Application Note: 10018

Drugs of Abuse by Direct Sample Probe Using Single Quadrupole GC/MS

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Key Words

- Direct Sample Probe
- Single Quadrupole GC/MS
- Drugs of Abuse
- Forensic Chemistry

Overview

Purpose

To evaluate a means of rapidly identifying unknown compounds using a direct sample injection as opposed to traditional gas chromatographic techniques. To compare two direct sample introduction methods with GC/MS and offer specific suggestions for operating parameters.

Methods

Simulated solid drug samples of cocaine and methamphetamine were prepared using commercial standards and a matrix that approximated "cutting" materials. A Thermo Scientific DSQ™ single quadrupole mass spectrometer and a Direct Sample Probe fitted with a direct exposure probe (DEP) or a direct insertion probe (DIP) were used for sample introduction and analysis. Drug samples were analyzed in powder form and as a methanolic solution.

Results

Both the DEP and the DIP proved useful for identification of cocaine and methamphetamine in powder and residue form. Sample preparation is minimal, particularly for the DIP, which utilized the raw powder, and the drug of interest is identified within two minutes of introduction into the mass spectrometer. The Direct Sample Probe, when used in conjunction with the DSQ, offers an additional tool for analysis of drugs of abuse.

Introduction

According to the United States Federal Bureau of Investigation Uniform Crime Report (FBI UCR) for 2002, there were estimated to be 1,538,800 state and local arrests for violation of drug laws. These arrests included charges of possession, manufacture/growth, and selling of illicit drugs.[1] Typically, the investigating officer performs the identification of seized drugs and evidence on a preliminary basis in the field, with confirmatory tests performed by crime laboratory drug chemists. Analytical techniques include chemical spot tests, thin layer chromatography, gas chromatography (GC-FID), Fourier Transform Infrared spectroscopy (FT-IR), and hyphenated techniques, such as gas chromatography-mass spectrometry (GC/MS) and liquid chromatography-mass spectrometry (LC/MS)[2]. Another available technique is direct sample probe analysis coupled with mass spectrometry.

Direct sample probe analysis allows the mass spectrometer user to bypass the GC or LC for sample introduction by inserting the sample directly into the source for ionization and analysis. The DSQ is a quadrupole mass spectrometer used with the Direct Sample Probe to analyze and identify unknown compounds directly via the probe. Figure 1 shows the mass spectrometer TRACE GC Ultra gas chromatograph, with an arrow pointing to the vacuum interlock. This vacuum interlock assembly allows insertion of the probe into the source. Since the probe is inserted through the vacuum interlock, the GC does not need to be separated from the mass spectrometer. There is minimal conversion time from probe mass spectrometer (MS) analysis to GC/MS analysis. This allows the user to perform direct probe analysis and GC/MS in the same instrument on subsequent analyses.

Figure 1: The DSQ GC/MS system, shown with the vacuum interlock.

The Direct Sample Probe (Figure 2) offers two means of sample introduction. The direct exposure probe (DEP) uses a filament through which current is passed. The current heats the filament wire rapidly, volatilizing the sample. Using a syringe, 1 µL of sample in solvent is placed on the wire. The solvent is allowed to evaporate at room temperature, and then the probe is inserted into the mass spectrometer. The user initiates the DEP program, which starts the mass spectrometer, and the sample is acquired. For the direct insertion probe (DIP), the sample is placed in a glass crucible that is heated at a programmed rate to volatilize the sample. After placing a small amount of sample in the crucible, the user

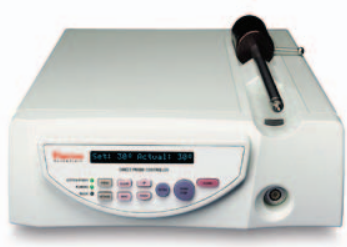

Figure 2: The Direct Sample Probe and controller. The keypad allows the User to enter method parameters and start and stop probe methods.

inserts the probe into the mass spectrometer, and starts the DIP program. The mass spectrometer then acquires the mass spectral data for the sample.

