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OVERVIEW

Purpose

To develop a reliable, quicker, and cost-saving in vitro method to accurately predict major human metabolite profile in vivo and to de-risk disproportional or unique human metabolites before a drug candidate nomination

Method

Using long-term animal and human hepatocyte co-cultures coupled with nontargeted MS/MS^{ALL} with SWATH acquisition by a UHPLC-QTOF system to generate metabolite profile information

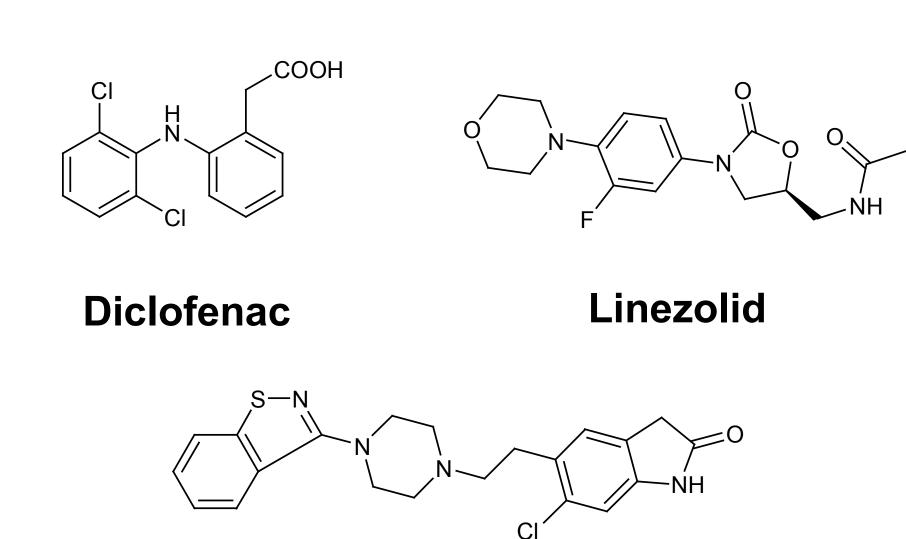
Results

Metabolites of the tested compounds identified in human hepatocyte co-cultures were also found in those of rat and/or monkey and the major human circulating and excreta metabolites of these compounds were also found in human and/or animal hepatocyte co-cultures. The proposed approach appears to be reliable.

INTRODUCTION

One of the main goals of *in vitro* species comparison studies is to assess whether there is adequate coverage from the preclinical species to humans with respect to disproportional and/or unique human metabolites. Also important is to accurately predict major human metabolite profile in vivo. Traditionally, this is performed with subcellular fractions and/or suspended hepatocytes; however, these shortterm in vitro systems do not usually provide multi-generation metabolites. [1, 2, 3, 4] In this study, we incubated selected compounds of diverse chemical structures (linezolid, ziprasidone, and diclofenac, Figure 1) that were subjected to a wide range of biotransformation pathways with long-term hepatocyte co-cultures model over an extended time period, and mined the metabolite information from the mass spectra generated by an UHPLC-QTOF-MS system through non-targeted MS/MS^{ALL} with SWATH acquisition to compare the metabolite profiles across species and to the major metabolite profile found in humans in vivo.

Figure 1. Structures of the Tested Drugs



METHODS

Ziprasidone (ZIP)

Sample Preparation

Linezolid, ziprasidone (ZIP), and diclofenac (@ 10 μM) were incubated with rat, monkey, or human HepatoPac™ co-cultures at 37°C in a 24-well format. Incubations with stromal cells served as the negative control. The plates were placed inside a humidified incubator over 168 hours. The enzymatic reactions were terminated by adding 400 µL of ice-cold acetonitrile solution directly to the well at 0, 4, 48, and 168 h. The mixture was vortex-mixed, centrifuged, and the supernatants were analyzed by UHPLC-MS/MS.

UHPLC-HRMS and UHPLC-MS/MS Conditions

The system used for metabolite identification and profiling consisted of a Shimadzu NexeraTM UHPLC system (**Table 1**) and a TripleTOFTM 5600 high resolution mass spectrometer (AB Sciex) controlled by Analyst TF^{TM} software (version 1.6). Mass spectrometric analysis was performed through MS/MS^{ALL} with Sequential Windowed Acquisition of all THeoretical Fragments (SWATH) acquisition (Table 2). The mass spectrometer data were mined with MetabolitePilotTM software (Version 1.6) using mass defect filtering, isotope pattern filtering, and background subtraction.

