

Overview

High resolution LC-MS/MS methods for targeted and non-targeted workflows were applied to the analysis of wastewater and river water samples taken from a heavily urbanized tidal river catchment area (London, UK).

Targeted and non-targeted workflows used a standardized LC-MS/MS method to increase reporting confidence in compound identification (reported analyses agree with a precursor mass accuracy error, isotopic pattern, retention time and library verification with product ion spectra).

1. Introduction

Quantitative monitoring of large panels of contaminants of emerging concern (CECs) in environmental samples is a key enabling tool to assess the impact of human exposure from prescription pharmaceuticals, lifestyle chemicals and illicit drugs. Although targeted mass spectrometry workflows have been successfully used in wastewater-based epidemiology (WBE) the challenge is to work with inherently complex samples and changing CEC usage.

In this work, both targeted and non-targeted workflows were used to identify a number of illicit drug and pharmaceutical compounds in river water and wastewater samples. Each target was confirmed using accurate mass, isotopic distribution, retention time and accurate mass fragment spectrum data. For non-targeted or suspect screening analysis, a series of tools were used including component detection, suspect screening search lists (to match molecular ion features) and to provide evidence for identification (fragment ion matching with external data bases using a fragment structure assignment application).

2. Materials and Methods

Samples of river water and waste were prepared by filtering using a PTFE 0.2µm filter (Millex-FG hydrophobic PTFE membrane, SLFGR04NL) and injected directly into a HRMS LC-MS/MS (LCMS-9030, Shimadzu Corporation, Japan). The same samples were also quantified using a validated triple quadrupole LC-MS/MS method (LCMS-8050, Shimadzu Corporation).

Table 1. HRMS LC-MS/MS parameters.

| HRMS LC-MS/MS method / LC parameters | |
|--------------------------------------|---|
| Sample injection | Direct injection; 40 µL |
| Column | Shim-pack Visto Rphényl (2.1 mm x 100 mm, 2.7µm) |
| Mobile phase A | 2 mM ammonium formate +0.02% formic acid |
| Mobile phase B | Methanol + 2 mM ammonium formate +0.02% formic acid |
| Flow rate | 0.3 mL/min |
| HRMS LC-MS/MS method / MS parameters | |
| Cycle time | 0.9 seconds for all mass scans |
| TOF survey | 100-600 Da; 100 mscans; positive ion |
| DA-MS/MS | 40-600 Da; 25 mscans for each mass scan; 32 DA-MS/MS mass scans; variable isolation width; CE 5-55V |
| Mass calibration | External mass calibration |
| Data processing | LabSolutions 5.99 and Insight 3.0 research application |

3. Results

3.1 Non-Targeted Workflows

The workflow involves the following steps:

1. **Detecting Components**, with Insight Analyze chromatographic deconvolution algorithm. This step generates a list of components as m/z, RT and ion abundance.
2. **Matching detected components with a search list** based on expected m/z, isotopic distribution (and within an expected RT window) within the search list.
3. **Verifying identified targets**: cross-referencing results to a highly curated high-resolution mass spectrometry library (table 2) generating a DoProd score.
4. **Reporting criteria**:

- * Precursor ion:
 - * Quantitation mass accuracy < 5 ppm
 - * Isotope distribution score > 30
 - * RT < 0.5 min
- * Product ion spectra (DA-MS/MS mass scan):
 - * Library similarity score (Similarity Index; SI) > 40 (default settings applied to DoProd weightings)

Table 2. Summary of Library Screening.

| Toxicology and Pesticide Libraries: | |
|-------------------------------------|--|
| Spectra in libraries | =1300 combined chromatographically separated authentic standards |
| CE spread | 5-55 V |
| Precursor isolation | 1 Da with (targeted MS/MS) |
| RT | Standardized LC with a Shim-pack Visto Rphényl column |
| Product ion spectra | MS/MS verified with Assign fragment annotation tool and curated for spectrum noise |
| File type | Searchable to built crowd sourced libraries |

3.2 Targeted workflows

Compounds identified in the non-targeted workflow were validated and quantified using authentic standards confirming identification (FPN/FMR).

1. Using a targeted QTOF method, previously identified components were used as a search list and quantified using authentic standards (Table 2). An example of the workflow and identification of cocaine in wastewater is shown in Figure 1.
2. Quantitative results from the Q-TOF were cross compared to results from an established validated triple quadrupole LC-MS/MS MRM method¹.

Comparison of quantitative results showed close agreement between both QTOF and LC-MS/MS measurements; plotting the analyte concentrations determined by the QTOF v TO resulted in a linear regression analysis with a slope close to unity (Figure 2).



Figure 1. Screenshot of LabSolutions Insight software highlighting cocaine detected in the wastewater sample which met the reporting criteria.

4. Conclusions

- * Non-target workflows using a standardized LC-MS/MS method with DA-MS/MS mass scans can be highly effective in screening environmental samples. In this study, melformin, cocaine and its primary metabolite benzoylcegonine were detected in both waste and river water samples at high concentrations. Interestingly levamisole, a known cutting agent was also detected. CECs from the suspect screening experiment included clozapine, citalopram, fluoxetine and sertraline.
- * As the data acquired are data independent, retrospective analysis for new or emerging analytes is possible for research purposes. A new or emerging analyte can be added to the search list or compound list and the mass accuracy, isotopic pattern, RT and product ion fragments are used to find suspect identifications.

Table 3. Comparison of component concentration in wastewater and river water quantified with QTOF method.

| Compound | Wastewater (ng/L) | River water (ng/L) |
|-----------------|-------------------|--------------------|
| Amoxicillin | 77 | |
| Benzoylcegonine | 134 | 96 |
| Benzoylcegonine | 1679 | 11 |
| Cabotamapine | 202 | 64 |
| Citalopram | 308 | |
| Clozapine | | 11 |
| Clozapine | 75 | |
| Cocaine | 464 | |
| Diclofenac | 96 | 78 |
| Fluoxetine | 35 | |
| Indinavir | 27 | 16 |
| Ketamine | 54 | |
| Ketoconazole | 101 | |
| Levamisole | 33 | 33 |
| Lidocaine | 67 | 15 |
| MEMA | 102 | |
| Melformin | +ULOD | 526 |
| Miconazole | 37 | |
| Morphine | 303 | |
| Nicotine | 2326 | |
| Oxamyl | | 63 |
| Oxycodone | 21 | 9 |
| Propofol | 50 | 20 |
| Sertraline | 167 | |
| Tamoxifen | 17 | |
| Tertbutyl | 24 | 78 |
| Tramadol | 214 | 78 |
| Trimethoprim | 176 | 21 |
| Verapamil | 194 | 57 |

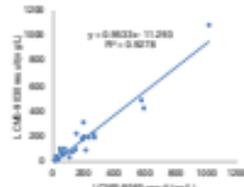


Figure 2. Comparison of quantitative results across two LC-MS/MS platforms: triple quadrupole (LCMS-8050) and Q-TOF (LCMS-9030) showed good correspondence.

5. References