



### **B43 A Proteomic Analysis of Human Hair From Various Body Sites**

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After attending this presentation, attendees will better understand that human hair is a biological link between its source and the forensic context in which it is found. This presentation will inform attendees regarding the proteomic information found within hair and how it can be exploited to render additional data regarding the anatomical location of human hair on the body.

This presentation will impact the forensic science community by informing attendees that forensic science is in critical need of new laboratory-based methods that provide a quantitative statistical association between an individual and a forensic context. If DNA is not available or is degraded, genetic information in protein may provide additional data.

Recent methodological advances in proteomic analysis offer the prospect of considerable improvement in the use of hair evidence for individual identification. An advantage is the supplementation of subjective findings from microscopic hair comparison with quantitative values amenable to probability estimates and experimentally determined error rates. Results to date are promising with respect to distinguishing among individuals by profiling protein expression levels in the hair shaft. Variations in expression level reflect variations in transcription factor levels, their affinities for response elements, and possibly epigenetic as well as genetic variation. Another form of variation is the presence of Genetically Variable Peptides (GVPs) that offer the prospect of even more discriminating analysis. GVPs are a consequence of non-synonymous single nucleotide polymorphisms that are translated as single amino acid polymorphisms. Increasingly well described by the database of single nucleotide polymorphisms in human DNA, the known non-synonymous mutations among them permit detection of GVPs in digests of hair proteins.

To maximize the usefulness of proteomic technology, two factors merit further exploration. First, optimization of hair processing, now very time consuming, is envisioned to increase the speed and sensitivity of the method so that eventually a single hair fragment will suffice for analysis. Progress in this optimization is occurring. Second, the relative value of hair from different anatomic sites remains to be assessed. The initial study indicated that the protein profiles of hair classes from four sites (axillary, beard, pubic, and scalp regions) are distinguishable. Current work addresses the relative discriminating ability of protein profiling of hair samples from these sites within and among individuals. Whether the profiles differ in a reproducible fashion according to site could be useful in assessing individual comparisons when a hair sample to be identified is of uncertain site origin. Complementing this direction, current work also addresses the yield of GVPs from hair from the different sites. Since GVPs from less abundant proteins are more likely to be observed with increased efficiency of hair digestion, optimization of the processing is envisioned to increase the number of GVP identifications and therefore increase the level of discrimination possible by this route.

#### **Body Hair, Proteomics, Genetically Variant Peptides**