Table 1. Liquid Chromatography Conditions

UHPLC Column	ACQUITY UPLC BEH C18 2.1 x 100 mm 1.7 μm
Column Temperature	40 °C
Flow rate	600 μL/min
Injection Volume	10 μL
Mobile Phase A	10 mM CH ₃ COONH ₄ in water, pH=5.0
Mobile Phase B	Acetonitrile containing 0.1% formic acid
UHPLC Gradient	5-5-40-50-95-95-5% of B @0.0-1.5-9.0-10.0-
	11.0-12.0-13.0-15.0 min

Table 2. TripleTOFTM 5600 Parameters

Parameter	Value		
Collision Gas (CAD)	6 Psig N ₂		
Curtain Gas (CUR)	30 Psig N ₂		
Ion Source Gas 1 (GS1)	60 Psig N ₂		
Ion Source Gas 2 (GS2)	60 Psig N ₂		
Ion Spray Voltage (IS)	5500 V		
Temperature (TEM)	550 °C		
Declustering Potential (EP)	80 V		
Full Scan TOF-MS Range	100-2000 Da		
SWATH MS/MS ALL Range	250-950 Da		
Accumulation Time	35 ms per 25 Da		
Collision Energy (CE)	35 V		
Collision Energy Spread (CES)	±15 V		

RESULTS

Incubation of ZIP with Hepatocyte Co-Culture

- 1. Three major human circulating and excreta metabolites Smethyl-dihydro-ZIP, ZIP sulfoxide, and N-dealkyl ZIP sulfone, [3-8] were identified in both monkey and human hepatocyte co-cultures (**Table 3**). S-Methyl-dihydro-ZIP and ZIP sulfoxide were also found in rat.
- 2. S-Methyl-dihydro-ZIP and S-Methyl-dihydro-ZIP-SO were the major metabolites in rat, monkey, and human hepatocyte co-cultures (Figure 2).
- 3. Metabolites identified in human were also found in animals.

Incubation of Linezolid with Hepatocyte Co-Culture

- 1. Two major human circulating and excreta metabolites, PNU-142586 and PNU-142300,^[9] were identified in both animal and human hepatocyte co-cultures as major or significant (**Table 3**).
- 2. Metabolite profiles were qualitatively similar across all species tested, with three morpholine ring-opened products PNU-142300, PNU-142586, and PNU-143010 as the major metabolites in human. PNU-142586, PNU-143131 the major PNU-142300 and monkey, while PNU-142618 were major metabolites in rat (Figure 3).
- 3. Metabolites identified in human were also found in animals.

Table 3. Generation of Major In Vivo Human Metabolites in Hepatocyte Co-Cultures of Rat, Monkey, and Human

Compound	Major <i>In Vivo</i> Human	Hepatocyte Co-Cultures		
Name	Metabolites	Rat	Monkey	Human
Ziprasidone	Ziprasidone sulfoxide	Yes	Yes	Yes
(ZIP)	(ZIP-SO)			
	S-Methyldihydroziprasidone	Yes	Yes	Yes
	(S-Methyl-dihydro-ZIP)			
	N-Dealkylziprasidone S-oxide	*	*	*
	(BITP-SO)			
	N-Dealkylziprasidone sulfone	No	Yes	Yes
	(BITP-SO ₂)			
Linezolid	O-Dealkylation/ring opening,	Yes	Yes	Yes
	carboxylic acid (PNU-142586)			
	N-Dealkylation/ring opening,	Yes	Yes	Yes
	carboxylic acid (PNU-142300)			
Diclofenac	4'-Hydroxydiclofenac	Yes	Yes	Yes
	5-Hydroxydiclofenac	Yes	Yes	Yes
	Acyl glucuronides	Yes	Yes	Yes

Figure 2. Major Metabolite Profiles of Ziprasidone in Hepatocyte Co-Cultures of Rat, Monkey, and Human

