H94 Proteogenomics: Shifting Touch Sample Analysis Paradigms

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Learning Overview: After attending this presentation, attendees will understand that it is possible to isolate both DNA and protein from human touch samples, providing a second meaningful source of genetic information on which forensic analysis can be based, in addition to traditional DNA analysis.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by aligning with the competencies of attendees who process trace forensic samples. Proteomic analysis is rapidly maturing, providing value to attendees focused on performance who are looking to implement these methods to derive additional value from these challenging sample types. These results demonstrate that this approach permits traditional DNA analysis and parallel protein analysis, highlighting the relevance to both the core competencies and performance requirements of typical attendees.

Human touch samples represent an increasing fraction of forensic casework analysis each year. Unfortunately, these samples are also among the most difficult to analyze effectively, especially with respect to traditional DNA analysis. Trace DNA in touch samples commonly leads to marker drop-out and other artifacts and can complicate analysis of DNA mixtures. Certain evidence types, such as brass shell casings, may further contribute to DNA degradation or inhibition. Proteins represent a separate, often overlooked, class of biomolecules in touch deposits that are both highly abundant and environmentally robust. The use of mass spectrometric-based proteomic analysis to identify Genetically Variable Peptides (GVPs) has been recently demonstrated to provide forensically relevant match probabilities to suspected individuals.

This study describes the application of a novel complete casework-oriented proteogenomic analysis method that encompasses sample preparation, DNA profiling, proteomic analysis, and a GVP-specific Random Match Probability (RMP) calculator specifically designed to use proteogenomic data sets. Using both human fingerprint samples as well as artificial fingerprints to standardize DNA and protein inputs, the study demonstrates that this approach maximizes DNA and protein yield across multiple surface types, including glass, plastic, laminate, and brass. Critically, the sample collection and extraction procedure stratifies and differentially extracts DNA and protein fractions, enabling parallel DNA and GVP analysis without significant loss of either fraction. This capability promotes future casework laboratory implementation by positioning GVP analysis as a complimentary tool and enhancement to standard DNA analysis (as opposed to promoting GVP analysis as a replacement of the current gold standard). Using this novel method, the current study demonstrates improved DNA yield in comparison to standard extraction methods. By extracting and analyzing protein markers from the same sample, these results further show that humans can be identified from touch samples with RMP values ranging from 10^{-5} to 10^{-16} regardless of DNA content. Taken together, this novel sample preparation strategy and custom analysis method provides a transformative capability for the analysis of touch samples.

Forensic Genomics, Forensic Proteomics, Touch Sample Analysis