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ISHI INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION

STARTING SEPTEMBER 13, 2021

September 2021

The ISHI Report

News from the World of DNA Forensics

Start Reading

What's inside:

Introduction

Letter from our Editorial Board

Technological Innovation Aids the Identification of Fallen Soldiers

How Do Our Phenotype Prediction Models Hold Up in Admixed Populations?

When the World Trade Center Towers Came Down, a Select Group of Forensic Experts Stood Up

A Leadership Perspective: From Bench Criminalist to Lab Director

Preventing Tomorrow's Victim

The Missing Piece: Rodney Johnson (Lake Stickney John Doe)

Get to Know the ISHI 32 Speakers

An Update from the Organization of Scientific Area Committees (OSAC) for Forensic Science

The Casework Direct System: Efficiently Process Sexual Assault Evidence and Property Crime Evidence

Calendar of Events



The ISHI Report

Letter from the Editor

Dear ISHI Report Readers,

We hope you are staying well as summer draws to a close.

There is still time to register for ISHI 32 with options to attend either in person at the Coronado Springs Resort in Orlando, Florida or virtually. Virtual attendees can choose to participate in the general session or select workshops for a nominal fee. Complete details can be found at www.ishinews.com.

This year's general session will feature some amazing talks including in depth accounts of the challenges posed when identifying casualties from the attacks on 9/11. We'll hear personal accounts from forensic scientists who worked with samples recovered from Ground Zero, the Pentagon and Flight 93. They will share lessons learned and describe advances made because of these efforts. Additional talks will cover the use of Forensic Genetic Genealogy to solve cold cases, real world applications of Rapid DNA analysis, and new forensic technologies. Visit the symposium website to see the complete list of speakers and topics.

Guest authors in this issue include Nicole Novroski who describes the research her lab is undertaking to explore how well phenotyping prediction models hold up in admixed populations. This work has important implications as phenotyping becomes more widely used in forensic science.

Ken Doyle explores how new technologies are resolving decades old cases at AFDIL, Armed Forces DNA Identification Lab. As new techniques are incorporated into AFDILs workflow, samples which previously provided no useful genetic information are leading to DNA identifications.

Finally, W. Mark Dale shares how the work of the KADAP committee, formed in the aftermath of the 9/11 attacks lead to recommendations useful for other mass disasters. Mr. Dale retired from the New York State Police after 30 years as the Director of Laboratories.

We hope you enjoy the September issue. As always, we welcome your ideas and written contributions to our publication.

Stay well,

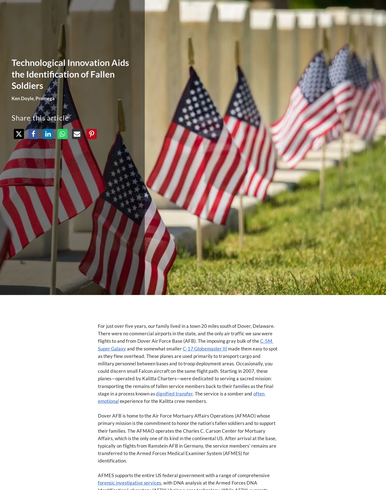
The Editorial Board

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Technological Innovation Aids the Identification of Fallen Soldiers

Ken Dovitch, Protect2

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For just over five years, our family lived in a town 20 miles south of Dover, Delaware. There were no commercial airports in the state, and the only air traffic we saw were flights to and from Dover Air Force Base (AFB). The imposing gray bulk of the C-5M Super Galaxy and the somewhat smaller C-17 Globemaster III made them easy to spot as they flew overhead. These planes are used primarily to transport cargo and military personnel between bases and to troop deployment areas. Occasionally, you could discern small Falcon aircraft on the same flight path. Starting in 2007, these planes—operated by Kalitta Charters—were dedicated to serving a sacred mission: transporting the remains of fallen service members back to their families as the final stage in a process known as dignified transfer. The service is a somber and often emotional experience for the Kalitta crew members.

Dover AFB is home to the Air Force Mortuary Affairs Operations (AFMAO) whose primary mission is the commitment to honor the nation's fallen soldiers and to support their families. The AFMAO operates the Charles C. Carson Center for Mortuary Affairs, which is the only one of its kind in the continental US. After arrival at the base, typically via flights from Ramstein AFB in Germany, the service members' remains are transferred to the Armed Forces Medical Examiner System (AFMES) for identification.

AFMES supports the entire US federal government with a range of comprehensive forensic investigative services, with DNA analysis at the Armed Forces DNA Identification Laboratory (AFDIL) being a core technology. While AFDIL supports AFMES with DNA identification for present-day operations, some of its most challenging work lies in identification of unknown soldiers or those missing in action from historical conflicts (known as past accounting).

Mitochondrial DNA

AFDIL began using mitochondrial DNA (mtDNA) analysis in the early 1990s to identify service members recovered from Vietnam. In July 1998, the laboratory used mtDNA analysis to assist in the identification of First Lieutenant Michael Joseph Blassie, who had died during the Vietnam War and laid to rest in the Tomb of the Unknown in Arlington National Cemetery. The identification process compared the mtDNA profile obtained from the unknown service member to mtDNA profiles from Lt. Blassie's mother and sister.

All nucleated human cells contain two types of DNA: nuclear and mitochondrial. The human nuclear DNA genome constitutes approximately 3.2 billion base pairs (bp) of linear DNA we spread into 23 pairs of autosomal chromosomes and one pair of sex chromosomes. The human mitochondrial genome is much smaller—approximately 16,500bp—and is a circular molecule. Different cell types contain different numbers of mitochondria in the cytoplasm, with oocytes containing up to 600,000, and each mitochondrion contains a single copy of mtDNA.



Jennifer Higginbotham, AFMES-AFDIL research DNA analyst, and Kerriann Meyers, AFMES-AFDIL supervisory DNA analyst, load samples onto the NGS instrument. (U.S. Navy photo by Mass Communication Specialist 2nd Class Samantha Thorpe, provided by AFMES).

Due to the high abundance of mtDNA compared to autosomal DNA, it can prove useful for analysis in degraded samples with limited amounts of DNA. Mitochondrial DNA is inherited only in the maternal lineage, making it easier to trace family relationships further back in time compared to nuclear DNA. In a similar fashion, Y-chromosomal DNA is valuable for tracing paternal lineage.

In contrast to short tandem repeat (STR) analysis that is typically conducted in forensic laboratories for nuclear DNA, mtDNA analysis relies on DNA sequencing to map individual base changes, or single nucleotide polymorphisms (SNPs), between samples. Technological advances over the years have made this method more powerful than ever.

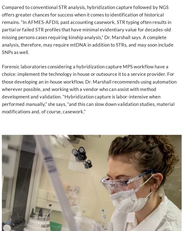
Technological Challenges

For 20 years, AFDIL has been working on identifying the remains of service members from the Korean War. These remains were transferred from North Korea to Japan in 1953 and were buried in the National Memorial Cemetery of the Pacific in Hawaii, colloquially known as the Punchbowl.

"Within the cemetery are known and unknown service members from World War II, Korea and Vietnam," says Timothy P. McMahon, PhD. He is the Director of DoD DNA Operations (AFDIL and AFRSSIR) AFMES. He serves as the chief scientist and scientific subject matter expert to the Armed Forces Medical Examiner, overseeing all human remains DNA testing and initiatives in support of the AFMES mission to identify fallen US service members from present and past accounting, as well as national disasters.

