White Paper 047
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Confident profiling of controlled substances using GC–TOF MS

This study describes the use of GC–TOF MS for comprehensive profiling of seized drug samples, for confident identification of controlled substances, as well as adulterants and cutting agents.

Introduction

The analysis of controlled substances, such as heroin and cocaine, is commonly performed using gas chromatography coupled with mass spectrometry (GC–MS). However, the quadrupole MS systems traditionally used for GC are restricted in terms of sensitivity when used for screening (i.e. in scan mode). Increased sensitivity may be obtained with selected ion monitoring (SIM) mode, but then whole-sample screening is not viable, resulting in compounds of interest being overlooked. The spectra obtained are also affected by the phenomenon of spectral skew, which could increase the potential for false-positive or false-negative results, as well as cause difficulties with spectral deconvolution.

These are important issues because forensic laboratories require unequivocal identification of any controlled substances present in a sample – a challenging prospect considering the ever-increasing list of target compounds and the novel 'designer' drugs that are now prevalent (e.g. synthetic cannabinoids).

Additionally, drug profiling involves the comparison of sample purity to determine whether two samples are from the same origin, as well as to assess the expected monetary value of the drug samples. This involves screening the entire sample for not only the target compounds (i.e. controlled substances), but also any adulterants or cutting agents that are present.

BenchTOF2™ time-of-flight mass spectrometers (TOF MS) can address these challenges by providing high-sensitivity screening, with excellent spectral fidelity, for confident identification of targets and non-targets in complex samples. In this study, we will demonstrate these advantages by the analysis of a selection of seized drug samples using GC–TOF MS. Furthermore, smart software tools will be demonstrated, which save time during data analysis for fast and simple comparisons of complex chromatograms.

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Experimental

Samples: Six seized drug samples, suspected to contain heroin, in methanol.

MS: BenchTOF2 (SepSolve Analytical) (Figure 1); Mass range: m/z 35–500.

Software: Instrument control and data processing by ChromSpace® 1D.

Please contact SepSolve for full analytical parameters.

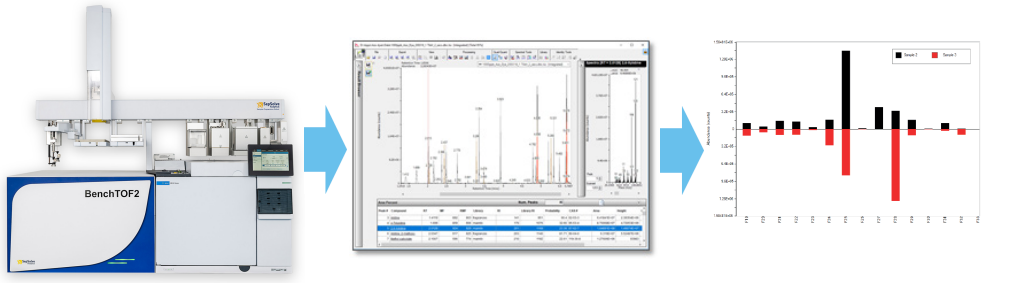

Figure 1

Schematic of the workflow for GC–TOF MS of controlled substances.

Results and discussion

The GC–TOF MS total ion chromatograms (TICs) obtained for the analysis of six seized drug samples are shown in Figure 2. Identifications are provided for the major peaks, which clearly indicate the presence of heroin (diacetylmorphine) in each sample. The identifications also show the presence of cutting agents in some of the samples, such as caffeine and acetaminophen (or paracetamol). The ability of TOF MS to collect all ions all the time ensures that high-sensitivity screening of the entire sample is achieved – both targets and unknowns.

In this study, the ChromSpace 1D software platform provided full instrument control, while also enabling real-time data processing to be employed during analysis. This allowed the chromatograms to be background-subtracted, integrated, deconvolved and library-searched while the samples were still acquiring, significantly reducing the amount of time spent on data analysis. Figure 3 shows the result of real-time data processing for Sample 4, with robust deconvolution enabling masked and co-eluting peaks to be identified automatically.

