

New Developments in HRMS Screening Method for Veterinary Drugs and Other Chemical Contaminants in Aquacultured Products

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133rd AOAC Annual Meeting September 9, 2019

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Previous Work



• Developed HRMS screening method for veterinary drug residues in aquacultured products

- Generic sample preparation with acidic acetonitrile extraction, pass-through SPE cleanup
- Q-Exactive Orbitrap coupled to C18 LC with acetonitrile/0.1% formic acid gradient
- Different types of data acquisition evaluated
- Validated method
 - Tested in 5 different types of aquacultured products with 70 veterinary drugs
 - Fortified at target testing levels and compared to one-point extracted calibration standard
 - Determined number of false positives/negatives (semi-quantitative limits test)

• Applied method to incurred and imported samples

- Monitored for both target analytes (70 compounds initially validated)
- Also compared to larger database (N > 500) to find new metabolites, unexpected residues
- Found new metabolite of amoxicillin in dosed fish and ofloxacin in croaker and eel sample





New Developments



1) Expansion of method to mixed contaminants



2) Improvement of method – data acquisition and processing



Expanding method

Validating for addition chemical contaminants

- Disinfectants/Antimicrobial Soaps
 - Benzalkonium chlorides, triclocarban, triclosan

Pesticides

- Few dozen likely to be found in aquaculture from agricultural run-off
- LC-MS compounds
- Human Pharmaceuticals/Emerging Contaminants
 - Those commonly found in surface water
 - Includes drugs for depression, hypertension, pain
- Additional Veterinary Drug Compounds
 - More antibiotics, anti-wormers, etc.







Example: Human drugs in tilapia





Example: Atrazine in shrimp



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Expanding method Validating for additional chemical contaminants



1,3-Dibromo-5,5-dimethylhydai	ntoin Atenolol	Gemfibrozil Ibuprofen Metformin Naproxen	Rifampin Aldicarb/Aldicarb sulfone/Aldicarb sulfoxide Methylene blue Acriflavine/Proflavine	
1,3-Dichloro-5,5-dimethylhydar	toin Caffeine			
Benzalkonium chlorides	Carbamazepine			
Triclocarban	Clarithromycin			
Triclosan	Clofibric acid	Propranolol	Rotenone	
Amitraz (degradant)	Diclofenac	Ranitidine	Thiabendazole	
Atrazine	Diltiazem	Sertraline	Sulfisoxazole	
Azadirachtin	Diphenhydramine Fluoxetine	Simvastatin Sotalol Valsartan	Rifaximin	
Azamethiphos			Roxithromycin	
Benzocaine			Marbofloxacin	
Carbaryl			Orbifloxacin	
Carbofuran			Baquiloprim	
Cypermethrin			Virginiamycin M1	
Dichlorvos	Initially ~ 60 additional compounds			
Etofenprox				
Fipronil/Fipronil sulfone Malathion Phoxim Praziguantel	 The majority worked well through the method, some were not detected, and others were detected only at higher levels Tested 4 different fish fortified at 100, 10 and 1 ng/g 			
Propazine Quinalphos				
Simazine	This increased the num	her of residu	es validated for our method	
Trichlorton	and expands the scope of the type of contaminants we are			
Trichloroisocyanuric acid				
Trifluralin	monitoring for in aquac	ulture.	ure.	
Quinoclamine			7_	

Food Addit. Contam. (2019)

Expanding method

Detection of additional chemical contaminants



Using HRMS screening method, several eel samples were initially presumptive positive for additional chemical contaminants. (HRMS identification criteria were met using non-targeted data acquisition)

- Further analysis (targeted MS² data acquisition, standard addition, analysis on separate QqQ method) confirmed thiabendazole (~ 6 ng/g) in one eel sample.
- Acriflavine was presumptive positive in many eel samples, but further analysis (targeted MS² data acquisition, standard addition) ruled out the presence of this compound.

Expanding method Confirmed thiabendazole in eel



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MS data acquisition



Thermo Q-Exactive Orbitrap High Resolution MS with a heated electrospray source (using both classic QE and QE-HF)

Full scan MS¹ data always collected (m/z 150-1000)

<u>Two types of MS² data acquisition programs were evaluated</u>:

Nontargeted: collect product ion data for all precursor ions. *All Ion Fragmentation* (*AIF*) or Data Independent Analysis (DIA)

Targeted: collect product ion data of targeted precursor ion on a list. *Data Dependent MS*² (DDMS²) or Parallel Reaction Monitoring (PRM) using inclusion lists



Types of data acquisition



Targeted acquisition



Non-targeted acquisition





Comparison of these methods similar to work done previously: Wang et al Analyt Bioanalyt Chem **2018** Wong et al J Ag Food Chem **2018**

Comparison of scan types

Sulfadoxine 10 ng/g in spiked eel





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Comparison of data acquisition



FDA identification criteria for exact mass data:

Identified = MH⁺ (5 ppm), one product ion (10 ppm), RT match

Nontargeted

- > 90% validation compounds detected and identified at 1X with AIF
- Most identified with AIF at much lower levels (0.1-0.5X of target testing level)
- Recently compared different DIA methods to AIF with similar results

Targeted

- ~ 70% of validation compounds identified with DDMS²
- Compounds with low target testing levels (dyes) or low method recovery(β-lactams) don't meet threshold to trigger DDMS²
- Some identified at higher levels
- Recently compared PRM (limited # of compounds) to DDMS² w/ better results (~90% of residues identified)

Comparison of Scan Types

Non-selective AIF data can lead to false positives

- Oxytetracycline (OTC) often "identified" in eel samples with AIF
- Less often detected using DIA; not usually confirmed by PRM, DDMS²

Example:

OTC initially identified in this eel at 37 ng/g – met exact mass criteria by AIF But...only one product ion found, mass accuracy worse than usual, retention off by 0.06 min





Comparison of Scan Types



Leucomalachite green (QqQ 214 ng/g)

Oxolinic Acid (QqQ 1950ppb)



- Residues found in imported eel sample
- DIA MS2 spectra can be easier to compare to on-line databases such as m/z cloud

Wu et al submitted to Rapid Commun. MS (2019)

Nontarget compound analysis



- Eel sample violative for several analytes including leucomalachite green investigated to look for additional compounds.
- Extracted ion chromatogram and MS² spectra for Des-LMG ($C_{22}H_{25}N_2$, m/z=317.20123) using AIF and DIA acquisition methods.
- Inserts show the annotated spectrum for the proposed structure using Compound Discoverer software to generate fragments for proposed structure and match the fragments observed in the unknown peak. Wu et al.

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Ongoing improvements to HRMS Screen



- Continue to keep evaluating data analysis work flow strategies (more non-targeted with using available software tools)
- > Work to transfer method to more routine analysis
- Evaluate alternative chromatography look at nanoflow interface to increase sensitivity, reduce matrix effects, simply extraction (similar to Alcántara-Durán et al, *Food Chemistry* 2018)





Acknowledgements



Co-authors (Animal Drugs Research Center/FDA Denver Laboratory)



FDA Denver Regulatory Laboratory

Thermo Scientific Application Scientists and Engineers



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