



NEAFS | MAAFS

joint meeting
KALAHARI RESORTS



Forensic Biology/DNA Session

Location: Kilimanjaro Ballroom Suite 7

NEAFS

Allyson Goble, Biology Session Chair

Timothy Goble, Biology Session Co-Chair

MAAFS

Kimberly Freeman, Biology Section Chair

Jonathan Forsberg, Biology Section Chair-Elect

Thursday, October 8

- 9:00 am** **Updates on Available Biology and DNA Standards with Strategies for Implementation**
Charlotte Word
- 9:30 am** **Strengthening DNA Analyst Training for Courtroom Testimony**
Amanda Murray, PhD - DNA Labs International
- 10:00 am** **Break**
- 10:45 am** **Evaluating miRNA expression level from burned bone and bone marrow for use in PMI estimation**
Dani Bailey - Towson University
- 11:00 am** **Evaluation of Different Collection Methods for Trace DNA Recovery on Fabrics**
Jesada Sanders, Ashley Morgan, PhD - University of New Haven
- 11:15 am** **Finding the Perfect Solution : Examining the Utility of Abrasive Wiping With Dilute Bleach Solutions as a Contamination Prevention Step in Forensic DNA Evidence Examination**
Morgan Christopherson, Katherine O'Connor - Hofstra University
- 11:30 am** **The Impact of Immigration on Forensic Databases: Preliminary Results from Mitochondrial DNA Analysis**
Filipa Simão, Ashley Gonzalez-Castro, Joan Oruitemeka, Amanda Hewitt - Towson University
- 11:45 am** **STRUCTURE and ForenSeq UAS Ancestry Predictions: A Comparison Study**
Melody Gokce, Büşra Tosun, Filipa Simão, Kelly M. Elkins - Towson University
- 12:00 pm** **Lunch**
- 2:00 pm** **Strategies to improve STR genotyping for forensic touch DNA samples collected from challenging surfaces**
Joseph Rahm, PhD - Lasell University



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- 2:30 pm** **Probabilistic searching of databases compared to binary CODIS eligibility: An improved methodology for maximizing investigative leads using STR DNA profiles**
Michael D. Coble, PhD - Center for Human Identification; Cesar Garza Sanchez, M.S.; Duncan Taylor, PhD; Curt Schuerman, B.S.; Tim Kalafut, PhD
- 3:00 pm** **Improving DNA Recovery from Multiple Fired Cartridge Cases Through Traditional and Automated Firearm-Based Grouping**
Savannah Koontz, M.S., Kayla Nichols, B.S., Elizabeth Reilly, Stephanie Walcott, M.S., Tracey Dawson Green, PhD - Virginia Commonwealth University
- 3:30 pm** **Break**
- 4:00 pm** **Scoring Multi-source Single-cell Forensic Evaluations when Clustering is a Latent Variable**
Catherine Grgicak, Desmond S. Lun; Gian Bates-Rudolph - Rutgers University Camden
- 4:30 pm** **Evaluation of Zar-Pro lifting strips as a mapping technique for the recovery of DNA from biological stains**
Meenakshi Anoop, Amy Brodeur - Boston University

Friday, October 9

- 9:00 am** **1952 Crash of C-124 Globemaster on Mount Gannett, Alaska: DNA Identification of Human Remains, 2012-2025**
Nancy Stokes - AFDIL - SNA International, Alexa Atencio, Deanna Ciampo, Kristen Dubyna, Brian Givens, Sherie Longshore, Miriam Narvaez, Rayna Ndongo, Jennifer Perez, Kathleen Tumblety, Malachi Weaver, Taylor Dickerson, and LTC Robert Nadeau
- 9:30 am** **From Backlog to Breakthrough: Lessons Learned from Baltimore Police Department's Historical SAFE Kit Project**
Lake Prescott, MSFS and Morgan Mack, MSFS - Baltimore Police Department
- 10:00 am** **Break**
- 10:45 am** **Performance Evaluation of the SERATEC® PAM Immunochromatographic Test for the Detection of Semen and Saliva in Forensic Samples**
Hannah Foor, BS; Charla Marshall, PhD; Sara R. Bodnar, MS; Coral Smith, MS - Center for Forensic Science Research and Education, Thomas Jefferson University
- 11:00 am** **Characterization of cell-free DNA in seminal plasma**
Francis Vu, M.S., Robin W. Cotton, PhD - Boston University
- 11:30 am** **Modernizing Forensic DNA Workflows Using Artificial Intelligence**
Amanda Fazi - DNA Labs International



