AN ASSESSMENT OF HEAD HAIR COMPARISON VIA PROTEIN PROFILING

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Recently, scientists from Lawrence Livermore National Laboratory's Forensic Science Center and other collaborators developed a hair shaft protein-based method for human identification. This method exploits genetic information preserved in hair proteins in the form of single amino acid polymorphisms (SAPs). As such, SAP profiling technique has the potential to play a critical role in our ability to complement forensic microscopic hair comparison. The goal of our research was to conduct a preliminary assessment of the efficacy and reliability of SAP profiling for its potential use in forensic casework. We conducted two preliminary studies: 1) determining the adequate hair shaft length required for analysis via SAP profiling using a protein extraction method developed in our laboratory and 2) evaluating the accuracy of current methods for identifying SAPs. On the first objective, a single hair from a single donor was serially sectioned into five hair lengths, from 2cm to 0.12cm. Our study identified 299 proteins and 130 proteins in 2cm and 0.12cm of hair shaft, respectively. Of these proteins, about 85% were non-keratins and 3% were hair keratins. Hair keratins were mostly resistant to a decrease in hair length. Thus, we determined hair segments of 2cm to 0.12cm are capable of providing enough information for proteomic analysis. The second objective of this study was to determine the best method to accurately identify SAPs from mass spectral data. Typical mass spectral analysis software does not have the ability to identify peptides that may vary from public protein reference sequence databases (i.e., genetically variant peptides or GVPs). Two alternative options to identify GVPs and SAPs are 1) to use an open software program called Global Proteome Machine (GPM), or 2) build a custom database of human protein sequences that mass spectral analysis software can search against. For this pilot study, we compiled SAP profiles of two keratin proteins (KRT86 and KRT35) derived from three human subjects using both methods. The GPM method created profiles that contained on average about twice as many SAPs than our custom database. Sequencing of nuclear DNA obtained from the three donors, which helps determine false positive and false negative rates, will also be presented. Based on our preliminary data, it is clear the main concern for the SAP profiling technique no longer lies with whether we can extract proteins from small hair lengths (e.g., 0.12cm), but it is now more focused on identifying a set of core SAPs that could be used for human hair shaft comparison.