

A172 Determination and Use of Optimized Techniques to Analyze Trace DNA From Fingernails

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After attending this presentation, attendees will recognize optimal methods for collection and processing of fingernail evidence and learn the importance these methods have for forensic practitioners.

This presentation will impact the forensic science community by introducing the best ways to collect and process trace evidence from fingernails in order to obtain the highest yields of exogenous DNA, along with the most genetic data. The results of this research have the potential to change the way forensic nurses, pathologists, and forensic biologists collect and process trace evidence from fingernails.

When two or more individuals come into contact with one another during a physical assault, a victim may fight back against the assailant, potentially resulting in the transfer of biological material, which has the potential to act as important evidence. In particular, a person struggling to free themselves from an assailant may grab and scratch that person, resulting in the deposition of cells beneath their fingernails. Given this, medical examiners, sexual assault nurse examiners, and others regularly collect fingernail evidence following assault, however, the manner in which they do so is highly variable, and the success in obtaining probative evidence is unknown.

Currently, various procedures are used for collecting biological evide nce from nails, including clipping the nail itself, scraping beneath the nail using a wooden applicator, and swabbing underneath the nail. In the first portion of this research, female volunteers donated fingernails, on which one microliter of blood from a male volunteer was deposited. DNA was isolated using an organic extraction, and male specific DNA was quantified using real-time PCR. Soaking the nails directly in digestion buffer yielded the highest levels of male DNA, while scraping recovered the least.

Next, different extraction methods were compared in order to optimize yields; a silica-based kit extraction was compared to the organic extraction, with the former yielding more DNA. Several aspects of the kit extraction were then optimized, including incorporating more than one elution and the volume used for elution.

Genetic analyses included comparing autosomal STRs and Y chromosome STRs. The soaking and swabbing procedures resulted in mixtures of nail and blood profiles, while the scraping procedure generally showed only male DNA, although allelic dropout often occurred. Assaying Y chromosome STRs produced clean, complete profiles from both soaked and swabbed nails, while scrapings again displayed dropout.

Crime laboratories often receive nails as a set, and process them together using a cumulative swab, in order to save time and resources. This has the potential to transfer material from a nail that harbors exogenous DNA to ones that do not, resulting in cross contamination and/or loss of valuable evidence. Male blood was placed on one or two female nails, which were then swabbed intermittent with nails without blood deposition. This cumulative swabbing led to cross contamination between nails, including full Y chromosome STR profiles from the nails without blood. In contrast, when nails with and without blood were transported together and then processed individually, no cross contamination occurred, although a substantial amount of male DNA was lost through transportation.

Finally, the fully optimized procedure was tested on actual scratchings. Female volunteers scratched male volunteers on the underside of the forearm, using the middle three fingers. The scale was tared with the forearm relaxed on the center, and the set amount of force was applied before scratching commenced. The nails were clipped or swabbed, and the resultant nail or swab head was soaked in the kit's digestion buffer overnight. Multiple elutions were used to recover DNA from the kit columns. Male DNA was quantified, and DNAs were assayed for both autosomal STRs and Y chromosome STRs.

Fingernails, DNA Analysis, Y-STRs