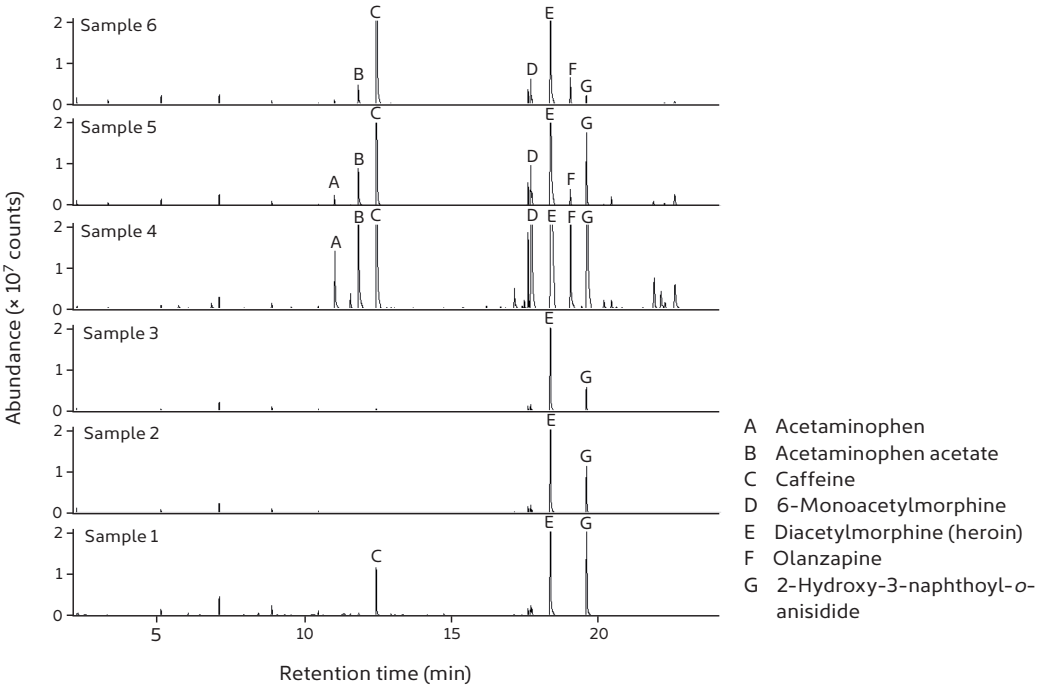

Figure 2

GC–TOF MS (TIC) chromatograms for six seized drug samples.

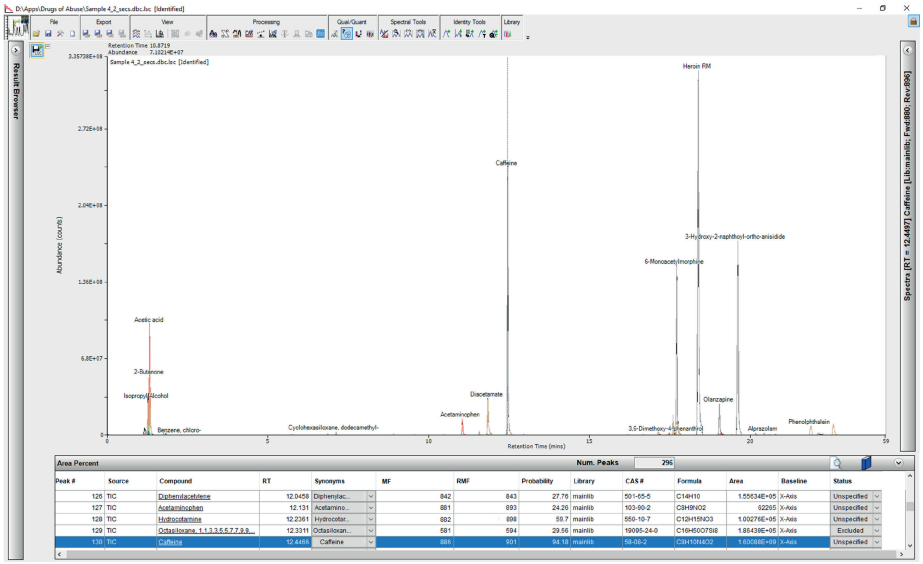

Figure 3

Real-time data processing in ChromSpace 1D software, showing deconvolution and identification applied to Sample 4 during acquisition.

