

Promega | Powered for 32 years

ISHI INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION

STARTING SEPTEMBER 13, 2021

February 2021

The ISHI Report

News from the World of DNA Forensics

Start Reading

What's inside:

Introduction

Letter from our Editorial Board

Bayes' Theorem: Can Statistics Help Guide a Verdict in the Courtroom?

Newly Launched G.O.L.D. Unit in Cuyahoga County: Using Forensic Genetic Genealogy to Identify Most-Wanted Cold Case Rapists

Former ISHI Student Ambassadors: Where are They Now?

Capillary Electrophoresis: Overcoming the Hurdles of Current Technologies

The Boundless Utility of Rapid DNA Identification

DNA Dead End? Protein Sequencing for Forensic Analysis

Tracing Roots: How the Transatlantic Slave Trade Impacted the Genetic Makeup of the Americas

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

ISHI 32 Workshops

Apply to be the Next ISHI Student Ambassador

Share Your Efforts or Nominate a Friend: Unsung Heroes

Calendar of Events



The ISHI Report

Letter from the Editor

Greetings from Madison, Wisconsin. This issue of The ISHI Report finds us looking forward to warmer weather and the beginning of the end of life under COVID.

The past year has been a slog for many of us. Some have experienced the loss of a friend or family member, financial hardships and emotional stress. During this difficult time, we know that many of you have stepped up to help in ways both great and small. To recognize and amplify these uplifting examples, we invite you to tell us how you have helped your community cope. Share your own efforts or nominate a friend. Look for details on the Unsung Heroes project in this issue to participate.

Additional features in the Spring ISHI Report include a conversation with Steven Micheletti, a population geneticist at 23andMe. We learned about his groundbreaking research on how the slave trade has impacted the genetic landscape of the Americas. He shares some surprising findings.

Rapid DNA has been successfully used for multiple applications including mass disasters, local DNA databases and providing quick relationship testing. Guest author Julie French shares her thoughts on the benefits of adopting Rapid DNA into a sample processing workflow and provides insights on how to get started in your own laboratory.

Our colleague Ken Doyle explores how Bayes' Theorem continues to be applied to forensic cases. Author Sharon Bertsch McGrayne further explores Bayes' Theorem in her book, *The Theory That Would Not Die: How Bayes' Rule Cracked the Enigma Code, Hunted Down Russian Submarines, and Emerged Triumphant from Two Centuries of Controversy*, and will be presenting on this topic during ISHI 32.

You too, can play a part at ISHI by presenting a scientific talk or interesting case study (abstract deadline June 14). If you prefer, submit an abstract for poster presentations (deadline July 12). All abstracts will be reviewed by an outside committee and selected based on perceived relevance for the forensic community. Abstracts can be submitted through this online portal.

If you are student in the forensic field, consider applying to become an ISHI Ambassador. Students selected for the program will receive free registration for ISHI 32 including workshops. Details on the application process can be found on page 11. We also caught up with our former Student Ambassadors on page 4 to hear more about what they are up to now.

You can find the latest information on plans for ISHI 32 by visiting the official symposium website, www.ishinews.com. Visit often to keep up with the latest news in DNA forensics. At this time we are moving forward with an in person event. If the situation changes so it becomes unsafe to hold an in person meeting, we will offer a virtual alternative. Answers to our most asked questions can be found here.

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

Stay well,

The Editorial Board

Contact ISHI

Newly Launched G.O.L.D. Unit in Cuyahoga County

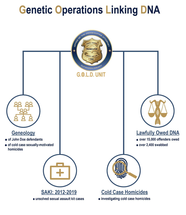
Using Forensic Genetic Genealogy to Identify Most-Wanted Cold Case Rapists

Interview written and condensed by Carol Bingham, Promega

Share this article

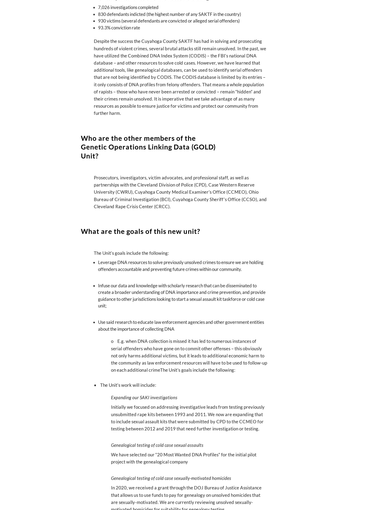
In 2013, the Cuyahoga County Prosecutor's Office (CCPO, Ohio) launched their Sexual Assault Kit Task Force (SAKTF) to investigate leads stemming from the testing of previously unsubmitted rape kits between 1993-2011. Over the years, the Task Force finalized over 7,000 investigations which resulted in indictment of 817 defendants and justice for 915 victims.

Last Fall, the CCPO was awarded a $1,000,000 grant from the U.S. Department of Justice to be used towards personnel staffing, victim advocacy and research partnerships, training, and other resources. This grant, in combination with prior DOJ funding helped to launch the office's Genetic Operations Linking DNA (G.O.L.D.) Unit, which will allow the CCPO to expand their efforts by utilizing forensic genetic genealogy.



Since the identification of the Golden State Killer in 2018, forensic genetic genealogy techniques have proven to be a powerful tool in closing cold cases and restoring identities to unidentified remains cases. Forensic genetic genealogy relies on genetic relationships between a DNA profile for an unknown person and profiles of known people in genealogy databases, such as GEDmatch, FamilyTreeDNA, or DNAdelves. 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 a candidate person 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.

To learn more about how the G.O.L.D. Unit is using forensic genetic genealogy to identify some of their most-wanted cold case rapists, we interviewed Mary Weston, Unit Supervisor of the Cold Case G.O.L.D. Unit (Genetic Operations Linking DNA) and project manager for the Cuyahoga County Sexual Assault Kit Taskforce (SAKTF). In her role, Mary oversees the unit which investigates and prosecutes sexual assaults and cold case homicides, consisting of prosecutors, investigators, victim advocates, and professional staff.



Mary, thank you for talking with us today.

I understand that CCPO has enjoyed great success with the Sexual Assault Kit Task Force that was formed several years ago. Since 2013 investigations from this team have resulted in 817 defendants indicted with a 93% conviction rate.

Given this success, what was the impetus for forming the GOLD unit?

The most updated numbers we have include the following:

- 7,026 investigations completed
- 830 defendants indicted (the highest number of any SAKTF in the country)
- 930 victims (several defendants are convicted or alleged serial offenders)
- 93.3% conviction rate

Despite the success the Cuyahoga County SAKTF has had in solving and prosecuting hundreds of violent crimes, several brutal attacks still remain unsolved. In the past, we have utilized the Combined DNA Index System (CODIS) – the FBI's national DNA database – and other resources to solve cold cases. However, we have learned that additional tools, like genealogical databases, can be used to identify serial offenders that are not being identified by CODIS. The CODIS database is limited by its entries – it only consists of DNA profiles from felony offenders. That means a whole population of rapists – those who have never been arrested or convicted – remain "hidden" and their crimes remain unsolved. It is imperative that we take advantage of as many resources as possible to ensure justice for victims and protect our community from further harm.

Who are the other members of the Genetic Operations Linking Data (GOLD) Unit?

Prosecutors, investigators, victim advocates, and professional staff, as well as partnerships with the Cleveland Division of Police (CPD), Case Western Reserve University (CWRU), Cuyahoga County Medical Examiner's Office (CCMEO), Ohio Bureau of Criminal Investigation (BCI), Cuyahoga County Sheriff's Office (CCSO), and Cleveland Rape Crisis Center (CRCC).

What are the goals of this new unit?

