A53 Application of mini-STRs to Low- Copy Number

Nicole M. Paes, BS, 2501 Lake Road, Apartment 34, Huntsville, TX 77340; and David A. Gangitano, PhD, 455 Wildwood Forest, Apartment 4206, Spring, TX 77380*

After attending this presentation, attendees will understand some principles regarding low-copy number DNA samples and where they can

be found in everyday scenarios. Attendees will also learn how to potentially increase the yield of DNA from such highly degraded samples using a novel method of collection, extraction, and amplification.

This presentation will impact the forensic science community by shedding light on a new method of collecting highly degraded DNA samples, such as those commonly found in crime scenes. The presentation will detail a novel collection method for low copy number DNA samples and possible ways to increase DNA yield from said samples.

This study tests the combination of mini-short tandem repeat (STR) polymerase chain reaction (PCR) amplification kits to low-copy number DNA samples, such as fingerprint residues, with the use of a double swab technique utilizing sodium dodecyl sulfate (SDS) on both swabs during collection to yield full DNA profiles for identification purposes.

DNA typing of low-copy number and degraded DNA samples can be problematic when using STR markers. Low-copy number DNA samples are typically categorized as being less than 200pg and complete amplification of all markers is difficult. The use of mini-STR markers, which employs smaller fragments, helps to increase the probability of complete amplification. The most common samples of low-copy number encountered are fingerprints. When a fingerprint is left, the residue is made up of sweat, oils, and epithelial cells from the individual. The use of SDS, which is a surfactant, is being explored for collection of fingerprint residues. A typical surfactant will absorb oils and fats, so its use for fingerprint residues will hypothetically increase DNA yield. It is theorized that the surfactant will break open the cells, which contain lipid membranes, to release the DNA and surround the oil residues of the print.

The addition of extra DNA polymerase, post-PCR purification using centrifugal filters, the use of increased purified sample during analysis, and an increased injection time were tested. Three different knife handles (wood, plastic, and metal) and a doorknob were handled by six individuals. Skin debris samples were taken from the neck of three female individuals in areas where moderate rubbing by a male individual had occurred hours earlier. This study used a double swab technique using 20% SDS on both swabs in combination with the mini-STR PCR amplification kit (D13S317, D7S820, D2S1338, D21S11, D16S539, D18S51, CSF1PO, and FGA).

The wood handled knife and doorknob obtained the most number of full profiles out of the objects tested for samples with and without clean- up methods (five and four out of six samples, respectively). For samples without clean-up, full DNA profiles were obtained from five of the six individuals tested and in the skin debris sample portion, no full male DNA profile was obtained. Full DNA profiles were observed in 14 out of 24 samples (58%) and six out of 24 (25%) showed no profile. The CSF1PO locus showed the greatest number of samples with successful amplification of all autosomal loci (17 out of 24), while D7S820 and FGA showed the lowest number (15 out of 24).

An increased injection time and use of increased purified sample for clean-up showed excess DNA for analysis. Only the techniques of additional DNA polymerase prior to PCR and post-PCR purification were used. After clean-up, full DNA profiles were also obtained for five out of the six individuals and one full male DNA profile was obtained for one set of individuals in the neck skin debris portion (16.67% ± 16.67%). The amount of full DNA profiles and no profile samples was unchanged from those seen with the regular mini-STR protocol. All autosomal loci showed successful amplification above 70% after the clean-up protocol, with AMEL being the only loci out of the nine loci tested showing a decrease after the clean-up protocol (17 to 15 out of 24 samples). No positive fingerprint samples were obtained for subject 01B.

Results indicate that the use of SDS and the mini-STR PCR amplification kit may give a full DNA profile from fingerprint residues and the use of the clean-up techniques studied did not increase the number of full DNA profiles obtained. Caution needs to be taken when dealing with low-copy number samples since there is an increased risk of contamination, allele drop-in and drop-out and heterozygote imbalance. **Mini-STRs, LCN, Fingerprints**

 ** Presenting Author*