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ISHI INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION

STARTING SEPTEMBER 13, 2021

May 2021

The ISHI Report

News from the World of DNA Forensics

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The ISHI Report

Letter from the Editor

Greetings from Madison, Wisconsin. We hope this edition of the ISHI Report finds you enjoying all that Spring has to offer including warmer weather and a slow return to normalcy as pandemic restrictions begin to lift.

Registration is open for ISHI 32 with options to attend either in person at the Coronado Springs Resort in Orlando, Florida or virtually. Attendance at the in-person meeting will be capped at 550 registrants to maintain social distancing requirements. 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.

Abstracts for oral or interesting case presentations at ISHI are due June 14. All abstracts will be reviewed by an outside panel of experts and selected based on perceived interest to the forensic community. Poster abstracts are due July 12. Abstracts not selected for oral presentation will be considered for poster presentation.

In this issue we check in on a pair of young people just embarking on careers in forensic science. Olivia McCarter and Eric Schubert are both contributing to efforts to identify unidentified remains using genetic genealogy databases. Despite their youth, both have helped solve previously intractable cases. Olivia will be attending this year's ISHI as a member of the student ambassadors. Speaking of this year's ambassadors, you can get to know all of them on page 9.

Our colleague Ken Doyle shares insights gained during interviews with two policy experts working on the problem of missing persons. Dr. Sara Katsanis and Dr. Jodie Ward are both working on the issue from different sides of the globe. Although the landscape is vastly different in the United States and Australia, the need to address this crisis knows no borders.

John Collins, one of the instructors at the ISHI workshop, *You Deserve a Cookie! Navigating the Challenging World of Leadership in Forensic Biology* pens an article advocating that leaders in forensic settings fully embrace their role. Participate in the workshop to learn from experts how to get the best from your staff and provide them with the support they need.

We are very excited to bring you the first episode of our video series ***The Missing Piece***, created in collaboration with Othram. This episode features Carla Walker, a 17 year-old abducted from a Fort Worth, Texas parking lot and murdered after a Valentine's Day dance in 1974. Her killer remained unidentified for nearly half a century before advanced DNA analysis and exceptional investigative work finally named him.

Michael Coble and Jessica Charak Lehrner tell us how life has changed (or not) due to the pandemic. Like many of us they have had to adjust to a new normal as they pivoted to remote work and the challenge of maintaining connections with colleagues via ZOOM.

Dr. Angie Ambers, Assistant Director of the *Henry C. Lee Institute of Forensic Science* and Mike Ware, Executive Director of the *Innocence Project of Texas* share the case of Lydell Grant, who was wrongfully convicted of a murder in Houston, Texas. The use of probabilistic genotyping helped to prove his innocence, though he is still waiting to be formally exonerated.

Finally, Lutz Roewer and Sascha Willuweit of the Institute of Legal Medicine and Forensic Sciences in Berlin, Germany explore the best ways to intrepret Y-STR evidence. If you'd like a copy of the YHRD Instruction Manual, please fill out the form on page 12.

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

Stay well,

The Editorial Board

Contact ISHI

Embracing the Challenges of Leadership in Forensic Biology

John M. Collins, Executive Leadership Coach

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Like you, I'm excited about ISHI 2021 while still sad about the impact that COVID-19 had on ISHI 2020 and so many other forensic science conferences. These conferences are critically important to the continued development of forensic science professionals and the nurturing of the community cohesiveness that marks most respected occupations - including forensic science.

The boards of directors and executive leaders responsible for the planning and hosting of our many forensic professional conferences over the last year were likely confronted with some of the most challenging and exhausting leadership decisions they've ever experienced. I, for one, am grateful for their service and am reminded, as we all should be, that leadership often comes with challenges that are both complex and unpredictable.

This is one of the many principles that my colleagues and I will be presenting in our one-day leadership workshop titled, ***You Deserve a Cookie: Navigating the Challenging World of Leadership in Forensic Biology***. As your facilitators, our goal is to elevate the awareness of our participants about the unique challenges of leading a forensic biology unit, while also presenting strategies and solutions for being more effective in a supervisory role.



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.

Learn more and register on our website: www.ishinews.com!

