

Case Summary

Case Synopsis:

Homicide, potentially gang related. Victim shot by a perpetrator wearing a hoodie. Perpetrator discarded hoodie and weapon while fleeing the scene. Initial DNA collection effort from the hoodie was completed utilizing the double swab method. Swabs were used to collect from all the areas on the hoodie that were likely to have the perpetrator's DNA material. Swabbing yielded a mixed, partial profile that had inconclusive results.

Challenge:

With a weak partial profile, the ties to a suspect were statistically inconclusive and the DNA results could not move the case forward. There were a number of challenges in collecting DNA material in the case. One was the fact that very little DNA material was available. Even after swabbing multiple areas on the hoodie, there was only enough DNA material to amplify a partial profile. Another challenge was the mixture, which combining all of the different areas on the hoodie increased the likelihood of detecting multiple donors. Compounding the issue, the hoodie had no visible stain, was a porous fabric substrate, and the target sampling area was relatively large. A mixture, the partial profile and the absence of a major contributor left the case without conclusive DNA evidence.

Processing:

The hoodie was processed for touch/contact DNA using the M-Vac wet-vacuum collection system. The evidence was reviewed by the detectives and the CSI serologist to identify the locations on the sweatshirt which were most likely to have been in contact by the wearer. Utilizing the M-Vac's higher collection efficiency, it was concluded that separate DNA samples should to be collected from the hoodie in four (4) primary regions. Each of those areas was sampled with a separate M-Vac. Approximately 200 mL of sterile surface rinse solution was sprayed down and collected from each region. Once each area had been collected, the liquid was concentrated using a 0.45 micrometer Nalgene disposable filter apparatus. The filters were covered, labeled and set aside to dry using standard chain of custody practices.

Laboratory Processing:

The evidence filters were sent to Sorenson Forensics for processing. The filter was removed from the filter apparatus and cut into small sections using a single use sterile scalpel to allow for extraction.. This substrate was then processed via modified organic extraction and quantitated using the Promega Plexor® HY rtPCR assay. The extracts were amplified with the Life Technologies AmpFℓSTR® Identifier® Plus PCR Amplification Kit and DNA mixture profiles were obtained.

Results:

A **significant** amount of DNA was recovered from each sample area (160ng – pocket, 4.0ng – forearm area, 107ng – chin area, 27.8ng – shoulder area). Subsequent amplification and genetic analysis resulted in two of the mixture profiles that were deemed suitable for comparison to known samples. As well, sufficient DNA collected via M-Vac sampling from the front of the hoodie where detectives suspected the wearer’s chin, neck and saliva had come in contact with the fabric that yielded a comparable profile that Sorenson Forensics was able to interpret as a “major” DNA profile. Comparison to known reference samples from an individual in this case generated an inclusion to this profile and a very significant statistical probability. Utilization of the M-Vac System in this case allowed a more focused and significantly higher sampling of wearer DNA to be obtained. This resulted in a comparison match statistical weight that was approximately 94.8% higher than that obtained from sampling with a swab.