Some of the unknown remains from the Punchbowl—approximately 800 soldiers—were chemically treated and are from the Korean War, while unknowns from World War II were not treated. The treatment methods caused significant damage to the DNA, complicating the identification process. "It took 16 years of research, and for science to catch up, to allow AFMES-AFDIL to identify that the average DNA length from Punchbowl samples was ~50bp," Dr. McMahon says. The small size of the recovered DNA made these samples recalcitrant to conventional Sanger sequencing techniques.

AFDIL's adoption of next-generation sequencing (NGS), also known as massively parallel sequencing (MPS), raised hopes for increasing the success rate of identification. NGS enables processing of many samples simultaneously, starting with extremely low amounts of DNA. However, there's another challenge with using this technology to analyze historical human remains, in addition to DNA degradation. Often, the extracted sample contains a large proportion of non-human DNA, much of which is bacterial DNA. To overcome these challenges, AFDIL turned to their emerging technology division headed by Dr. Charla Marshall. She is currently Chief of the Emerging Technologies Section, DNA International, and a contractor supporting AFMES-AFDIL. In 2015, her team validated a modification of the typical NGS workflow, known as hybridization capture or target enrichment.



AFMES-AFDIL DNA analysts place samples into cartridges before loading them into the NGS instrument. (U.S. Air Force photo by Staff Sgt. Nicole Leidholm, provided by AFMES).

"This was the first NGS method to be implemented in an accredited forensic laboratory worldwide," Dr. Marshall says. The procedure has since been used to obtain DNA profiles from the most severely degraded and forensic-preserved remains from World War II, the Korean War and Vietnam, leading to hundreds of NGS-based identifications. Dr. Marshall points to the average length of DNA fragments from Punchbowl samples of 50bp. "This fragmented nature of the DNA led to polymerase chain reaction (PCR) amplification failure of both STR and SNP targets," she says, because most PCR primers were situated >100 base pairs apart. However, the use of hybridization capture and NGS allows analysts to obtain a usable DNA profile.

Hybridization Capture and Sequencing

How does this approach work? In a standard hybridization capture workflow, NGS libraries containing a mixture of human and non-human DNA sequences are treated with specially designed DNA or RNA probes or "baits" that contain sequences of interest. In the validated AFDIL technique, the probes would include human mtDNA sequences spanning the entire mitochondrial genome. The probes hybridize to complementary DNA sequences in the sample libraries and are attached to a solid surface, such as magnetic beads or a microarray. Non-hybridized, unwanted DNA is washed away, leaving only the desired DNA that can then be amplified and sequenced. In the case of highly degraded DNA samples, which may contain a lot of bacterial or fungal DNA, a hybridization capture step may help enrich for human DNA targets.

Hybridization capture technology "successfully allowed for the first identification of a Punchbowl unknown on March 17, 2016," Dr. McMahon says. Over the last 5 years, the success rate of the NGS method has increased from 28% to 68%, according to Dr. McMahon. "We have run 2,365 tests and written over 400 DNA comparison reports, of which 175 have supported new identifications." He adds that these 175 individuals would have remained unidentified without the use of hybridization capture and NGS technology.

Compared to conventional STR analysis, hybridization capture followed by NGS offers greater chances for success when it comes to identification of historical remains. "In AFMES-AFDIL past accounting casework, STR typing often results in partial or failed STR profiles that have minimal evidentiary value for decades-old missing persons cases requiring kinship analysis," Dr. Marshall says. A complete analysis, therefore, may require mtDNA in addition to STRs, and may soon include SNPs as well.

Forensic laboratories considering a hybridization capture MPS workflow have a choice: implement the technology in-house or outsource it to a service provider. For those developing an in-house workflow, Dr. Marshall recommends using automation wherever possible, and working with a vendor who can assist with method development and validation. "Hybridization capture is labor intensive when performed manually," she says, "and this can slow down validation studies, material modifications and, of course, casework."

Shannon Ryan, AFMES-DoD DNA Operations DNA analyst, sands a vertebra to get rid of any external contaminant before DNA extraction. (U.S. Air Force photo by Staff Sgt. Nicole Leidholm, provided by AFMES).

Forensic Genetic Genealogy

Although mtDNA is more abundant, nuclear DNA provides more information, because the much larger genome contains more SNPs. To compensate for the relatively low proportion of nuclear DNA in degraded samples, it can be enriched for regions of interest using hybridization capture. "SNP capture allows us to focus our sequencing efforts on identity-informative SNPs for improved coverage and higher confidence in the genotypes obtained from the sample," Dr. Marshall says.

This type of information could be especially useful for identification using forensic genetic genealogy (FGG)—a method that has gained attention in high-profile criminal investigations after it was used to capture the Golden State Killer. In a nutshell, after developing a DNA profile, analysts use it to construct family trees using public genealogical DNA databases, which could eventually lead them to the identity of the suspect.

Dr. McMahon adds that AFMES-AFDIL has partnered with Parabon NanoLabs to develop genealogically relevant SNP panels that could enable anyone within four generations of a missing service member, regardless of relationship, to provide a viable reference sample. Initial development tested existing commercial SNP panels that did not work with AFDIL's typical casework samples. The research team and Parabon developed new SNP hybridization capture panels and analytical software specially designed for highly degraded, low-coverage samples. The process is currently undergoing extensive internal validation that meets all Federal Bureau of Investigation (FBI) Quality Assurance Standards and ISO-17025 Forensic Accreditation Standards. "The method developed will have the ability to utilize all current references that have been collected for our missing service members, as well as any future collections," Dr. McMahon says.

While controversy still surrounds the use of FGG in criminal investigations, Dr. McMahon notes that it is important not to confuse that application with its potential use in identifying missing service members or historical remains. "FGG is simply a process that uses genetic similarities between two individuals to establish familial relationships to generate the investigative leads," he says. Once the technology is perfected, the next step will be to develop policies that address the unique needs of implementing FGG to identify historical remains of service members. These policies must take into account the forensic community's concerns associated with the use of genealogical DNA information.

Next Steps

What does the future hold for the identification of historical remains at AFMES-AFDIL? Both Dr. Marshall and Dr. McMahon agree that workflow automation will play a major part. Dr. Marshall would like to see "an automated workflow from bone powder digestion through sequencing setup."

"The assay we are developing and publishing will work across all sample types from highly degraded historical remains to highly copy modern samples," Dr. McMahon explains. He lists workflow automation as essential to increasing sample throughput and making the process cost-effective. In addition, Dr. Marshall and Dr. McMahon identified the need for a core set of identity-informative SNPs to be standardized and admissible for CODIS—the centralized DNA database developed and maintained by the FBI.

For commercially developed kits, Dr. McMahon hopes to see the availability of "a highly tailorable kit that has SNPs, mtDNA, autosomal STRs, and Y-STRs, with protocols on how to just target individual sets, or to combine two or more together to get more results at one time." These innovations, together with well-defined policies surrounding the use of FGG, will provide new hope to the families of missing service members and, ultimately, give names to those simply listed as "unknown soldiers."

How Do Our Phenotype Prediction Models Hold Up in Admixed Populations?