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Updates on Available Biology and DNA Standards with Strategies for Implementation

Charlotte Word

By the time of the joint MAAFS/NEAFS meeting, ~32 Standards, Best Practice Recommendations and Technical Guidance Documents will be available for implementation in Biology and DNA sections of forensic testing laboratories. An organized summary of the various documents available for training, validation, protocol development, statistics, contamination and familial searching using serological and DNA testing methods along with strategies for laboratory implementation will be presented. Basics on the standards development process, information on the 5 year updates, and the various ways for laboratories and individuals to get involved will be presented. These documents are available free of charge on the websites for the American Academy of Forensic Sciences Academy Standards Board (ASB)¹ and the Organization of Forensic Science Committees for Forensic Science (OSAC)².

¹<https://www.nist.gov/osac/registry>

²<https://www.aafs.org/academy-standards-board>

Strengthening DNA Analyst Training for Courtroom Testimony

Amanda Murray, PhD - DNA Labs International

As forensic DNA interpretation continues to advance, courtroom testimony has become increasingly complex. Modern DNA analysts are now expected to clearly explain probabilistic genotyping results, statistical weight of evidence, and the implications of emerging technologies to judges, attorneys, and juries with varying levels of scientific literacy. Despite these growing demands, initial training programs for new DNA analysts have historically emphasized laboratory methods and technical interpretation, often placing courtroom preparation as a secondary focus. As a result, many analysts enter casework with limited formal training in testimony and are left to develop courtroom skills reactively through on-the-job experience. This approach can leave analysts underprepared for challenging cross-examinations, complex legal questions, and evolving expectations regarding transparency and communication of uncertainty. This presentation examines the expanding scope of DNA testimony and identifies key gaps in traditional analyst training programs. Practical recommendations are provided for



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better integration of courtroom-focused education into initial analyst training, including early exposure to legal concepts, structured communication training, and more extensive use of moot court exercises. Emphasis is placed on building confidence, consistency, and clarity in testimony before analysts appear in court. Strengthening courtroom preparation during initial training can enhance analyst performance, support scientific integrity, and improve the effective communication of DNA evidence within the justice system.

Evaluating miRNA expression level from burned bone and bone marrow for use in PMI estimation

Dani Bailey - Towson University

Generally, postmortem interval is estimated utilizing rigor mortis, body temperature, concentration of potassium in the vitreous humor, and insect activity. More recent studies have found the ability to use decreasing RNA expression analysis as a method of PMI estimation, however it is only accurate up to 30 days after death. The purpose of this project is to evaluate the use of miRNA in estimating postmortem interval from burned bones and bone marrow. RNA was extracted using TRIzol organic extraction method for both burned and unburned bone and bone marrow, then RT-qPCR was performed using purchased primers targeting miRNA for RNA quantitation. The statistical analysis will determine if it is likely miRNA degradation is able to be used in estimating postmortem interval from burned bones and bone marrow.

Evaluation of Different Collection Methods for Trace DNA Recovery on Fabrics

Jesada Sanders and Ashley Morgan, PhD - University of New Haven

Since trace DNA may be the only evidence available in a case, the selection of the best collection method is critical to the success of subsequent DNA typing. The porosity of the substrate can affect DNA recovery success, as the adherence of trace DNA to the material could lead to difficulties in its subsequent release from the material. In this experiment, trace DNA was collected from three donors, deposited onto natural and synthetic fiber towel swatches, and five different collection methods: double swabbing, single swabbing, dry vacuum, scraping, and cuttings, were used and compared to one another. Key findings related to sample preparation, towel material, collection method, and their impacts on DNA recovery success will be discussed.

Finding the Perfect Solution : Examining the Utility of Abrasive Wiping With Dilute Bleach



Solutions as a Contamination Prevention Step in Forensic DNA Evidence Examination

Morgan Christopherson and Katherine O'Connor - Hofstra University

Contamination in a DNA laboratory is a detrimental situation; however, there is no formal standard for how multi-use metallic tools used in evidence examination procedures prior to DNA extraction should be cleaned. This study aims to determine the efficacy of abrasive wiping combined with a dilute bleach solution as a cleaning procedure for these tools. Metallic scissors and tweezers were abrasively wiped with a KimWipe soaked with a dilute bleach solution for various amounts of time, and were immediately swabbed for residual DNA. The residual DNA was then extracted and quantified, following applicable standard manuals. The data was then analyzed for any observable trends.