To evaluate the utility of the Direct Sample Probe as a sample introduction technique, simulated drug samples were created in a matrix reflecting typical cutting agents. Cocaine and methamphetamine samples were analyzed, both in a powder form and as a methanolic rinse of residue from a container, and the selection of sample probe tip corresponded to the sample type. The powder forms were tested using the DIP, and the methanolic solutions were analyzed with the DEP. Data were acquired using the DSQ GC/MS in electron impact (EI) mode at 70 eV to generate library-searchable mass spectra. Instrument performance was verified prior to the test using a full Autotune, and performance was also checked following sample analysis to determine method ruggedness. Additionally, the potential for carryover was evaluated by running blank acquisitions after each sample.

The Direct Sample Probe, when used in conjunction with the DSQ GC/MS, provides an alternate means of sample introduction that reduces or eliminates sample preparation time. The technique also requires a minimal sample amount for testing. There was no carryover observed for either the DIP or the DEP, showing that the filament and crucible could both be re-used as needed for more samples. Mass spectral data provided high quality library matches, and instrument performance was robust. All of the testing was performed with the gas chromatograph still in place, which allowed rapid return to GC/MS operation. Overall, direct sample probe analysis offers increased utility in confirmation analysis of drugs of abuse.

Methods

Sample Preparation

Drug standards for cocaine and methamphetamine were obtained from Cerilliant Corporation (Round Rock, TX). "Cutting" agents included baking soda, powdered (confectioners') sugar, and powdered skim milk. These were mixed together at a 1:1:1 ratio. Then, approximately 0.5 grams of this mixture were measured into an aluminum weigh tray. For the cocaine sample, four vials of 1.0 mg/mL standard were added to the mix and allowed to evaporate. The final concentration of cocaine in powder was approximately 0.8%. Similarly, four vials of methamphetamine standard were added to a different tray with 0.5 g of the mixture, again resulting in a concentration in matrix of approximately 0.8%. The powdered samples were transferred to individual vials for storage, and the trays were scraped to clean them. Each tray was rinsed with about 1 mL of methanol, with care taken to rinse only about half of the tray, thereby preserving the other half of the tray. The methanol rinses were transferred to appropriately labeled autosampler vials with caps.

Instrumental Analysis

A DSQ single quadrupole GC/MS with a 250 L/s turbopump and an Ion Bright™ source was selected for this analysis. The instrument was tuned and calibrated using a full EI Autotune for classical ion ratios (Figure 3). The GC/MS system was set up for gas chromatographic analysis; however, there was no need to detach the GC from the mass spectrometer for this analysis, so the column remained installed in the transfer line, and the mass spectrometer was not vented. After tuning, the standard EI ion volume was removed via the vacuum interlock, and an ion volume for probe work was installed. The MS was ready for probe analysis within 3 minutes.

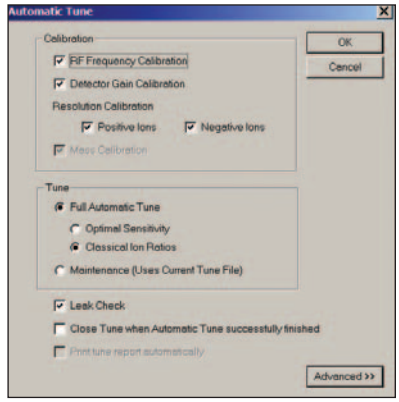

Figure 3: DSQ tune and calibration selections, used both pre- and post-probe sample analysis.

The MS instrument method parameters are summarized in Table 1. Different filament delay times were necessary for the differing probe tips due to variations in volatilization rates. Table 1 also includes the probe methods. The user creates probe methods directly on the keypad of the probe (Figure 2), while the method for the mass spectrometer is developed within Xcalibur™ Instrument Setup.

