Screening of 300 Drugs in Blood Utilizing Second Generation Exactive Plus High-Resolution, Accurate Mass Spectrometer and ExactFinder Software

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Overview

Purpose: Evaluate Thermo Scientific Exactive Plus high performance bench-top mass spectrometer for drug screening of whole blood for forensic toxicology purposes.

Methods: Whole blood samples were processed by precipitation with ZnSO₄/ methanol. Samples were injected onto an HPLC under gradient conditions and detected on an ExactiveTM Plus mass spectrometer. Results were analyzed with Thermo Scientific ExactFinder software.

 $\textbf{Results:} \ \, \text{Over 400 drugs were detected at LODs ranging from 5-100 ng/mL in whole blood.}$

Introduction

Forensic scientists and toxicologists need to search for many different compounds in samples of human blood. Endogenous matrix components and the wide variety of possible compounds make the task daunting. The second generation Exactive Plus high-resolution accurate mass spectrometer with fast polarity switching enables identification of compounds in a wide chemical space with minimum interference from endogenous compounds. Additionally, full scan data allows for retrospective analysis of data for previously unknown compounds.

Methods

Sample Preparatio

Mix 50 μ L of blood with 5 μ L of internal standard solution containing reserpine and tolbutamide-d9. Add 150 μ L of 40mM ZnSO₄ in 66% methanol and vortex immediately. Place samples in a –20°C freezer for 20-30 minutes. Centrifuge at 13,000 rpm for 10 minutes. Transfer supernatant to and autosampler vial, cap, and inject 20 μ L onto HPLC system.

Liquid Chromatography

The HPLC used is a Thermo Scientific Accela 600 pump with Accela TM open autosampler. Mobile phases are 10 mM ammonium acetate in water (A), 0.1% formic acid in acetonitrile (B), and acetonitrile:1-propanol:acetone (45:45:10) (C). The HPLC column used is a Thermo Hypersil GOLD, 5 μm , 100 x 3 mm run under the gradient shown in Figure 1.

FIGURE 1. HPLC gradient method

Start (min)	Sec	Flow (mL/min)	%A	%В	%C
0.00	60	0.50	95	5	
1.0	660	0.50		100	
12.0	60	0.75		100	
13.0	30	1.00			100
13.5	60	2.00	95	5	
14.5	30	0.50	95	5	

Mass Spectrometry

Compounds are detected on a Exactive Plus high performance bench-top mass spectrometer equipped with an Orbitrap™ mass analyzer. A schematic diagram of the Exactive Plus instrument is illustrated in Figure 2.

An atmospheric pressure chemical ionization (APCI) probe was used as an ion source. The instrument was operating in alternating positive and negative full-scan and all-ion fragmentation (AIF) mode with fast polarity switching at a resolution of 70,000 to 35,000 (FWHM) at m/2 200.

The Exactive Plus has an S-lens for improved ion transmission. The performance and robustness of the Automatic Gain Control (AGC) is improved using a C-Trap charge detector (CTCD). The higher-energy collisional dissociation (HCD) cell collects fragment-rich spectra similar to those generated in the collision cell of a triple stage quadrupole instrument. Relevant scan and source parameters are shown in Figure 3 and 4.

FIGURE 2. Schematic diagram of the Exactive Plus high-resolution accurate mass henchton mass spectrometer

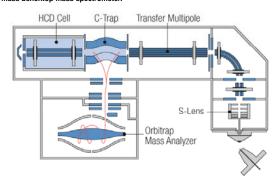


FIGURE 3. Scan Parameters for Exactive Plus Mass Spectrometer

Parameter	Value	
Full MS		
Micro scans	1	
Resolution	70,000	
AGC Target	3e6	
Maximum IT	200 msec	
Scan Range	m/z 120-1200	
AIF		
Micro scans	1	
Resolution	35,000	
AGC Target	3e6	
Maximum IT	100 msec	
NCE	35.0	
Scan Range	m/z 80-1200	

FIGURE 4. Source Parameters for APCI Probe.

