

FRAGMENTED NUCLEAR DNA IS THE PREDOMINANT GENETIC MATERIAL IN HUMAN HAIR SHAFTS

Michael D. Brandhagen, Odile Loreille, and Jodi A. Irwin
Federal Bureau of Investigation, Laboratory Division

While shed hairs are one of the most commonly encountered evidence types, they are among the most limited in terms of DNA quantity and quality. As a result, nuclear DNA short tandem repeat (STR) profiling is generally unsuccessful and DNA testing of shed hair is instead performed by targeting the mitochondrial DNA control region. Although the high copy number of mitochondrial DNA relative to nuclear DNA routinely permits the recovery of mitochondrial DNA (mtDNA) data in these cases, mtDNA profiles do not offer the discriminatory power of nuclear DNA profiles. In order to better understand the total content and degradation state of DNA in single shed hairs and assess the feasibility of recovering highly discriminatory nuclear DNA data from this common evidence type, high throughput shotgun sequencing was performed on both recently collected and aged (approximately 50-year-old) hair samples. The data reflect trends that have been demonstrated previously with other technologies, namely that mtDNA quantity and quality decrease along the length of the hair shaft. In addition, the shotgun data reveal that nuclear DNA is present in shed hair and surprisingly abundant relative to mitochondrial DNA, even in the most distal fragments. Nuclear DNA comprised, at minimum, 88% of the total human reads in any given sample, and generally more than 95%. This presentation provides a characterization of both the nuclear and mitochondrial DNA content of shed hairs and a discussion of the implications of these data for forensic investigations.