Having practiced as a leadership instructor and executive coach for almost 8 years now, I've had the opportunity to coach laboratory directors, system directors, quality assurance managers, and unit supervisors in forensic science. But I can say without hesitation that the forensic biology supervisors and DNA technical leaders I've coached have taught me that the leadership challenges in forensic biology have elements of uniqueness and complexity that make them worthy of great respect.

One might argue, correctly so, that every forensic discipline is unique in its own way because the technologies, methods, and expertise are all unique. But there's something about life in a forensic biology unit that sets it apart from not only the other forensic science disciplines, but also from other fields of professional endeavor both inside and outside of forensic science.

You might be surprised to hear that among the most challenging of leadership issues in forensic biology actually has nothing to do with science, work volumes, method validations, or difficulties with personnel. Instead, what I find to be a challenge of remarkable complexity and nuance is the hesitation of supervisors and technical leaders in forensic biology to fully commit to their leadership roles. This is easier said than done, of course. There is something almost addictive about the power that our scientific experience and expertise afford us. We worked hard for it. We were really good at what we did. We enjoyed making good use of it. And, not surprisingly, it became part of our individual sense of self-worth and identity. So to just give it all up for the enormous and seemingly thankless burdens of leadership is a big risk to take.



This hesitation, however, is costly because it impairs the leader's ability to fully commit to the responsibilities of leadership with which he or she has been entrusted. And because he or she is keeping one foot in the casework sandbox while attempting to manage the affairs of the unit, the supervisory responsibilities aren't met with the degree of commitment and energy needed to do it right. This adversely impacts the unit and its employees, and it makes leadership a much more frustrating experience than it should be. And, like a vicious feedback loop, this frustration causes the forensic biology leader to become even less committed to the leadership role.

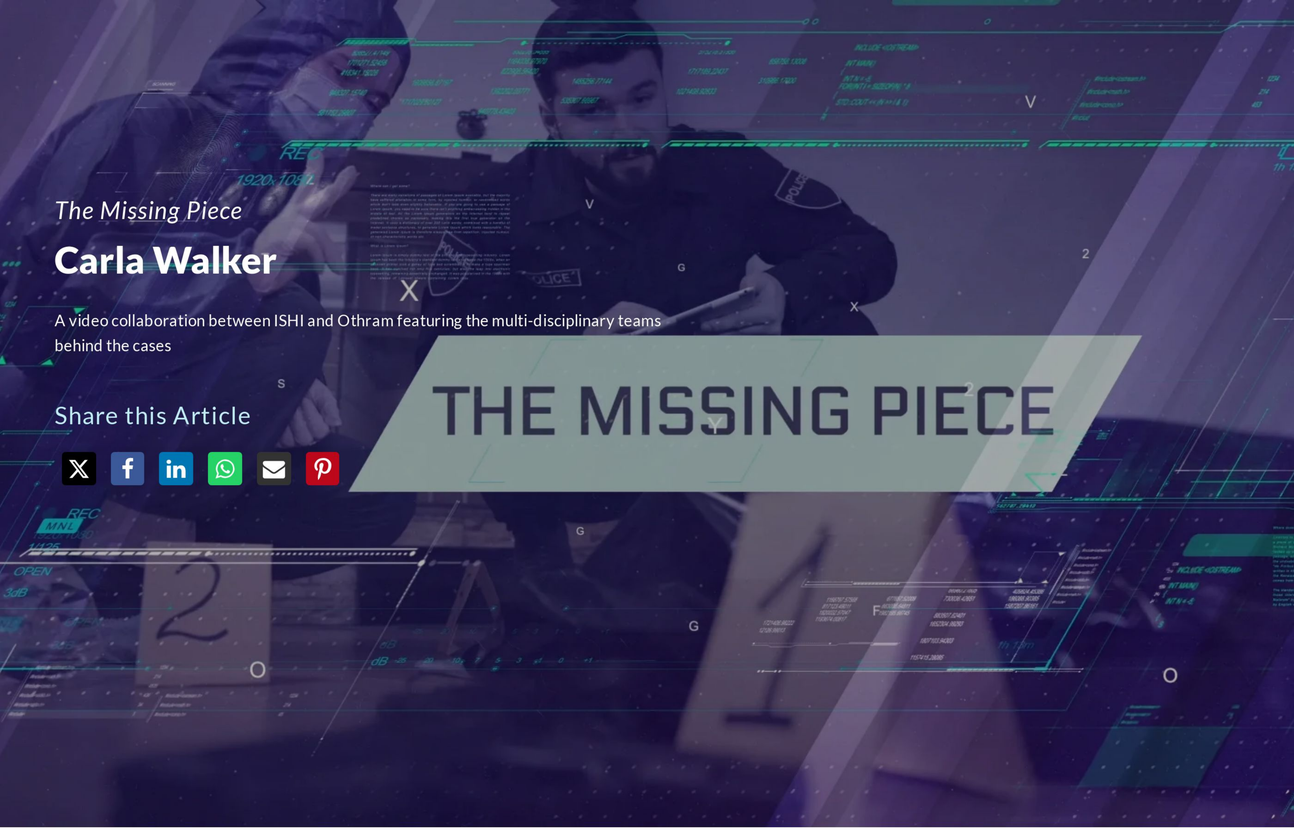
The issues and challenges that we'll explore in ***You Deserve a Cookie*** are not easy to manage on a daily basis. In fact, they can be quite exhausting at times. But leadership is an expertise of its own sort, one that comes with even more influence and power than what the forensic biology leader ever had as a casework scientist. Even though you might still feel a strong pull to work cases to the extent that it impedes your ability to fully commit to your leadership responsibilities, give yourself permission to fully embrace your leadership role. Trust me, it's worth it. If working cases is not necessary for you and your laboratory, stop doing it. Instead, enjoy the rewards and satisfaction that come from completing cases through your people. That is, after all, what leadership is all about.

