B60 Primary Ion Middle Ion Structure Analysis (PIMISA®) -Enabled Direct Analysis in Real-Time (DART®) QDa Mass Spectrometer (MS): The Latest Development in Forensic Analysis Efficiency

Rachel C. Beck, PhD, 504 Rolling Hills Drive, Chelsea, AL 35043; Frederick Li, MS, Ionsense Incorporated, 999 Broadway, Ste 404, Saugus, MA 01906; and Brian Musselman, PhD, IonSense, Inc., 999 Broadway, Ste 404, Saugus, MA 01906*

The goals of this presentation are to: (1) describe the reverse search data analysis software, PIMISA®; (2) understand the capabilities of the DART® source, Waters Acquity QDa mass detector, and PIMISA® software; and, (3) recommend workflow that allows scientists to produce high-quality, efficient, and economic drug screening analyses in minutes.

This presentation will impact the forensic science community by introducing an innovative and cost-effective drug screening approach, PIMISA®-enabled DART® Acquity QDa® mass detector, and by recommending a potential workflow for increased efficiency.

The new combination of the reverse search library program, PIMISA®, and DART® -equipped compact mass detector offers an efficient, highly selective, and cost-effective drug screening approach for compound identification in forensic laboratories.

PIMISA®-enabled DART® QDa MS is evaluated for implementation into forensic workflow. The instrument exploits Collision Induced Dissociation (CID) to collect four spectra with varied fragmentation. The PIMISA® program analyzes these spectra, identifying analytes through library matching. The library contained spectra for 170 certified reference materials. This approach was evaluated through accuracy, specificity, limit of detection, experienced versus inexperienced users, and correlation studies. In all studies, samples were analyzed in triplicate with an analysis time of two to five minutes per sample, including data analysis.

Accuracy studies were performed through analyses of 70 adjudicated case specimens (pills, powders, plant materials, etc.) over a 4-day period by an experienced user. Samples were previously analyzed by traditional methodologies (visual identification, microscopy, gas chromatography/mass spectrometry, etc.) and reported to contain up to four drugs. The specificity study was evaluated for six sets of analytes, two pairs in three categories, at concentration ratios ranging from 10:1 to 1:10. Categories were determined by molecular ion differences of 1, 2, and 10s of daltons. Analyte pairs included methadone/alprazolam, codeine/temazepam, methamphetamine/CMP, hydrocodone/oxymorphone, hydrocodone/acetaminophen, and cocaine/procaine. The Limit Of Detection (LOD) study was performed for six analytes representing the Alabama casework population with varying polarities. Two scientists, a novice user (<1 year experience) and an experienced user (5^{+} years experience), and two sample introduction methods (semi-automated versus manual) were compared for 20 randomly selected, adjudicated cases (not included in the previous 70) in the blind study. The semi-automated sample introduction method utilized wire mesh consumable (QuickStrip®) cards, while the manual method used fused capillaries. The correlation study was designed to compare a DART® Time Of Flight (TOF) /MS with the PIMISA®-enabled DART® QDa MS. An experienced user re-analyzed 20 of the 70 adjudicated case samples on the DART® TOF/MS and compared the data.

Results of the selectivity studies were calculated as percentages of “analyte detection” versus “negative” and

ranged from 81% to 100%. In the specificity study, analyte identification of molecular ions within 1 and 2 daltons was not observed at certain concentration ratio differences and this ratio varied between analyte pairs. For the 1 dalton separation pairs, observed interference began at concentration ratios of 2:1 for methadone/alprazolam and 4:1 and 1:10 for codeine/temazepam. Concentration ratio interference for methamphetamine/CMP was observed at 2:1, while hydrocodone/oxycodone was observed at 5:1. No concentration ratio interference was observed for cocaine/procaine; however, hydrocodone/acetaminophen was observed at 4:1. The LOD study included analysis of methamphetamine, diphenhydramine, cocaine, alprazolam, methadone, and THC. The cutoff concentration results varied between 0.5µg/mL and 10µg/mL. The robustness of the approach was demonstrated by both sample introduction and user experience during the blind study. Results for the experienced user were consistent between both sample introduction methods with a screening acceptability (accuracy and false positive) of 90%. Results for the novice user ranged from 70% to 80% screening acceptability with manual sampling preferred. Data comparisons of the PIMISA®-enabled DART® QDa MS to the DART® TOF/MS resulted in 89% accuracy.

The DART® Waters Acquity QDa mass detector enabled with PIMISA® demonstrated capabilities for detection of multicomponent mixtures in minutes. With screening acceptability exceeding 70% and selectivity results above 80%, the approach is determined to be robust and highly selective. Additionally, the platform is shown to be comparable to existing DART® TOF/MS workflows at half the capital investment. Therefore, the DART® QDa MS and PIMISA® approach is an efficient, highly selective, and economic platform for forensic drug screening.

DART® MS, PIMISA® Software, Forensic Drug Screening