Nicole M.M. Novroski, PhD, Assistant Professor and Forensic Geneticist, Forensic Science Program, Department of Anthropology, University of Toronto Mississauga

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Forensic DNA phenotyping (FDP) is becoming an increasingly popular tool within criminal and civil investigations. When little to no information about an individual is known, the generation of a FDP profile has the potential to provide insight into what externally visible characteristics (EVCs) an individual may possess [1]. Specifically, many FDP tools focus on skin pigmentation, hair color, eye color and freckling and associate a confidence, or prediction accuracy, for every EVC reported in the phenotypic profile. While FDP models have demonstrated an *acceptable* level of accuracy in discrete populations, very few studies focus on how the prediction of hair color, eye color and skin pigmentation may be impacted if an individual has admixed ancestry.

Our lab performed a preliminary evaluation of the ForenSeq DNA Signature Prep Kit for phenotype prediction accuracy in a subset of first-generation or second-generation admixed Canadian individuals (n=100), where participants provided a DNA sample and self-identified for hair color, eye color, and ancestry on their mother's and father's side [4]. While there exist many tools for modeling phenotypic traits, the ForenSeq DNA Signature Prep Kit is a commercially-available multiplex that has been validated for forensic casework in many laboratories worldwide. The ForenSeq Signature DNA Prep Kit is a multiplex developed for use with the Forensic Genomics (FGx) massively parallel sequencing platform and includes 27 global autosomal STRs, 24 Y-STRs, 7 X-STRs, 94 identity SNPs (iiSNPs), 22 phenotypic SNPs (piSNPs) and 56 biogeographical ancestry SNPs (aiSNPs) [2]. In contrast to STRs, which were selected in part due to their presence in non-coding regions of the human genome, SNPs used to infer ancestral and phenotypic information can often be found within or near coding regions. As an example, 11 of the piSNPs included in the ForenSeq DNA Signature Prep Kit are located in the melanocortin 1 receptor (MC1R) gene, which has vast implications in human pigmentation [3]. Specifically, variants of the MC1R gene are known to cause loss of function in eumelanin production, and haplotypes in this gene have been strongly associated with red hair color. Conversely, normal function of the MC1R gene typically indicates dark pigmentation and aids in the prediction of black and brown hair color. The remaining piSNPs included in the ForenSeq panel are located in other key pigmentation genes, including HERC2, OCA2, SLC45A2, TYR, TYRP1, IRF4, and EXOC2. HERC2, which is located upstream of pigmentation gene OCA2, is thought to be a regulator for OCA2. SNP haplotypes across these two genes have been found to predict blue and brown eye color extremely well when variants are in their homozygous state. Phenotype prediction panels such as IrisPlex utilize rs12913832, located in the HERC2 gene, as the major branch point between light and dark iris pigmentation [1,3].

Using the 22 piSNPs and two common SNPs within the DPMB (DNA Primer Mix B) of the ForenSeq DNA Signature Prep Kit, phenotype predictions were generated by the ForenSeq Universal Analysis Software (UAS). The phenotype predictions then were interpreted and each sample was assigned a predicted hair color (blonde, red, black, or brown) and a predicted eye color (brown, blue, or intermediate). The ForenSeq UAS provides phenotype predictions as numerical results out of a maximum value of 1.0 in each trait. For example, **Figure 1** illustrates how phenotype prediction estimates are displayed by the ForenSeq UAS. It is commonplace to use a cut-off of 0.70 to assign hair and eye color predictions. We decided, however, to evaluate the prediction metrics with and without a threshold value.



Figure 1. An example of a phenotype prediction estimate from an individual of admixed ancestry using the ForenSeq UAS. If a threshold of 0.7 were used, this individual would have a predicted hair color of *undetermined* and a predicted eye color of *blue*. If no threshold is used, this individual would have a predicted hair color of *brown* and a predicted eye color of *blue*.

When comparing phenotype predictions against the self-identified EVCs provided by each participant, we established some baseline designations. A correct prediction designation was applied when the self-identified phenotype and predicted phenotype generated by the ForenSeq UAS were concordant. An incorrect prediction designation was applied when the self-identified phenotype and predicted phenotype generated by the ForenSeq UAS were discordant. We found that, when no interpretation threshold was utilized, 77% of eye color predictions were correct (**Figure 2**), while only 47% of hair color predictions were correct (**Figure 3**).

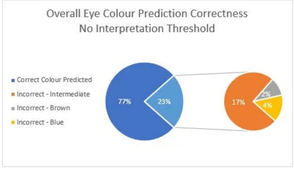


Figure 2. Summary of correct and incorrect eye color predictions as percentages when no interpretation threshold was applied. Incorrect predictions are displayed to the right (smaller pie chart) and are grouped based on their true phenotype to demonstrate which eye color is most often incorrectly predicted.

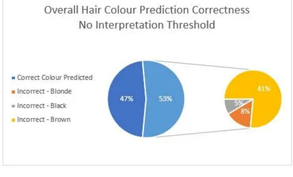


Figure 3. Summary of correct and incorrect hair color predictions as percentages when no interpretation threshold was applied. Incorrect predictions are displayed to the right (smaller pie chart) and are grouped based on their true phenotype to demonstrate which eye color is most often incorrectly predicted.

While the use of an interpretation threshold did raise the percentage of correct phenotype calls for both hair and eye color, we found that many of the same patterns (i.e., difficulty predicting intermediate eye color; black versus brown hair color) were consistent with and without a threshold applied.

Overall, our preliminary findings highlight that FDP predictive power remains challenging for individuals of admixed ancestry, when compared to individuals whose ancestry is more homogenous in nature. While the field continues to develop refined panels and approaches to predicting and modeling EVCs, it is our belief that admixed samples (which comprise a growing number of individuals in the global population) will continue to remain challenging under our current prediction constructs. We look forward to exploring additional forensic tools for EVC prediction in admixed samples in the coming months and publishing our findings accordingly.

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When the World Trade Center Towers Came Down, a Select Group of Forensic Experts Stood Up

W. Mark Dale, MBA, ASQCQA
Inspector, New York State Police (retired)

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On September 11, 2001, I was the Inspector in Charge of the New York State Police Laboratory System. September 11 started similar to most days at 7:00 AM meeting with staff to discuss expedited cases, backlogs, upcoming trials, FOIA requests, accreditation QCARs and QPARS, training, professional meetings, DNA databank, Laboratory Information Management System (LIMS) implementation, new hirings, retirements and the never ending daily tours. At 8:14 AM United Airlines flight 175 departed from Logan airport in Boston with 56 passengers, 7 flight attendants and two pilots. The Boeing 767-222 was scheduled to fly from Boston to Los Angeles. At approximately 8:42 AM flight 175 at 30,000 feet almost directly over the NYSP laboratory in Albany, New York went off course and made a left turn headed south to New York City. (Board, 2002)

At 9:03 AM flight 175 collided with the south tower of the World Trade Center. All laboratory staff were speechless fixated in horror watching the tragedy unfold on any television or computer monitor that could be found in the laboratory.

On September 12, I contacted Dr. Bob Shaler, Director of the NYC Office of Medical Examiner DNA laboratory, and asked how the NYSP laboratory could provide assistance. Bob suggested a visit to review laboratory operations.