The Unit's goals include the following:

- Leverage DNA resources to solve previously unsolved crimes to ensure we are holding offenders accountable and preventing future crimes within our community.
- Infuse our data and knowledge with scholarly research that can be disseminated to create a broader understanding of DNA importance and crime prevention, and provide guidance to other jurisdictions looking to start a sexual assault kit taskforce or cold case unit.
- Use said research to educate law enforcement agencies and other government entities about the importance of collecting DNA
    - E.g. when DNA collection is missed it has led to numerous instances of serial offenders who have gone on to commit other offenses – this obviously not only harms additional victims, but it leads to additional economic harm to the community as law enforcement resources will have to be used to follow-up on each additional crime The Unit's goals include the following:
- The Unit's work will include:

    Expanding our SAKI investigations

    Initially we focused on addressing investigative leads from testing previously unsubmitted rape kits between 1993 and 2011. We now are expanding that to include sexual assault kits that were submitted by CPD to the CCMEO for investigative leads between 2012 and 2019 that need further investigation or testing.

    Genealogical testing of cold case sexual assaults

    We have selected our "20 Most Wanted DNA Profiles" for the initial pilot project with the genealogical company

    Genealogical testing of cold case sexually-motivated homicides

    In 2020, we received a grant through the DOJ Bureau of Justice Assistance that allows us to use funds to pay for genealogy on unsolved homicides that are sexually-motivated. We are currently reviewing unsolved sexually motivated homicides for suitability for genealogy testing.

    Continuing the Lawfully Owned DNA project

    Continue to collect DNA on those offenders who lawfully owe it to law enforcement; out of the 13,371 offenders we have identified who lawfully owe DNA, we have swabbed 2,441 to date – 87 of which produced a CODIS "hit" to another crime (including murder, sexual assault, robbery, & others)

Why did you elect to use an outside company to process these cases instead of using in-house resources?

Our office currently does not have those capabilities as we do not have access to genealogy databases that the public has put their DNA into. Up until now, if we identified a DNA profile on a piece of evidence, the best we could hope for was that the profile was eligible to be uploaded to the CODIS database. However, the CODIS database is limited because it only consists of DNA profiles from felony offenders. Now, with this new funding, we will expand our pool of DNA profiles to catch these previously "hidden" offenders through genealogy.

How will you decide which cases the unit will work first?

The CCPO formed a committee of prosecutors and investigators with the aim of producing a list of 20 Indicted John Doe defendants most suitable for investigative genetic genealogy. The committee went through an extremely thorough vetting process in which it reviewed all the Task Force's indicted John Doe cases and ranked them, considering such factors as (a) whether the unknown DNA profile was linked to multiple crimes (i.e. serial offenders); (b) DNA results (i.e. the quality and quantity of the DNA); and (c) the facts of the case (i.e. the case's solvability in the event genealogy produced results, including witness availability). The CCPO wanted to ensure that if genealogy solved the case, the case would be immediately highly prosecutable.



Have any challenges arisen during the creation of the GOLD unit?

How did you overcome these challenges?

Your instinct is that you want to submit all of your unsolved cases for genealogy to bring justice for every single victim. However, genealogy is cost-prohibitive. In 2019, we applied for and received a grant from the Department of Justice's Bureau of Justice Assistance Programs Sexual Assault Kit Initiative. The grant provided enough funding for us to submit 20 unsolved sexual assault cases for genealogy. To overcome the challenge of limiting our pool to 20 cases, we focused on which cases involved unidentified serial offenders and which involved the most violent crimes. Solving these cases first will make our significantly community safer and bring justice for these victims. We are grateful that in 2020, we applied for and received funding that we will use to test even more cases.

What advice do you have for other jurisdictions considering implementing genetic genealogy?

Set up a committee to review the largest pool of cases that can be considered for genealogy. Look at your lab reports and determine suitability for genealogy based on location of the DNA on the evidence and whether the DNA is single source or a mixture. Review the facts of the case and make sure parties are still available to determine the case's solvability if genealogy produces results. You want to ensure that if genealogy solves the case, the case will result in a successful prosecution.

Does the task force have an expiration date, or will it continue as long as it produces results?

We are committed to continuing this project for as long as we can. As long as there are cases that need to be solved and victims that are waiting for justice, we will continue to seek funding so we can hold these "hidden" offenders accountable.

Have any of your cases already been solved through use of genetic genealogy?

Not yet. We are very excited to announce that we have dropped our first batch of cases to our genealogy lab and are awaiting results. These cases are all unsolved "John Doe" rape cases, meaning a grand jury has returned an indictment against a DNA profile that represents the rapist, but the person with that DNA profile has not yet been identified.

Can you describe the details of some of the cases that you are hoping to solve through genetic genealogy?

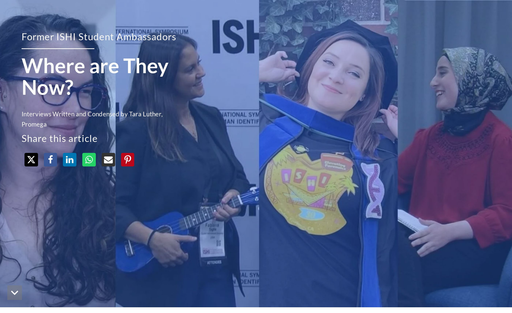
We cannot discuss the particulars of any open investigations, but we can say that our first batch of genealogy cases represents our unsolved serial offenders and most violent stranger rapes.

Former ISHI Student Ambassadors

Where are They Now?

Interviews Written and Condensed by Tara Luther, Promega

Share this article



In 2019, for the 30th anniversary of ISHI, we launched the Student Ambassador program. We knew that the next generation of forensic scientists were doing amazing things, but we never imagined just how inspirational they'd truly be.

As we begin our search for the next batch of Student Ambassadors, we thought there was no better time to catch up with the ladies who started it all to see what they were up to now.

For this article we interviewed:

- **Allison Sherier,** Ph.D. Candidate, University of North Texas Health Science Center
- **Mirna Ghemrawi,** Teaching Assistant and Ph.D. Student, Florida International University
- **Fabiana Taglia,** Ph.D. Candidate, Florida International University
- **Rachel Kieser,** Postdoctoral Fellow, Houston Methodist Research Institute | Weill Cornell Medical College of Cornell University

If you know someone who would be interested in becoming an ISHI Student Ambassador, or would like to submit an application yourself, you can learn more here.

How has life changed for you over the past year and a half?

Allie: Since ISHI 2019 in beautiful Palm Springs, CA a lot has changed. The world as we know it has drastically changed. Personally, I have continued working on my PhD and received a National Institute of Justice Fellowship in 2020. I am excited to have received this wonderful award and look forward to spending my time focusing on my dissertation work.

Mirna: I guess the main change is that life became quieter and more isolated (for everyone). Although it slowed down many milestones, I was able to finish my course requirements and I am aiming to apply for my candidacy exam this semester. It also gave me time to write two manuscripts: The genital microbiome and its potential for detecting sexual assault, which was published, and the other is being reviewed. Two more papers are almost ready too!

Fabiana: My life has changed a lot in the last year. I passed my candidacy exam on April 2020. I've been assigned to a very interesting project and hopefully I will graduate this Fall 2021.

Rachel: In my time since being an ISHI Ambassador, almost every aspect of my life has changed. This change extends beyond simply the impact of a global pandemic, yet that did not help in the least. In the past year and a half, I earned my doctorate and am "PhinishedⓇ." I moved across the great state of Texas and began a new career in the field of single cell genomics as a postdoctoral fellow.

Has your career path changed since we first met you?

Allie: I do not want to say my career path has changed because I am still learning about new opportunities. I am still actively looking at post-doctoral positions, government, and private industry jobs. My main goal for my career is to enjoy my work and support others in their forensic endeavors.

Mirna: My career goal didn't shift from academia but I am also open to industry, particularly research and development. I am working on widening my professional network in the forensic community, and thanks to opportunities like ISHI ambassadorship, I gained more confidence in approaching people and connecting with other scientists in the field. Additionally, I also started to work on my science communication writing skills (still an amateur) so I was delighted to contribute to three blogs that were shared on ISHI News website: How to Choose a Research Thesis Topic, No Nuclear DNA in Rootless Hair: Myth or Fact?, and PhDs: From Distressing to De-Stressing.

