*}, Hyenjong Kim¹ and Kwang-Yeop Jahng²¹National Agricultural Products Quality Management Service, Seoul 150-804, Korea²Division of Biological Sciences and Basic Science Research Institute, Chonbuk National University, Korea

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Abstract

Mycotoxins are potentially dangerous contaminants of livestock feeds. In this study, we measured the levels of fumonisin B₁ and glycated fumonisin B₁ in feedstuffs and then investigated the ability of the extrusion heating regimen to convert the most prevalent mycotoxin contaminant, fumonisin B₁, to a less toxic glycated form. All feed samples were analyzed with fully validated methods. All measured concentrations of fumonisin B₁ were below harmful thresholds, including European Union-recommended levels or US Food and Drug Administration action levels.

Because fumonisin B₁ was highly contaminated mycotoxin in our present investigation and fumonisin B₁ has been shown to be less toxic following Maillard type reaction with reducing sugar, we examined the formation of fumonisin B₁ derivatives by Maillard reaction under extrusion process conditions. We employed a variety of tandem mass spectrometric methodologies to selectively detect fumonisin B₁ derivatives and to elucidate their structures partially. We found that compounds of *m/z* 736 were more likely artifacts or side reaction products rather than glycation products. N-(carboxymethyl) fumonisin B₁ of *m/z* 780 and other major glycation products of *m/z* 794 and 810 were not detected, and only negligible amounts of methylene fumonisin B₁ was found in 10 extruded feed samples. Therefore, either the tested extrusion conditions did not induce fumonisin B₁ glycation or the glycation products simply could not be detected by the method employed in this study.

Introduction

Mycotoxins are secondary fungal metabolites generated in various agricultural commodities during standing crop, harvest, and post-harvest stages. Mycotoxins have adverse health effects on livestock as well as humans. Out of more than 300 mycotoxins, Aflatoxins (AFs), Ochratoxin A (OTA), and Fumonisin Bs (FBs) are considered to present the most serious economic setback as well as risk factors to animals (Figure 1). *Fusarium* genera produce approximately 170 trichothecenes including DON, NIV, T-2, and, fumonisins. Ingestion of FB₁, which is frequently found in corn crops worldwide, has been associated with leucoencephalomalacia in both horses and rabbits, pulmonary edema in pigs, and nephrotoxicity and liver cancer in rats [1-4]. Interestingly, various reports have highlighted the possibility that FB₁ toxicity might be reduced by a Maillard type reaction of the FB₁ amino group with reducing sugar [5-7]. For example, Lu et al. [6] reported that a FB₁-fructose reaction mixture fed to diethyl nitrosamine-initiated Fischer344/N rats resulted in significantly less hepatic cancer promotion than FB₁ alone.

In this study, we had two aims. First, we generated data on contamination of feedstuffs by fumonisin B₁ as of 2013. All samples were analyzed with fully validated methods. Secondly, we studied the ability of a heating regime to reduce FB₁ toxicity, since glycation of FB₁ has been suggested as a decontamination process. We investigated the presence of FB₁ analogues transformed by glycation during extrusion processing from commercial feedstuffs.

The key to the second experimental set was to unambiguously identify glycated FB₁ from a model reaction [6]. Tandem mass spectrometry combined with liquid chromatography (LC-MS/MS) is a powerful technique for studying drug metabolites. In this technique, a parent compound undergoes alteration on a certain moiety, such as oxidation or conjugation, while maintaining its basic structure [7-9]. Likewise, FB₁ was assumed to experience modification of its amino group during the glycation process. Hence, a similar approach to the characterization of drug metabolites was adopted in this study.

