A QUANTITATIVE METHOD FOR SELECTING A HAIR FOR NULEAR DNA ANALYSIS

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Human hairs roots exhibiting a variety of growth stages are often recovered at a crime scene. Forensic hair examiners rely on a qualitative method, high magnification microscopy, to select hairs that are likely to result in successful nuclear (nu) DNA analysis. Currently, the potential of hairs to contain sufficient amounts of native nuDNA is based on the microscopic visual inspection of two independent factors – the growth phase and the presence of adherent soft tissue surrounding the root where the hair was once anchored in epidermal follicles. This tissue is often observed in the roots of actively growing (anagen) hairs and is typically absent in quiescent (telogen) hair roots, the latter of which constitute the majority of hair evidence found at crime scenes. The assumption is that the presence of tissue will lead to successful nuDNA typing. Furthermore, regardless of whether or not tissue is present, anagen roots are still sent to nuDNA analysis. However, neither hair roots bearing soft tissue nor anagen hairs guarantee successful results. The implementation of a method to better inform the potential for successful nuDNA typing could mitigate this assumption. At present, there is no commercially available kit that allows forensic examiners to determine the initial amount of native DNA in hair roots prior to DNA extraction. In this study, we evaluate a quantitative method, using the minor-groove binding dye 4', 6-diamidino-2-phenylindole (DAPI). First, our procedure was successful in staining, visualizing and counting the number of nuclei in hair roots. Second, our findings indicate no evidence of DAPI inhibition on PCR amplification as cycle threshold values of quantitative PCR internal positive controls and relative fluorescent unit of the short tandem repeat (STR) loci analyzed remained relatively constant. Third, based on a combination of nuclei visualization and STR analysis, we propose a preliminary threshold of ≥100 nuclei for full STR profiles, regardless of hair growth phase and tissue amount. Experiments to determine the lowest nuclei count threshold (<100 nuclei) for full STR profiles will be presented. When validated, this simple, quick, and quantitative screening method can be used to select a hair for nuDNA analysis.