B6 Assessing Alternative Polymerases for Amplifying Mitochondrial DNA From Shed Hairs

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After attending this presentation, attendees will better understand that the choice of DNA polymerase used in Polymerase Chain Reaction (PCR) can influence the yield of products substantially. Additionally, attendees should be able to identify the importance of selecting an efficient and robust polymerase for use in the PCR, so that yields necessary for downstream sequencing are routinely obtained from hairs representing a range of treatments and biogeographic ancestries.

This presentation will impact the forensic science community by identifying efficient and robust DNA polymerases that can be used to amplify DNA from forensic-type samples.

Forensic DNA analysis of hair evidence typically involves the amplification and sequencing of the Whole Control Region (WCR) 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 WCR, Hypervariable Region II (HV2), and Hypervariable Region II-B (HV2B). This initial assessment was performed using total genomic DNA extracted from 2cm of hair adjacent to the root from three donors. Two polymerases were identified that consistently resulted in significantly higher yields ($p<0.05$) for all three regions, when compared to the currently used 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 biogeographic ancestries (i.e., Caucasian, Hispanic, African American, Asian, and 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 currently used polymerase (13- and 7-fold increase in yield). The results from this study highlight that novel commercially available polymerases could greatly assist with the analysis of mitochondrial DNA, especially from the challenging hair samples encountered in evidence.

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