On September 13, NYSP Superintendent James McMahon, Administrative Officer William Callahan and I were on a NYSP helicopter headed straight down the Hudson River headed for NY city. Eerily, similar to the same flight path as United Flight 175. As we approached the Manhattan west side landing facility it was apparent that air space was secured and limited to only military and law enforcement traffic. US Navy and Coast Guard gun boats patrolled the Hudson River. The plume of heave smoke from the collapsed towers was drifting eastward over Manhattan and Queens. There were significant concerns the plume could contain debris from a dirty bomb with radiological, chemical hazards or bacterial pathogens.

We first met with Dr. Bob Shaler and Dr. Charles Hirsch (NYCOME Chief Medical Examiner). Dr. Hirsch was seated at his desk in a casual short sleeved shirt exposing his forearms covered with stitches that resulted from being struck by debris from the collapse of the second tower. Dr. Hirsch is one of many that left his office and rushed towards the scene of the collapse of the first tower in an effort to provide assistance. He was struck by debris from the collapse of the second tower. We asked how the NYSP laboratory could provide assistance to his laboratory in an effort to identify victims. Dr. Hirsch replied "Mark, just take a look around and suggest how you can help in any way". His response was the first step of a massive interagency collaboration of laboratory resources.

We started our "look around" on 30 street next to the NYCOME building. There were approximately 10 autopsy tables with overhead tent canopies and ME staff removing victims from body bags and conducting autopsies. Approximately every hour refrigerated box trucks would deliver more victims from ground zero. Autopsies would stop and all NYCOME staff and bystanders would salute the approach of each additional truck loaded with victims.

I noticed the staff performing the autopsies would extract a small tissue sample from a victim, place the sample in a test tube, place the tube in a rack and affix an adhesive bar code to each tube. We decided to follow the rack. A technician took the rack up the elevator to the 6th floor DNA laboratory. At the entrance to the DNA laboratory a staff member wrote the barcode number into a bound leger. At that point I realized the NYCOME required a Laboratory Information Management System with bar code capabilities. The NYSP laboratory had just completed the installation of a LIMS with full bar code and document management capabilities.

I advised Superintendent James McMahon we could install a LIMS similar to ours for management of victim samples and control exemplars for comparison. Superintendent McMahon advised: "Do it and let me know whatever you need to get it done."

Three weeks later we drove to NYCOME with a dozen computers, bar code readers, printers and scanners all loaded with LIMS software. The PorterLee Beast™ LIMS system supported by PorterLee™, IT contractors, NYSP IT, NYSP laboratory scientists, and University at Albany MBA IT management graduate student interns are all responsible for making this happen. Laboratory staff, including Dr. Allison Eastman, travelled to NYCOME and keyboard entered thousands of exemplars in the LIMS system. Within one month the WTC LIMS sample databank was current.

The next challenge was performing complex mixture and familial DNA profile comparisons between dirty, degraded mixtures from WTC victims and victim known exemplars extracted from victim's personal items. In 2001 familial source attribution statistical analyses comparisons were not commonly performed in any forensic laboratory. The solution was for the NYSP laboratory in Albany to receive and analyze all known exemplars submitted from victims' families such as toothbrushes, razor blades, hats, combs etc. The NYCOME laboratory would perform analyses on all tissue samples collected from autopsies. A CODIS similar network and software was then established between the NYCOME and NYSP laboratories to be used for comparisons. False identifications or exclusions were not an option.

We immediately became aware that the number of sample analyses and statistical familial comparisons between victim samples and known exemplars from personal belongings had never been done before on this scale or scope. We required immediate assistance from experts from the forensic laboratory and academic communities specializing in forensic molecular biology, statistics and IT management. We also needed assistance to coordinate the collaboration of this select forensic expert community in the most efficient and effective manner. A call was made to NIJ to provide assistance assembling and facilitating this unprecedented effort of mass disaster victim identification. NIJ immediately delivered the support needed to nurture and sustain KADAP (Kinship and Data Analyses Panel) and software tools which continue to this day identifying WTC911 victims bringing closure to families of the WTC911 disaster.

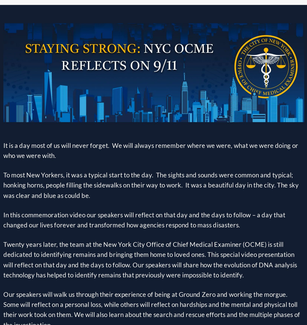


Members of the KADAP team

A Promise Kept: Commitment to World Trade Center Identification

The 20th Anniversary of the September 11th terrorist attacks marks a moment in the history of the United States like no other. The attacks cast a shadow over American life and defined the new century and a war on terror. The aftermath of these attacks was not confined to weeks or months but continues today. The opening presentation at ISHI 32 given by Mark Desire (Assistant Director of the New York City Office of Chief Medical Examiner) and Mary Fetchet (Executive Director and President of the Voices Center for Resilience) will walk along the hardship and perseverance through the eyes of the team and families of the victims. This commitment to identify all of those who lost their lives has not wavered.

Later that day a panel presentation will discuss lessons learned from 9/11. Bruce Budowle (Director for the Center for Human Identification) will moderate and is joined by Mark Desire, Alan Giusti (forensic examiner in the DNA casework unit of the FBI Laboratory) and Timothy McMahon (Director of DoD DNA Operations at the Armed Forces Medical Examiner System). Panelists will be discussing how their agencies worked to identify both victims and perpetrators of the 9/11 attack, and will reflect on the advances in forensic science that have come about in the aftermath of the event.



It is a day most of us will never forget. We will always remember where we were, what we were doing or who we were with.

To most New Yorkers, it was a typical start to the day. The sights and sounds were common and typical; honking horns, people filling the sidewalks on their way to work. It was a beautiful day in the city. The sky was clear and blue as could be.

In this commemoration video our speakers will reflect on that day and the days to follow – a day that changed our lives forever and transformed how agencies respond to mass disasters.

Twenty years later, the team at the New York City Office of Chief Medical Examiner (OCME) is still dedicated to identifying remains and bringing them home to loved ones. This special video presentation will reflect on that day and the days to follow. Our speakers will share how the evolution of DNA analysis technology has helped to identify remains that previously were impossible to identify.

Our speakers will walk us through their experience of being at Ground Zero and working the morgue. Some will reflect on a personal loss, while others will reflect on hardships and the mental and physical toll their work took on them. We will also learn about the search and rescue efforts and the multiple phases of the investigation.

In the end, what stands out is their continued dedication to the city and the work they do.

This exclusive content will premiere on Friday, September 10, 2021 at 10 AM ET / 9 AM CT. After registering, you will receive an email with a link where you can access the video starting at that time.

Register to Attend



A Leadership Perspective

From Bench Criminalist to Lab Director

Interview Written and Condensed by Ann MacPhetridge, Promega

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Brian Hoey, the Lab Director at the Missouri State Highway Patrol, recently presented at one of our Tech Tours held in Seattle. In his talk, he shared insights from his lengthy career in forensics. He is a twenty-eight-year veteran of the Missouri State Highway Patrol Crime Laboratory. Brian worked much of his career as a DNA analyst and served as the DNA technical Leader for 8 years. Brian is currently the Director of the laboratory system.

He holds a Bachelors and Masters degree in Biology from Northern Illinois University, as well as an MBA from William Woods University.

