

A NOVEL DATA-INDEPENDENT ACQUISITION STRATEGY FOR NON-TARGETED ACCURATE MASS CONTAMINANT SCREENING

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THE SCIENCE OF WHAT'S POSSIBLE.®

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INTRODUCTION

Some people call them Non-Targeted acquisitions, some Data Independent Acquisitions (DIA). What does Non-Targeted screening mean to you? Here, we discuss the use of a novel DIA method, SONAR, where precursor and product ion data are acquired with a sliding quadrupole window. We compare results of a SONAR acquisition, developed primarily for 'omic' experiments, to traditional DIA acquisition strategies such as full scan low and high collision energy acquisition (MS^E[1]), and its ion-mobility enhanced variant (HDMS^E) for use in contaminant screening.

METHODS



Reported Residues	Reprtd (ng/g)	UPLC-TQS micro	APGC-TQS micro	UPLC-Vion	Xevo G2-XS Sonar
Azoxystrobin	21	-	-	-	✓
Bifenthrin*	161	✓	✓	✓	✓
Boscalid	131	✓	✓	✓	✓
Captan*	30	✓	✓	✓	✓
Cypermethrin*	34	-	-	-	✓
Fenhexamid	116	✓	✓	✓	✓
Imidacloprid	T	✓	✓	✓	✓
Iprodione*	51	-	-	-	✓
Pyraclostrobin	18	✓	✓	✓	✓

* GC Amenable

Excellent results correlation for all samples (Blackberry shown) using 3 different systems, 5 acquisition types

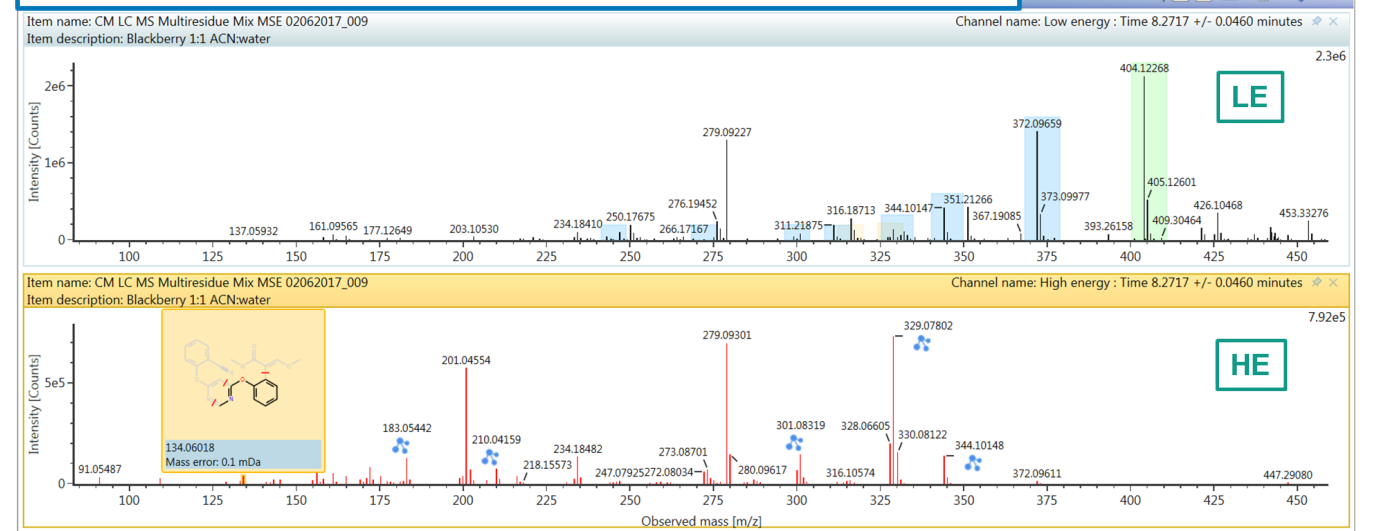
Tandem Quad (TQ-S micro) LC and APGC MSMS
 Non-IMS Enabled ToF (Xevo G2-XS) MS^E and SONAR
 IMS Enabled ToF (VION) HDMS^E