Fabiana: The career path didn't change since we met. I'm still in Dr.McCord's lab .

Rachel: Although my career path has altered from its original trajectory, I feel that my career can only benefit from this difference in perspective. Currently, I am navigating the world of single cell genomics and its application to cancer genetics and cardiovascular research. It may be at times an intimidating transition, but it is fascinating. I was fortunate to have been selected as the first postdoctoral fellow to a new team under the mentorship of Dr. Rui Gao at the Houston Methodist Research Institute and its affiliated academic institution, Weill Cornell College of Medicine at Cornell University. Dr. Gao is known for her groundbreaking contributions to the field of single cell genomics. I cannot wait to see what the future holds for our group.

Did being an ISHI Student Ambassador assist you in your career?

Allie: Of course! A career is so closely tied to your ability to network. Being an ISHI Ambassador allowed me to meet and talk to so many people. There is no way I would have been able to meet so many elite people if I had not been selected as an ISHI Ambassador. I wish ISHI would let me be an Ambassador again!

Mirna: Yes, it definitely did. Other than the networking and interviewing skills I gained, being an ISHI Ambassador gave me some "fame". I got featured twice on FIU CASE News (college of Arts, Sciences and Education), one of which is with Fabi <3 [1,2]. I was also selected to be part of the young investigator community at QIAGEN and got featured on their website that was later shared on "QIAGEN Life Sciences" official LinkedIn account [3]. I was one of the few who got recognized by my alma mater university on its 65th anniversary as part of their "Meet our Alumni" series [4]. Last but not least, I got invited twice to give an online workshop on how to apply for scholarships, the does and don'ts, and how to prepare to become a strong candidate for scholarship applications. I was delighted to share my experience and to motivate students back home [5,6].

Fabiana: It will help me for sure, since I'm working with a lawyer to apply for a green card via the National Interest Waiver petition, which is related to scientific merit. Therefore the importance of the work I am doing and any accomplishments I reached will assist.

Rachel: Being an ISHI Ambassador was an unforgettable opportunity as it afforded me the chance to really show what I was capable of as a young investigator. As any PhD student knows, your research becomes such a huge part of your life in those years of hard work. One of the most meaningful takeaways from the ISHI ambassadorship was that it allowed me to showcase my completed doctoral work. In addition, I was honored to be a female scientist interviewed for Ann MacPhetridge's "A Passion for Science: Women in Forensic Science" article. Above all, as an ISHI Ambassador, I gained invaluable connections and friendships. It was an experience that I will never forget and to Promega, I am most thankful.

What's new on the personal side?

Allie: My little boy is turning two in May. So, any parent can appreciate how crazy it was working from home multiple times with no childcare in 2020. He is a smart boy who loves animals and constantly keeps us on our toes. Both of my dogs are still doing well and have loved me working from home.

Rachel: Outside academics, I finally moved in with my husband (as long distance for 8 years was more than enough) and we built our dream house, all just in time to quarantine with the rest of the world.

How have you been navigating the pandemic? What challenges did that present for you and how have you overcome?

Allie: As mentioned above, no childcare at times has been a struggle in our house. As far as my personal work, the pandemic has allowed me to work from home and spend more time with my family. It has been a long learning process and my work 'desk' has changed from the living room couch, to my bed, to hiding in the kitchen floor, to finally setting up the visitor's bedroom as a more permanent office space.

Like so many, we sadly lost two family members this year. One was due to COVID complications. Nothing can replace the family members we lost but we are doing all we can to help our son know these wonderful people that were lost too soon.

My co-workers have made the pandemic a little easier by having Teams/Message groups to stay in contact whether that is work related or just talking about our lives during the pandemic. While there is no good time for a pandemic, I think my lab has been great about supporting each other and checking in with each other regularly.

Mirna: When everything suddenly shut down, the idea of wearing and seeing people with masks was weird and I felt that I was in an "outdoor hospital". But school wise, I had time to reflect on my progress and shift my focus to reading and writing. So, I invested the first chunk of the pandemic in working on grant proposals and research paper writing. The "wet lab" work was slowed down because of COVID, but we started to schedule our time in a way that only 1 or 2 individuals are in the lab at the same time. It is challenging, especially when you are social and you like to have people around you. But all in all, other than feeling lonely at work, we are thankfully still working towards our milestones.

Fabiana: Physically and mentally, the pandemic affected everyone a lot. In my case, I spent 3 months at home working and studying. The challenge was preparing my candidacy exam studying at home with a baby boy of 3 years old. The struggle was real, but thankfully, the help of my husband allowed me to take time to focus and I passed the exam.

What does the future hold for you?

Allie: Writing? Yes, I am positive more writing. That is what academics do, right?

Mirna: I am afraid I don't have an answer because of all the uncertainties around me. Luckily, we now see the light at the end of the tunnel regarding COVID-19 and vaccination. But, on a personal level, I am still reluctant about stability and the future back in Lebanon. Regardless, I still have hopes, and I know that God has the best plan for everyone. So, I've got to be patient and have full faith in my creator who will guide me to what is best for me. I am hoping and working towards a brighter future.

Fabiana: In the near future, I hope to attend the next ISHI Symposium in person, and overall, my greatest expectation is to get a job! I can't wait to start new professional experiences.

Anything else you'd like to include?

Allie: I want to say thank you to Promega. There are so many employees at Promega that have reached out to me over the past two years to see how I was doing. The opportunity to be an ISHI Ambassador was like nothing else I have experienced at a conference. That experience was due to Promega as a company and the wonderful people that developed the ISHI Ambassador position.

Fabiana: I just can't wait to see my family, especially my parents, again. They are all in Italy, and due to this pandemic It's more than a year since I've last seen them.

Advertorial

Capillary Electrophoresis: Overcoming the Hurdles of Current Technologies

Gabriela Saldanha and Ann MacPhetridge, Promega

Share this article

The vast majority of the human genome is identical among diverse individuals. However, there are small regions of variation, especially in areas with repetitive sequences. One example is short tandem repeats (STRs) that can vary in length among individuals, with each repeat consisting of three to five nucleotides of DNA. Analysis of these repeats reveals a characteristic pattern for each individual that is inherited from paternal and maternal DNA. Forensic DNA databases use these patterns of STRs for human identification, and each national database has requirements for specific STR loci that are included.

To characterize these STR patterns, or DNA profiles, human genomic DNA is amplified using the polymerase chain reaction (PCR) with sets of primers for each STR being tested. The primers are labeled with fluorescent dyes, and the amplified products are separated according to size by capillary electrophoresis (CE). Fluorescence imaging by the CE instrument results in a set of peaks for each dye channel, which together constitute an electropherogram that serves as a DNA "profile" for that individual. Statistical analysis of the DNA profile and comparison to reference databases can predict whether the individual matches a known DNA profile, with a high power of discrimination.

CE instruments therefore play a key role in forensics labs, as they help enable scientists to generate DNA profiles. With this information, casework labs can help investigators to confirm or challenge the accounts of those involved in a crime and rule suspects in or out. Casework labs work with extremely challenging samples due to the conditions under which the DNA is collected. These labs require very sensitive, robust STR kits that work in the presence of inhibitors. The DNA evidence they produce often plays a critical role in the conviction or acquittal of those who are put on trial, so the stakes could not be higher.

In the case of database labs, they process a high volume of samples taken from convicted felons, felony arrestees, and misdemeanor arrestees. Paternity laboratories process samples to determine a characteristic pattern inherited from maternal and paternal DNA, which requires speed and cost-effective analysis. All of these laboratories require sensitive, flexible and cost-effective CE instruments, but to date, the choice available to them has been limited.

Drawbacks of existing technologies

The existing CE instruments are costly to purchase and run – and are designed for high throughput environments (with 96 well plate capacity). Subsequently in many forensics labs, particularly smaller ones, scientists currently have to work around the availability of the CE instrument. Oftentimes they have to batch their samples together and wait until other analyses are completed, which causes challenges, particularly with turnaround times and scheduling. Scientists might even be forced to carry out partial plate runs, which has a negative impact on cost due to wastage of array, polymer, reagents etc. Due to the critical and time-pressured nature of their work, this situation is far from ideal.