	DSQ MS		DIRECT SAMPLE PROBE		
COCAINE FULL SCAN MS METHOD	Acquisition Time:	Probe Run Time	Initial Current:	0 mA	DIRECT EXPOSURE PROBE (DEP) METHOD
	Source Temp:	250 °C	Initial Hold:	15 sec	
	Start Time:	0.25 min	Ramp:	20 mA/sec	
	Electron Energy:	-70.0 eV	Final Current:	1,000 mA	
	Emission Current:	100.0 µA	Hold:	30 sec	
	Detector gain:	1 x 10^5			
	Scan Event 1				
	Scan Mode:	Full Scan			
	Scan Rate:	500.00 amu/sec			
	First Mass:	40.0			
	Last Mass:	450.0			
METHAMPHETAMINE FULL SCAN MS METHOD	Acquisition Time:	Probe Run Time	Initial Temp:	30 °C	DIRECT INSERTION PROBE (DIP) METHOD
	Source Temp:	250 °C	Initial Hold:	0 sec	
	Start Time:	0.00 min	Ramp:	Max	
	Electron Energy:	-70.0 eV	Final Temp:	450 °C	
	Emission Current:	100.0 µA	Hold:	30 sec	
	Detector gain:	1 x 10^5			
	Scan Event 1				
	Scan Mode:	Full Scan			
	Scan Rate:	500.00 amu/sec			
	First Mass:	45.0			
	Last Mass:	450.0			

Table 1: Method parameters for the DSQ, the DEP and the DIP.

Sample Analysis

DEP: For the direct exposure probe, the methanolic rinses of the weigh trays were analyzed. Using a clean autosampler syringe, 1 µL of the rinse from the cocaine tray was placed on the filament. The DEP filament design incorporates a loop that catches the droplet (Figure 4).[3] The solvent was allowed to evaporate at room temperature, and when the droplet was no longer visible, the probe was inserted into the analyzer via the vacuum interlock.

Figure 4: The direct insertion filament, shown with the loop on the end. A 1 µL sample is placed on the loop and the liquid allowed to evaporate prior to inserting the probe into the source.

A software tool, shown in Figure 5, guides the user through the steps of inserting the probe. These steps prevent accidental venting of the analyzer. Once the probe is in place, the sample line in the Xcalibur sequence is initiated, which prepares the instrument for analysis. When the mass spectrometer goes to a status of "Waiting for contact closure…", the user presses the *Start* button on the probe controller. This begins the DEP and MS method. The DEP ramps the current through the filament and volatilizes the sample. When the probe method is complete, the MS method ends. After analyzing the cocaine sample, the method was repeated to check for carryover. Then, the methamphetamine methanol rinse was analyzed using the same procedure. After the methamphetamine analysis, the filament was again checked for carryover.

DIP: After completing the DEP analysis, the probe was changed to the DIP. The probe controller automatically senses the probe type and changes the method parameters accordingly. The DEP uses current passed through the filament, whereas the DIP uses direct temperature. A clean glass crucible was inserted into the probe (Figure 6), and then a clean disposable glass Pasteur pipette was used to collect a few grains of the solid powder. The powder was transferred to the crucible, and an appropriate method was programmed into the probe controller.

Figure 6: Insertion of the DIP crucible into the probe end. The crucible contains the powder sample.

The DIP was inserted into the mass spectrometer using the same procedure as described above, with sample acquisition proceeding in the same manner as the DEP. After the powder was analyzed, the DIP was heated again to check for carryover. The crucible was removed and replaced with a new one before analyzing the next powder.

After checking the crucible for carryover, the probe ion volume was removed, and the standard ion volume was reinserted. Then, instrument performance was verified again by performing a full Autotune and calibration using the same settings as the initial tune.