The expansion (Figure 4) shows an example of this, with two co-eluting components confidently identified using the excellent spectral quality of BenchTOF2 instruments, which, unlike other TOF mass spectrometers, are free from mass discrimination.

The combination of highly sensitive detection, excellent spectral fidelity and smart software tools ensures that comprehensive profiling of the sample is achieved. For example, Figure 5 shows a wide range of trace impurities and cutting agents identified in Sample 5 using this GC–TOF MS approach.

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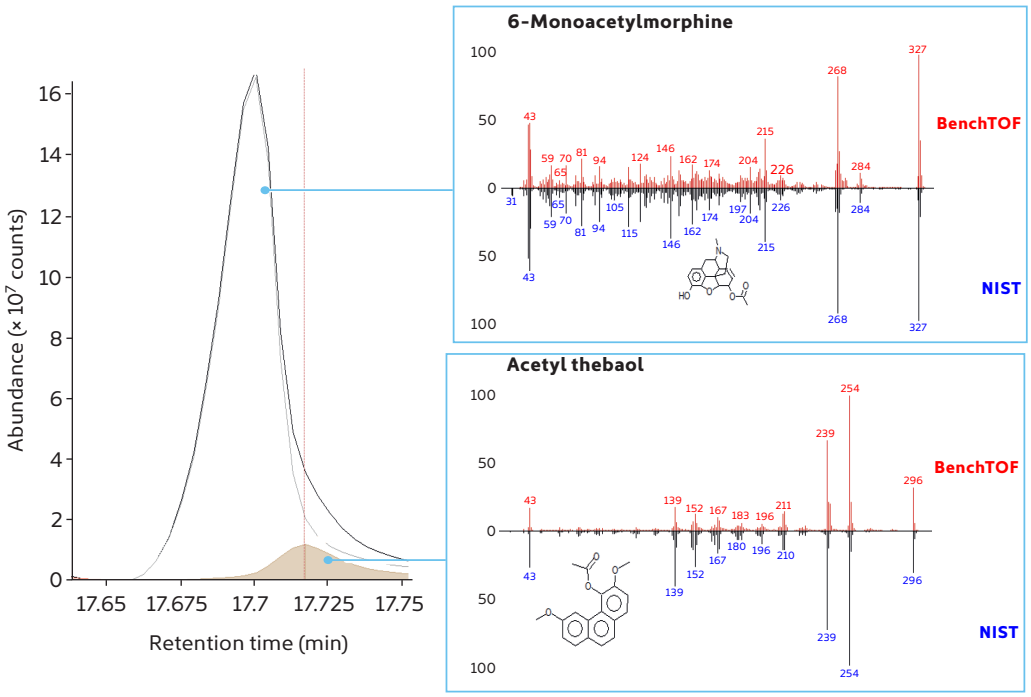

Figure 4

Deconvolution in ChromSpace 1D for two co-eluting peaks found in Sample 4, with identifications using BenchTOF2 mass spectra.