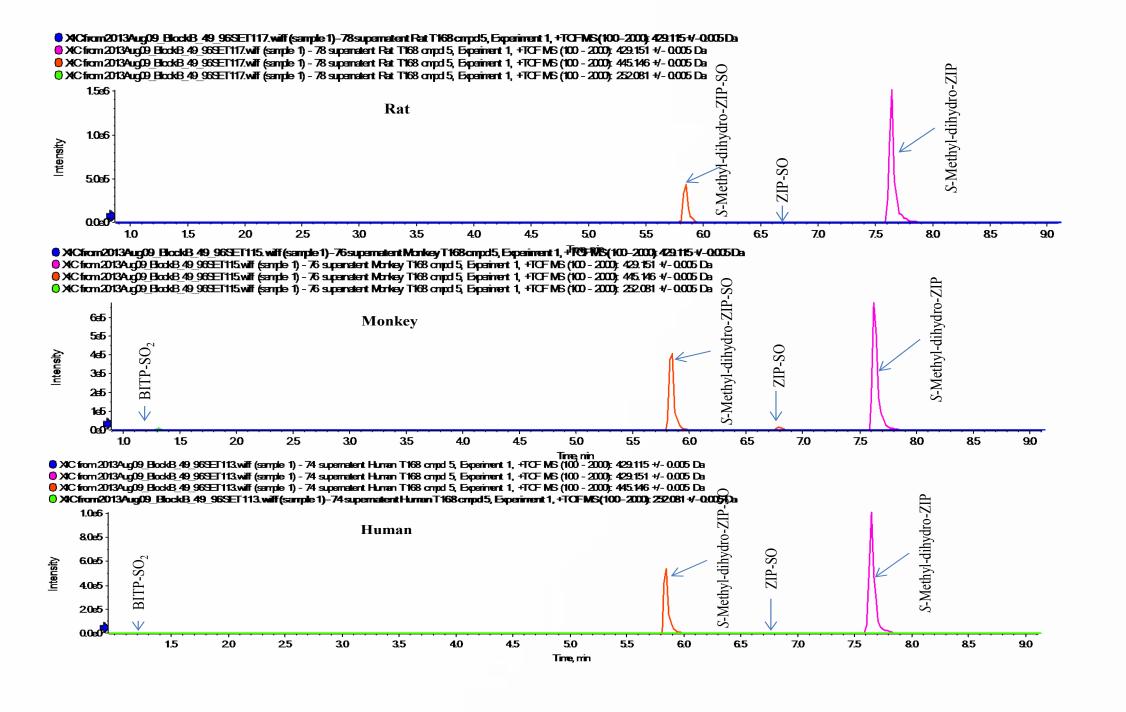


Figure 3. Major Metabolite Profiles of Linezoid in **Hepatocyte Co-Cultures of Rat, Monkey, and Human**

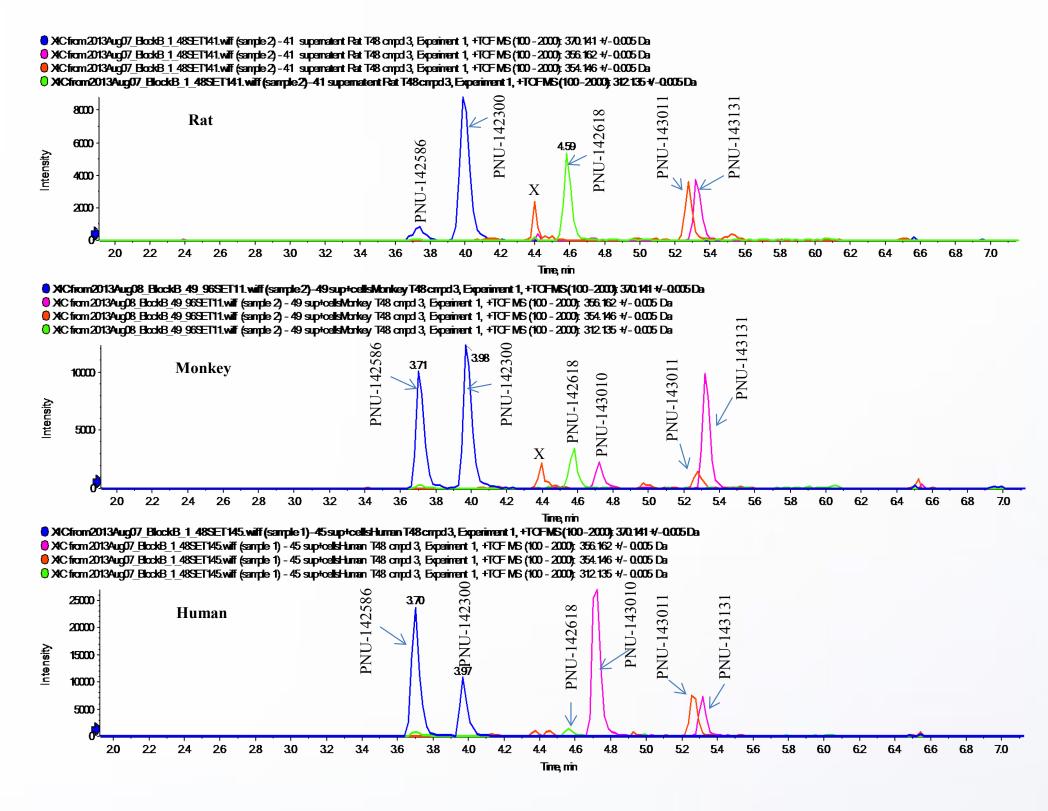
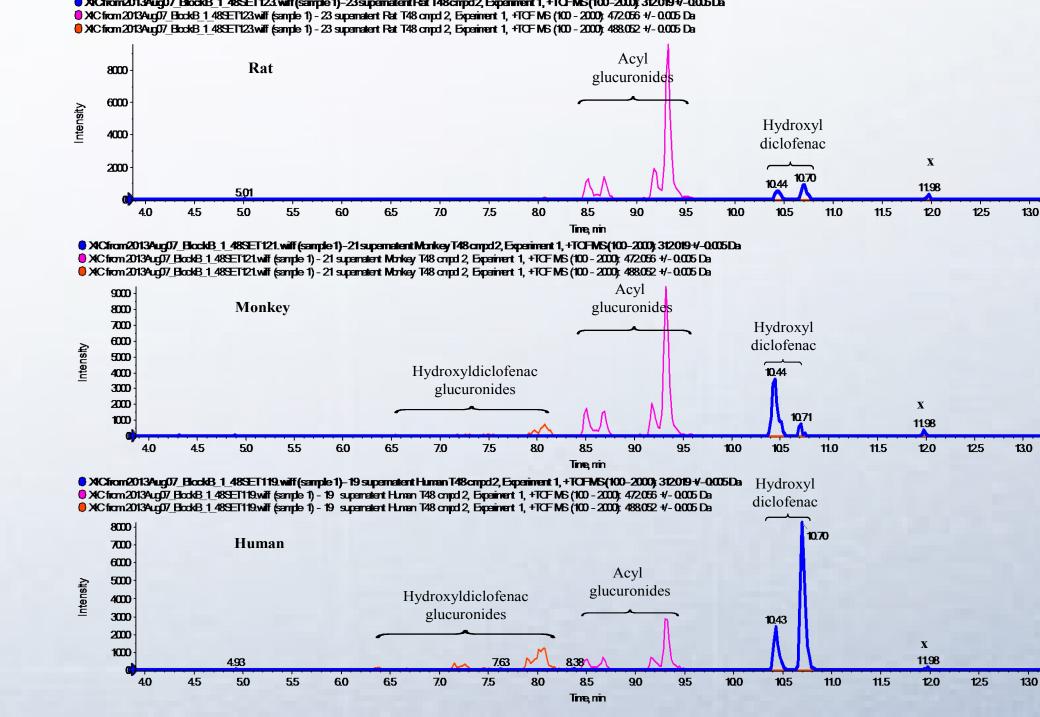


