Cold Case File: The Ben Lomond Strangler
Captain Andrew Armando and Cindy Anzalone, San Mateo County Sheriff’s Office, San Mateo, CA

In 1986, tourists found 17-year old Annette Thur's body on State Highway 35 in a remote part of San Mateo County. She was partially clothed and strangled to death. "Walter" was last seen with Thur as he gave her a ride from a party to his residence, where he wanted to have sex. Thur was not interested and left "Walter's" residence, likely hitchhiking. After extensive work, investigators could not obtain any leads that would have brought them to a final conclusion on the murder. The case was suspended and went cold. In 2012, San Mateo County Sheriff's Office Detectives met with the San Mateo County Forensic Laboratory regarding an unrelated murder. By chance, the evidence from Thur's homicide was discussed and the case was re-opened for DNA testing. Using DNA technology that did not exist at the time of Thur's death, the serial killer was eventually identified and linked to other murders in California.

What happens to touch evidence when a gun is fired? Improved methods for sampling and processing touch evidence from bullet casings
Dr. Glendon Parker and Ashlee Lynch, U.C. Davis, Forensic Science Program

DNA analysis of touch evidence on fired cartridge cases is highly probative but can be difficult to obtain despite numerous attempts to improve collection and extraction methods. There are numerous factors that reduce the amount of material on a bullet casing including how it was handled, the sheer forces of firing and metal in the casing that reacts with DNA. Protein is also a major component of biological touch evidence, that is more robust than DNA and also contains genetic and contextual information that may be useful to investigators. Combined extraction and analysis of both DNA and proteins in will provide the maximum amount of genetic information obtainable from a bullet casing. Currently the best practice is to use a wet followed by dry cotton swab. This study evaluated the efficiency of transferring known amounts of DNA and protein from artificial fingerprints on a glass microscope slide into the analytical workflow for seven different collection and transfer methods. The standard wet-dry cotton swab was compared with, a Copan microFLOQ® swab, with and without lysing agent, and with and without extraction buffer, a cell scraper, and adhesive silicone gel-film sheets. Based on the results obtained it was determined that the Copan microFLOQ® swab was the overall most efficient and consistent with an average transfer of 58% efficiency for DNA and 55% for protein compared to 28% DNA and 25% protein yields when using cotton swabs respectively. The evaluation was taken a step further to measure transfer of DNA and protein from real fingerprints on a glass microscope slide to the workflow. It was determined that the Copan microFLOQ® swab collected an average of 15.7 ng of total DNA and 2300 RDU of total relative protein density, while the cotton swab collected 11.8 ng of total DNA and 1200 RDU of total relative protein density. When normalized for individuals the Copan microFLOQ® increased yields by 1.7 fold (p=0.23) for DNA and 1.9 fold (p=0.02) for protein. The last evaluation was to mimic real-life scenarios where the Copan microFLOQ® swab was used to transfer DNA and protein from unfired and fired cartridge cases into the technical workflow. When the Copan microFLOQ® was compared to wet/dry cotton swabs material transfer increased 3.2-fold (p=0.03) for DNA and 2.0-fold (p=0.06) for protein when unfired cartridge casings were tested and 3.7-fold (p=0.09) for DNA and 1.6-fold (p=0.24) for protein when fired casings were tested. This indicates that the firing process was harsher on DNA then protein. When normalized for individuals, 55% of protein was lost, whereas 76% of DNA was lost. Protein therefore was almost twice as stable as DNA on fired bullet casings. The genetic information in protein therefore is more likely to persist on fired casings, and could be a valuable source of probative genetic and contextual evidence on this type of challenging trace evidence.

