



B42 The Forensic Value of Processed Human Hair Extensions

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After attending this presentation, attendees will better understand the probative value of processed human hair extensions in forensic casework. Specifically, this presentation will address the inability to identify a hair as an extension using microscopic and genetic techniques and the associated forensic implications.

This presentation will impact the forensic science community by indicating the forensic value of processed human hair extensions and emphasizing the implications associated with not identifying a human hair as an extension in casework.

The human hair extension industry has grown immensely with revenues exceeding nine billion dollars each year. Statistics indicate that more than 60% of women have at some point invested in hair extensions and that they are even becoming popular with men.¹ In spite of the expansion of the extension consumer market, human hair extensions have never been evaluated for their evidentiary value in a forensic case. A human hair extension collected from a crime scene would be evaluated as a shed human telogen hair and analyzed using microscopic techniques and mitochondrial DNA (mtDNA).² Sequencing of mtDNA from the extension would place the hair donor, not the suspect, at the scene. Although it is not likely that the mtDNA sequence would be matched to the donor's maternal lineage, the evidence would be misleading. Hair extensions collected from a crime scene would misdirect an investigation and result in a misuse of time and resources. The ability to identify a human hair as an extension would be invaluable during an investigation and might exclude the hair as probative evidence.

In this study, three brands of processed human hair extensions were evaluated microscopically and genetically for their probative value in forensic casework. Microscopic analysis of hair morphology by transmitted light microscopy and Scanning Electron Microscopy (SEM) determined that the internal and surface characteristics of the human hair extensions were consistent with human head hair and failed to identify any distinguishing features (pitting, striations, indentations, or internal variations) that differentiated the extensions from natural human hair. Chemical analysis by an Energy Dispersive X-Ray (EDX) detector in conjunction with an SEM identified carbon, oxygen, sulfur, aluminum, and calcium as the main elemental components of the processed human hair extensions, which is consistent with human hair. No elements unique to the extensions were detected.

MtDNA extracted from the hair extensions was sequenced and compared to the revised Cambridge Sequence (rCRS) to identify Single Nucleotide Polymorphisms (SNPs).³ SNPs were used to assign haplotypes and distinguish regional affiliations associated with the extensions in an attempt to establish the ethnicity of the hair donor's maternal lineage.³ Haplotype assignments for the hair extensions were based on Hypervariable region 2 (HV2) genetic polymorphisms and represented multiple geographic regions and a large portion of the population. HV2 sequences were not restrictive enough to determine regional affiliations for particular extension brands or processed human hair extensions as a whole. More definitive haplotype assignments would be possible with Hypervariable region 1 (HV1) SNP discrimination. Also, sequence variation between hair extensions of the same brand indicated that the hair within a single package of extensions was from multiple donors. This has significant implications in forensic analysis.



Reference(s):

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3. Allocco D.J., Song Q., Gibbons G.H., Ramoni M.F., Kohane I.S. (2007). Geography and Genography: Prediction of Continental Origin Using Randomly Selected Single Nucleotide Polymorphisms. *BMC Genomics*, 8: 68.

Mitochondrial DNA, Haplotype, Hair Microscopy