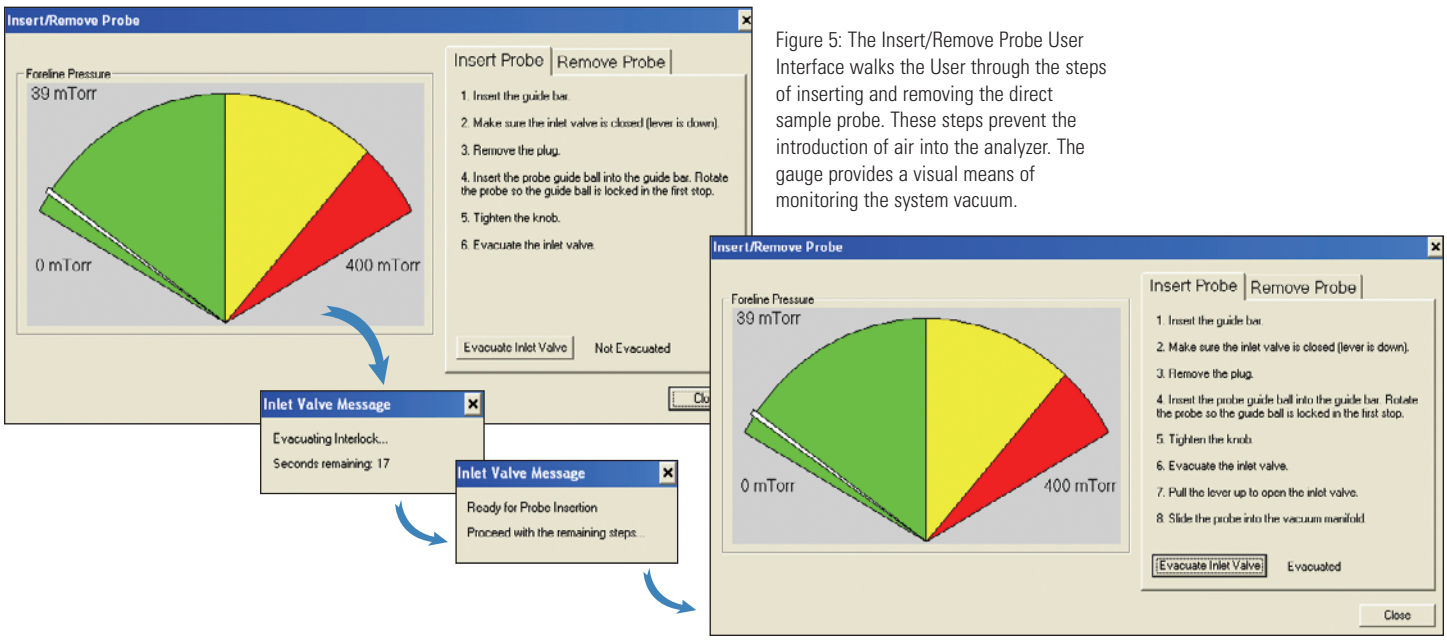

Figure 5: The Insert/Remove Probe User Interface walks the User through the steps of inserting and removing the direct sample probe. These steps prevent the introduction of air into the analyzer. The gauge provides a visual means of monitoring the system vacuum.

Results

Cocaine was successfully identified in both the powder form and the residue rinse. Methamphetamine was not compatible with the DEP due to the faster heating profile of the DEP, so it was not identified at the low concentration using the DEP. However, by using the DIP to analyze methamphetamine in powder form, the methamphetamine was identifiable. Chromatograms and associated mass spectra for the DEP analyses of the cocaine residue, along with the blank run for carryover evaluation, are shown in Figure 7. Additionally, the NIST 2.0 library match is displayed for cocaine.

