COMPARISON OF POLYMERASES THROUGH AMPLIFICATION OF MITOCHONDRIAL DNA FROM HAIRS REPRESENTING VARIOUS ETHNICITIES AND TREATMENTS

Natalie Damaso[1], Emily C. Ashe[1], Kelly A. Meiklejohn[1], Mark F. Kavlick[2], James M. Robertson[2]
[1]Visiting Scientist Program, Counterterrorism and Forensic Science Research Unit, Federal Bureau of Investigation Laboratory Division
[2]Counterterrorism and Forensic Science Research Unit, Federal Bureau of Investigation Laboratory Division

Forensic DNA analysis of hair evidence typically involves the amplification and sequencing of the whole control region of the mitochondrial (mt) genome. In compromised hair samples, such as shed hairs, the number of mt genome copies could be low; thus, it is imperative that the polymerase used in PCR is efficient to ensure the maximum recovery of information. Considering this, the first phase of this study compared the yields obtained from 12 polymerases (sourced from a range of commercial companies) when amplifying the whole control region (WCR), hyper variable region II (HV2), and hyper variable region II-B (HV2B). This initial assessment was performed using total genomic DNA extracted from 2 cm of hair adjacent to the root from three donors of differing ethnicities and hair color/texture. Two polymerases were identified that consistently resulted in significantly higher yields ($p<0.05$) for all three regions, when compared to the current SOP polymerase (6 and 4 fold increase in yield). The second phase of this project was focused on assessing the broad utility of these top two performing polymerases for amplifying the WCR and HV2B from hair samples representing diverse ethnic backgrounds (i.e., Caucasian, Hispanic, African American, Asian, Native American), treatments (i.e., bleached, dyed, and chemically straightened), and anatomical locations (e.g., head and genitalia hairs) (n, 41). The results indicated that regardless of sample type, the top two polymerases still significantly ($p<0.05$) outperformed the SOP polymerase (13 and 7 fold increase in yield). The results from this study highlight that enhanced commercially available polymerases, could greatly assist with the recovery of mitochondrial DNA from challenging hair samples encountered in evidence.