Brian served as a Member of the Scientific Working Group on DNA Analysis Methods (SWGDAM) for 8 years as well as served on it's on the Executive Board for 3 years. Brian is a Member of the Midwestern Association of Forensic Scientists (MAFS) where he served on the Board of Directors as the Treasurer for three years (2008-2011) and President (2013). Brian was awarded MAFS Outstanding Scientist in 2016. Brian is a certified facilitator for Police Leadership: The West Point Model. Brian is also a member of the American Academy of Forensic Sciences (AAFS) and The American Society of Crime Laboratory Directors (ASCLD).

How would you sum up your leadership path?

I have had a very fulfilling career. Leadership was not something I sought. To be honest, I had some bad leaders, and that motivated me to think I could do better. However, leadership for me happened rather organically and with a lot of luck. I truly was in the right place at the right time, but success is a perfectly timed collision between luck and skill. I suppose I was at least skillful enough to be in a particular position when luck happened. I was also fortunate enough to have good mentors who chose to work with me and show me that even as an informal leader, people were following me.

In your presentation at the Promega Technology Tour earlier this year, you talked about how your leadership approach has changed dramatically from the early days...What was your leadership style then? How would you describe your leadership style now?

My father was a football coach, I was really into sports and the early part of my life was largely influenced by sports coaches; consequently, my original leadership style was very "Mike Ditka" oriented. I don't recall screaming and yelling, but I was mercurial and tried to bend situations to my will. I screwed up a lot of humans. Today, I've learned that leadership is not about me, it's about the needs of the people I lead and aligning those needs with the purpose and mission of my organization.

What's the biggest mistake leaders often make?

I think it may be hubris that if we are successful in our career then we are certain to be a successful leader. We frequently see very successful athletes become terrible coaches, or successful business women and men be bad leaders. And in our profession, we frequently see good bench scientists be challenged as leaders.

You've had a lengthy career in forensics, did you feel prepared to take over as Lab Director? If not, how did you get up to speed?

I thought I was prepared for it with the same hubris as mentioned above. I was fortunate however - for lack of a better word- that I failed early in my formal leadership career (although my followers probably didn't feel so fortunate). My failure caused me to learn. I sought to achieve a similar, if not the same, formal training as I did to become a successful Forensic Biologist; I took a bunch of classes, trainings, etc. and even sat for my MBA.

What was the most unexpected challenge you faced when you became Lab Director? How did you handle it?

As with most promotions I've received, the unexpected challenge was exactly that, ...the unexpected. The grass is always greener... Things like the legislative schedule, political pressure and financial cycles were new challenges. I handled them like I've done so many times in my career, I learned, failed and learned again. And I'm still learning and practicing. One very important lesson I learned when learning how to handle it is that I can't do it all, nor know it all; I've got great people that help and take on much of the heavy lifting. My administrative staff is great at helping me see the outside view, things that I don't see through my own, often self-important lens. I, like many others, frequently put myself in a box and fail to see the outside view. Being surrounded by loyal "no-sirs" is very helpful; being willing to listen and rethink is a must.

In your opinion, what qualities make a good leader? Can these be learned? Or are they something you're just born with?

Competence, character, compassion. and commitment. Nature vs. nurture is an age-old debate when it comes to these discussions. I believe it is both. Michael Jordan was certainly born talented, but was also cut from his high school varsity team (although that story is a bit nuanced). The point is that Jordan practiced, was relentless about it and the rest is history. Like anything else we do, leadership qualities can be learned, but it takes practice. I am still practicing.

How do you think management/leadership today can best support their teams, especially in times of crisis, like the COVID pandemic?

You can never over communicate, and you must empathically listen. Communication and listening begin with mutual respect, mutual purpose, and making the communication safe to have. We all know that COVID created fear and uncertainty, particularly early on. Some felt like it was nothing, while others felt completely unsafe in the workplace. As leaders, we need to respect both opinions and make the environment safe so our followers can express their feelings and opinions to us. We need to listen to our followers and make them feel felt. We also need to communicate the mutual purpose we all share with the organization's purpose and mission; people need to know the why. That mantra should be the same and consistent whether it is giving someone a performance appraisal, dealing with a crisis or even a once in a lifetime global pandemic.

What advice do you have for new leaders who are feeling unprepared for their new roles?

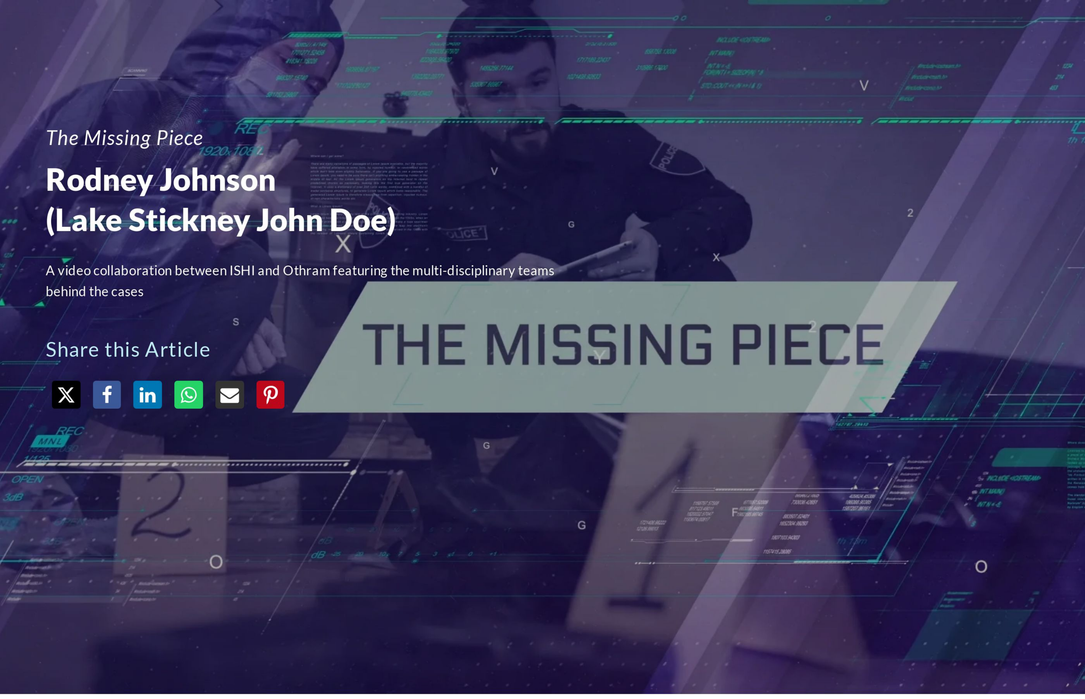
Learn and practice. Know that you don't know it all, and never will. Put as much effort into learning leadership as you did to learn molecular biology and mixture interpretation. Be the Scientist that you are- hypothesize, test it, and be willing to be flexible when you are wrong. Then analyze where you went wrong and learn from it. Most importantly, as you would with a case, be radically transparent.

What's the most rewarding thing about leading your team?

Organizations are collections of people. Successful leaders meet the needs of people while furthering the purpose and mission of the organization. If leaders can do that, you give people the tools to succeed, and it is like capturing lightening in a bottle. It is rewarding when your followers and organizations succeed. If I had even the slightest hand in leading someone to success, it is very rewarding. Leadership is a gift.

For more on how to lead in the laboratory, consider attending the *You Deserve a Cookie! Navigating the Challenging World of Leadership in Forensic Biology* workshop at ISHI 32. Learn more and register on our website.