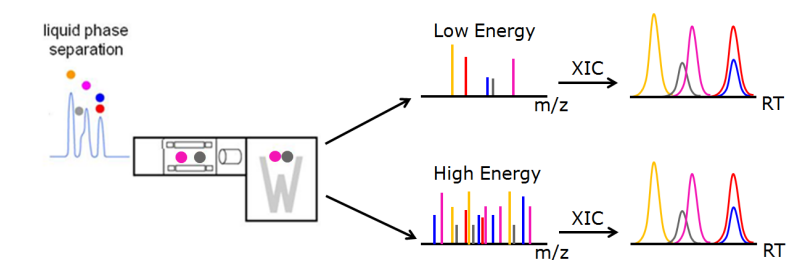
All accurate mass data was Apex peak picked and componentized [2] in UNIFI software. Utilizing informatics to align and display data across all channels results in cleaner spectra



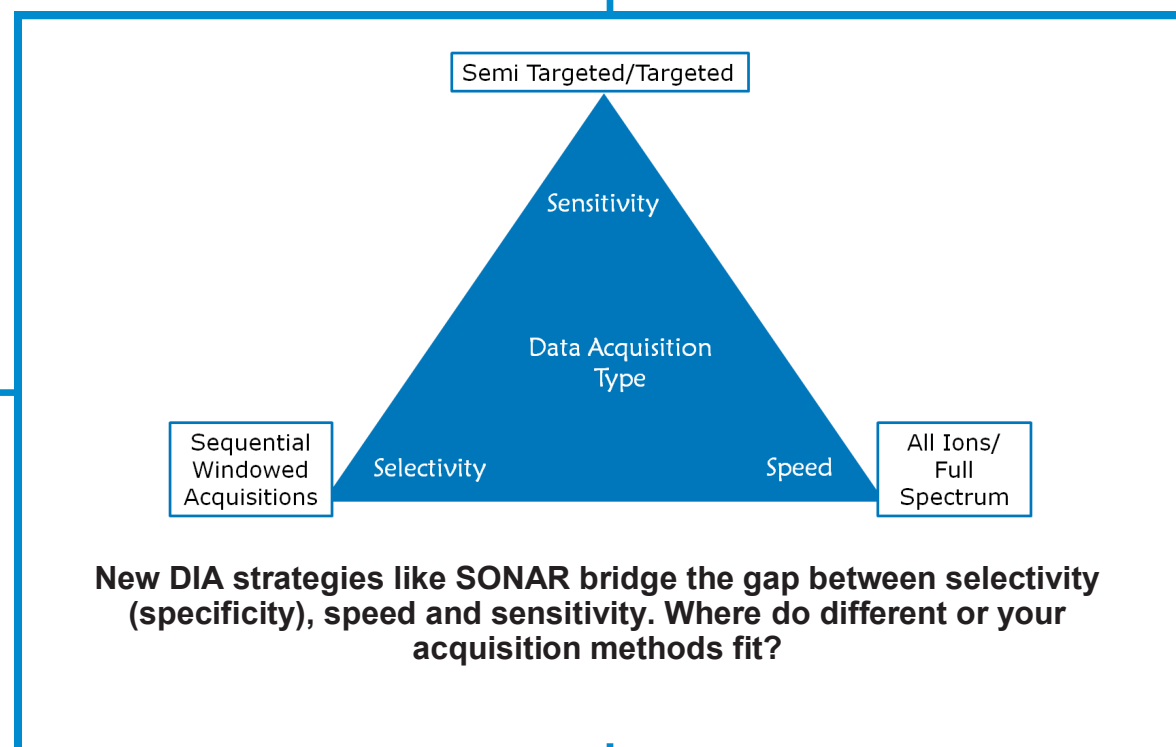
21 ng/g Azoxystrobin in Blackberry - Xevo G2 XS - MS^E



DIA



Focus! All MS data shown here is for 21 ng/g azoxystrobin in blackberries using MS^E, HDMS^E and SONAR acquisitions



New DIA strategies like SONAR bridge the gap between selectivity (specificity), speed and sensitivity. Where do different or your acquisition methods fit?

