A HOLISTIC APPROACH, USING UPLC-MS/MS AND CHEMICALLY INTELLIGENT SOFTWARE TO FULLY PROFILE METABOLIC BIOTRANSFORMATIONS OF NEW CHEMICAL ENTITIES

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INTRODUCTION

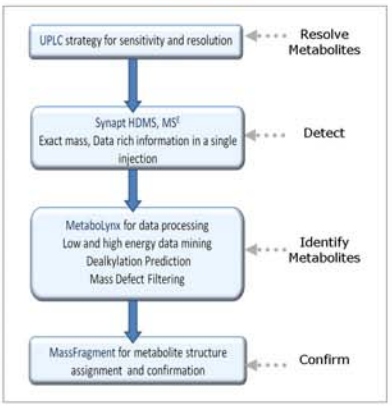
Typically, metabolite identification studies generate vast amounts of information rich LC/MS data which can be time consuming to decipher. Rigorous investigation of the data is essential to ensure that endogenous matrix peaks are eliminated from the sample data and that expected and unexpected metabolites are correctly identified. As the cost of developing New Chemical Entities (NCEs) in drug discovery increases there is a need to employ holistic approaches, involving automation and intelligent software, to improve efficiency and productivity.

Here a workflow, describing an holistic approach to discovery Metabolic Profiling, is presented and employed in the identification of phase I metabolites of the anti-depressant drug Nefazodone. Following Ultra Performance Liquid Chromatogrpahy (UPLC) and exact mass MS^E data acquisition on a Synapt HDMS mass spectrometer (figure 1), the data is processed using MetaboLynx, a software algorithm for metabolite identification. The automated Data mining process is complemented by mass defect filtering capabilities and uses compound specific expected metabolite information generated by a chemically intelligent tool to predict dealkylated metabolites.

The automated metabolite profiling process is completed through the use of a fragmentation interpretation software tool, MassFragment to enable software driven assignment of metabolite structures from fragmentation patterns.

Figure 1. Waters UPLC/Synapt HDMS system.

WORKFLOW



EXPERIMENTAL CONDITIONS

Incubations

Nefazodone was incubated at 10 uM in rat liver micrososmes (1mg/ml protein, 1% MeCN, 1mL total volume) in the presence of 1 mM NADPH. Following 60 minute incubation the reaction was terminated by addition of equal volume of Acetonitrile and then centrifuged. The supernatant was diluted 1:1 in mobile phase A prior to injection.

Chromatography

Column	ACQUITY UPLCTM HSS 1x150mm
Flow rate	200 uL min-1
Mobile phase A	5 mM Ammonium Acetate
Mobile phase B	MeCN
Gradient	5 minute gradient, 0-60% B

Mass Spectrometry Conditions

MS System:	Waters SYNAPT HDMS
Ionization Mode:	ESI Positive (V)
Capillary Voltage:	3 KV
Cone Voltage:	25 V
Desolvation Temp:	250 °C
Desolvation Gas:	800 L/Hr
Source Temp:	120 °C
Acquisition Range:	50-1000 m/z

RESULTS AND DISCUSSION

Chromatographic resolution and detection of metabolites

The base peak intensity chromatograph, figure 2, indicates the presence of numerous metabolites requiring identification and structural elucidation. Exact mass MS^E data acquisition recorded both low and high collision energy data in the same injection. Considerably reducing analysis time required for metabolism studies of this kind.

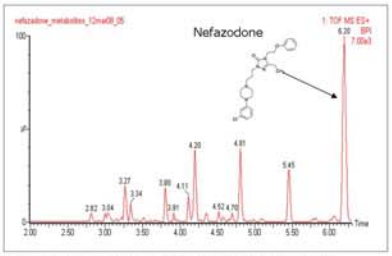


Figure 2. Low Energy MS^E BPI chromatogram displaying resolved metabolite peaks of Nefazodone.

MetaboLynx for Metabolite Identification

MetaboLynx mines the MS data and correlates *m/z*, retention time and intensity of peaks in the sample to control peaks and a list of predicted or 'Expected' metabolites. The specific Dealkylated metabolites of Nefazodone were also incorporated into the list of expected metabolites, through the use of a dealkylation tool within the MetaboLynx method (figure 3).

Figure 3. Building the 'Expected' list of Metabolites, including Specific dealkylations, into the MetaboLynx Method.

Mass Defect Filtering

A filter, based on the mass defect of the metabolite compared to mass of Nefazadone, was applied to the data to eliminate endogenous matrix peaks. As the mass defect of Nefazadone metabolites displays a non linear relationship to nominal mass (figure 4) it is difficult to predict the filter window to apply, especially when searching for dealkylated metabolites. To allow for this, a moving automatic mass defect filter window, specific to the predicted metabolites of Nefazadone (figure 5), was activated in the MetaboLynx method.

