



### A38 Assessing Touch DNA Collection Methodologies for Obtaining a Genetic Profile

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After attending this presentation, attendees will have learned about the collection of Touch DNA using three chemical surfactants, a tape lift methodology, and a combination of surfactant followed by a lift technique.

This presentation will impact the forensic sciences community by demonstrating that this new method could be useful in many crime labs for optimal collection of touch DNA, used in conjunction with double-swabbing techniques.

Attendees of this presentation will learn about the collection of Touch DNA using three chemical surfactants, a tape lift methodology, and a combination of surfactant followed by a lift technique. Touch DNA is DNA obtained from epithelial cells which have been shed or sloughed. The following collection methodologies were used: double swabbing technique using ddH<sub>2</sub>O (control); 1:1 EtOH; 20% SDS; hydrophilic tape; and a combination of the hydrophilic tape lift followed by the most successful swabbing surfactant. This study hopes to impact the forensic science community by demonstrating that this new method could be useful in many crime labs for optimal collection of touch DNA, used in conjunction with double-swabbing techniques.

A total of twenty test subjects were used; ten of each sex, each asked to wear a t-shirt for one twelve hour period. The t-shirts were purchased, washed once and given to the participants in a paper bag with wear and handling instructions. The study participants were blinded to the experiment, and were from an age cohort of 20-25 years old. The t-shirts were stored in their individual brown paper bags in the pre-PCR laboratory at room temperature until they were processed.

The shoulder area of the t-shirt was used for the swabbing/lift experiment. This work builds on an earlier study conducted in our laboratory (Schantz, et al AAFS Feb '09), and a pilot study conducted by the first two authors. The previous work indicated that the shoulder area from the seam down towards the torso (9 cm from the shoulder seam on the front and back of shirt) was in consistent contact with the wearer. Moreover, the treatment condition for swabbing and lifting where

randomly assigned to one of six quadrants laid out in on a template, prior to cutting for each t-shirt. This allowed all treatments to be evaluated with different cutting areas from each t-shirt.

After each swab or lift, the sample was digested at 55°C with Proteinase K and a stain lysis buffer. It was found that a longer digestion time, thirty-six hours rather than the standard overnight incubation increased DNA recovery. Swab tops, or tape pieces were taken from their digestion tube and placed in a spin basket in a new 2.0 ml tube, then the digested lysis material was then carefully pipetted into the new tube. The tubes were centrifuged for two minutes at 4,500 g, the flow through was used as the starting material for an organic extraction. A standard organic (P:C:I) extraction was performed, along with a microcon concentration step. Samples were quantified and then amplified with ProfilerPlus, and run on a 3100 Avant Genetic Analyzer. Samples were examined for each treatment condition, by sex, and by individual. Reference samples were then processed to confirm the allelic base pair (bp) sizes.

#### **Touch DNA, Surfactant, Genotyping**