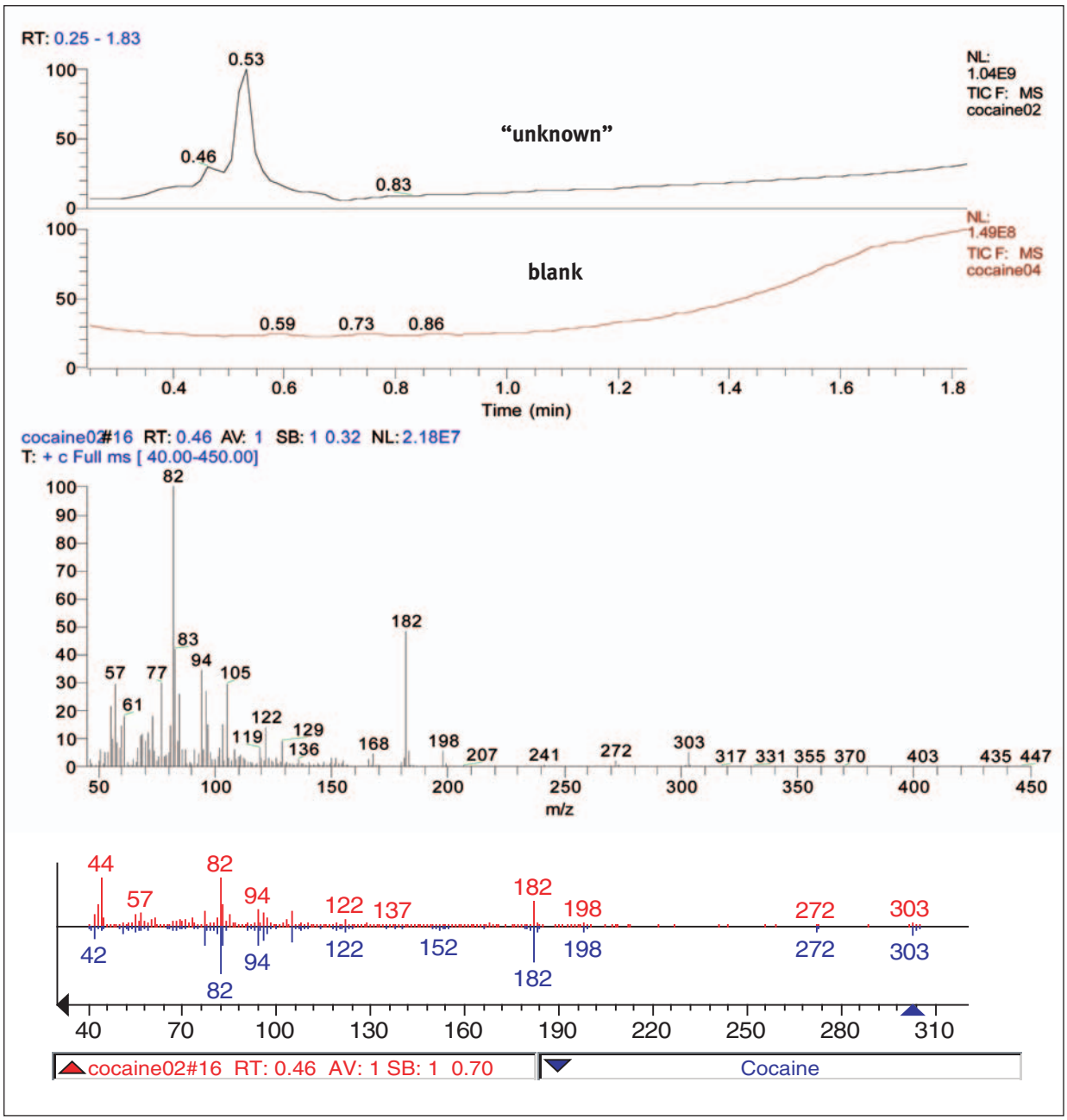

Figure 7: Cocaine residue analysis by DEP. The top chromatogram shows the residue, with cocaine at 0.46 min. The second trace (maroon) is a blank run. The spectrum for cocaine is also displayed. The NIST 2.0 library search result compares the "unknown" (red) to the library entry (blue).