The burdens and challenges of forensic biology leadership don't come with many tangible perks and incentives. The work is difficult, often frustrating, and the pressures are high. But my colleagues and I are going to teach you how to make it less difficult, less frustrating, and less pressure-packed. More important, we're going to teach you how to engage more effectively with your entire team.

If you are a forensic biology leader, you do, in fact, deserve a cookie. You actually deserve a whole lot more, but the knowledge and perspective we're going to give you in our workshop will be worth much more than that. The cookie we're going to be sharing with you has a very sweet and enticing flavor that I like to call *confidence*.



John M. Collins is an executive leadership coach specializing in working with professionals in positions of public trust. Now based in Southfield, Michigan, John enjoyed a stellar 20-year career working in state, local, and federal forensic science laboratories, including his role as the director of forensic science for the state of Michigan. He is the author of 3 books on leadership, policy, and professionalism in forensic science. For more information about John and his practice, please visit https://criticalvictories.com/



The Missing Piece

Carla Walker

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.

Full of life and with a bright future ahead, Carla Walker was just 17 when she was abducted from a Fort Worth parking lot and murdered in February of 1974. Carla and her boyfriend stopped by a local bowling alley to use the restrooms after attending a Valentine's Day dance. The perpetrator jerked open the passenger side door and dragged Carla out of the car, threatening her boyfriend with a gun and beating him unconscious. Carla's body was found in a culvert three days later; she had been raped, beaten, and strangled.

This brutal crime remained unsolved for nearly a half-century, with all available leads exhausted, including conventional forensic DNA testing. In April 2020, Carla's story was featured on Oxygen's "The DNA of Murder with Paul Holes." Shortly after the Carla Walker episode aired, Holes connected Fort Worth PD Detectives Leah Wagner and Jeff Bennett with Othram to discuss the case. Within weeks, Othram's advanced DNA analysis paired with exceptional investigative work from the detectives led to the identification of a suspect.



UPDATE: On May 6, 2021, the Tarrant County District Attorney's Office announced they aim to seek a life sentence for Carla Walker's killer and not the death penalty - a decision supported by Carla's family. The pretrial date for Glen McCurley has been set for June 16.

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Work Interrupted

How the COVID-19 Pandemic Impacted Life in the Lab

Interview Written and Condensed by Carol Bingham, Promega

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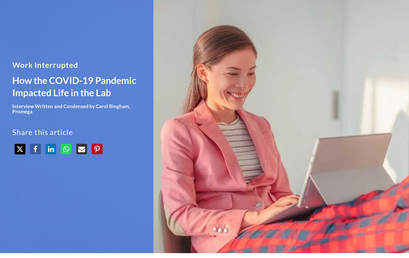

We caught up with workshop chairs Michael Coble and Jessica Charak Lehrner to gain their perspective on weathering the pandemic. Read on to see how both made it through the last year eager to take on 2021.

What is your current job title? How long have you worked there and in the field of forensic DNA?

