

Workflow and Proof of Concept for Non-Targeted Analysis of Environmental Samples by LC-MS/MS

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SETAC North America 36th Annual Meeting, Salt Lake City, November 2015 Advanced Analytical Methods for Contaminant Discovery



# **The Chemical Universe**

We live in a chemical sea of continually changing composition – comprising both anthropogenic and naturally occurring chemical stressors.

Unlike biota, chemical pollutants have no boundaries in their global distribution – "*everything is everywhere*," only the concentrations vary.





## **Background/Problem**

 Human 'exposome' – "At its most complete, the exposome encompasses life-course environmental exposures (including lifestyle factors) from the prenatal period onwards" Chris Wild, Cancer Epidemiology Biomarkers 2005.



U.S. Environmental Protection Agency Office of Research and Development National Exposure Research Laboratory Environmental Sciences Division Environmental Chemistry Branch

#### **Biological Systems and Stressors** "Toxicant (Totality, Tolerance, Trajectory", 4T'ss





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- Rapid assessment and screening of these chemicals is a difficult challenge facing EPA in its mission to protect public health and the environment.
- Need a variety of methods and models to understand and predict exposures.
  - o Tools to advance knowledge of chemicals to which we are exposed, and at what concentrations.
  - o "Ground truth" various high-throughput exposure models.

## **The Chemical Universe**

### The KNOWN Universe

# As of October 2015, over 105 million commercially available chemicals.

(indexed by the American Chemical Society's Chemical Abstracts Service in their CAS Registry; excluding bio-sequences such as proteins and nucleotides: http://www.cas.org/content/chemical-substances/)

Of these millions of known chemicals, only 344K+ are inventoried or regulated by government bodies worldwide - representing only 0.3% of those that are commercially available,

Approximately 15,000 new substances are added each day.





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## **Analytical Instrumentation**











## **Objectives**

 Develop a non-targeted analysis utilizing existing lab capabilities

- Accurate mass- HPLC/TOF-MS
- Fragmentation- UPLC-tandem MS

 Demonstrate the usefulness of this analysis in identifying non-targeted compounds.



# **UPLC** conditions

- Acquity® UPLC BEH C<sub>8</sub> 1.7 μm, 2.1 x 50 mm analytical column
- Acquity® UPLC BEH C<sub>8</sub> 1.7 μm, 2.1 x 5 mm Vanguard pre-column
- Mobile phase: A 5:95 MeOH/DI water 0.4 mM ammonium formate
   B 95:5 MeOH/DI water 0.4 mM ammonium formate
- Flow rate 0.41 mL/min
- Gradient translated from HPLC/ToF method



# **UPLC gradient**



**HPLC** Retention Time (min)



Survey Switch		Survey Switch		
Switch From Scan Type MS Scan  Method Ionization Mode ES.  Data Centroid  Mass (m/z) Start 80 End 700 Scan Duration (secs) Scan Time 0.15 Cone Voltage Cone Voltage (V) 30 Collision Energy 4 Time (Mins) Start 0.1	Switch To Scan Type Daughter Scan Method Ionization Mode ES- Dgta Centroid Mass (m/z) Start 80 Eng 700 Scan Duration (secs) Scan Time 0.15 Collision Energy 1 Collision Energy 1 Eng 25	Activation Criteria Trigger Criteria Trigger Criteria Trigger Activation Delay (Mins) Trigger Sensitivity Trigger Threshold Max. Masses of interest per survey scan Resume Criteria Total Time in Switched Scan Mode (s) Detected Precursor Inclusion Re-include after Time (s) Exclusion Window +/- (Da) Isotope Cluster Range (Da) Specific Mass Selection Include Masses Exclude Masses	Image: second	Determines m/ inclusion
	OK Cancel Help		OK Cancel	Help
			NUM	

### **MS** Parameters Kerriment Setup - c:\masslynx\dust\_ahhs\_20150309.pro\acqudb\neg\_dust\_ahhs\_20150504\_survey\_30cv\_15\_45\_2s\_tt2.exp

