B2 Implementing Hematoxylin Into Casework at the North Carolina State Crime Laboratory

Lindsey Admire, MS, North Carolina State Crime Laboratory, Raleigh, NC 27603; Kristen Crawford, MS, North Carolina State Crime Laboratory, Raleigh, NC 27603; Melanie Carson, BS, Raleigh, NC 27603; Samantha McDonald, BS, East Carolina University, Greenville, NC 27858; David M. Freehling, BS, North Carolina State Crime Laboratory, Raleigh, NC 27603*

Learning Overview: After attending this presentation, attendees will understand the growth phases of human hair, the type of hair that may be left behind at a crime scene, and how the presence of telogen hair roots can potentially impact DNA results obtained from hair.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by providing an overview of the internal hematoxylin study performed at the North Carolina State Crime Laboratory and how implementation of the hematoxylin staining technique will ensure that only hair roots with the best potential to develop a DNA profile are sent for DNA analysis.

When a hair root is sent for DNA analysis, the hair examiner has determined that this hair may provide valuable information to the investigators. Hair analysis and DNA analysis complement each other in that DNA may be able to provide a potential identification for the source of a hair that the examiner deemed important. However, sending a hair root for DNA analysis is a destructive test and no further information can be obtained from that root if a profile is not developed. The hair examiners in the trace evidence section noticed over the past several years that hair roots being sent for DNA analysis were not yielding DNA profiles as expected. The recent advancements in the forensic biology section's detection limits prompted the trace evidence hair examiners to begin researching whether changes needed to be made to the current hair root removal protocol to increase the likelihood of developing a DNA profile from a hair root.

Several staining methods for determining the presence of nuclei within a hair root have been tested and published in scientific journals, as well as validated within other crime laboratories. Based on these studies, the trace evidence hair examiners decided to validate the method of hematoxylin staining for use in screening roots in the telogen growth phase for DNA analysis. In this study, more than 700 head hairs from approximately 15 living donors were examined for the presence of telogen roots. Those roots were then stained using hematoxylin and examined for the presence of nuclei. The roots were separated into one of six groups based on the number of nuclei present: Group 0 (0 nuclei), Group 1 (1 to 10 nuclei), Group 2 (11 to 20 nuclei), Group 3 (21 to 30 nuclei), Group 4 (31 to 40 nuclei), and Group 5 (41 or greater nuclei). A set of 64 hair roots, including the negative control group (Group 0) and a positive control group (anagen or catagen growth phase hair roots), were sent for quantitative analysis in the forensic biology section. The quantitative data showed a clear delineation between Groups 1 and 2, where 36% of Group 1 verses 80% of Group 2 passed the quantification cutoff. All samples in Group 0, Group 1, and the positive control group were then amplified along with a representative sample in Groups 2, 3, 4, and 5. After amplification, the delineation between the results of Groups 1 and 2 maintained constant with 27% of Group 1 obtaining DNA profiles verses 89% of Group 2 obtaining DNA profiles. This showed that the cutoff for the minimum number of nuclei required in order to obtain a potential DNA profile at the North Carolina State Crime Laboratory is 11 or more nuclei.

Hair, Hematoxylin, Telogen