Materials and Methods

Samples and Chemicals

Thirty samples of compound feed were collected at manufacturing sites and submitted to our laboratory by field officers. Acetonitrile (HPLC grade) was obtained from Fisher Scientific

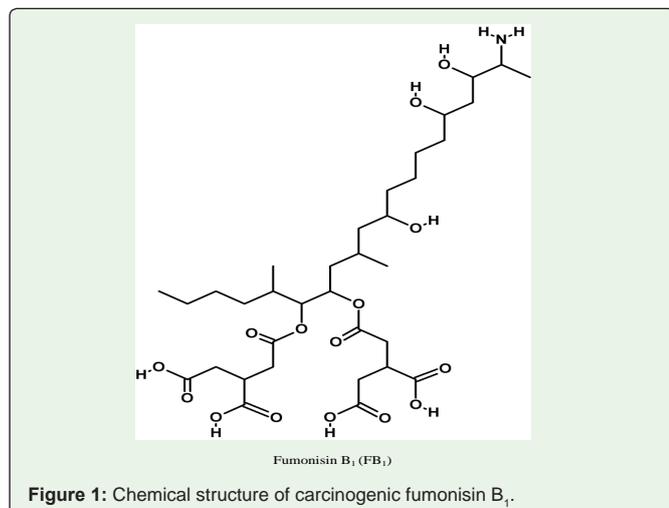


Figure 1: Chemical structure of carcinogenic fumonisin B₁.

(Schwerte, Germany), water for the HPLC mobile phase was distilled twice, and glucose and formic acid were obtained from Merck (Darmstadt, Germany). Fumonisin B₁ standards and internal standards, ¹³C₃₄-FB₁ was purchased from Biopure GmbH (Tulln, Austria). O-Phthaldialdehyde (OPA) 2-mercaptoethanol and a phosphate-buffered saline (PBS, pH 7.4) were purchased from Sigma-Aldrich (Seoul, Korea). Fumoniprep (Rbiopharm, Glasgow, UK) were used for Immunoaffinity Column (IAC) cleanup. All other solvents and reagents were analytical grade or High Performance Liquid Chromatography (HPLC) grade as appropriate.

Quantification of FB₁ with LC-MS/MS after IAC Enrichment

Each 20-g feed sample with 40 ng ¹³C-labeled FB₁ in 50 mL of ACN-MeOH-water (25+25+50, V/V/V) was shaken for 20 min on an orbital shaker in a 250-mL centrifuge bottle. The mixture was then centrifuged at 2500 × g for 2 min. The supernatant (10 mL) was mixed with PBS (40 mL) in a 100-mL flask and filtered with a microfiber filter. Filtrate (10 mL) was applied to each IAC by gravity and then washed with 10 mL PBS. Adsorbed FB₁ on IAC was eluted with 1.5 mL LC grade methanol by back-flushing at least three times. Sample volume was adjusted to 3 mL by passing 1.5 mL water through the column. Each 10-μL sample was injected into an Agilent HPLC 1200 series and separated over an A 150 × 4.6 mm Hypersil GOLD ODS column (5-μm particle size, Thermo Fisher, Runcorn, UK) at 35°C. The system was programmed to elute with a gradient of 0.2% formic acid in water (mobile phase A) and 0.2% formic acid in ACN (mobile phase B) for a run time of 22 min at a flow rate of 0.9 mL/min according to the following schedule: 2 min, 95% A; 10 min, 50% A; 2 min, 0% A; 4 min, 0% A; 2 min, 95% A; and 4 min, 95% A. The HPLC was coupled through a turbo ion source to a Qtrap tandem mass spectrometer (AB 3200 Qtrap, Toronto, Canada). Infusion of each standard solution was conducted to optimize parameters for Electro Spray Ionization (ESI) acquisition. Parameters were 30 psi curtain gas, medium collision gas, 5.2-kV ion spray voltage, and 600°C turbo gas temperature. Additional parameters are listed in Table 1 and Recovery of fumonisin B₁ in feed are listed in Table 2.

Model Experiment of Fb₁ Incubation for Maillard Reaction

One mL solution containing 139 μM FB₁ and 100 mM d-glucose with 50 mM phosphate buffer (pH 7.4) was prepared in a 30-mL headspace vial and cooked for 48 h at 80°C [6]. The aqueous reaction

Table 1: Optimized parameters of LC-MS/MS.

Mycotoxins	Q1	Q3	Declustering potential	Entrance potential	Collision energy
FB ₁	722.4	334.5	91	8	53
	722.4	352.4	91	8	43
¹³ C ₃₄ -FB ₁ ^a	756.4	356.5	91	8	53
	756.4	374.5	91	8	43

¹³C₃₄-FB₁^a: Internal standard for fumonisin B₁.