In the case of Y-STR analysis or mitochondrial DNA sequencing, some labs currently partner with an outside organisation, making the testing protocol lengthier and more complex. Critically, this means the chain of custody of the sample can be more complicated, and it can add complexity in the courtroom too, with more than one lab potentially having to testify, which should be avoided wherever possible.

What is needed is a more flexible instrument that can fit more seamlessly into the workflow of the forensics lab and enable all analysis to be done on site in the lab, when it is needed.

Emerging technologies

More innovative, affordable personal CE instruments are coming into the market, that are specifically designed to overcome some of the challenges forensics labs are facing. They have a smaller footprint, fit into the workflows more seamlessly and allow greater flexibility in sample batch sizes. They provide a lower cost alternative, but with the capabilities of their bigger counterparts, making them an ideal alternative.

The technical capabilities of new CE instruments are also improving, with eight dye color options on the horizon, enabling amplification and detection of more loci from challenging casework samples for better analysis of inhibited and degraded DNA (see Figure 1). Ultimately, this level of analysis provides more information about the sample, allowing scientists to be more confident and make better decisions.

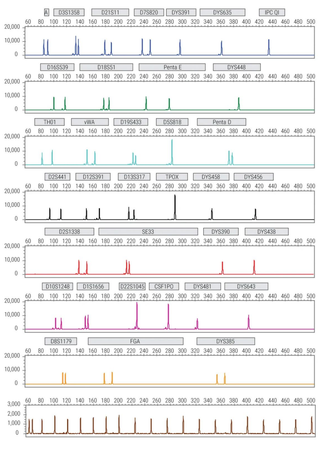


Figure 1: DNA amplification with eight dye colors using a CE System.

With the caseload on forensics labs ever increasing, more convenient and easier to use technologies are going to help to ease the burden and streamline analysis. The growing choice for forensics labs of CE instruments – whether they have a high or low throughput of samples – is going to bring about important efficiencies in the near future.

In the longer term, CE analysis is likely going to remain the "gold standard" for generating STR profiles in the forensics market for years to come. While massively parallel sequencing offers some key advantages, wide adoption by forensic laboratories isn't expected in the near future given the challenges of bioinformatics, a lack of training resources, funding constraints and the cost per sample. In the meantime, CE instruments and their associated STR kits will continue to enable laboratories involved in human identification applications to get meaningful information from precious samples.

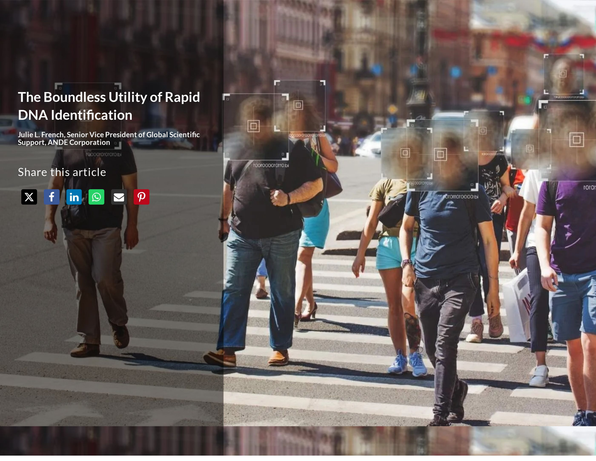
About Promega Corporation

Promega Corporation is a leader in providing innovative solutions and technical support to the life sciences industry. Our product portfolio of over 4,000 products support a range of life science work across areas such as cell biology; DNA, RNA and protein analysis; drug development; human identification and molecular diagnostics. For over 40 years these tools and technologies have grown in their application and are used today by scientists and technicians in labs for academic and government research, forensics, pharmaceuticals, clinical diagnostics and agricultural and environmental testing. Promega is headquartered in Madison, WI, USA with branches in 16 countries and over 50 global distributors. For more information, visit www.promega.com.

The Boundless Utility of Rapid DNA Identification

Julie L. French, Senior Vice President of Global Scientific Support, ANDE Corporation

Share this article



Rapid DNA Identification has been successfully used by agencies around the world for over 10 years. Even so, sometimes it is still referred to as a new technology – why is that? Perhaps the answer lies in the countless different uses for rapid DNA, and each time it is applied in a new way, it seems, well…new. This article will present an overview of the most common applications for rapid DNA and discuss how to implement a rapid DNA program with confidence. Let's start with the application that was first NDIS-approved back in 2016 – ANDE Rapid DNA testing in an accredited forensic laboratory.



Forensic Laboratory Use of Rapid DNA

Databasing laboratories are approved to use rapid DNA to test reference buccal swabs for direct upload into the FBI's National DNA Index System (NDIS). This can be a complementary technology used to increase sample throughput, or a tool that allows work to continue when analysts have limited lab time or have to work from alternate locations – such as when COVID-19 restrictions are in place. Also, CODIS hit confirmations are always time sensitive and typically consist of small batches of samples – a perfect fit for rapid DNA testing.

The practicality of rapid DNA testing in casework laboratories is often undervalued. Most labs have methods optimized to process large batches of samples. This works well because, with DNA being a powerful tool for criminal prosecution, labs continue to be inundated with a large volume of cases. But, what about that small number of samples that need to be quickly tested to eliminate possible suspects in a high-profile, time-sensitive case? Rapid DNA offers significant value because samples can be processed quickly without disrupting the casework batch processing already underway.

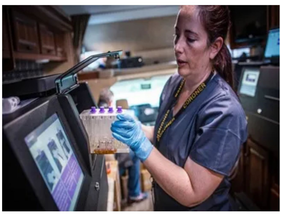
Laboratory applications for rapid DNA have continued to expand with testing of samples from sexual assault cases. As presented at the 2019 ISHI meeting, the Kentucky State Police has been at the forefront of rapid DNA use; testing post coital swabs followed by searching of the resultant profiles against their state data. Accelerating the testing of sexual assault evidence is solving cases faster. Every step taken to help victims of sexual assault and violence is an important one and one worth taking. Today this processing is happening in the lab, but the simplicity of rapid DNA means a transition to medical facilities is within reach.

Booking Stations and Arrestee Enrollments

Next, let's move to the booking station where history was made the first week of February 2021 when the ANDE Series G System became the first rapid DNA system approved by the FBI for use in law enforcement booking stations. During the booking process, arrested individuals are moved through biometric capture stations where fingerprints, mugshots, and other biometric data is recorded. In many states, DNA is one of those biometrics and the DNA samples have historically been collected and mailed to forensic laboratories for processing. Now, those samples can be processed right at the point of collection. The results are automatically sent to NDIS where matches can be made to unsolved cases and results returned to the booking station while the individual is still in custody. This will make our communities safer.

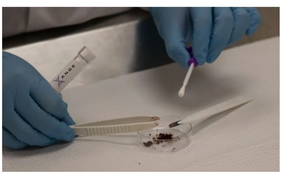
DNA Identification of Decedents

A quick DNA test is useful to Medical Examiners and Coroners in every case; this technology helps bring answers to the families in times of tragedy. Rapid DNA can generate a DNA profile from blood, tissue, or bone to be compared with family members who have donated their buccal swabs. Rapid DNA results can also allow the reassociation of limbs that may have become separated during vehicle accidents or other non-criminal or criminal acts. In the event of disaster events such as fires, hurricanes, or airline crashes, the rapid DNA instrument can be mobilized to the scene for fast processing of samples from unidentified human remains. Since the operation of the system is simple, just-in-time training for operation of the system can be provided right on site. The days of waiting a year or more to generate DNA results from a single bone needs to be a thing of the past.