Visit the ISHI Website



The Missing Piece

Rodney Johnson (Lake Stickney John Doe)

A video collaboration between ISHI and Othram featuring the multi-disciplinary teams behind the cases

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For years, victims were listed on cold case files in law enforcement evidence boxes. While never forgotten, limitations in forensic science prevented their cases from being closed. Families waited decades for answers and justice while their killers remained unidentified.

In 2018, a new tool for crime solving rose to prominence as the notorious Golden State Killer was finally unmasked; forensic genetic genealogy. To begin, investigators upload their unknown DNA profile to the site, which generates a list of the closest genetic matches, based on how many centimorgans (cM) of DNA are shared with the unknown person. Next, investigators will begin to build back the unknown person's family tree until a common ancestor is uncovered. Then, they will build the family trees forward, identifying every descendent possible, using traditional genealogy techniques. Once the trees have been fully built out, investigators look to identify candidate persons that might match the unknown person. Once a person of interest has been identified, new DNA can be collected to compare to the original forensic sample.



The search for answers began in 1994 when a fisherman discovered a body in the lake. The Snohomish County Medical Examiner's office determined the deceased to be between 25 and 35 years old and the victim of a violent homicide. Multiple varied facial reconstructions were made for the victim over the years, in part because ethnicity assessment was inconclusive. Each artistic rendition was shared with the public in hopes that someone would recognize the victim and come forward with information.

Detective Scharf and Investigator Jorgensen reached out to Othram to perform DNA testing. Despite having less than a fifth of a nanogram (less than 20 cell's worth) of badly degraded and heavily contaminated human DNA to work with (a scenario currently inaccessible by any other forensic lab), Othram's scientists were able to reconstruct a genealogical profile.

After uploading the genealogical profile to a public genealogical database, a match was identified, allowing Othram's internal laboratory team and investigators to establish an identification: Rodney Johnson.

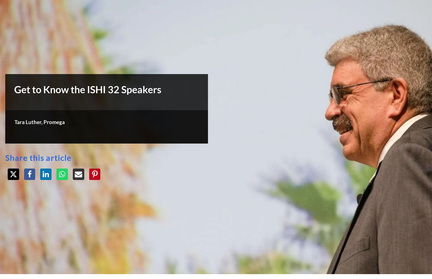
Usually, one match is not enough to point to a single person. However, this match had included another clue in their public database profile. They belonged to a distinctive direct maternal lineage. The high-resolution profile developed by Othram allowed investigators to perfectly match up this uncommon maternal lineage signature.

The investigators then found a record for a missing person that appeared to match Mr. Johnson. Interestingly, although the missing person was reported in 1996, the Mr. Johnson had last been seen in 1987. He was only 25 years old. It's likely that the Lake Stickney John Doe had been in the lake for as many as seven years before being discovered.

Investigators reached out to next-of-kin and used legacy DNA testing to confirm the identity established from the genealogical profile. Investigators are now working to better understand what might have happened in the days leading up the Johnson's death.

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Get to Know the ISHI 32 Speakers

Tara Luther, Promega

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Before heading to ISHI (or logging on virtually) this year, let's get to know some of the ISHI General Sessions speakers a little better.

What tips would you give to someone who is just starting out in the field of forensics, or what is the best advice that you've received?

Ed Green: If you already know the answer, don't bother doing that experiment. Think of a better one.

Allison Sherier: Graduate school is always a big decision. The best advice I suggest is to treat it like a job. Make yourself deadlines and goals and stick to them. The typical week should be working on your classes, research, and writing from 8 am to 5 pm Monday through Friday. Focusing on graduate school as a job meant that I had time for myself and my family. This approach also helped me prevent burnout early on in my program.

Dane Plaza: Work hard and be innovative. The forensics field can be demanding and stressful, but a strong work ethic and positive attitude can take you far in your career. Don't be afraid to bring up new ideas as some of the most impactful programs/research I have been a part of started as blue sky ideas that resulted in successful and impactful projects.

Emily Simek and Lies Janssens:

- Be open to change because forensic science is an ever-evolving field.
- Own up to your mistakes, and don't be afraid to ask questions.
- If you have a passion for forensics, keep up with it.

Tarah Nieroda: The best advice I ever received also happens to be the same advice that I give today. To never give up and keep on trying, that once you get your foot in the door even if it is at the bottom of the barrel in an entry level position that is all you need to start a career in this industry.

Rachel Oefelein: Take every opportunity! Candidates with at least some experience tend to shine, not to mention many interns end up getting hired by their host laboratory.

Elena Zavala: The best advice that I received when I first decided I wanted to study forensics over fifteen years ago was to first get a strong foundation in the natural sciences. As you begin to identify your area of interest I would recommend talking to as many people as possible who do what you want to do. This will help you learn how to follow their path and/or gain better insights into the reality of their job.

Curt Hewitt: I'm on the R&D side of things, so the most important advice I can give is to be creative in how you approach problems and constantly check your assumptions against the data.

Laurence Devasse: I would say that passion for the topic goes a long way in the field of forensics, and you're likely to meet a lot of very passionate people. Try to network as much as possible. Every person I have met in the field has given me fresh insights and inspired me. One of the best pieces of advice I was ever given was to always take any opportunity to present your work – even if you're nervous, each presentation is practice for the next one.

Lawrence Wein: While in graduate school at Stanford, the late Sam Karlin told me: To be a good applied mathematician, you need to know ten times as much math as you are going to use.

Jianye Ge: Learn new technologies and listen to your seasoned colleagues.

Has there been anything good that came out of the pandemic that you'll continue doing going forward?

Ed Green: Travel less.

Allison Sherier: The pandemic changed many things, but it did force me to be more intentional about time for myself. Working from home allows me to have more time (not commuting), but I quickly realized I was working a ton of extra hours. I finally had to start scheduling my day a little more closely and adding specific time to go work out or take walking breaks. I hope to keep up this extra separate time as I start to work full time on campus.

Dane Plaza: We have further enhanced our reachback center and training program using the tools that have become more available during the pandemic. Much of our staff is more comfortable and experienced with virtual support and training, which is a large part of the Rapid program. While we recognize every mission is different, we believe we have an amazing infrastructure and baseline to further enhance our remote support for future operations.

Emily Simek and Lies Janssens: We have a bigger appreciation for our health as well as our coworkers. Working from home, although nice, made us miss our inter-office relationships.

Tarah Nieroda: I have started roller blading and bike riding with my family so now on weekends we make sure to spend as much time outdoors as possible.

Rachel Oefelein: Lots more FaceTime, Zoom, Skype, etc. I think being able to see someone's face is so important in communication and I will continue more 'video chat' both personally and professionally.

Elena Zavala: I hope to be better about balancing my time. I found that there are certain tasks and areas of work that are easier when working from home and others that are essential for in person. Hopefully I can maintain this balance in the future.

Curt Hewitt: I think I will better appreciate not being in a pandemic once the pandemic is over!

Lawrence Wein: I am a Senior Associate Dean who oversees 130 Ph.D. students at Stanford. During the pandemic, my staff aggressively engaged with these students in an effort to maintain good mental health. We will continue this practice as we emerge from the pandemic.

Jianye Ge: Zoom meeting can be very productive if we spend time to learn how to use it. I particularly like the functions like recording and white board.



