NOVEL METHODS TO OBTAIN NUCLEAR DNA PROFILES FROM ROOTLESS HAIR SHAFTS

Gina Pineda Murphy, M.S[1], Hiromi Brown, Ph.D.[1], Anne H. Montgomery, M.S.[1], Sudhir K. Sinha, Ph.D.[1], Jonathan Tabak, B.A.[1], Kelly S. Grisedale, Ph.D.[2], Mark R. Wilson, Ph.D.[2]

[1] InnoGenomics Technologies; 1441 Canal Street, Suite 307; New Orleans, LA 70112
[2] Western Carolina University, 136C Stillwell Science Building 111 Memorial Drive, Cullowhee, NC 28723

Hair samples are a common form of trace evidence in many forensic laboratories, and can oftentimes link an individual to a crime or crime scene. Forensic laboratories typically first analyze hair evidence for the presence of root material. If present, nuclear DNA (nuDNA) profiling may be attempted with conventional methods, such as STR typing. If root material is lacking, forensic laboratories often do not process the sample, or submit it for mitochondrial DNA (mtDNA) sequencing, which has typically been more successful than nuDNA on hair shafts. However, mtDNA analysis has several limitations; most significantly, it is maternally inherited and thus cannot differentiate between maternal relatives. Additionally, the mtDNA process is labor intensive, and although useful, does not provide a high statistical power. While typing of nuDNA from hair shafts has often been unsuccessful previously, the presence of some nucleated biologically dead cells or keratinocytes in their last stage of differentiation on a hair shaft make it possible to extract nuDNA. This DNA is both degraded and low in copy number, however, making it difficult to obtain informative profiles with conventional nuDNA testing methods.

We report here utilization of a recently developed technology to improve the success rate for obtaining informative results from forensic samples, including highly compromised, degraded and trace samples such as hair shafts. The InnoTyper™ 21 kit is a small amplicon retrotransposon marker DNA typing system that is compatible with currently used PCR/Capillary Electrophoresis instrument platforms. The system contains 20 *Alu* retrotransposon element bi-allelic markers, ranging in size from 60-125 bp, making the assay highly sensitive for extremely degraded and/or low-level forensic samples, and enabling recovery of discriminating results from samples that would typically require mtDNA sequencing. The application of the InnoTyper™ system to rootless hair shafts will be presented. The present study focused on 60 hairs from various individuals. Two centimeter hair shaft samples, with follicular tags removed, were cleaned in a series of wash steps before complete digestion and purification using commercial buffers. The resultant DNA extracts were quantitated using degradation assessment qPCR quantitation kits, and amplified using both a next generation STR kit as well as the novel small amplicon system InnoTyper™. Comparative results including statistical analysis of the resultant profiles will be presented, demonstrating the ability to produce highly discriminatory nuDNA results from rootless hair shafts.