MS^E Summary

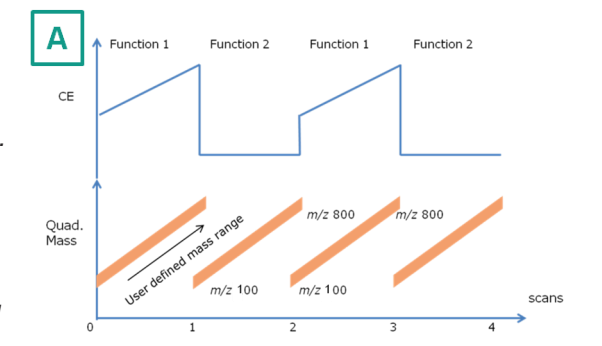
- Fast Acquisition: GC and UPLC compatible
- Accurate mass precursor and fragment ions
- Spectral Cleanup with Apex Peak picking
- Most sensitive Data Independent Acquisition



HDMS^E Summary

- Orthogonal separation of all parent ions using ion mobility - potential separation of isomeric species
- Fast Acquisition: GC and UPLC compatible
- Accurate mass precursor and fragment ions
- Spectral Cleanup with Apex Peak picking, RT alignment and Drift Time alignment
- Library searchable spectra
- Speedy target list screening data review
- Aids in elucidation of unknowns

(A) SONAR acquisition schematic. Consists of 1 scan at a high collision energy (CE) followed by another at low CE. During each period the quadrupole is swept over a predetermined mass range, with a defined mass window.



(B) Schematic of the scanning quadrupole and alignment of the precursor and fragment ions.