What is your favorite Disney character and why, or which Disney character do you most relate to and why?

Ed Green: Queen Elsa from Frozen. I love her songs!

Allison Sherier: Alice in Wonderland has always been a favorite of mine. Alice is just a young girl trying to work through her life and the world around her. She meets a bunch of super unusual characters that shape her experiences and guide her. A very close second is the Cheshire cat.

Dane Plaza: While a bit obscure, it's Heimlich from A Bug's Life. His dialogue and overall presence in the movie make me laugh every time.

Emily Simek: WALL-E (from "WALL-E"). I like that he is optimistic, curious, and he really cares about plants. He is a plant hobbyist just like me.

Lies Janssens: Belle (from "Beauty and the Beast"). I like that she is independent, smart, and adventurous. The movie is set in France, and that just reminds me of my childhood in France.

Tarah Nieroda: My favorite Disney Character is Princess Aurora, I love her story from the movie Maleficent because it shows her as a fun, life loving individual who also looks for the best in people and is the ultimate optimist. She is my favorite enough that I named my daughter after her.

Rachel Oefelein: Ariel, she has the best songs and I love being in the water :D I relate to how important love is to her and her inquisitive mind.

Elena Zavala: My favorite Disney character has always been Pluto.

Laurence Devasse: There was a mouse in Cinderella, I think his name was Gus? There was a scene where he tried to carry too much cheese – it makes me laugh every time I think of it.

Curt Hewitt: Probably Wall-E. I feel like we are equally amazed by and oblivious to much of the world around us.

Lawrence Wein: I have a pet California rabbit (white with red eyes) who lives in my living room and has been a good companion during the pandemic. So I guess I would choose White Rabbit from Alice in Wonderland (it is also a great song).

Jianye Ge: Mickey Mouse. Mickey was the first Disney character I saw in the TV.

If you could have one superpower, what would it be and why?

Ed Green: To be able to sing like Idina Menzel.

Allison Sherier: I am an animal lover. So above all else, the ability to talk to animals would be my pick.

Dane Plaza: The ability to bypass all traffic. If you have ever driven in the Northern Virginia area, you would agree!

Emily Simek: the ability to fly because I hate traffic especially rush hour.

Lies Janssens: the ability to teleport because it would cheaper and easier to see my family and friends overseas.

Tarah Nieroda: I could detect when someone was lying, honesty is something that is very important to me in both my personal and professional life. Although if I could detect lying, I should probably be an officer or a lawyer instead of a scientist.

Rachel Oefelein: Teleportation so I would never have to sit in traffic or be on a bad flight again! Plus, you could see all the people you love whenever you want!

Elena Zavala: Despite or perhaps because of my fear of heights, I would love to be able to fly.

Laurence Devasse: Time travel, so that I could go back in time to chat to loved ones and a few famous scientists. A hop into the future to read my finished thesis wouldn't go amiss either.

Curt Hewitt: Time travel. Barring any universe ending paradoxes, when wouldn't that be useful?

Jianye Ge: Make the Texas summer cool.

What's one thing that others may not know about you?

Ed Green: I think most people don't know anything about me. One random thing is that I religiously read the local newspaper from Nashville, Georgia (The Berrien Press) – a city where my 3x great-grandfather lived but I've never lived myself – for reasons that don't make sense to anybody, including me.

Allison Sherier: I used to show Brahman cattle in high school and managed a show cattle ranch in Oklahoma for a year during my bachelor's degree. For the people not familiar with show cattle, you raise a heifer (female) or steer (altered male) and show them at county fairs or stock shows. The heifers are typically shown at multiple shows until they have their first calf, and steers are generally shown at one big show. While managing the show cattle farm, at 19 years old, I oversaw halter breaking heifers and steers from a few months of age up to 2 years. I also managed their daily needs and did essential work to prepare them for shows.

Dane Plaza: I grew up raising cranberries for Ocean Spray in Northern Wisconsin on our family's marshbog.

Emily Simek: My free-lance makeup work was published in Utah's "Rocky Mountain Bride" magazine.

Lies Janssens: I was a flautist and backing vocalist in a Jazz band named "Tourist in Paradise".

Tarah Nieroda: I am not one of those individuals that wanted to be a scientist their whole lives. I wanted to be an artist until I was 17 and had already been accepted to multiple art colleges before changing my mind.

Rachel Oefelein: I find dolphins terrifying but happily swim with sharks!

Elena Zavala: I also have a degree in music and play both the viola and piano.

Curt Hewitt: I grew up racing go karts and I'm entirely comfortable going 90 mph three-quarters of an inch above the ground.

Laurence Devasse: I grew up in Belgium, and my first language is actually French. When I first moved to England for university, a lot of people thought I was a Belgian princess (I'm not!).

Lawrence Wein: I don't think anyone in this community knows me or anything about me – I don't know anyone aside from my two amazing co-authors. I am not a forensic scientist. I am an applied mathematician, and in the years after the September 11, 2001 attack, my research on avoiding or mitigating catastrophic events was implemented nationwide on a number of issues (nuclear, smallpox, anthrax, botulinum toxin, US-VISIT Program, pandemics). In the last few years, I have become interested in crime solving via ballistic imaging, sexual assault kits and FGG.

Jianye Ge: I am a computer scientist, but not a statistician.

An Update from the Organization of Scientific Area Committees (OSAC) for Forensic Science

Robyn Ragsdale, Chair of OSAC's Biology Scientific Area Committee and Beth Ordeman, Chair of OSAC's Human Forensic Biology Subcommittee

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The Organization of Scientific Area Committees (OSAC) for Forensic Science's Human Forensic Biology Subcommittee continues to move forward regardless of the pandemic! The subcommittee currently has 18 documents at the AAFS Academy Standards Board (ASB), two of which may be published shortly. Furthermore, we have posted as OSAC Proposed Standards, OSAC 2020-S-0004, ***Standard for Interpreting, Comparing and Reporting DNA Test Results Associated with Failed Controls and Contamination Events*** and OSAC 2020-N-0007, ***Best Practice Recommendations for the Management and Use of Quality Assurance DNA Elimination Databases in Forensic DNA Analysis***. Both have been sent to ASB for further development and publication. Additionally, OSAC 2021-S-0021, ***Forensic Autosomal STR DNA Statistical analyses – General Protocol, Protocol Verification, and Case Record Requirements*** recently completed its open comment period and OSAC 2021-S-003, ***Standard for Setting Analytical and Stochastic Thresholds for Application to Forensic Casework Using Electrophoretic Systems*** should be posted for open comment in September.

In August, four new DNA standards were added to the Registry and include:

- ANSI/ASB Standard 023, ***Standard for Training in Forensic DNA Isolation and Purification Methods***, First Edition, 2020.
- ANSI/ASB Standard 110, ***Standards for Training in Forensic Serological Methods***, First Edition, 2020.
- ANSI/ASB Standard 115, ***Standard for Training in Forensic Short Tandem Repeat Typing Methods using Amplification, DNA Separation, and Allele Detection***, First Edition, 2020.
- ANSI/ASB Standard 116, ***Standard for Training in Forensic DNA Quantification Methods***, First Edition, 2020.

Three additional ASB published standards are under consideration for the Registry and three more standards, originally proposed by OSAC, are in the open comment period at ASB.