The Impact of Immigration on Forensic Databases: Preliminary Results from Mitochondrial DNA Analysis

Filipa Simão, Ashley Gonzalez-Castro, Joan Oruitemeka, Amanda Hewitt - Towson University

Mitochondrial DNA (mtDNA) is widely used in forensic genetics, particularly when nuclear DNA is highly degraded or unavailable. The statistical weight of a mtDNA match depends on the frequency of the profile within reference populations. However, migration may influence these frequencies, as genetic lineages introduced through immigration are not always well represented in forensic databases. This study evaluates the impact of generational migration on mtDNA diversity in the United States. Buccal swabs were collected from Maryland residents following informed consent, and information on mother and maternal grandmother birthplaces was recorded. The mtDNA control region was sequenced using Sanger sequencing, and haplogroups were assigned through the EMPOP database. Preliminary analysis of 19 samples showed that 53% belonged to haplogroups of Eurasian origin. Lineages from the three continental backgrounds – Eurasian, Native American and African - were identified among first-generation U.S. residents (individuals whose mothers were born outside the United States), indicating recent introduction of diverse genetic backgrounds through migration. Although the current sample size is limited, these findings highlight the diverse maternal ancestry present within the U.S. population. A larger, ongoing study will enable evaluation of whether recent immigrants and long-established resident populations differ in their mtDNA composition and assess the potential impact of these differences on the representativeness of forensic mtDNA databases.

STRUCTURE and ForenSeq UAS Ancestry Predictions: A Comparison Study



Melody Gokce, Büşra Tosun, Filipa Simão, Kelly M. Elkins - Towson University

Ancestry predictions can be useful for guiding criminal investigations. In this project, we compared software predictions for ancestry using a dataset collected at an American university in the Mid-Atlantic. Buccal swabs were collected from deidentified donors with approval from the Institution Review Board (IRB). DNA was extracted using an EZ1 instrument (Qiagen) and quantified using qPCR. Libraries were prepared using the ForenSeq Signature Prep kit Primer Set B (Qiagen) and sequenced on a MiSeq FGx instrument, following the manufacturer's protocol. Genotypes were assigned within the ForenSeq Universal Analysis Software (UAS) software. Ancestry predictions generated by UAS and STRUCTURE were compared. For UAS output, the four ancestry groups reported by the software - Admixed American, African, East Asian, European – were evaluated using Principal Component Analysis (PCA) plots. Using the STRUCTURE software, ancestry proportions were estimated using four continental groups as reference: African, European, Native American and Asian. For samples classified as Admixed American by the UAS, more detailed ancestry composition was outputted by STRUCTURE which provided proportional estimates of the ancestry. This additional resolution provides more specificity and granularity, uniquely informing investigations.

Strategies to improve STR genotyping for forensic touch DNA samples collected from challenging surfaces

Joseph Rahm, PhD - Lasell University

Over the last thirty years, DNA amplification with polymerase chain reaction has revolutionized forensic DNA profiling for human identification. The prevalence of touch DNA, small amounts of skin cells and cell free DNAs left on surfaces and objects left after contact, has highlighted the challenges associated with each step of the DNA profiling process. First, the use of the cotton swab during the collection step limits the success of DNA profiling, especially when used to collect from challenging surfaces like stainless steel and brick material as cotton swabs tend to rip and tear on rough surfaces which is destructive to the sample. The cotton swab was compared to the novel Venturi Vacuum Device with a Polycarbonate Filter for collection of touch DNA from steel and brick. Second, extraction efficiencies for samples collected from cotton swabs have a wide range of recovery (20-80%) due to the swab's inability to properly release cellular material when collected. Therefore, a DNA extraction workflow was compared to a direct amplification workflow for HID. Skipping the extraction step in favor of direct amplification seemed promising but the analytical issues and more complex profiles associated with PCR persist.



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Probabilistic searching of databases compared to binary CODIS eligibility: An improved methodology for maximizing investigative leads using STR DNA profiles

Michael D. Coble, Ph.D. - Center for Human Identification; Cesar Garza Sanchez, M.S.; Duncan Taylor, Ph.D.; Curt Schuerman, B.S.; Tim Kalafut, PhD

Probabilistic methods of DNA mixture interpretation have improved our ability to deconvolve complex mixtures for subsequent searching of POIs in a DNA database. Current approaches use a summarization of obligate alleles or genotypes based on a threshold (e.g. 99% genotype weights). We compared the effectiveness of directly searching a database of mock offender DNA profiles versus the current criteria for searching CODIS. We show the use of an alternative searching strategy (such as the software DBLR) has great potential to identify true donors in a database compared to current binary methods for searching.