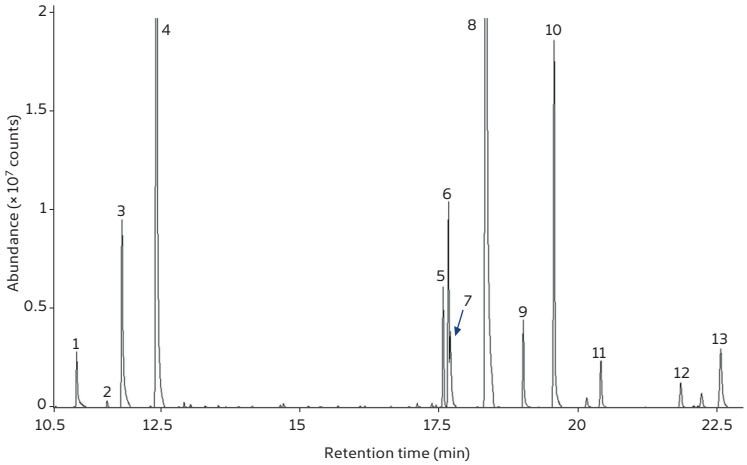

Figure 5

Expanded region of the GC–TOF MS (TIC) chromatogram for Sample 5, with peak identifications provided in the table.[1]

Peak no.	Identification	Description
1	Acetaminophen	Cutting agent (analgesic)
2	Meconin	Trace impurity
3	Acetaminophen acetate	Cutting agent
4	Caffeine	Cutting agent (CNS stimulant)
5	6-Acetylcodeine	Trace impurity
6	6-Monoacetylmorphine	Trace impurity
7	Acetyl thebaol	Trace impurity
8	Heroin	Controlled substance
9	Olanzapine	Cutting agent (antipsychotic)
10	Azonaphthol OA	Synthetic dye
11	Alprazolam	Cutting agent (benzodiazepine)
12	Phenolphthalein	Cutting agent (laxative)
13	Phenolphthalein 2AC	Cutting agent

The identification of cutting agents, impurities and diluents is an important aspect of drug profiling as it can often provide information on the origin of the drug, as well as distribution networks and manufacturing techniques.

The ChromCompare® module in ChromSpace 1D is a useful tool in drug profiling studies for automated comparison of samples. ChromCompare provides rapid and objective comparisons of multiple data files based on relative abundances of identified compounds (Figure 6) – displaying a simple matrix of pairwise match factors (between 1 and 1000) to make it easier to identify trends.

In Figure 6, the comparison of two of the seized drug samples is shown in ChromCompare, using a suite of identified impurities, adulterants and cutting agents. It can be seen that Samples 4 and 1 have a high match factor of 902, indicating similar profiles. However, the histogram plot (or H-plot) also highlights where differences exist, such as the presence of acetaminophen (and its impurities, e.g. acetaminophen acetate) in Sample 4 only.

Figure 6

ChromCompare H-plot showing the comparison of two of the seized samples.

In a similar way to spectral libraries, ChromCompare databases can be created for these H-plots, meaning that subsequent drug samples can be screened quickly and easily. In other words, the match factor will quickly show whether the new sample is similar to an existing entry in the database, which could help to indicate the same source.

It is important to note that if targeted analysis is performed for specific drugs and impurities, using instruments such as single quadrupole MS (SIM mode) or triple quadrupole MS, important compounds may be overlooked. On the other hand, TOF MS provides comprehensive screening of the entire sample in a single analysis, meaning that all of the information is available for robust profiling and retrospective analysis.

Conclusions

This white paper has described how GC–TOF MS can be used for comprehensive profiling of seized drug samples, specifically:

- BenchTOF2 provides the speed, sensitivity, selectivity, stability and spectral quality required for unparalleled confidence in forensic analyses.
- Comprehensive profiling of the entire sample in a single analysis, with robust deconvolution of co-eluting peaks.
- Real-time data processing in ChromSpace 1D for immediate results and streamlined reporting.
- ChromCompare enables fast and objective comparison of cutting agents and trace impurities present in seized drug samples to help identify samples from the same supplier or distribution network.

For more information on this application, or any of the techniques or products used, please contact SepSolve.

References

[1] UN Office on Drugs and Crime, Methods for impurity profiling of heroin and cocaine, 2005, https://www.unodc.org/pdf/publications/report_st-nar-35.pdf.

Acknowledgements

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Applications were performed under the stated analytical conditions. Operation under different conditions, or with incompatible sample matrices, may impact the performance shown.

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