Several documents, including and 2021-S-0029, ***Standard for Familial Searching*** and 2021-S-0028, ***Standards for the Analytic Procedures and Report Writing of Forensic Serological Methods*** are currently being reviewed by a scientific and technical review panel (STRP) and open for public comment until September 6. Fourteen other documents are also under development. Several of them, including standards for training and validation, massively parallel sequencing, and testimony propositions, are close to completion. An assessment/ implementation document related to ANSI/ASB Standard 040, ***Standard for Forensic DNA Interpretation and Comparison Protocols***, First Edition, 2019, is also in process.

The Biology Scientific Area Committee has also recently posted a list of informative literature for forensic biology covering both the human and wildlife disciplines. A list of current research needs will be posted shortly as well.

Please visit the OSAC website and view our monthly Standards Bulletin to see the standards that are open for comment. OSAC's Biology Scientific Area Committee (SAC) and Human Forensic Biology Subcommittee need your expertise and input to help make these standards as strong as possible! We also encourage you to review and use the standards that are listed on the Registry. If you have any questions about any of these standards, please contact the OSAC Biology SAC Chair (robynragsdale@fdle.state.fl.us) or Human Forensic Biology Subcommittee Chair (bordeman@co.pinellas.fl.us).

- Join our email list to receive the OSAC Standards Bulletin, news and other updates.
- Follow us on LinkedIn.
- If you have relevant expertise, consider applying to become an OSAC member.



The Casework Direct System

Efficiently Process Sexual Assault Evidence and Property Crime Evidence

Ann MacPhetridge, Promega

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In recent years, the overwhelming number of property crime and sexual assault evidentiary samples submitted to forensic laboratories has resulted in a significant need for improved solutions for processing these challenging sample types. The Casework Direct System is designed to rapidly process swabs from casework samples or cuttings of sexual assault swabs and stained fabric prior to quantification of human DNA using the PowerQuant® System, and amplification of normalized template using PowerPlex® Systems for STR analyses. For casework samples, no further purification of the Casework Direct lysate is required prior to STR amplification unless data from the quantification step suggests that PCR inhibitors may be present.

- Generates amplification-ready lysates in less than 1 hour
- Improves efficiency for Y-screening and selection of evidentiary samples for STR testing
- Optimized for use with PowerQuant®, Plexor® HY and PowerPlex® Systems

When used specifically with the PowerQuant® System, additional valuable information on the quality and integrity of the DNA can also be obtained, helping laboratories to quickly determine which samples may be the most optimal for moving on to STR analysis.

With a brief incubation step followed by centrifugation, the protocol is straightforward. The resulting lysate is ready for use in a quantification assay and STR amplification.



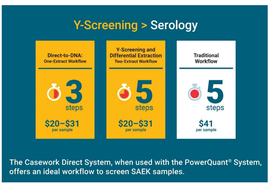
How it Works: Y-Screening Application

Sexual Assault Kits (SAK) account for a substantial percentage of backlogged cases in forensic laboratories. However, traditional methods require hours to complete and are often laborious, while providing insufficient sensitivity when compared to male DNA detection by amplification. Additionally, conventional screening results offer analysts little predictive power as to what DNA profile may result. Recognizing the limitations and challenges associated with traditional serology methods, SWGDAM recommendations are now instructing the use of a "direct to DNA" approach, where DNA analysis is performed before serology to maximize the chances of obtaining CODIS eligible profiles. The Casework Direct System is highly sensitive, enabling detection of male DNA in the presence of high amounts of female DNA (see Table 1).

Table 1. Serology, PowerQuant® System quantification and STR percent profile results for vaginal swabs obtained at varying post-coitus time intervals.

Sample	AP	PSA	Mens	[Quant] (ng/µl)	[Y] (ng/µl)	[Auto][Y]	% Male Profile PowerPlex® Fusion 6C System	% Profile PowerPlex® Y23 System
8 hours	+	+	+	25.2410	1.7284	14.59	100%	100%
24 hours	+	+	+	126.4271	8.4182	288.59	11%	100%
48 hours	–	–	+	178.0133	0.0271	6,572.58	8%	87%
72 hours	–	–	–	38.2087	0.0030	19,828.22	0%	81%
96 hours	–	–	–	24.5140	–	–	0%	0%

By using Casework Direct System to perform this "direct to DNA" amplification, laboratories can reduce the overall turnaround time for SAK sample processing in addition to minimizing the potential DNA loss typically seen in the DNA extraction step.

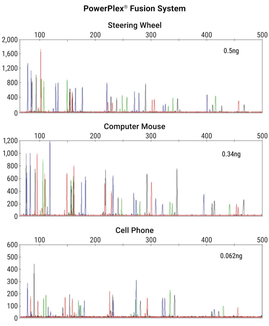


How it Works: Touch DNA Samples

When DNA is found at a property crime scene, laboratories may be able to match the evidence to a known offender's sample in CODIS, and these profiles could be connected to other types of offenses. Because of these successes, crime investigators will submit numerous "touch DNA" samples to their forensic laboratories, causing the laboratory to use significant resources for property crime cases by testing evidence for "touch DNA". These samples tend to contain very little DNA, so running them through a typical DNA extraction protocol can also result in further loss of DNA, which can lead to an unusable profile.

Integration of the Casework Direct System into a laboratory's workflow provides a rapid and cost-effective means to generate high-quality STR profiles from precious, low-abundance DNA samples with minimal hands-on time.

Panel A.



Panel B.

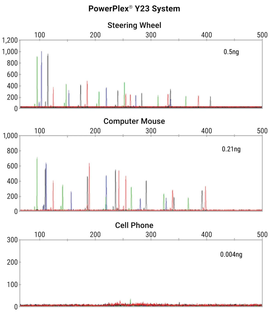


Figure 2. The Casework Direct System generates high-quality STR profiles from touch DNA samples. Cotton swabs were used to collect touch DNA samples from steering wheel, computer mouse and cell phone surfaces. For each sample, 400µl of Casework Direct Solution was added to the swab placed in a spin basket assembly, incubated at 70°C for 30 minutes and centrifuged at 16,000 × g for 5 minutes to recover the lysate. The amount of human amplifiable DNA was quantified from 2µl of lysate using the PowerQuant® System, and 0.5ng or the maximum volume of lysate was used for STR amplification using the PowerPlex® Fusion and PowerPlex® Y23 Systems. The amplified products were electrophoresed on the Applied Biosystems® 3500xL Genetic Analyzer using POP4 with 3kV, 5-second injection and analyzed on GeneMapper® IDv3.2 with an analysis threshold of 50 RFU.

In conclusion, with the ever-increasing workloads seen by forensic casework laboratories, solutions such as the Casework Direct System, which can provide a more efficient method to triage samples to ensure that the samples processed have a high probability of providing a usable profile, are a welcome answer to the challenge of finding ways to work smarter, not harder.

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There's Still Time to Register for ISHI 32!

There's still time to register to attend the 32nd International Symposium on Human Identification; whether you'd like to join us in person at Disney's Coronado Springs Resort or attend virtually.

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tara.luther@promega.com

DNA Solutions from Spent Shell Casings and Rootless Hairs

Bode X-traction technology enables DNA recovery from spent shell casings and rootless hairs. Advanced sampling methods developed from the ATF[8] combined with technology developed at Bode enable analysts to obtain **~10 X more DNA from spent shell casings** and obtain useable nuclear **DNA profiles from a single hair**.