Michael Coble:

I am an Associate Director of the Center for Human Identification (CHI) at the University of North Texas Health Science Center. I am also an Associate Professor in the Graduate School of Biological Sciences Department of Microbiology, Immunology and Genetics. I have been at the University for over 3 years now.

Jessica Charak Lehrner:

I have been the DNA Technical Leader of the Las Vegas Metropolitan Police Department's Biology/DNA Detail for the past 7.5 years. Prior to moving to Vegas, I worked as a Senior DNA Analyst for the Prince George's County Police Department in Maryland for 7 years and as a DNA Analyst with the Armed Forces DNA Identification Laboratory (AFDIL) for another 4.

How did your daily work change as a result of COVID-19?

Michael Coble:

Fortunately, for me, my daily work routine did not change drastically. I am no longer working in the laboratory every day, so being able to connect remotely through my desktop computer each day was easy. All of the in-person training and teaching I do for the CHI had to be moved to an online format. Our analysts working in the laboratory had to adjust schedules and monitor their distance when working in close proximity.

Jessica Charak Lehrner:

Working for the police department, we are considered essential personnel and therefore were required to continue to report to the office each day. For safety, all in-person meetings and trainings were canceled, and we shift adjusted our large group in an attempt to spread out our work schedules as much as possible, including allowing for work on Saturdays and Sundays. We had several internal validation projects which were slated to begin shortly after Nevada declared a state of emergency in March. These projects were postponed several times over several months as it became more apparent that the pandemic would not soon be coming to an end.



What challenges (if any) did you encounter feeling part of your team at work?

Michael Coble:

I think the most challenging aspect of the pandemic was the loss of the in-person social interactions with coworkers and colleagues. Video feeds on "Zoom" or "Teams" only go so far. My friend and coworker Dawn Boswell had just moved into her new office next door to me in January before we started working remotely in March last year. I think everyone at the CHI is looking forward to returning to normal at some point in the near future.

Jessica Charak Lehrner:

All of our in-person team meetings were canceled and we converted to the use of a virtual agenda. I am one that likes to communicate and I really enjoy the social aspects of working together as a team. I found it challenging to keep people updated when relying mainly on email, and to continue to collaborate and receive input/feedback from the group.

What was the most challenging work-related hurdle that you encountered as a result of the pandemic?

Jessica Charak Lehrner:

In January 2020, we pre-planned and locked in dates for our required external casework and databasing QAS audits to occur in the spring, well ahead of the July 1st revision of the standards going into effect. However, due to all business-related travel being suspended by both agencies, the logistics of having an onsite external audit were not on our side. Ultimately, we were able to receive permission for a virtual audit to take place, albeit after July 1st. We shuffled our priorities and pushed to modify and implement our policies to ensure complete compliance with the new audit documents prior to the virtual audit occurring. In the end, I am pleased to say that we did not have any findings on either audit document. It was a reminder that sometimes we are forced to abandon and pivot from ever-our best laid plans.

Were there benefits to working remotely?

Michael Coble:

Teaching in an online format can be much more challenging in some respects than teaching in person. Although the online audience may (not always) have their cameras turned on, it can be difficult to gauge their facial expressions while trying to teach. I find that I am always thinking of how to improve my presentations and adding new content, so that will help in the future.

What have been the most challenging aspects of juggling family and work duties?

Michael Coble:

Finding that work-life balance was a challenge since it was easy to spend more time at the computer when there was no longer a need to commute to the office daily or spend time in an airport/airplane fly to a meeting. Setting boundaries was important at the beginning as it was easy to start feeling burnout after the first few weeks adjusting to the new schedule.

Jessica Charak Lehrner:

While I continued to go into the office each day somewhat business as usual, my husband was relegated to working from home with our two pups. He works in an environment that is typically filled with social events and networking and he thrives off of public interactions and personal relationships. When I came home each night, he was more than ready to finally spend time talking to someone in person, whereas I still needed a little of my usual decompression time that I previously had while he was out being a people-person. There was a learning curve while we adjusted to our new normal, but in the end, we were able to compromise to ensure that both of our needs were being met.



What are you most looking forward to in a post-pandemic world?

Michael Coble:

Seeing friends again. That is the only thing on my top ten list for now.