Investigative Leads for Criminal Cases

With a focus on improving public safety and aiding investigations, the use of rapid DNA testing on evidentiary samples, even without access to a large database, is an incredibly powerful tool. An agency can control their own investigation by deciding to test multiple samples from a scene to determine if they match the victim, the homeowner, or if they are from a possible perpetrator. Obtaining this information in near real time, while the crime scene is still under the control of the agency, can be the key to ultimately solving the case. It may also result in fewer samples submitted to the laboratory, focusing their efforts only on those samples needed for prosecution of the case. Immediate DNA results not only steer the investigation - but suspects frequently plead guilty when presented with the results from rapid DNA testing.



Training and Implementation – A Key to Success

It is critical to have a training and implementation plan, not only to ensure proper sample collection and system operation, but also to provide foundational knowledge and support for the establishment of a successful rapid DNA program. Operating the instrument is incredibly simple and can be demonstrated in less time than it took to read this article. Beyond operational training, it is important that users review all published standards, best practice recommendations and guidelines related to rapid DNA issued by the FBI, SWGDAM, OSAC, and other working groups. Other implementation activities may include evaluating existing sample collection procedures, conducting an internal validation, discussion of peer-reviewed publications, and collaborating with other agencies currently using rapid DNA.

Once the foundation is set, those tasked with writing policies and procedures should keep it simple – writing straightforward, clear procedures and policies about who, when and how rapid DNA and the resulting matches will be used. When drafting policies, topics to consider include case selection, duplicate swab collection, sample naming conventions, and tracking metrics related to the use of rapid DNA. Current users are often happy to share their policies and this can be a great starting point for new programs.

In addition to the use of a proven underlying technology, successful rapid DNA programs consist of trained users, clear policies and procedures, and an active interest in advancing investigations immediately. The utility of rapid DNA is limited only by the artificial constraints imposed on it. In practice, any time a fast biometric comparison would make the world a safer place is a great time to utilize rapid DNA.

DNA Dead End? Protein Sequencing for Forensic Analysis

Curt Hewitt, Signature Science, LLC

Share this article

Introduction

A crime scene. A suspect. A brass shell casing to tie them together. The trace amount of DNA collected is too degraded for DNA profile generation. With that, the suspect walks away, free to strike again. Reaching a dead end like this one in the forensic laboratory is not uncommon and frustrates even the most seasoned analysts and law enforcement officials. In recent years, however, the use of next generation sequencing and genetic genealogy techniques to generate investigational leads have shown us that advancements in forensic science can inject hope into cold cases. In the case of our shell casing, can we find another way in the forensic laboratory to exploit the same and identify the suspect? Protein molecules, abundant and relatively robust against degradation in touch samples offer significant potential. Signature Science's team has been working to develop methods to enable protein sequencing for human identity analysis with funding from the U.S. government's Intelligence Advanced Research Projects Activity (IARPA's) Proteos program. Based on our research to date, protein sequencing has significant potential as a forensic tool.

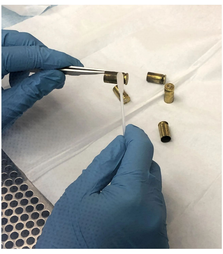
Background

Pioneers of protein sequencing for human forensics, or forensic proteogenomics, showed that polymorphisms in the amino acid sequence of proteins could be used to infer the underlying single nucleotide polymorphisms (SNPs) which gave rise to them during the process of transcription and translation.[1] In essence, these protein variants can be used as a SNP genotyping tool complementary to other forensic SNP genotyping methods like DNA sequencing or microarrays. Early protein sequence characterization focused on rootless hair shafts, a forensic sample type notorious for poor DNA yields. More recently, bone, teeth, fingernails, and even archeological samples containing badly degraded DNA have been studied.



Touch Samples

Signature Science's IARPA-funded work focuses on touch samples which, while occasionally containing sufficient DNA to produce a complete STR profile, more often result in no profile or in a complex mixture of partial profiles. The difference between touch samples and other common forensic samples, such a blood, cannot be overstated, as significant portion of the DNA in touch samples is extracellular.[2] Unlike DNA present in samples like dried blood, which remain encapsulated in lipids and protein, much of the touch DNA we collect has been exposed to harsher environments which include nucleases, UV radiation, and reactive chemical species. A significant number of the cells left behind on a touch sample, conversely, lack DNA. These keratinocytes lose their nuclei as they transit to the skin surface, resulting in a dead, dried cell composed primarily of protein and lipids.



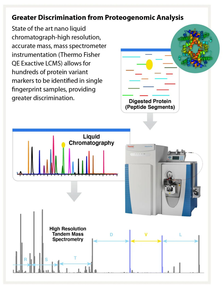
Sample Collection and Extraction

Developing an extraction protocol to enable both DNA and protein analyses presented challenges. Signature Science's team faced two largely incompatible workflows to capture two different biomarkers from the same sample. Forensic DNA extraction methods focus on maximizing DNA yield. To free the DNA from other cellular material, strong surfactants and enzymes are employed to degrade nucleases and structural proteins. Protein sequence analysis is impossible following this step. Conversely, if a laboratory were to prioritize protein analysis, the harsh denaturation conditions would likely degrade any DNA present in the process. A simple approach to enable parallel DNA and protein analysis would be to split the sample in half; however, a 50% decrease in DNA yield from a trace sample can be the difference between success and failure in generating a DNA profile. For this reason, it is not feasible to expect forensic laboratories to sacrifice potential DNA yield based on the chance that a set of protein markers may also be collected.

Signature Science's team worked for more than two years to develop collection and extraction protocols which collect DNA with equivalent quality, quantity, and methodologies currently used in forensic laboratories.[3,4] The result is a workflow that enables protein to be recovered from fractions of the sample previously discarded as waste. Better still, this recovered protein can be stored frozen while traditional DNA analysis takes place. If the resulting DNA profile is sufficient for matching, the protein can be discarded. If insufficient DNA is collected, the lab has the option to thaw and analyze the protein. We routinely produce robust protein marker profiles (more than 60 markers per sample) from as little as 1 microgram of protein collected from a touch sample.

Sample Analysis

As part of the Proteos program, Signature Science has analyzed numerous touch samples prepared both internally and by an independent third party that were deposited across a range of nonporous substrates such as glass and plastic, porous surfaces like laminate or wood, or even some especially challenging forensic sample types like brass shell casings. Our proteomic analysis methods have routinely resulted in the accurate identification of the correct contributor from a panel of 51 potential donors from as little as 140 ng of total protein, a common yield for even trace touch samples. Our methods have also successfully identified individuals within a mixture, a critical capability when considering touch samples.



It is important to note that proteomic analysis has some fundamental differences compared to conventional DNA genotyping. Most of these differences are caused by the process of transcription and translation. For DNA analysis, the absence of a marker can be as informative as its presence. This is because most forensic markers will have two copies in the genome and produce a concordant signal during analysis. Protein markers, on the other hand, will only be present if the gene is expressed in the appropriate tissue (e.g., skin). Even if the gene is expressed, there is no guarantee that both copies of the gene contributed equally to its expression. Further, variation in amino acid sequence between proteins can profoundly impact the detectability of a given protein variant using LC-MS, sometimes precluding the detection of one allele altogether. With these limitations in mind, Signature Science's team has designed and developed statistical tools to calculate forensic match statistics that consider the unique nature of protein markers. We can calculate accurate random match probabilities (RMPs) and likelihood ratios (LRs) that reflect the specific nature of both protein markers and proteomic analysis. While we hope that the future holds a protein marker database analogous to CODIS, for now, these match statistics can be used to establish the likelihood that a protein profile from one sample matches another or that it matches to a specific suspect's genome.

Conclusion

We hope that our research and development efforts, alongside the work of other proteomic researchers, have established a strong foundation toward a future forensic capability. As the Proteos program concludes, we are eager to identify collaborators to further develop this emerging capability. Future efforts will help to inform the limitations of these methods and to identify the cases where protein sequencing could succeed when DNA analysis fails.