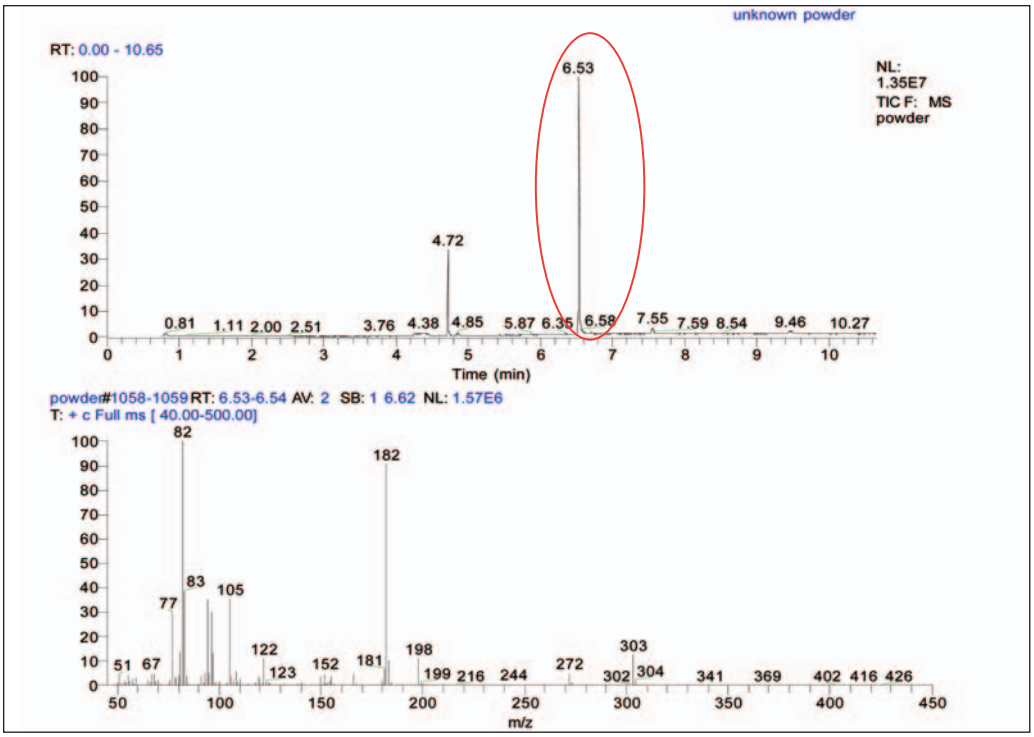

Figure 8: The same methanol rinse of the cocaine residue was analyzed by full-scan GC/MS. The retention time for cocaine is 6.53 min, using a 20 m x 0.18 mm i.d. x 0.4 µm Rtx®-5MS column and an oven ramp from 65-270 at 40 °C/min.