Daughters

🖉 Neutral Loss 🛛 🖉 Survey

10

Time

File Edit View Options Toolbars Functions Help

MS Scan

Information

Survey Scan, Time 0.10 to 25.00, Mass 80.00 to 700.00 ES-

Parents

D 🖻 🖬 🎒 🗭 🗙

Total Run Time: 25.00 ↔

SIR Points Per Peak: 25.000

No. Type

U

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MRM

20mins

nited States Environmental Protection

Agency



### MS Scan of Blinded Sample



### **ESI** Positive





#### **ESI** Negative





## **Mass Spectra**

uM DSS Tox  50501_cgr_03 2699 (9.452)	XEVO-TQD#QCA699	01-May-2015	
<b>D</b>			
	·····································		
	MS scan onl	MS scan only method	
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	359.66		
113.06			
69.23 91.07 162.16			
196-16			
93,30 175,12 258,24.			
	399.15		
100 120 140 160 180 200 220 240 260 280	300 320 340 360 380 400 420 420 460 460 500 520 540 56	0 580 600 620 640 660 680	
um DSS Tox 50504_cgr_02 2603 (9.439)	XEVO-TQD#QCA699	04-May-2015 1	
	3/6.28		
	INIS scan from	survey method	
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	369.08		
	339 0.0		
	339° 00		
	359 0.8		
	3390 008 318 366 318 366 365 .09		



# **Library Search and Match**





Compounds from the blinded sample confirmed using LC-MS/MS with accurate mass from ToF, RT and spectral library matches.

Accurate mass	Retention Time (min) (+ or - ESI)	Compound name
266.163	0.67 (+)	Atenolol
162.1157	0.72 (+)	Nicotine
306.1041	1.35 (±)	Fluconazole
218.1055	1.36 (+)	Primidone
152.0473	1.77 (-)	Methyl paraben
351.0347	1.91 (±)	Meloxicam
206.1518	2.33 (+)	Ethanol, 2-[2-(2- Butoxyethoxy)ethoxy]-
221.1052	2.96 (+)	Carbofuran
276.1209	3.10 (+)	Triethyl citrate
201.079	3.23 (+)	Carbaryl
236.095	3.60 (+)	Carbamazepine
180.0786	4.15 (-)	Propyl paraben
191.131	4.43 (+)	Diethyltoluamide
222.0892	4.55 (+)	Diethyl phthalate
346.2144	4.92 (±)	Corticosterone
298.1933	5.82 (+)	Norethindrone
285.1365	6.36 (+)	Piperine
250.1205	6.93 (+)	Dipropyl phthalate
313.978	8.72 (±)	Triclocarban

U.S. Environmental Protection Agency



## **Results/Conclusions**

- Gradient successfully migrated from HPLC to UPLC decreasing run time from 45 to 25 minutes (linear relationship between RTs).
- While MS Full Scan mode was necessary to acquire for every sample, Survey Scan mode provided an easy way to automatically find fragment ions (threshold setting plays an important role in method development).
  - ~20 compounds were confirmed using this workflow (slide #11).
- TOF accurate masses were very helpful for finding peaks through extracted ion chromatograms.
  - Additional 30 compounds were tentatively identified but not confirmed due to a limited database.



# Conclusions (cont'd)

- Commercial MS/MS libraries are very limited and are instrument software specific.
- This process is not automated and can be very time consuming.
- LC-MS/MS has a place in non-targeted analysis/suspect screening.
  - Cannot do the job alone (accurate mass is important).
  - Will be useful to develop targeted methods allowing high resolution instruments to focus on more difficult aspects.
  - Excellent instrument for confirming with authentic standards.



### References

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### Acknowledgement



Thank You!

#### Prepared for the

SETAC North America 36<sup>st</sup> Annual Meeting November 1-5, 2015 Salt Lake City, Utah Workflow and Proof of Concept for Non-Targeted Analysis of Environmental Samples by LC-MS/MS

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