Table 2: Recovery of fumonisin B₁ in feed.

Mycotoxins	Recovery (%)	Mean ± SD	%RSD	Spiked (μg/kg)	LOD (μg/kg)	LOQ (μg/kg)
FB ₁ (N=3)	91.33	45.66±3.05	6.69	50	0.07	0.22
	98.26	245.66±26.54	10.80	250		

mixture was lyophilized immediately after being cooled to room temperature. The resultant dry matter was reconstituted in 1 mL of acetonitrile-distilled water (50+50, v/v) and stored at 4°C until analysis.

Detection of Fb₁ Analogues Derived by Maillard Reaction

All samples were filtered through a 4-μm microfiber filter before loading into a column. Precolumn derivatization with OPA was conducted according to a previously described methodology [1]. Chromatographic separation was performed on a Phenomenex ultracarb 5 ODS (150 × 4.6 mm, 5-μm, Torrance, CA, USA). Gradient elution was employed for satisfactory separation as follows: initial elution with solvent A (0.2% formic acid in water), a 5-min isocratic step, a linear increase in solvent B (0.2% in acetonitrile) over 35 min until the column was saturated with solvent B, and a final 10-min step. The flow rate was 300 μL/min.

To identify and measure FB analogues semi-quantitatively, precursor ion scans, neutral loss scans, product ion scans, and multiple reaction monitoring scans were performed with Qtrap combined with chromatographic separation. The optimized parameters for FB₁ were used equally for the detection of FB analogues. The sample preparation method described by Seefelder, et al. [5] was followed to determine FB₁ derivatives in extruded samples.

Results and Discussion

Contamination of Feedstuffs by Mycotoxins

The major ingredients of many livestock feeds are imported and then manufactured into various compound feeds in Korea. When main ingredients were imported, analysis-based certification of their quality is usually required by the trading company. Therefore, legislative framework or guidance implemented by the importing country is very important to ensure that feeds of poor quality are not circulated freely in the market. Regulation limits for AFB₁ and OTA are set to 20 and 50 μg/kg, respectively, in compound feeds in Korea, Table 3.

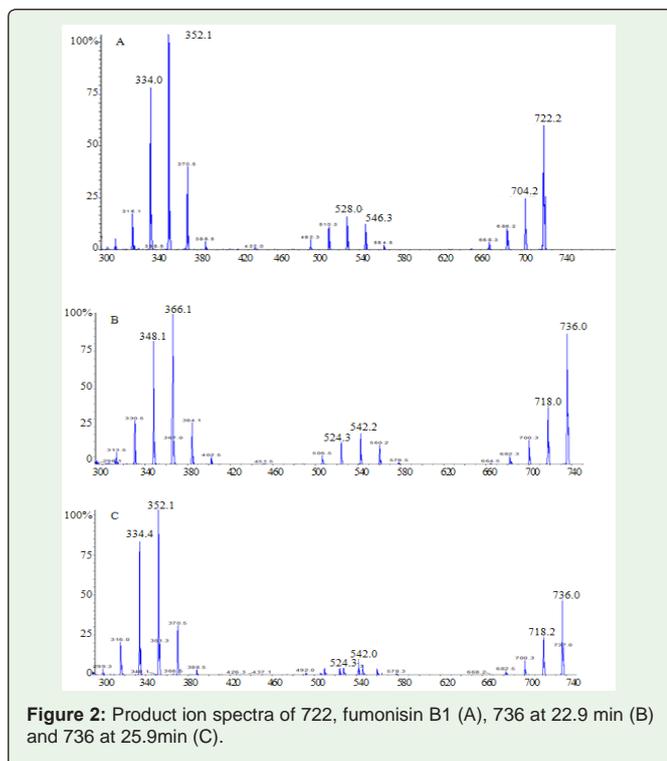
In the preliminary trial (n=30), we examined levels of FB₁ that remained unregulated as of 2013 in Korea. All compound feeds (n=30) were contaminated predominantly by FB₁. FB₁ was detected in all test samples at concentrations ranging from 52.45 to 1580.20 μg/kg. FB₁ was evenly distributed irrespective of sample types such as pig, poultry and cattle feed. Therefore, we designed and carried out a pilot study to detect the glycation of FB₁ in extruded feeds, which has been suggested to be an effective decontamination process [13-15].