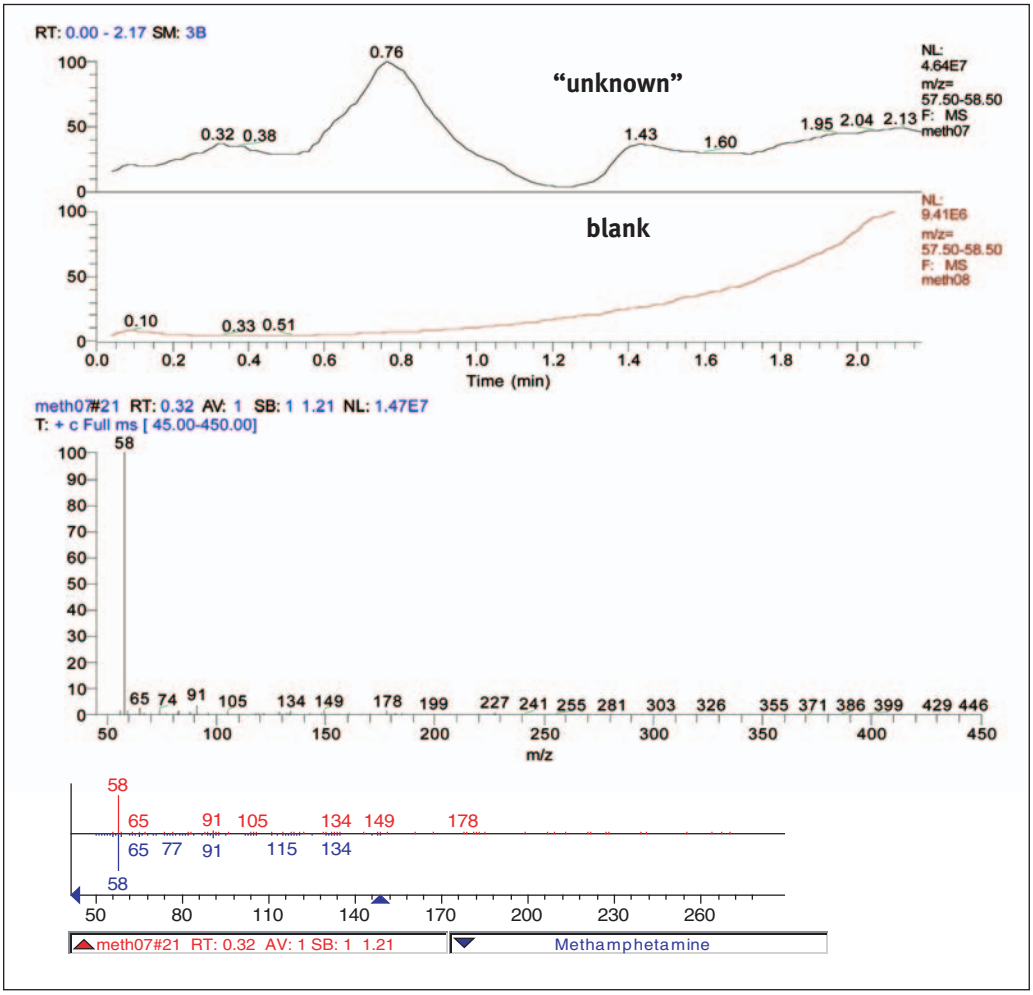

Figure 9: Methamphetamine powder analysis by DIP. The top chromatogram shows the residue, with meth at 0.32 min. The second trace (maroon) is a blank run. The spectrum for meth is also displayed. The NIST 2.0 library search result compares the "unknown" (red) to the library entry (blue).

The chromatogram resulting from direct sample probe analysis differs from a standard GC chromatogram. First of all, the analysis time is significantly shorter with the use of the probe. As Figure 8 shows, cocaine elutes at 6.53 minutes using a narrow bore column (20 m x 0.18 mm i.d. x 0.4 µm film 5% phenyl column. Using the probe to analyze the same solution, cocaine comes out at 0.46 min. Additionally, the chromatogram does not reflect chromatographic separation, since samples are separated based upon volatility. As soon as the samples are volatized, the compounds are ionized. Figure 9 summarizes the results of the methamphetamine powder analysis using the DIP, including the NIST 2.0 library search match for methamphetamine. Methamphetamine was the top library hit.

Probe analysis offers sufficient sensitivity, with concentrations of methamphetamine and cocaine in powder at approximately 0.8%. No carryover was seen after each analysis. The filament, with a maximum current of 1400 mA, is self-cleaning and can be used repeatedly until it wears out. The crucibles for the DIP, on the other hand, tend to fill up with non-volatile components and must be replaced regularly (Figure 10). However, volatilization of the target component is complete after one run, as shown in the blank run following the sample.

One important consideration of direct sample probe analysis is its effect on the source. Contamination of the source can lead to decreased sensitivity and an increased need for maintenance. However, the presence of the Ion Bright source ensures more than enough sensitivity for continued use. Removable ion volumes also allow for convenient, routine instrument maintenance without the need to vent the analyzer.

Figure 10: Direct Insertion Probe (DIP) tips. The crucibles on the left are new, while the crucibles on the right contain the non-volatile by-products of heating that were left over after analysis of the methamphetamine and cocaine powders.

Conclusions

The Direct Sample Probe offers an excellent alternative to GC and LC for mass spectral analysis of solid drugs and drug residues. The DSQ single quadrupole MS, via the vacuum interlock, provides high-quality mass spectral data for identification of unknown compounds. This direct analysis offers rapid identification of unknowns. When coupled with a TRACE GC Ultra, the combination of direct sample probe-MS and GC/MS offers an additional tool for drug analysis. Further research will pursue other drug classes and types, such as pills and liquids. The use of chemical ionization in conjunction with the direct sample probe may offer more conclusive identification of drugs with indistinct EI mass spectra, such as methamphetamine and amphetamine.

References

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Acknowledgement

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