B145 Genotyping of Nuclear Loci From Telogenic Hair Shafts Using mini-STRs

Michael D. Coble, PhD, Peter M. Vallone, PhD, and John M. Butler, PhD, National Institute of Standards and Technology, 100 Bureau Drive, Mail Stop 8311, Gaithersburg, MD 20899-8311*

After attending this presentation, attendees will learn an approach to increasing the successful typing of nuclear DNA from telogenic hair samples using miniSTRs for both CODIS and non-CODIS markers will be described.

This presentation will impact the forensic community and/or humanity by demonstrating how the successful typing of even a small number of nuclear loci from shed hairs can greatly increase the forensic discrimination of the sample compared to mtDNA testing alone, where a significant number of common types are present in the population.

Forensic DNA analysts often perform short tandem repeat (STR) typing on highly degraded biological material and then turn to mitochondrial DNA (mtDNA) testing, which is less variable but more likely to obtain a result due to higher copy numbers in cells, if many or all of the STRs fail. MtDNA typing of hair shafts is a particularly important application as shed hairs are commonly found as sources of evidence. Currently, forensic hair comparisons of evidentiary and reference specimens are based upon a set of morphological characteristics. These analyses tend to be subjective, relying on the experience and judgment of the examiner.[1]

A number of studies have demonstrated that successful analysis of degraded DNA specimens from mass disasters or forensic evidence improves with smaller sized polymerase chain reaction (PCR) products.[2] By moving PCR primers closer to the STR repeat region, it is possible to obtain fully concordant results to the commercial kits while improving successful analysis of degraded DNA with smaller PCR products or miniSTRs[2]. However, many of the CODIS core loci have large allele ranges (e.g., D21S11 and FGA) that make it impossible to create small PCR products. The authors are also going beyond the CODIS core loci and examining a battery of new potential STR loci that can be made less than 100 bp in size and would therefore be helpful in testing highly degraded DNA samples.[3]

Methods and Materials: Hairs were digested using either a standard micro-tissue grinding protocol or a complete digestion protocol.[4] DNA template was purified with phenol/chloroform/water followed by microcon concentration or via binding/elution using a Qiagen column. PCR reactions using STR miniplex markers of CODIS markers (TH01, FGA, D18S51, D16S539) along with the D2S1338 marker and Amelogenin were evaluated. An additional miniplex containing non-CODIS markers (D10S1248, D14S1434, and D22S1045) was also evaluated.

Summary of Results: A set of two miniSTR multiplexes containing CODIS and non-CODIS markers have been evaluated for their ability to genotype degraded DNA. A number of the miniSTR markers were used to successfully type nuclear DNA from hairs belonging to multiple individuals.

Conclusions: The selection of STR loci that have a narrow allele range (e.g., less than 50 bp) and can be made smaller than 100 bp works well with degraded DNA samples. The successful typing of even a small number of nuclear loci from shed hairs can greatly increase the forensic discrimination of the sample compared to mtDNA testing alone, where a significant number of common types are present in the population.

References:

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(2) Butler, J.M., Shen, Y., McCord, B.R. (2003) The development of reduced size STR amplicons as tools for analysis of degraded DNA. *J. Forensic Sci.,* 48(5): 1054-1064.

(3) Coble, M.D. and Butler, J.M. (2004) Characterization of new miniSTR loci to aid analysis of degraded DNA., *submitted.*

(4) Hellmann, A., Rohleder, U., Schmitter, H., Wittig, M. (2001) STR typing of human telogen hairs – a new approach. *Int. J. Legal Med.*, 114: 269-273.

Short Tandem Repeat DNA Typing, Degraded DNA, Reduced Size PCR Products

 ** Presenting Author*