Table 3: Contamination of feeds by mycotoxins.

Mycotoxins	Products (sample no)	Positive (%)	Maximum ($\mu\text{g}/\text{kg}$)	Mean \pm SD ($\mu\text{g}/\text{kg}$)
FB ₁	Cattle (n=10)	100.00	1580.20	528.07 \pm 298.88
	Pig (n=10)	100.00	1394.45	606.89 \pm 557.74
	Chicken (n=10)	100.00	936.62	368.23 \pm 406.73

Table 4: CAD fragmentation of reaction products in comparison to that of 722, FB₁

[M+H] ⁺ (m/z)	Retention (min)	[M+H-nH ₂ O] ⁺	[M+H-TCA ^a -nH ₂ O] ⁺	[M+H-2TCA-nH ₂ O] ⁺	BC ^c
		[M+H-r-nH ₂ O] ⁺	[M+H-TCA-r ^b -nH ₂ O] ⁺	[M+H-2TCA-r-nH ₂ O] ⁺	
722	25.6	704, 686, 668	564, 546, 528, 510, 492	406, 388, 370, 352, 334, 316	299
736	22.8	718, 700, 682	578, 560, 542, 524, 506	420, 406, 384, 366, 348, 330	313
736	25.9	718, 700, 682	578, 560, 542, 524, 506, 564, 546, 528, 510, 492	406, 388, 370, 352, 334, 316	299
780	26.6	762, 744, 726	622, 604, 586, 568, 550	464, 446, 428, 410, 392, 374	299
794	26.7	776, 758, 740	636, 618, 600, 582, 564	478, 460, 442, 424, 406, 388	299
810	26.7	792, 774, 756	652, 634, 616, 598, 580	494, 476, 458, 440, 422, 404	299

TCA^a: Tricarballic acid side chainr^b: Mass adductionBC^c: Fragment ion representing backbone carbon chain.**Figure 2:** Product ion spectra of 722, fumonisin B1 (A), 736 at 22.9 min (B) and 736 at 25.9min (C).

The measured concentrations of fumonisin B₁ were below all harmful thresholds, such as European Union-recommended levels or U.S. Food and Drug Administration action levels [16,17]. However, as a short-term strategy, manufacturers should use only a restricted ratio of ingredients that represent highly potential hazards, such as corn gluten, and authorities must establish acceptable limits for such ingredients.

Selective Detection of Fb₁ Analogues from Reaction Mixtures Using Precursor Ion and Neutral Loss Scans

FB₁ generates a Schiff base when heated with glucose or fructose as in other glycation processes where a free amino group on an amino acid, peptide, or protein reacts with the carbonyl group of reducing sugars. N-(deoxy-N-fructose-1-yl) FB₁ was reported [6] to be a stable initial product, and presumably this Schiff base undergoes further oxidation during an extended heating time or at a higher temperature.

The mass spectrum of FB₁ shows prominent [M+H]⁺ ions in comparison to sodium atoms, potassium atoms, or solvent adduct ions in acidic mobile phase. Product ion spectra of protonated FB₁, which are obtained at Q3 after collisionally-activated dissociation of selected mass 722, are depicted in Figure 2A. Fragmentation of protonated FB₁ brought three salient ion bunches to the product ion spectrum. Three consecutive losses of water from the molecule led to *m/z* 704, 686, and 668. Loss of one side chain and sequential dehydrations were represented by *m/z* 564, 546, 528, 510, and 492. In addition, the lowest *m/z* group, including *m/z* 370, 352, 334, and 316, can be explained by two Tricarballic Acid (TCA) losses and subsequent water deletion (Table 4).

A precursor ion scan of *m/z* 352 representing two side chains losses and a concomitant dehydration was used to screen methyl esterified FB₁ compounds or FB₁ impurities that have a different side chain from TCA. However, if Maillard type reaction of a free amino group occurs at the backbone, a neutral loss scan of two side chains, *m/z* 370, is more plausible than a precursor ion scan of 352 to determine the molecular weight of the protonated FB₁ glycation products in the incubation mixture. Several ions were detected by the neutral loss scan of 370, although two major peaks were presented in the chromatogram. The retention times of these ions were so similar that they were hardly resolved even with slow gradient elution. Therefore, these ions were selected for the multiple reactions monitoring mode. The chromatographic elution profiles of each ion were compared to avoid a misleading data interpretation that would most likely be due to in-source fragmentation, solvent, or metallic ion adducts added to the compound.