Parameter	Value
Sheath Gas	35
Aux gas	15
Sweep gas	1
Discharge current	4
Capillary temp	320
S-Lens RF Level	60
Vaporizer Temp	350

Study Design

Parameters are the same for

To determine LOD for each compound, aliquots of whole blood were spiked with sets of compound at 5, 10, 20, 50, and 100 ng/ml. Matrix effects were determined by processing a sample spiked in water in place of blood.

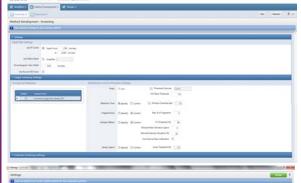
Data Analysis

Chromatograms are reconstructed with a mass tolerance of 5 ppm. Compounds are identified based on exact mass and retention time; confirmation is with fragments and isotopic pattern using ExactFinder™ software. Figure 5 shows the ExactFinder method used in this study along with the compound database.

Results

Over 400 different compounds were tested in this study: 487 were detected at 5 ng/mL, 39 at 10 ng/mL, 10 at 20 ng/mL, 18 at 50 ng/mL, and 7 at 100 ng/mL. Figure 6 shows a representative chromatogram. Fast polarity switching enabled identification of both positively and negatively charged species in one analytical run. Average mass accuracy was <3 ppm. Figure 7 shows the limits of detection of compounds in this

FIGURE 5. ExactFinder processing method and database.



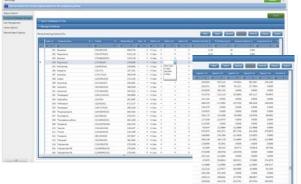


FIGURE 6. Chromatograms reconstructed with a 5 ppm mass window at 5 ng/mL.

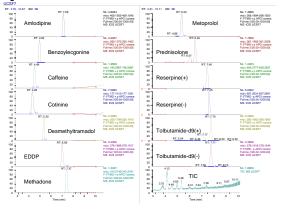
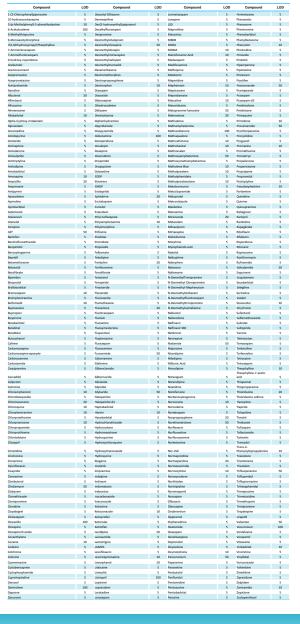


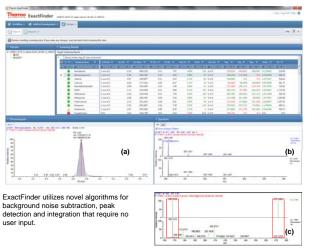
FIGURE 7. LODs for around 490 compounds



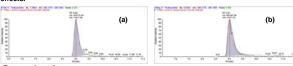
For targeted screening, ExactFinder uses parameters set in processing method to identify and confirm the presence of compound based on database values. Figure 8 shows data review results for one donor sample. In this method, compounds were identified by accurate mass within 5 ppm and retention time. Identity was further confirmed by isotopic pattern and presence of known fragments.

Matrix effects were observed to be compound dependent and were generally within $\pm 50\%$. Figure 9 shows peaks for hydrocodone in water and blood to compare effect of matrix on signal intensity.

FIGURE 8. ExactFinder results page showing XIC chromatogram reconstructed wit h 5 ppm mass window (a), isotopic pattern (b) and fragment ion confirmatior (c). Fragment mass deviation is 1.5 ppm.



effects.



Conclusion

- We have developed a screening method for over 400 compounds in whole blood with LODs of 5-100 ng/mL.
- Matrix effects are compound dependent and ±50%.
- Combination of high-resolution, accurate mass and fast polarity switching allows for rapid and confident identification in whole blood matrix for forensic toxicology purposes.

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