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# LC-MS/MS Determination of Nitrofurantoin Metabolite Residues in Honey

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# Abstract

This application note describes an LC-MS/MS method for the quantification of nitrofurantoin metabolite residues (AOZ, AMOZ, 1-Aminohydantoin(AH), Semicarbazide (SC)) in commercially available honey.

## Introduction

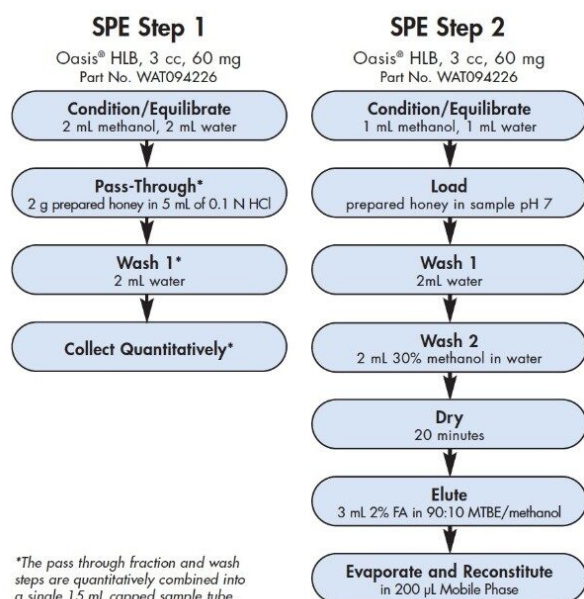
Apiculture relies on antibiotics to prevent disease propagating through the densely populated bee colonies. The overuse of antibiotics in honey bee colonies can cause high levels of residues in honey products, which becomes a public health issue. Additionally, bacteria that have developed resistance to the applied antibiotics can pose an increased threat to both human and animal health. Consequently, antibiotics become less effective against bacteria and there will be fewer alternatives available for the successful treatment of infection. Unscrupulous producers search for these alternative antibiotics such as nitrofurans to treat disease.

Nitrofurantoin antibiotics metabolize rapidly with an in vivo half-life in the order of hours, making parent drug detection ineffective. An LC-MS/MS method is described for the quantification of nitrofurantoin metabolite residues (AOZ, AMOZ, 1-Aminohydantoin(AH), Semicarbazide (SC)) in commercially available honey. The metabolite residues were extracted from the honey samples by first dissolving the honey in HCl. The samples were cleaned, derivatized and then enriched using Oasis HLB solid phase extraction devices. The metabolite residues were resolved chromatographically using a XTerra MS C<sub>18</sub> analytical Column. Positive ion electrospray mass spectrometry was used to quantify and confirm the parent ion [M+H]<sup>+</sup> and fragments for each target analyte.

## Experimental

### Preparation of Honey Samples

The honey samples were prepared for analysis using a two step SPE process (Figure 1). The first step provides a simple pass through clean-up to fractionate the analytes from the bulk of the matrix. This dramatically improves the subsequent derivatization procedure. The second SPE protocol provides additional clean-up as well as providing a sample enrichment factor of 10 to 1 (2g Honey into 200 µL).



## Nitrofuran Derivative Structures

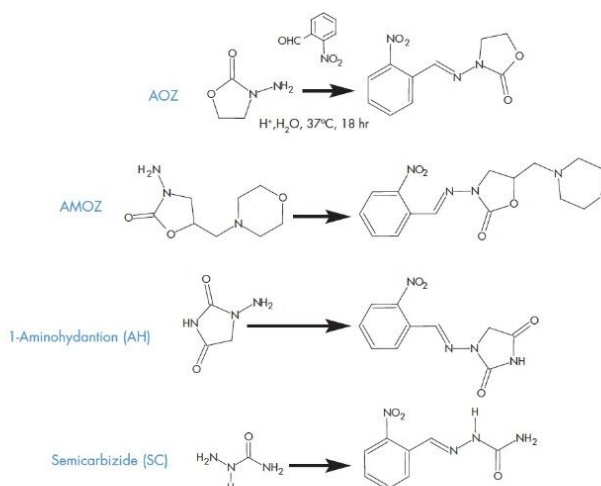


Figure 1. SPE Protocol Summary.

