

## USE OF PROTEINS TO OBTAIN MEASURE OF IDENTITY IN THE ABSENCE OF USABLE DNA

Melissa Huntzinger, Daniel Fairbanks, Glendon Parker  
Utah Valley University

The use of nuclear DNA to provide matches between a forensic sample and an individual has revolutionized forensic science. DNA matches may have less than a 1 in  $10^{13}$  probability of occurring randomly in the population. Unfortunately DNA is chemically and physiologically labile. In certain contexts, such as in hair shafts, degraded forensic samples, or in contaminated samples such as rape kits, amplification of DNA and subsequent DNA-typing is difficult or not possible due absence of usable DNA. Protein however can theoretically substitute for DNA: the sequence of amino acids is a record of the template DNA and incorporates in the primary amino acid sequence non-synonymous single-nucleotide polymorphisms (SNPs). There are 185,000 non-synonymous SNPs in the human genome (an average of 9 per protein). Many of these single amino acid polymorphisms (SAPs) can be detected through mass spectrometry. We ground together three hairs from one individual and digested with 20  $\mu$ g trypsin (Promega) overnight in the presence of 1% ProteaseMax (Promega). Three aliquots of 0.5% of the sample were then applied to a maXis™ LC/MS/MS (qTOF) mass spectrometry instrument. A total of 18154 peptides were detected, 1694 of which were unique and not redundant. This corresponded to 285 proteins. Polymorphic peptides with corresponding allelic dbSNP frequencies from the Utahn and Northern European populations were identified in eighty proteins. Using loci from 14 of these proteins a measure of identity, or the chance that one person would have that profile, was calculated at  $5.8 \times 10^{-5}$  (or 1 in 17000). These loci require additional level of scrutiny, such as comparison with synthetic peptide standards, confirmation of inferred SNPs using a SNP-chip and confirmation of the robustness of the analysis by repetition with hair samples from additional individuals. Higher levels of discrimination are probable with the use of custom reference protein databases. This methodology has the potential to contribute to the probative forensic information gained from protein samples in the absence of usable DNA template.