According to these results, *m/z* 736, 780, 794, and 810 were determined tentatively to represent modified FB₁s derived from incubation and have been previously reported as N-methyl FB₁, N-carboxymethyl FB₁, N-(3-hydroxyacetyl) FB₁, and N-(2-hydroxy, 2-carboxyethyl) FB₁, respectively. However, only N-carboxymethyl FB₁ has been characterized substantially with mass spectral and NMR data. Therefore, we studied these four ions in detail to obtain structural information from the product ion spectra.

Identification of Fb₁ Analogues from Reaction Mixtures Using Products Ion Scans

The product ion scan of m/z 736 resulted in several peaks on the chromatogram with two different types of daughter ion spectra (Figure 2B and C). Peaks between 22 min and 25 min showed identical spectra where all major ions were shifted higher by 14 amu than those of Fb₁, indicating that the modification occurs at the backbone. Because we could not speculate on which moiety is different from the original Fb₁ with this information, the OPA derivatization method was employed to check whether the free amino group was affected. All these peaks disappeared following OPA derivatization of the sample, and the standard solution itself contained a considerable amount of these substances. However, the solution of Fb₁ without glucose remained quantitatively constant, which means that these peaks did not arise from a Maillard reaction and that the substances were vulnerable to a nonenzymatic browning reaction as well. Therefore, these peaks are assumed to be modified Fb₁ with an additive methylene group that has been reported previously as an impurity of the Fb₁ standard [18].

Another group of peaks between 25 min and 27 min having $[M+H]^+$ 736 gave similar daughter ion spectra to that of Fb₁. Ions accounting for the backbone, 388, and sequential dehydration had the same masses as those of Fb₁, whereas ion groups that were assumed to have one or two TCA were shifted higher by 14 amu. These could be identified as Fb₁ methyl esters that are methylated on one of four carboxyl groups of two TCA side chains. These peaks were phased out by OPA, which mean these compounds still had free amino groups. These peaks might be generated by a side reaction other than glycation.

The peak at 26.6 min with a precursor ion of m/z 780 gave a product spectrum identical to that of standard Fb₁ except that all the ions were shifted higher by 58 amu, indicating that mass adduction had occurred in the backbone. Howard, et al. [13] identified this as N-(carboxymethyl) Fb₁ and suggested that prominent fragmentation at m/z 132.1 arose from cleavage between C3 and C4 to yield stable C₅H₉NO₃. Two other m/z 794 and 810 previously identified by Lu, et al. [6] belong to the same category of mass spectra as those of N-(carboxymethyl) Fb₁. Lu, et al. [6] characterized these unknown compounds as N-(3-hydroxyacetyl) Fb₁ and N-(2-hydroxyl, 2-carboxyethyl) Fb₁, respectively, according to the general scheme of the Maillard reaction. Now we present supportive additional information on diagnostic product ions, 146.2 of N-(3-hydroxyacetyl) Fb₁ and 162.1 of N-(2-hydroxyl, 2-carboxyethyl) Fb₁ corresponding to 132.1 of Fb₁.

Detection of Fb₁ Analogues from Real Extruded Samples Using Multi Reaction Monitoring (MRM)

We attempted to measure glycated Fb₁ from real extruded feeds using the sample preparation method of Seefelder, et al. [5] and even after only extraction without SPE clean-up. N-(carboxymethyl) Fb₁ and other glycation products were not detected in 10 samples. Only negligible amounts of methylene Fb₁ were found. These results imply that conventional extrusion conditions, including temperature, pressure, and reactants with reducing groups, were not effective at generating glycated Fb₁. However, the possibility that Fb₁ underwent glycation successfully but was not extractable in bound forms cannot be excluded, since there is much evidence that thermal activation

enables Fb₁ to bind to food components such as starch and protein via Fb₁'s two TCA side chains [15,19].

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