Improving DNA Recovery from Multiple Fired Cartridge Cases Through Traditional and Automated Firearm-Based Grouping

Savannah Koontz, M.S., Kayla Nichols, B.S., Elizabeth Reilly, Stephanie Walcott, M.S., Tracey Dawson Green, Ph.D. - Virginia Commonwealth University

Fired cartridge cases (FCCs) represent a valuable source of both firearm identification evidence and trace DNA, although DNA recovered following discharge is frequently low-template and results in incomplete STR profiles. This study evaluated whether grouping FCCs associated with the same firearm using traditional firearm examination or the Ballistics IQ automated comparison system prior to DNA analysis could improve DNA recovery and STR profile quality while assessing the effects of cartridge case metal type and caliber. Traditional firearm examination achieved 97.91% grouping accuracy, and Ballistics IQ achieved 92.59%, with neither method producing incorrect firearm associations, while grouping significantly increased total DNA yield ($p < 0.05$); aluminium cartridge cases and 9 mm ammunition produced the most complete STR profiles ($p \leq 0.05$). These findings demonstrate that firearm-based grouping strategies can improve DNA recovery while maintaining reliable firearm associations and support integrating firearm examination with forensic DNA analysis as a practical multidisciplinary workflow. Adoption of this approach has the potential to improve laboratory efficiency, maximize the evidentiary value of fired cartridge case evidence, and increase the likelihood of obtaining informative STR profiles in forensic casework.

Scoring Multi-source Single-cell Forensic Evaluations when Clustering is a Latent Variable

Catherine Grgicak, Desmond S. Lun, Gian Bates-Rudolph - Rutgers University Camden

Bulk DNA signatures do not deliver source (cell type) evaluations, instead yielding sub source LRs about DNA that sometimes fail to well discriminate between H1 and H2, affecting evaluative reporting and database search effectiveness.

With each cell being imaged and clustered by their cell-type and genetic signatures, single cell analysis offers a way forward. Prior works show forensic-aware clustering methods outperformed general purpose approaches but assuming a single clustering, nevertheless, remains insufficient when scEPGs are low fidelity.



In this presentation we explain a new method that assigns a probability to each clustering, motivate its use and evaluate its performance using the log loss scoring rule that was decomposed into its CALibration and REFinement elements, which offers a valued verification strategy.

Results showed that when single-cell data are coupled with probabilistic clustering and high resolution imaging, they yield source level evaluations that behave like single source profiles, potentially reshaping the way biological evidence is generated, interpreted and understood.

Evaluation of Zar-Pro lifting strips as a mapping technique for the recovery of DNA from biological stains

Meenakshi Anoop and Amy Brodeur - Boston University

Forensic alternate light sources (ALS) are commonly used to detect latent biological stains by fluorescence, but their effectiveness depends on the substrate, as certain fabrics can interfere with visualization. This limitation can result in biological evidence being overlooked and reduce opportunities for DNA recovery. This study evaluated the use of Zar-Pro™ lifting strips to transfer latent semen and saliva stains from ALS-incompatible substrates onto the strips, thereby aiding in mapping the location of stains and subsequent DNA recovery. The lifting strips demonstrated some success transferring both types of biological stains, with better performance observed for semen. Additionally, some of the transferred stains remained suitable for DNA recovery, demonstrating the potential of Zar-Pro™ lifting strips as a possible alternative screening method for challenging substrates.

1952 Crash of C-124 Globemaster on Mount Gannett, Alaska: DNA Identification of Human Remains, 2012-2025

Nancy Stokes - AFDIL - SNA International, Alexa Atencio, Deanna Ciampo, Kristen Dubyna, Brian Givens, Sherie Longshore, Miriam Narvaez, Rayna Ndongo, Jennifer Perez, Kathleen Tumblety, Malachi Weaver, Taylor Dickerson, and LTC Robert Nadeau

A C-124 Globemaster carrying 52 servicemen from McChord AFB, WA to Elmendorf AFB, AK crashed in bad weather on Mount Gannett, Alaska, on November 22, 1952 and shortly after the plane wreckage was lost in Colony Glacier. Observations of debris on the glacier in 2012 resulted in re-discovery of the C-124 crash site and efforts for recovery of human remains and personal effects were initiated that year. All human remains were delivered to the Armed Forces Medical Examiner System (AFMES) for identification by fingerprint comparisons or DNA processing and kinship analyses with family reference samples. After 14 years of annual search & recovery events (2012-2025), a total of 7,082 samples of bone, soft tissue, teeth, hair, and nails were processed for auSTR, Y-STR, and/or mtDNA by the Armed Forces DNA Identification Laboratory (AFDIL). Despite difficult search conditions on the receding glacier and overall poor quality of the samples recovered, by 2025 - 73 years after the crash - all 52 servicemen had been identified.



