



## Pathology Biology Section – 2006

### G65 Quantification and Amplification of MtDNA From Chemically Treated Hair

Rayna L. Hebard, BS\*, and Bruce R. McCord, PhD, Florida International University, International Forensic Research Institute, 11200 SW 8th Street, Miami, FL 33199; and DeEtta K. Mills, PhD, Florida International University, Forensic DNA Profiling Facility, 11200 SW 8th Street, Miami, FL 33199

After attending this presentation, attendees will learn of some of the techniques used to extract, quantify, and amplify mtDNA from telogen hair shafts that have been chemically treated. The attendee will also be aware of how these chemical treatments affect the quantity and quality of DNA amplified.

This presentation will impact the forensic community and/or humanity by providing knowledge of whether chemical processes cause degradation to DNA in hair shafts and to what extent that damage may be. This knowledge can help the forensic community to establish ways in which to overcome this difficulty so as to enhance mtDNA extraction and amplification from hair so that genetic profiles can be more sufficiently attainable, as hair forensics is becoming increasingly significant in forensics and law.

Evidentiary collection at crime scenes and mass disaster typically include hair strands that later undergo DNA typing that can identify victims and assailants. This presentation will impact the forensic community and/or humanity by demonstrating the effect that various beautification processes have on the quantity and quality of amplifiable mtDNA extracted from hair shafts.

Millions of people, both men and women, subject their hair to different chemical treatments, such as bleaching, coloring, and perming. As such, it is reasonable to assume that hair recovered from a crime scene may have come from a person who utilizes one or more of these popular processes.

Nuclear DNA extraction is typically done on hair strands with growing root tissue. However, telogen hairs, hair strands that are naturally shed, do not contain roots. The shafts of hair are not suitable for nuclear DNA due to the degradation that occurs because of the keratinization process. However, mitochondria are present in abundance in hair shaft. Therefore, mitochondrial DNA is typically extracted from the myriad of mitochondria that are still present in cells. There have been several studies on the efficiency of mtDNA extraction from hair. While the consensus among these studies is that adequate amounts of mtDNA can be extracted from hair and other types of degraded samples, the quality and quantity of the genetic material recovered has not been directly addressed. Within some of these same studies, researchers agreed that damage to hair caused by fire or environmental conditions can significantly affect the amount of DNA extracted. However, there has not been any published research that examines how normal chemical conditioning of hair affects DNA recovery. With the advent of real time PCR, this DNA can be quantified at the picogram level and by examining the effect of amplicon size, the level of degradation can be evaluated.

In this research project, DNA was extracted from telogen hairs from volunteers who used chemical treatments and those who did not. Ten to fifteen hairs, approximately 2-3 cm long, were extracted from each volunteer using the published phenol chloroform separation method and purification of the DNA. The recovered DNA was quantified with real time PCR. Amplification was done using published mtDNA primers and primers specifically designed for this research. The primers utilized amplified conserved areas of the coding region of mtDNA, as these areas have the least amount of variability. Sequencing was done on selected samples with noncoding, control region primers for the hypervariable 1 and 2 regions. The resulting electropherograms were compared to the known reference samples to determine if adequate amount of quality mtDNA was amplified in order to yield a genetic profile.

The amount of mtDNA recovered varied from person to person, but preliminary results revealed that the quantity and quality of mtDNA recovered from individuals without chemical hair treatments exceeds that which comes from treated hair. However, those hairs subjected to treatments can undergo successful mtDNA amplification and sequencing which can then be used to obtain a genetic profile.

**Mitochondrial DNA, Real Time PCR, Telogen Hair**