B21 Body Fluid Identification by Mass Spectrometry From Sexual Assault Evidence

Kevin M. Legg, 2300 Stratford Avenue, Willow Grove, PA 19090; Heather E. Mazzanti, MSFS, 450 S Easton Road, Glenside, PA 19038; Christian G. Westring, PhD, 2300 Stratford Avenue, Willow Grove, PA 19090; and Phillip Danielson, PhD, Department of Biology, 2101 E Wesley Avenue, Lab 223, Denver, CO 80210*

After attending this presentation, attendees will be aware of a novel workflow for screening of biological material originating from sexual assault kits through the use of targeted mass spectrometry.

This presentation will impact the forensic science community by illustrating how this work has the potential to significantly improve serological screening of forensic evidence. Not only will practitioners be able to obtain unambiguous test results for saliva and seminal fluid, but the multiplex design will eliminate the need to perform separate tests on an unknown stain. In short, the successful completion and implementation of this technology will provide a powerful tool for screening and prioritization of sexual assault-type samples for laboratory processing and criminal investigation.

While DNA profiling makes it possible to individualize biological stains, the accurate characterization of the biological material present can provide critical information to prioritize samples for subsequent microscopic and DNA analyses. Currently, the technologies used for the confirmation of seminal fluid and saliva (critical fluids for screening sexual assault evidence) are primarily based on antibody and enzyme activity-based assays.

Contrary to the marketing claims made by some commercial providers, the identification of seminal fluid and saliva by these methods is based on a presumptive indication of the presence of a body fluid. Positive results with non-target body fluids, false positives with non-biological materials, and antibody cross-reactivity with non-human sources have been well documented in the forensic literature.

Thus, it is recognized that there is clear value in developing alternative approaches that are both sensitive and accurate for the identification of human biological stains. To date, a proteomics-based analysis of human body fluid proteomes have identified multiple protein biomarkers for six forensically relevant body fluids — including seminal fluid and saliva. The specificity of each biomarker, the reliability with which it can be detected, and the degree of inter-individual variability in expression has already been demonstrated across a large sample population of human subjects.

These biomarkers have been incorporated into a targeted mass spectrometry assay for the identification of human seminal fluid and saliva. The work described here employs simulated sexual assault swabs in order to compare the sensitivities of the mass spectrometry approach relative to several commercial immunochromatographic tests for the detection of seminal fluid and saliva. To assess this, simulated sexual assault swabs were prepared by spotting varying quantities of semen and saliva onto blank semen-free vaginal swabs. Each dilution was assayed using commercial immunochomatographic systems for saliva (RSID™ Saliva) and semen (RSID™ Semen and Abacus Diagnostics® ABAcard® p30) as well as by targeted mass spectrometry on a triple quadrupole mass spectrometer. All targeted biomarkers for both seminal fluid and saliva were reliably detected (based on response ratios, retention times, peak shape, and symmetry as compared to a known positive control) at all dilution levels by the mass spectrometry method. Conversely, several immunochromatographic systems produced erroneous weak positive results due to the hook effect while yielding only weakly positive results at the lowest quantities of spotted body fluid.

Based on these results, the mass spectrometry-based approach offers a superior detection platform while consuming less evidentiary material. In addition, the mass spectrometry-based approach is well suited for simultaneous fluid identification, is compatible with batch analyses in multi-well plate formats, and offers automated data processing and reporting of true confirmatory results.

Serology, Mass Spectrometry, Proteomics