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From Backlog to Breakthrough: Lessons Learned from Baltimore Police Department's Historical SAFE Kit Project

Lake Prescott, MSFS and Morgan Mack, MSFS - Baltimore Police Department

A prominent challenge facing many forensic DNA laboratories is a backlog of untested historic Sexual Assault Forensic Examination (SAFE) kits that must be addressed, in addition to all other case types that come through the laboratory. The Forensic Biology Unit (FBU) of the Baltimore Police Department set out to address this issue through strategic planning and workflow optimizations, including streamlined batching schedules, a direct-to-DNA approach, and adopting a Y-screening protocol. This presentation will provide data to demonstrate how these adjustments successfully eliminated the backlog of historic SAFE kits, while also having a lasting impact on the unit's routine casework. Attendees will learn how BPD is continually refining and improving DNA workflows to achieve a notable decrease in casework turnaround time and how to implement these strategies within their laboratories, with a long-term goal of reaching real-time analysis.

Performance Evaluation of the SERATEC® PAM Immunochromatographic Test for the Detection of Semen and Saliva in Forensic Samples

Hannah Foor, BS; Charla Marshall, PhD; Sara R. Bodnar, MS; Coral Smith, MS - Center for Forensic Science Research and Education, Thomas Jefferson University

The SERATEC® PAM assay is a multiplex immunochromatographic test that simultaneously detects prostate-specific antigen and α -amylase for the identification of semen and saliva. However, its performance under extreme antigen concentrations has not been fully characterized. This study evaluated the analytical sensitivity of the SERATEC® PAM assay, investigates its susceptibility to the high-dose hook effect for both semen and saliva, and assesses its performance using controlled semen-saliva mixtures and mock casework samples across a range of forensically relevant conditions. This research will provide additional data regarding the capabilities and limitations of the SERATEC® PAM assay and its application in forensic body fluid identification.

Characterization of cell-free DNA in seminal plasma

Francis Vu, M.S. and Robin W. Cotton, PhD - Boston University

Cell-free DNA (cfDNA) has been reported in multiple biological fluids in both medical and forensic literature, but forensic research has mainly classified its relevance as a source of DNA to be recovered from touch deposits. Beyond the DNA that is found in sperm, cell-free DNA occurs in semen at a high enough concentration to generate populated electropherograms. With no use of an extraction kit, 34 unique unpurified seminal cfDNA samples were quantitated by qPCR and 33 of those samples were amplified for capillary electrophoresis, resulting in electropherograms displaying 13 full profiles, 14 partial profiles, and 6 null profiles. DNA extraction methods employed in forensic laboratories can incur excessive cfDNA loss, but successful purification, especially with other kits designed to capture small



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DNA fragments, has been shown to improve electropherogram quality. Preliminary data also shows that seminal cell-free DNA is recovered from a sterile swab in the epithelial cell fraction after differential extraction with the EZ1® DNA Investigator® Kit.

Modernizing Forensic DNA Workflows Using Artificial Intelligence

Amanda Fazi - DNA Labs International

The integration of artificial intelligence (AI) into forensic DNA laboratory workflows offers opportunities to improve efficiency, consistency, and analytical throughput while maintaining rigorous scientific and ethical standards. This presentation outlines practical implementation considerations, ethical safeguards, and an example of a successfully deployed AI-enabled workflow suitable for international forensic collaboration. AI can support multiple stages of the forensic DNA pipeline, including sample triage, contamination-risk assessment, data interpretation, and reporting. Machine-learning models trained on validated datasets can identify low-quality samples, inform amplification strategies, and promote consistency in mixture interpretation. When responsibly implemented, these tools reduce analyst workload, minimize inter-analyst variability, and accelerate turnaround times without replacing expert judgment. Ethical deployment requires transparency, auditability, and continuous human oversight. Models must be trained on representative data to mitigate bias, and AI-generated outputs must remain interpretable, reviewable, and subject to challenge by qualified analysts. Laboratories implementing AI-assisted interpretation alongside probabilistic genotyping have demonstrated reduced review time, improved reproducibility, and clearer documentation of analytical decisions. These outcomes illustrate how AI can responsibly augment forensic DNA workflows while preserving human experts as the final decision-makers.