Jessica Charak Lehrner:

My family does not live in Las Vegas and I have not been able to see them in person since November 2019. This feels like an eternity and is the longest I have ever gone without spending time with them. I cannot wait until we are all comfortable to travel so I can finally hug my parents, sister and brother-in-law, and niece and nephew.

Have there been any silver linings that you didn't foresee?

Michael Coble:

I am very fortunate to have a loving and supportive family, and recently became a grandfather to my grandson Steven. It has been great being able to spend some extra time with him and watch him grow.

Jessica Charak Lehrner:

The cancellation of all in-person meetings and postponement of validations led me to have more time available to spend with two recently promoted Forensic Scientists who were learning DNA analysis, binary interpretation, and STRmix for the very first time. I felt that the pandemic allowed me to focus more personal one-on-one time training in the inner-workings and foundations of STRmix, in a manner that was more well organized and meaningful than if I had been juggling the trainings with regular hectic schedules. I also saw the bottom of my Outlook inbox for the first time in 7.5 years.

Jessica, you will be chairing the Tech Leader Meeting at ISHI 32. Can you tell us what subjects will be covered?

Jessica Charak Lehrner:

As the DNA community continues to move towards probabilistic genotyping, I thought it would be helpful to discuss how to train new analysts in both binary and prob gen interpretations. There will also be material regarding experiences preparing for the different legal challenges surrounding the use of probabilistic genotyping. An important note: the agenda has not yet been finalized as it is pending travel approval from speaker agencies.

Michael, you will be chairing a workshop on likelihood ratios at ISHI 32. Can you tell us why the topic is important and why people should sign up?

Michael Coble:

I have used a slide in previous presentations on the movement of laboratories from "binary" methods of DNA interpretation to probabilistic methods of interpretation where a man jumps from one rocky ledge to another with a canyon in between. Taking such a leap can be scary when using a new software for interpretation.

I then mention that there should actually be another rocky ledge in the middle of these two interpretation methods to represent the "Likelihood Ratio (LR)" rock, as it is important to understand the foundations of LRs as they are used to report the statistical output of the probabilistic software.

Although over-one-half of the forensic DNA community has made that jump to probabilistic methods and have become accustomed to using LRs, (a Bright line colleague and co-presenter) and I would like to take a moment to bring a refresher for those labs already using LRs, and introduce laboratories looking to move to probabilistic methods in the near future. Unlike previous LR workshops hosted at ISHI, we plan to present material beyond the "basics" and work through more advanced examples. Attendees should have a solid understanding of algebra and bring a calculator to the workshop.

Advertorial

Successful Forensic Lab Automation: The Journey to Modularity

Written by: Kevin W.P. Miller, Ph.D., Hamilton Company

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In a previous ISHI Report article titled, "Successful Forensic Lab Automation Starts Here" we discussed practical insights to help you to develop a healthy automated ecosystem within your forensic DNA laboratory. After one year, some of you have taken the insights to heart as you developed and reaped the benefits of your own automated ecosystems. Congratulations!

Others, it seems, may remain hesitant to jump into this new automated world; or even the first step that involves taking a modular approach. This journey to modularity doesn't have to instill feelings of dread, and we are here to guide you through the path.

First, let's set the stage.

Think Modular

As you may recall from the previous article, modularity is about choosing universal robotic solutions that reduce touch points from one step to the next within a given workflow while also increasing reproducibility. Universal robotic platforms expand the contribution that each instrument can make to an overall workflow, therefore decreasing the number of instruments required. Modular instruments also share common deck accessories, programming language, and even consumable products, enabling flexibility in assay chemistry choice and workflow direction. This enhances the lifespan of your capital purchase.

"We already validated our semi-automated workflow that includes instruments dedicated to a single step," I hear you say, "it works just fine, so what's the benefit of replacing instruments now?"

Good question, and the answer lies with the samples coming into your lab.



Consistency is key to successful automation, and when it comes to the forensic DNA lab, consistent sample type, dependable parameters, and documented environmental conditions are the stuff of – dreams! We all know that the only thing that is consistent about evidentiary samples is that they are not at all consistent. Rather, they are challenging on so many levels.

DNA is more difficult to extract from some evidence types compared to others. Limited supply, environmental exposure, substrate interference, and even collection technique can add additional challenges to the successful extraction of high yield, high quality DNA from samples. So how is that dedicated "plug-and-play" automated extraction platform working for you in context of sample variety and challenges?