Figure 4. Major Metabolite Profiles of Diclofenac in Hepatocyte Co-Cultures of Rat, Monkey, and Human



Incubation of Diclofenac with Hepatocyte Co-Cultures

- 1. The major human circulating and excreta metabolites, four acyl glucuronides, 4'-hydroxyl and 5-hydroxyl diclofenac,[10,11] were identified in both animal and human hepatocyte co-cultures as major or significant (Table 3).
- 2. Four diclofenac acyl glucuronides were the major metabolites in all species at 4 h. At 48 h, acyl glucuronides were the major metabolites in rat and monkey, while acyl glucuronides and 4'-hydroxyl and 5hydroxyl diclofenac were major metabolites in human (Figure 4). At 168 h, 4'-hydroxyl and 5-hydroxyl diclofenac were the major metabolites in monkey and human, while acyl glucuronides and 4'-hydroxyl and 5hydroxyl diclofenac were major metabolites in rat.
- 3. In addition, multiple hydroxyldiclofenac glucuronides and a dehydrogenated diclofenac (detected in negative mode) were also identified in animal and/or human.
- 4. Metabolites identified in human were also found in animals.

CONCLUSIONS

- Major human circulating and excreta metabolites of the three compounds were found in human hepatocyte cocultures.
- Metabolites of the three compounds identified in human hepatocyte co-cultures were also found in those of rat and/or monkey.
- The non-targeted MS/MS^{ALL} with SWATH acquisition enables a comprehensive qualitative and quantitative analysis of all components within the dynamic range interrogated. High resolution MS and MS/MS spectrum of every analyte in the sample reduce potential for interferences, therefore provide high quality data. The ability of re-interrogation of the MS data of all analytes allows the update of metabolite profile information without additional experiments.
- This approach of long-term hepatocyte co-cultures coupled with non-targeted MS/MS^{ALL} with SWATH acquisition by UHPLC-QTOF-MS provides a reliable, quicker, and cost-saving method to accurately predict major human circulating and excreta metabolites as well as to compare metabolite profiles across species in order to de-risk unique or disproportional human metabolites before drug candidate nomination.

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