DIA with IMS

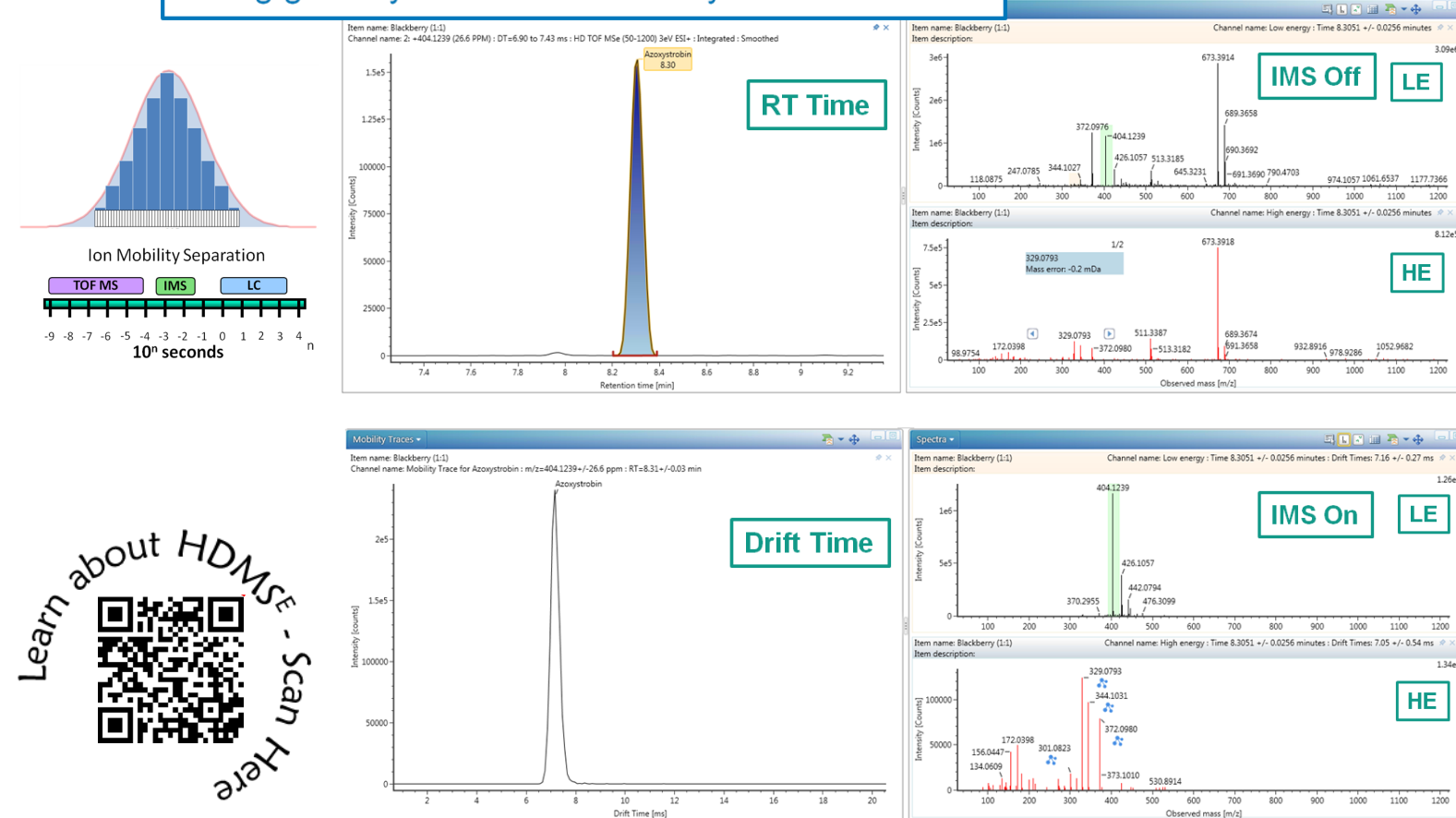
DIA Scanning Quad

SONAR Summary

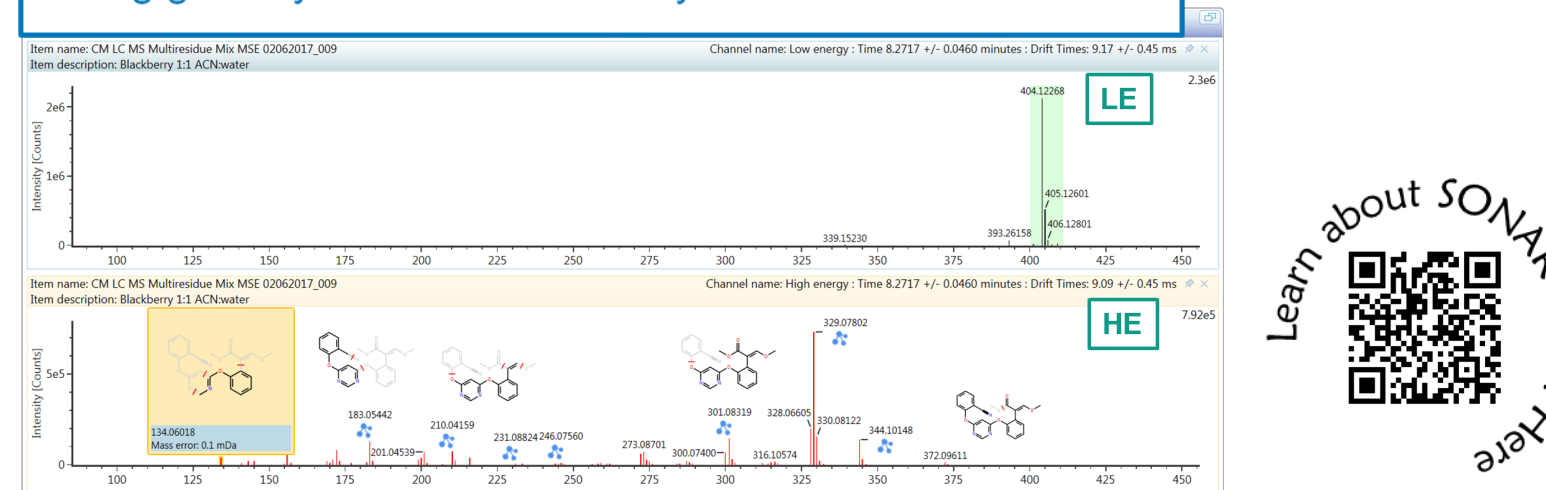
- Fast Acquisition: GC and UPLC compatible
- Accurate mass precursor and fragment ions
- Spectral Cleanup with Apex Peak picking and quadrupole scanning windows
- Library searchable spectra
- Speedy target list screening data review
- Aids in elucidation of unknowns

SONAR™

21 ng/g Azoxystrobin in Blackberry - VION - HDMS^E



21 ng/g Azoxystrobin in Blackberry - Xevo G2 XS - SONAR



CONCLUSIONS

- Data independent acquisition strategies afford a robust, generic approach which generate rich, comprehensive datasets amenable to automated analysis such as contaminant screening.
- On ion mobility enabled instruments, HDMS^E experiments enable clean up of data in more complex matrices via drift time correlation of precursor and of product ions.
- On non-ion mobility instruments, as well as established strategies such as MS^E, swept scan approaches such as SONAR— while primarily targeted for 'omic' experiments—do offer the scope for an intermediate level of specificity between MS^E and targeted MSMS. To this end, the next steps should be to perform a validation to establish SONAR as a fit for purpose method for contaminant screening.

REFERENCES

- MS^E White Paper: <http://www.waters.com/webassets/cms/library/docs/720004036en.pdf>
- Componentization White Paper <http://www.waters.com/webassets/cms/library/docs/720004597en.pdf>

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