References

1. Parker, G. J. et al. Demonstration of Protein-Based Human Identification Using the Hair Shaft Proteome. PLoS ONE 11, e0160653 (2016).
2. Stanciu, C. E., Philpott, M. K., Kwon, Y. J., Bustamante, E. E. & Ehrhardt, C. J. Optical characterization of epidermal cells and their relationship to DNA recovery from touch samples. F1000Research (2015) doi:10.12688/f1000research.7385.1.
3. LeSassier, D. S. et al. Artificial fingerprints for cross-comparison of forensic DNA and protein recovery methods. PLOS ONE 14, e0223170 (2019).
4. Schulte, K. Q. et al. Fractionation of DNA and protein from individual latent fingerprints for forensic analysis. Forensic Science International: Genetics 50, 102405 (2021).

Acknowledgements

This research is based upon work supported in part by the Office of the Director of National Intelligence (ODNI), Intelligence Advanced Research Projects Activity (IARPA), via contract number 2018-18041000003. The views and conclusions contained herein are those of the authors and should not be interpreted as necessarily representing the official policies, either expressed or implied, of ODNI, IARPA, or the U.S. Government. The U.S. Government is authorized to reproduce and distribute reprints for governmental purposes notwithstanding any copyright annotation therein.



Curt Hewitt, Ph.D.

Curt Hewitt, Ph.D. is one of the Principal Investigators leading Signature Science's research and development efforts supporting IARPA's Proteos program. He also leads applied research initiatives for Signature Science's Center for Advanced Genomics. Beyond proteogenomics, Dr. Hewitt is currently focused on projects in synthetic biology, to include microbial engineering and coronavirus research, and human and microbial forensics.
For more information, please contact chewitt@signaturescience.com.

Tracing Roots

How the Transatlantic Slave Trade Impacted the Genetic Makeup of the Americas

Interview Written and Condensed by Ken Doyle, Promega

Share this article



Historical records on transatlantic slavery show that an estimated 12.5 million people were forcibly taken from Africa and sent to the Americas between 1515 and 1865. More than one and a half centuries after slavery was abolished, a study led by Steven Micheletti, a Population Geneticist at 23andMe, examines how the slave trade impacted the genetic landscape of the Americas.

During the course of the study, Micheletti, et al, analyzed genotype array data from over 50,000 research participants representing the major slave trading regions of Atlantic Africa, Europe, and the Americas and compared the results with shipping manifests and other historical documents. This comparison allows those who are descendants of slaves to learn more about their roots, but it also illuminates the extent to which slavery still impacts the gene pool today.

Micheletti, et al, primarily focused on participants who were 23andMe customers whose grandparents were born in one of the geographic regions of trans-Atlantic slavery. Using this database allowed the researchers to ask focused questions of the participants and garner data that academics are typically not privy to.

To learn more about the study, we interviewed Steven Micheletti. Below, he shares the inspiration behind the study, challenges that arose, and surprises that were found when comparing historical records to the genetic information gathered.

What factors inspired the origin of this project, and how did you personally become involved?

Our mission is to help people access, understand, and benefit from the human genome. The foundations of this study began almost 13 years ago by Joanna Mountain, senior author on the paper, out of a recognized need to further understand the ancestral history of African Americans. Personally, my interest in population genetics, historical migrations, and the potential of helping people better understand their ancestral origins drew me to this project. Over the years, we eventually acquired enough study participants to have sufficient genetic representation of people from countries across the Atlantic and could make inferences about the genetic landscape that resulted from the transatlantic slave trade.

What were the main challenges with integrating the data from the 23andMe genetic database with the other databases used in the study?

The historical records we used, such as the Slave Voyages, describe events that impacted millions of people up to 500 years ago. Therefore, we carefully included study participants from the Americas that are possible descendants of the people that the historical records describe. This specifically meant selecting a subset of our millions of study participants who had ancestry originating from Atlantic Africa as well as deep historical ties to geographic regions involved in the transatlantic slave trade. In Africa, we included study participants self-identifying from ethnolinguistic groups that were directly impacted by the transatlantic slave trade, as described by historians. After selecting our study participants, it was a matter of determining the genetic connections between people of the Americas and Africa and comparing those results with records describing regional slavery practices. Perhaps not surprising, historical literature describing the atrocities of slavery and inhumane treatment of enslaved people best described resulting genetic patterns in people of African descent today.

Does next-generation sequencing (NGS) offer any advantages, compared to the SNP arrays used in this study?

Higher density genetic data produced by NGS offers the potential advantage of identifying more distant genetic connections by identifying smaller shared genetic segments that were passed down by common ancestors. This would be useful for more distant historical events; however, for the purpose of identifying population structure and genetic connections originating from, at most, 500 years ago, our arrays containing 500,000 - 1.2 million genetic variants suffice.

Given the size of the Slave Voyages database, how did your team approach the problem of finding the relevant data?

With a collection of over 35,000 historical shipping manifests, we had to curate data from Slave Voyages so that they could be directly mapped and aggregated by contemporary geographic locations. This meant determining which country and state each historical port in Africa and the Americas is located in today and determining the number of Africans that were forced between each embarkment and disembarkment port. Similarly, we used geographic locations of study participants' grandparents to determine the likely ports where their enslaved ancestors disembarked. Once we mapped all of the ports, we aggregated additional variables of interest, such as the proportion of men, women, and children on each voyage. Together, this painted a picture of how many enslaved people were being transported between regions of Africa and the Americas and what composition were women and children.

Additionally, we collaborated with historians and African American studies scholars to put genetic results into historical context.

How did the study's results compare with the historical records? Were there any unexpected results?

In general, ancestral connections between slave trading regions of Africa and the Americas mirror the proportion of individuals forcibly moved between those regions. People of African descent in the Americas share the most recent common ancestors with people of West Central Africa. This is consistent with records indicating West Central Africa experienced the largest proportion of deportations in the mid-1800s.

However, there were some key differences:

- We observed an over-representation of Nigerian ancestry in many parts of the Americas compared to what shipping records show. This most likely reflects the often under-discussed active trade that moved slaves within the Americas, even after the slave trade had been banned by several European nations.
- Senegambia appears to be underrepresented given the overall proportion of enslaved people who were deported from this region into the Americas. This may be because Senegambians were transported to rice plantations in the United States which were often rampant with malaria, resulting in an extremely high death rate.
- Latin American individuals had strikingly lower African ancestry proportions compared to those from the United States and British Caribbean. The proportion of people with greater than 5% African ancestry was five times lower in Latin America, despite Latin, Central, and South America receiving roughly 70% of all disembarked African slaves.
- This could be due to higher mortality and smaller effective population sizes in enslaved people brought to Latin America. Another factor to consider is that many Latin American countries promoted the dilution of African heritage through intermarriage between fair-skinned Europeans and women of African descent.
- Confirming other studies, we saw a bias towards African female contributions to the gene pools of the Americas due to generations of rape and exploitation. This is particularly evident in Latin America where we estimated about 15 African women reproduced for each African man in Central America and estimated similar values for South America and the Latin Caribbean. The evidence that African females contributed to the gene pools of the Americas to a much greater extent than did African males is surprising given that the majority of enslaved individuals were male.

Read the full article in the August 2020 issue of the American Journal of Human Genetics.

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

Share this article

On January 20, 2021 the Organization of Scientific Area Committees (OSAC) for Forensic Science, the American Academy of Forensic Sciences (AAFS) Academy Standards Board (ASB) and Promega held the fourth webinar in a series aimed at providing information on new standards and best practice recommendations for forensic biology and DNA testing laboratories. Part four of this series highlighted ANSI/ASB Standard 018, Standard for Validation of Probabilistic Genotyping Systems, First Edition, 2020 and described how this document was developed, it's key requirements, and implementation strategies. This standard was initially drafted by OSAC's Human Forensic Biology Subcommittee (formerly the Biological Data Interpretation & Reporting Subcommittee) and was published by ASB this summer.

If you missed any of the webinars in this series, or would like to watch them again, you can view them on-demand on the Promega website.