SPE Step 1 removes polyphenolic constituents, waxes, and organic contaminants. The sugars and the underivatized nitrofuran metabolites pass through the cartridge. This cartridge is discarded. The sugars are removed post derivitization in SPE Step 2 before the final SPE elution of the derivitized nitrofuran metabolites.

A 2 g sample of honey was diluted with 5 mL of 0.12 M HCl and prepared using the procedure outlined in Figure 1. The eluent was quantitatively collected and 300 µL of 50 mM 2-nitrobenzaldehyde in DMSO is added for derivitization. The sample was hydrolyzed and derivitized for 18 hours at 37 °C. The sample was cooled to room temperature and adjusted to pH 7 by addition of 6 mL of 0.1 M K<sub>2</sub>HPO<sub>4</sub> prior to SPE Step 2.

## HPLC Conditions

Instrument:	Alliance 2695 Separations Module
Column:	Xterra MS C <sub>18</sub> , 3.5 µm, 2.1 x 100 mm
Part number:	186000404
Flow rate:	0.20 mL/min
Mobile phase:	Isocratic 70% 20 mM ammonium formate pH 4.0, 30% ACN

Inj.volume: 20.0 µL

Temperature: 30 °C

## MS Conditions

Instrument: Waters Micromass Quattro micro

Interface: Positive Electrospray (ESI+)

Optics: Capillary - 2.9kV

Extractor - 4V

RF Lens - 0.1V

Source Block Temperature - 150 °C

Desolvation Temperature - 350 °C

## MRM Parameters

Analyte	MRM	Cone (V)	Collision (V)
AOZ	236 → 134	28	12
AMAZ	335 → 291	28	12
SC	209 → 192	25	10
AH	249 → 178	28	15

## Materials

The part listing is based on the analysis of 1000 honey samples and does not include the reagents.

### Waters Equipment

Part	Part Number	Quantity Needed
Oasis HLB 3cc, 60 mg	WAT094226	2000
Extraction Manifold	WAT200607	1
Manifold Rack	WAT200681	1
SPE Reservoir (30 mL)	WAT011390	48
Adaptors	WAT054260	24
Vacuum Pump (110V)	WAT085114	1
XTerra MS C <sub>18</sub> 2.1x100 3.5 µm	186000404	1
Syringe Filters (PTFE, 0.45 µm)	WAT200508	1000
Qsert Vials	186001126	1000

### Non-Waters Equipment

Part	Quantity Needed
Syringes 1cc	1000
Test Tubes 13x100mm borosilicate glass	1000
15 mL Caped Polypropylene Tubes	1000
Nitrogen Evaporator	1
Sample Heater/Reactor/Water bath	1
Vortex Mixer	1
Volumetric pipettes and tips	As Needed