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Josh Abernathy, MSFS, QIAGEN, Germantown, MD

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At your discretion, Y-STR stats using discrete Laplace
Steven Myers, CA DOJ DNA Laboratory, Richmond, CA

For over a decade, forensic scientists in the United States relied upon the US Y-STR Database for their reporting statistics. Users could compare single-source evidentiary profiles to a data set that grew to over 32,000 profiles representing five major population groups (African American, Asian, Caucasian, Hispanic, and Native American). The results of the search were presented using the counting method and a 95% Upper Confidence Interval statistics. As of 2014, SWGDAM match probabilities were also reported. Beginning in 2018, the US Y-STR Database was absorbed into the Y-Chromosome Haplotype Reference Database (YHRD), and the US Y-STR Database was decommissioned in 2019. To maintain consistency with previous practice, YHRD maintained the US dataset as a “National Database (with Subpopulations) - United States.” Counting method and 95% UCI statistics, as well as SWGDAM 2014 match probabilities, are reported as well.

The preferred statistic at YHRD and of the DNA Commission of the ISFG is not, however, based upon the counting method. Instead, they suggest using the discrete Laplace method developed by Andersen et al., Journal of Theoretical Biology 329 (2013) 39–51. This method overcomes the counting method’s reliance upon database size by allowing for the multiplication of probabilities across multiple loci in a Y-STR haplotype. This presentation will discuss the math and assumptions behind the discrete Laplace statistic, its benefits and limitations, and the implementation of the method at YHRD.

STRmix topic TBD
Daniela Cuenca, CA DOJ DNA Laboratory, Richmond, CA

Hamilton Company: The latest updates in liquid handling excellence
Taylor Dibble, Hamilton Company, Reno, NV

Hamilton Company specializes in the development, manufacturing and customization of precision measurement devices, automated liquid handling workstations, and sample management systems. As Sales Manager of Hamilton in Northern CA, Taylor Dibble will briefly speak about Hamilton’s history, current status amid the COVID-19 pandemic, and updates on Hamilton’s forensic solutions.

Comparison of the ANDE 6C Rapid DNA Instrument and the Applied Biosystems RapidHit ID Instrument
Nichole Tuscher, Contra Costa County Crime Laboratory, Martinez, CA

Rapid DNA has been presented as a potential solution to the increased DNA evidence sample processing demand. This presentation will detail the trials and tribulations of the validation process between the two instruments. The strengths and limitations of each instrument will be discussed.

Application Innovations and Lab Efficiency: What’s New at Thermo Fisher Scientific?
Danielle Jardel and Kellie Fenesan, Thermo Fisher Scientific, South San Francisco, CA

Let’s catch up on the latest and greatest chemistry and application innovations from Thermo Fisher Scientific. Our STR chemistries are going beyond the CODIS core loci and are being developed to meet the needs of the most challenging forensic casework globally. From the easy identification of potential inhibitors and degradation of the The Applied Biosystems GlobalFiler IQC system to the additional loci in The Applied Biosystems VeriFiler Plus PCR Amplification Kit, dramatically increasing its discrimination power. We also have some exciting news surrounding our Applied Biosystems RapidHIT ID System including U.S. Federal Bureau of Investigation (FBI) approvals.

Individual application updates are great but they’re only as useful as the lab efficiency. The ID NIMBUS® Presto Assay Ready Workstation is as simple as an Automate Express DNA Extraction System but with more processing power with magnetic particles deliver superior yield and quality of DNA from most forensic sample types and allows for more customized workflows solutions.

Case presentation – A child’s toy, a man’s malice
Steven Crotti, CA DOJ DNA Laboratory, Richmond, CA

Extracting Better Outcomes from Forensic Samples - Making Your Life Easier with Next-Generation Sequencing
Dr. Meredith Turnbough, Verogen Inc, San Diego, CA
Sequencing STRs means cleaner data, fewer artifacts, fewer overlapping alleles, and more confidence in your data. See how you can upgrade your data and simplify interpretation with NGS and the MainstAY kit.

**Legislative Update**  
*Michael Chamberlain, Deputy Attorney General, CA DOJ DNA Laboratory, Richmond, CA*

This presentation will provide attendees with updated information on pending and enacted legislation--both in California and nationally--related to various aspects of forensic science, including genetic genealogy and expert witness testimony.