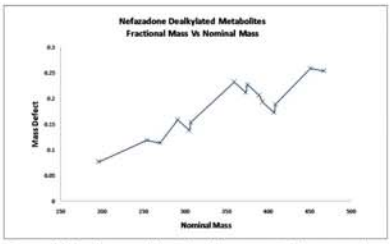


Figure 4. Non Linear relationship between nominal mass and mass defect for dealkylated Nefazodone metabolites.

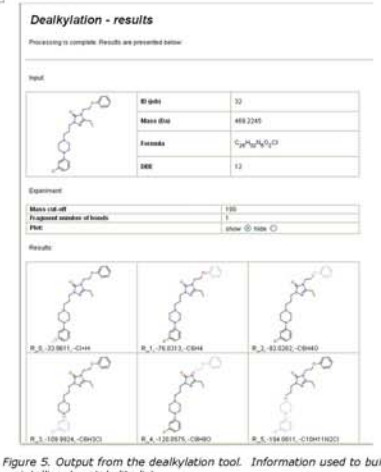


Figure 5. Output from the dealkylation tool. Information used to build an intelligent metabolite list.

Identification of Metabolites

Using this method MetaboLynx identified 25 metabolites of Nefazodone in the Low energy MS^E data (Figure 6). These metabolites included expected phase I, dealkylated and combined metabolites. Mass accuracy for the identified peaks was 2.9 RMS.

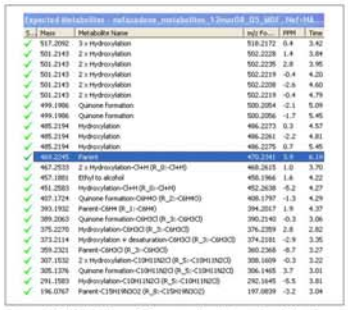


Figure 6. MetaboLynx Browser displaying identified

High Energy MS^E Data Mining

The High collision energy data provided fragmentation information for the detected Nefazodone metabolites. The fragments were analysed by MetaboLynx and viewed through the MetaboLynx browser. Common fragments and Neutral losses information, also displayed in the browser, aided throughput of metabolite structure assignment.

Assignment of Fragment Ions and Structure Elucidation

The fragments of Nefazodone in the high energy MS^E spectra were identified by the software tool MassFragment (Figure 7). MassFragment predicts fragment structures based on systematic bond disconnections and a scoring principle. Using MassFragment the key fragments of Nefazodone, were assigned within seconds. The assigned fragments consequently aided throughput of complete identification of metabolites.

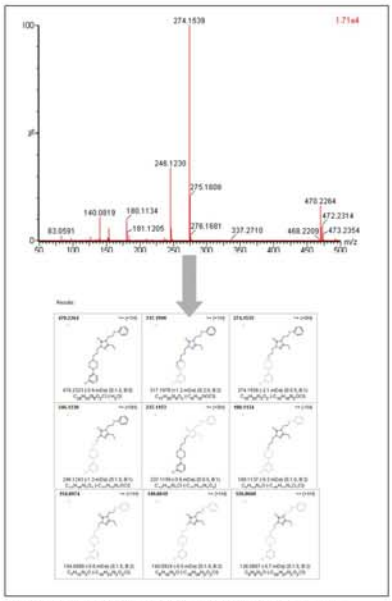


Figure 7. High energy spectrum of nefazodone and MassFragment report showing proposed structures of fragment ions.

CONCLUSIONS

- **A holistic approach to discovery metabolite profiling is described and applied to metabolic profiling of Nefazodone.**
- **UPLC was employed for rapid resolution of 25 metabolites over a 5 minute gradient.**
- **Low and high collision energy MS data acquired using MS^E acquisition capabilities of the Synapt HDMS**
- **Automated data mining software, MetaboLynx, with mass defect filtering and dealkylation prediction tool enabled timely, accurate identification of metabolites.**
- **MassFragment , a chemically intelligent software tool, enabled automated assignment of fragment ions from the high energy data. Enabling efficient metabolite structure elucidation.**
- **This workflow offers a complete and automated solution for discovery metabolite identification, from generation of raw data to elucidation of metabolite structures.**

References:
1)Bateman *et al.*, ***Rapid Comms. in Mass Spectrom.*** 21 [9], 1485-96. 2007
2)Wrona *et al.* ***Rapid Comms. in Mass Spectrom.*** 19 [18], 2597-602 2005
3)Zhang *et al.* ***J. Mass Spectrom.*** 38 [10], 1110-12, 2003
4)*Zhu et al.* ***Anal. Chem.*** 79 [21], 8333-41, 2007
5)Hortsihire-Smith *et al.* **Poster** (Generic Dealkylation: A Tool for Increasing the Hit-Rate of Metabolite Identification and Customizing Mass Defect Filters) **ASMS 2007**

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