## Results and Discussion

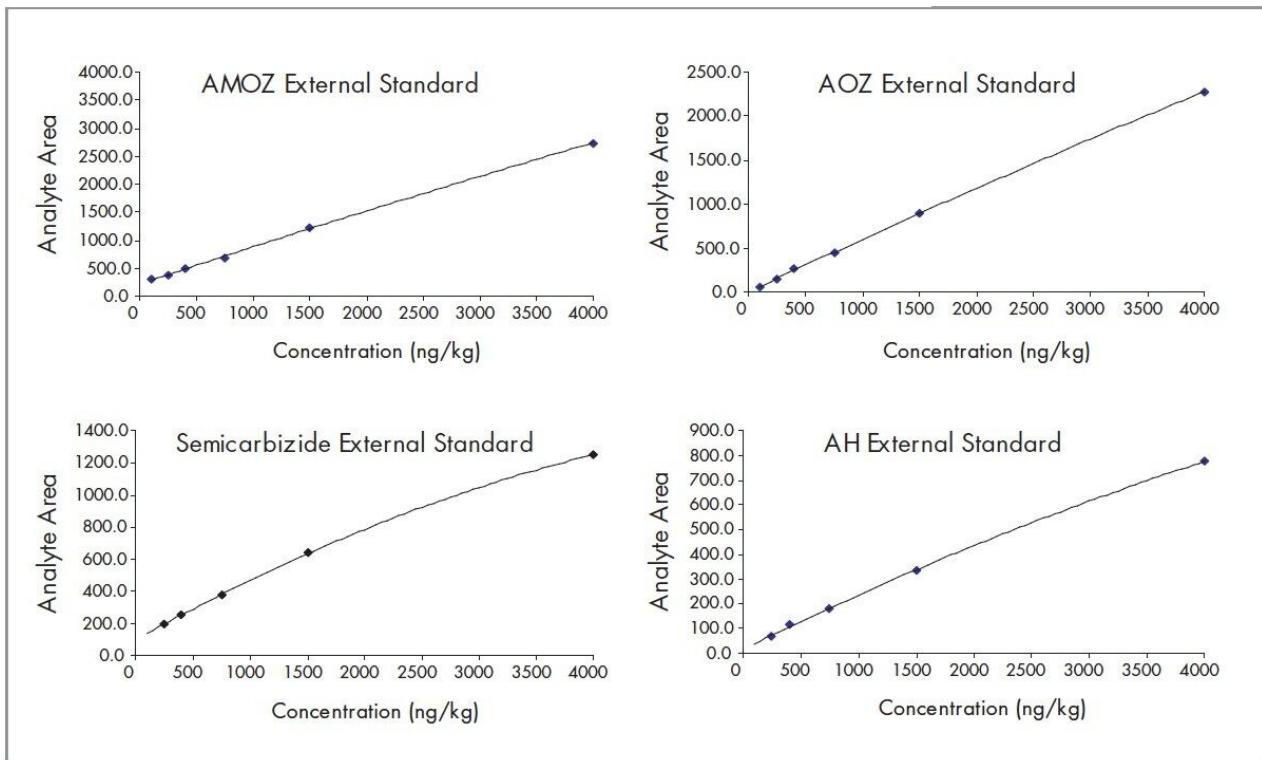


Figure 2. Representative calibration curves spiked into blank honey. Note: Suitable deuterated internal standards were not available at the time of this study. The resulting non-linear calibration curves for SC and AH were fit to a quadratic function.

## SPE Step 1

## SPE Step 2



Figure 3. Left

Side Column (SPE Step 1): The column on the left shows the retained matrix resulting from the initial sample pass-through. This column is discarded and the passed-through sample is then derivatized. Right Side Column (SPE Step 2): The column on the right shows the sample clean-up after the final analyte elution.