- Part 1: Development and Publication of New Standards and Best Practices – The Process
- Part 2: Mixture Interpretation Validation, and Protocol Development and Verification
- Part 3: Training Standards Overview
- Part 4: ANSI/ASB Standard 018, Standard for Validation of Probabilistic Genotyping Systems, First Edition, 2020

Be sure to check out the OSAC Standards Bulletin for a monthly update on the DNA standards moving through the development and OSAC Registry processes!

- 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.



ISHI 32 Workshops

Share this article

Pre and post-conference workshops have been announced for the 32nd International Symposium on Human Identification. Topics covered include probabilistic genotyping, forensic genetic genealogy, leadership, cold cases, and more.

Registration is limited, so claim your spot early!

Shortened descriptions, dates, and costs are included below. For more information on any of the workshops, including speakers, visit our website.

Sunday, September 12

9:00 - 12:00

AABB Meeting

This workshop will address AABB accreditation related topics, including the accreditation process, Relationship Testing Standards, proficiency testing, validations, and calculations.

Cost

There is no charge for this workshop, but pre-registration is requested.

1:00 - 4:00

Practical Application of the Likelihood Ratio

This workshop will give the audience an introduction to the assignment of the likelihood ratios (LR) for single source and mixed DNA profiles. Attendees will become familiar with the mathematical models and calculations for LRs from probabilistic genotyping software. Advanced examples including LRs for small pedigrees will be explored. We will cover how to report LRs with emphasis on avoiding fallacies (including the transposed conditional or prosecutor's fallacy). Worked examples will help the attendees understand the theoretical concepts. Attendees should have a solid understanding of algebra and bring a calculator to the workshop. Handouts will be provided.

Cost

$100

Monday, September 13

8:30 - 5:00

You Deserve a Cookie! Navigating The Challenging World of Leadership in Forensic Biology

Managers in forensic science are often ill-prepared for the demands of their job, as most originated from positions as autonomous analysts. Managing in a forensic DNA laboratory has its own unique complications. This interactive workshop is designed for individuals in these leader positions, offering them management and leadership tools that they can implement in their operations. The workshop will also offer attendees an opportunity to bring their own challenges and questions to their peer group for advice or solution. Instructional material includes: DiSC assessment, PowerPoints, resource lists, post-it-notes, and cookies.

Cost

Early Registration - $250

Standard Registration - $275

8:30 - 5:00

Unusual Collaboration and Techniques to Solve a Cold Case Homicide

Presentation of the challenges and obstacles faced in solving a 47 year old cold case kidnapping, sexual assault and homicide of an eleven year old girl. Unusual collaboration between numerous law enforcement agencies, medical examiner offices, forensic anthropologist, public and private forensic/DNA laboratories, unique investigative techniques and Genetic Genealogy were used to solve this case. Several generations of DNA technologies, CODIS, familial searching, genetic genealogy and human remains exhumation were utilized over sixteen years. Participants will benefit from lessons learned, new forensic approaches to solve cold cases as well as the requirements for successful prosecution of these cases.

Cost

Early Registration - $250

Standard Registration - $275

9:00 - 5:00

Grupo Cientifico Latino-Americano de Trabajo Sobre Identificacion Humana

This workshop will be held entirely in Spanish. Description and details on how to submit abstracts for consideration to follow.

Cost

Standard Registration - $100

Thursday, September 16

1:00 - 4:00

Lawyer Proof Your Lab

The last decade has brought about significant changes in forensic DNA analysis that are being challenged in courts across the country. As forensic technologies have become more sensitive, the threat of contamination has increased, and mixture interpretation has become more complex. To deal with this complexity, labs have implemented new statistical software that use probabilistic modelling. This has led to great changes in the language of expert opinions. There have also been significant changes in standards and best practices, including the FBI-QAS and the SWGDAM guidelines. In this workshop, independent forensic DNA experts will discuss some of the problems they see when reviewing work from laboratories around the country, and will offer methods to reduce common errors that result in courtroom challenges.

Cost

Early Registration - $190

Standard Registration - $210

1:00 - 4:00

Technological Considerations for Responsibly Implementing a Forensic Genetic Genealogy Workflow with NGS

Forensic genetic genealogy (FGG) is a powerful tool for investigative lead generation for the identification of unknown remains, solving cold cases, and innocence projects. The FGG workflow combines a DNA profile generated using microarrays, whole genome sequencing (WGS) and/or targeted SNP sequencing methodologies with a database like GEDmatch PRO to identify genetic relatives and finally performing confirmatory testing with traditional STR assays. These data generation methods face inherent challenges typing SNPs across forensic samples such as skeletal remains (bones and teeth), sexual assault evidence and other body fluids which are frequently degraded, inhibited, and low input. The choice of data generation technologies, in turn, have implications for kinship outcomes.

Cost

Early Registration - $190

Standard Registration - $210

1:00 - 4:00

Technical Leaders Meeting

Description to be announced.

Cost

Early Registration - $190

Standard Registration - $210



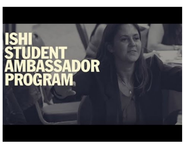
Are you a student pursuing a degree in forensic science?

Are you passionate about sharing your research with future generations?

Can you "hashtag this" quicker than you can pipette?

Would you like to win free registration for ISHI 32 at Disney's Coronado Springs Resort in Orlando, FL?

If so, we invite you to apply to become an ISHI Student Ambassador.



CONNECTION

As a student, you know that it's important to network with those in the field who can further your research or assist you in obtaining a job after you graduate. But networking can be intimidating! As an ISHI Student Ambassador, you'll make connections before you even arrive in Orlando. We will introduce you and your research on our website and social channels, introducing you to other attendees and jumpstarting the networking process.

Is there an expert in the field that you'd love to meet? Let us introduce you!

You'll also have access to all networking functions, including the Welcome Event and Wednesday Night Event.

Allison Sherier
University of North Texas Health Science Center

"This is a great conference to attend to find Ph.D. and post-doctoral positions. The number of people from private, public, and research labs is fantastic for networking. If I had to pick only one meeting to attend each year, ISHI would definitely be my choice. There is just so much information and the people are so friendly to new people in the industry."



OPPORTUNITY

As an ISHI Student Ambassador, you'll attend the largest conference focused entirely on DNA forensics. Learn about the latest techniques and technologies over two and a half days in the general sessions. You'll also be granted complimentary registration to the pre and post-conference workshops, which will provide you with information that you can take back to the lab with you.

Is the stress of looking for a job after you graduate wearing on you? Each year, ISHI hosts a large number of vendors in our exhibit hall. You'll have access to the exhibition area to chat with potential employers and being an ambassador will look great on your resume!

Mirna Ghemrawi
Florida International University

"I highly recommend this conference to other students because I have no doubt that it will be beyond what is expected. Throughout the whole conference, I was on the edge of my seat listening to real casework's.

I was honored to meet experts from the federal, local and international crime labs as well as researchers from other institutions. As students and new scientists in the field, it is very important to explore and build connections. Who knows? Maybe you meet your future boss."



INSPIRATION

You're never too young to make a difference! As an ISHI Student Ambassador, you'll have a chance to share your passion for forensic DNA with your peers and future generations. Present your scientific poster to an in-person audience, including mentors you'll be able to take selfies with later.

We'll also record a video interview of your poster presentation to be shared on our social channels later, leading to further connections.

Rachel Kieser
University of North Texas Health Science Center
(formerly)

"If you are able to attend ISHI....GO! ISHI is the top conference to attend as a student or young investigator seeking a profession within the forensic genetics community as well as finding lifetime friends and collaborators.

Additionally, the position of ISHI Ambassador offers students funding to attend the conference where they can experience networking and exposure to research."



THE NEXT STEPS

Interested in applying? Here's what you need to do.

Draft a written essay answering the following questions using between 500 to 750 words total.

- Forensic science can be a demanding career. The work may be exacting and tedious without a bit of recognition or a job well done. How did you decide that forensic science was the career for you? What aspirations do you have for your career after graduation and what is your scientific area of focus?
- If you are selected to attend this year's ISHI in Orlando, what do you hope to gain from your participation? What impact might participation in ISHI have on your personal and career growth?
- If you are awarded free conference registration, you will be asked to present a scientific poster. Briefly describe what your scientific poster will be about.