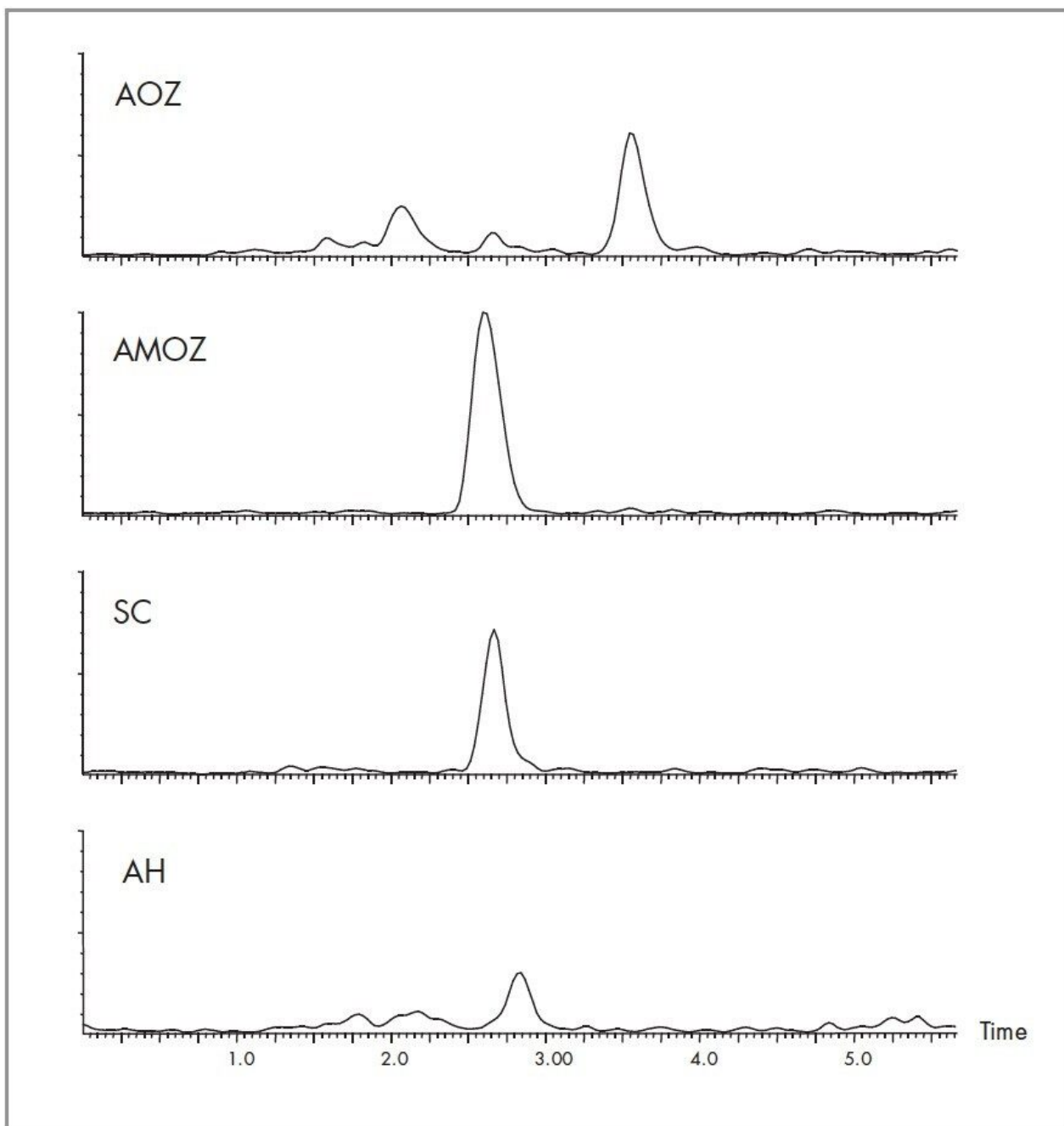


Figure 4. Representative chromatograms of a 400 ng/Kg spiked honey sample.

Honey Sample 1		Honey Sample 2		LOQ (ng/kg)
Analyte	RSD (%)*	Analyte	RSD (%)*	
Semicarbizide	9.8	Semicarbizide	9.7	200
AOZ	13.9	AOZ	9.6	200
AMOZ	3.8	AMOZ	2.9	300
AH	14.0	AH	3.8	200

Table 1. Relative standard deviation obtained from two different lots of honey spiked at 500 ng/kg (ppt). Sample 1 is raw wild flower honey and Sample 2 is buckwheat honey, both commercially available. Metabolite recovery was greater than 85% postderivatization for each analyte. The blanks used for spiking tested negative before the study.

## Conclusion

The SPE protocol described in this paper provides sample enrichment and cleanup acceptable for the routine determination of nitrofurantoin metabolites in honey. Results obtained from fortified honey samples indicate that the limit of quantification (LOQ) was below 300 ng/kg.

Sample derivatization is necessary for chromatographic retention for the small, polar nitrofurantoin metabolites. Unfortunately, derivatization in the presence of unwanted matrix reduces the reaction efficiency and may increase matrix side-reactions that can interfere with the LC analysis. The two-step SPE procedure described in this method was optimized to minimize the matrix effects prior to derivatization. This procedure reduced the undesirable matrix interferences while minimizing the amount of derivatization reagent required to achieve a successful reaction.

## References

Determination of Nitrofurantoin Veterinary Drug Residues Using Waters Micromass Quattro Premier: Tandem Mass Spectrometer, Waters Application Note [720000847EN <https://www.waters.com/nextgen/us/en/library/application-notes/2004/determination-of-nitrofurantoin-veterinary-drug-residues-using-waters-micromass-quattro-premier-tandem-mass-spectrometer.html>](https://www.waters.com/nextgen/us/en/library/application-notes/2004/determination-of-nitrofurantoin-veterinary-drug-residues-using-waters-micromass-quattro-premier-tandem-mass-spectrometer.html).

A Method for the Determination of Nitrofurantoin Veterinary Drug Residues by LC/MS/MS, Waters Application Note [720000705EN <https://www.waters.com/nextgen/us/en/library/application-notes/2003/%20a-method-for-the-determination-of-nitrofurantoin-veterinary-drug-residues-by-lc-ms-ms.html>](https://www.waters.com/nextgen/us/en/library/application-notes/2003/%20a-method-for-the-determination-of-nitrofurantoin-veterinary-drug-residues-by-lc-ms-ms.html).

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· [Alliance HPLC System <https://www.waters.com/534293>](https://www.waters.com/534293)

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