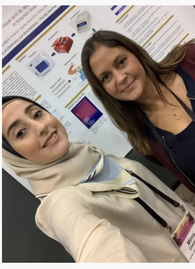
Prepare a video recording between 30 seconds and 2 minutes long.

The video should explain why you would like to participate in this year's ISHI in Orlando, FL. It can elaborate on any aspects of the conference that especially appeal to you (i.e., meeting a certain speaker, attending a specific workshop, participation in networking events, etc.). Don't be afraid to let your personality show through. The committee is looking for candidates who can communicate their excitement for forensic science to fellow students.

Four winners will be selected by a group of reviewers from the ISHI Committee. Selected students will receive waived registration for ISHI 32 and any additional workshops held at ISHI (~Travel and hotel accommodations are the responsibility of the student.)

Fabiana Tagila
Florida International University

"First, prepare to be surprised and to meet great researchers from all around the world. My only advice is that for everyone working in forensic DNA, ISHI must be the meeting to attend. If you have any doubt, go, and you will realize once the conference starts."



The students awarded free registration will be asked to provide the ISHI committee with the following materials to be shared on social media by ISHI show management:

- A headshot or photo of the student.
- A day in the life series to be shared on our Instagram stories.
- A 500-word blog post before the ISHI symposium about what the student's plans are for the meeting in Orlando.
- Photos to be shared on the student's social media channels of you preparing for the conference.
- A scientific poster presentation at ISHI (abstract due July 12, 2021).
- Social media posts each day of the ISHI conference.
- Onsite interviews at the symposium with the ISHI media team including (but not limited to) sharing of the student's scientific poster, and what they hope to learn/have learned while in attendance.
- A handful of photos taken at the event.
- A 500-word blog post after ISHI about what the student learned at the meeting.

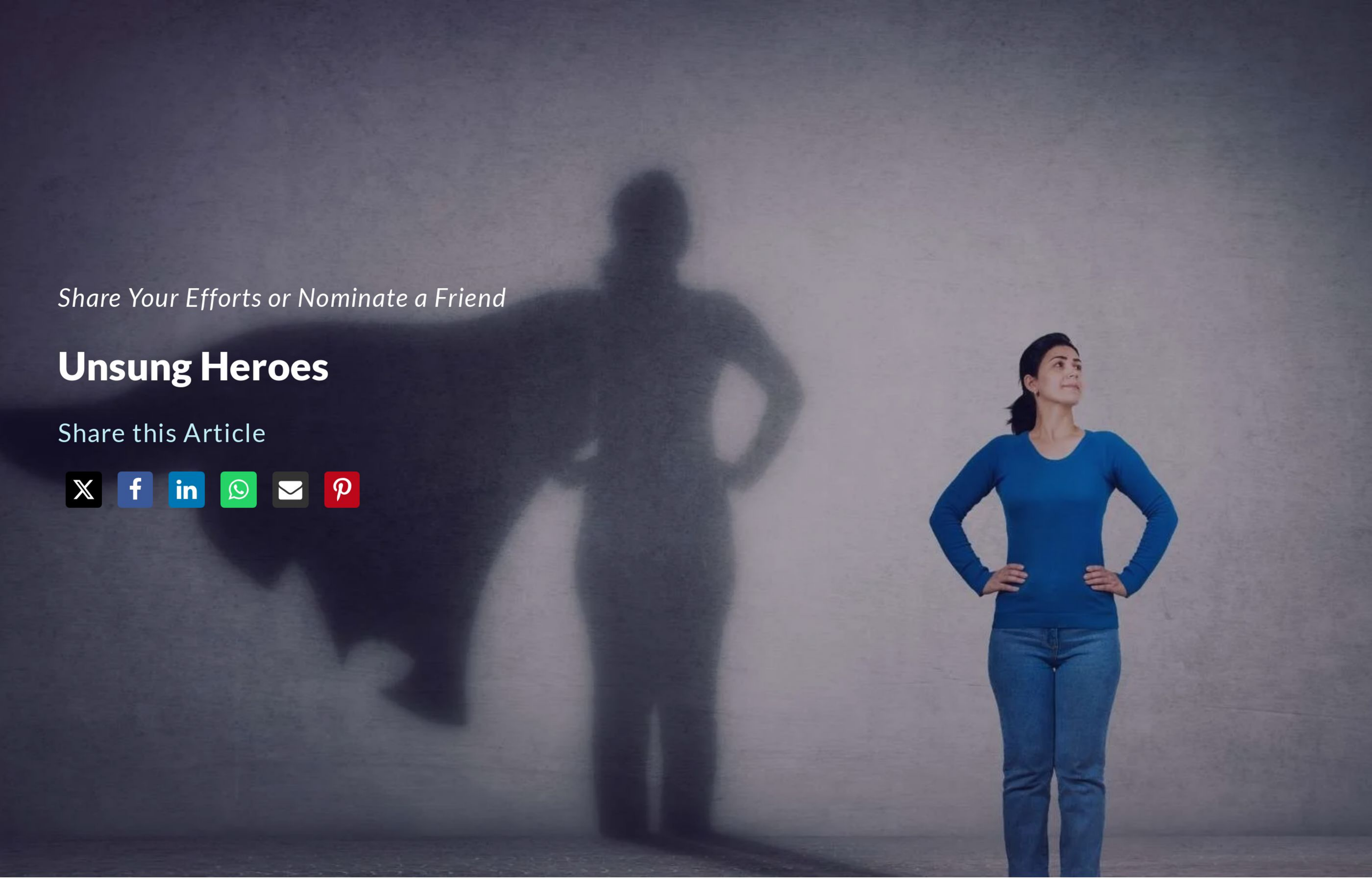


ELIGIBILITY REQUIREMENTS & CONTEST RULES

- This contest is open to students currently enrolled in a forensic science (or a similarly named program) at the undergraduate or graduate levels.
- Applicant must have a public Facebook and Instagram page to allow for sharing of content.
- All videos and essays must be submitted by the submission deadline of April 11, 2021.
- All submissions must be original and not previously published elsewhere.
- By submitting an entry and video clip to the contest, each entrant gives ISHI all rights, including copyright, to the entry and express permission to edit and publish the entry in all media listed above without limitation and without any other notice.

ALL APPLICATIONS MUST BE RECEIVED BY APRIL 11, 2021

Learn More and Apply



Share Your Efforts or Nominate a Friend

Unsung Heroes

Share this Article

What does a hero look like to you? They are unlikely to be wearing a cape, but may be wearing a uniform, or camouflaged in plain clothes. During the COVID pandemic many of our friends and co-workers have become de facto heroes by helping others in ways both great and small.

During the pandemic many of our neighbors have suffered profound losses, from the death of someone dear to financial hardships or the stress of job loss. How have you/your colleagues/organization helped to make live better for the community? Perhaps you have delivered groceries to the elderly or organized a food pantry, whatever it is, we would like to hear. Tell us about your efforts or nominate a friend or colleague. Your work might inspire others and will serve to spread some good news in the dark time.

Tell us how you or your friends have helped lighten the load and we'll share your good works with the forensic community. As a token of appreciation we'll gift you a nifty t-shirt so you can share your message of hope with others.

Submit an Unsung Hero







Calendar of Events

Deadlines

March 2021

ISHI Registration Opens

June 14, 2021

Oral Abstracts Due

June 14, 2021

Interesting Case Abstracts Due

July 12, 2021

Poster Abstracts due

July 12, 2021

Early Registration Deadline

Sign up to receive future issues

First name

Last name

Email

Company

Country

I consent to adding my name to the ISHI mailing list

Submit

Do you like what you see in ISHI Magazine?

Your customers do too. Consider advertising in an upcoming issue and reach a targeted forensic audience of more than 5,000 people (US and international combined)

Contact Tara Luther to inquire about rates and specifications. Space is strictly limited.

tara.luther@promega.com