Think Fresh

Perhaps a transition to a plug-and-play system is how you start your journey to modularity. It's a longer journey, but it may alleviate anxiety among those who dread the idea of automation. In this case, we can still help you to improve capabilities, capacity, and functionality compared to your current instrument or manual method.

The ID NIMBUS Presto assay ready workstation from Hamilton Company can be used as a plug-and-play system for automated sample extraction and purification or incorporated into a more-encompassing automated DNA sample processing workflow. It performs the same nucleotide extraction processes that you know and love, but wait, there's more…there are two important twists.



First, ID NIMBUS Presto works with the Applied Biosystems™ PrepFiler™ Automated Forensic DNA Extraction Kit as well as the Applied Biosystems™ PrepFiler™ BTA Automated Forensic DNA Extraction Kit, both from Thermo Fisher Scientific. As you know, the former assay chemistry is used for a broad range of evidentiary DNA samples, while the latter is especially suited for use with samples that are calcified (bone and teeth) or that include adhesives (cigarette butts, tape lifts, envelope flaps). Both assay chemistries use uniquely structured magnetic particles and a multi-component surface chemistry to extract high yield, high quality DNA, but now they can be performed on a single instrument in batches of up to 96 samples at a time.

Second, the Thermo Scientific™ KingFisher™ Presto Purification System is mounted on the ID NIMBUS Presto deck. The KingFisher Presto system was designed in concert with the assay chemistry's unique nature. Here, rods sheathed in a disposable tip comb transfer magnetic beads bound with DNA from lysed samples to plates containing specific reagents. By moving magnetic particle-affixed samples instead of liquids, DNA moves from one clean reagent to the next. At the same time, fresh reagents are independently pipetted to labware in a "just-in-time" fashion, enabling next steps in the procedure.

Together, all of this means that DNA extraction is rapidly completed, regardless of the nature of the starting material.

The ID NIMBUS Presto processes sample volumes ranging from 50 – 5000 µL, and is pre-programmed for use with both extraction chemistries. This latter feature is important for three reasons.



The first is a matter of time. Pre-programmed protocols developed in collaboration with the chemistry manufacturer help to ease assay setup and streamline internal laboratory validation requirements.

The second reason is a matter of convenience and cost-management. By enabling the processing of two kit chemistries on one automated workstation, the entire range of forensic samples – from simple to challenging – can be extracted on a single unit. Forensic labs don't have to incur the cost, maintenance and service requirements, and physical space needs of separate, dedicated systems for each assay chemistry.

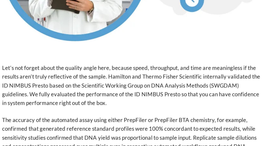
The third reason supports our advice – Don't Let Your Samples Control You – from last year's article. The pre-programmed ID NIMBUS Presto reigns in sample chaos by enabling users to combine separate workflows on the same instrument. The system also allows a variety of non-proprietary labware to be used, so you can use whatever combination of input and output tubes and plates that is right for you, allowing you to concentrate on the issues that really matter – tackling backlog and turnaround time.

Think Confidence

We also previously noted that (Deck) Real Estate is King, and so ID NIMBUS Presto, based on the Microlab NIMBUS automated liquid handler, makes best use of the deck space to drive walkaway efficiency. This includes integrating a barcode reader to eliminate transcription errors and facilitate a complete chain of custody, and exclusive Compressed O-Ring Expansion (CO-RE®) technology that enables exceptional pipetting accuracy and precision, and also permits enhanced functionality such as the use of on-deck gripper paddles that transport samples around the deck.

Time savers such as rapid assay formats, flexibility, and batched samples of up to 96 samples per run really add up. Paperwork is also streamlined. Hooking up to your lab's LIMS to create worklists and store results –and tracking all robotic actions associated with a sample and analyst for output as a standardized document in a case file – help to put time back on the analyst's clock.

Speaking of the analyst's valuable time, the big benefit of an automated workflow is regaining time that you used to spend on low value activities like pipetting. This time can now be applied elsewhere. Think of what you can accomplish with this newly found freedom. You could take a small break, perhaps grabbing coffee or fresh air to recharge your brain, or you could forge ahead with high value activities like data interpretation. The choice is yours. Either way, through automation, the overall lab can accomplish much more in a day, week, or month compared to manual methods.



Let's not forget about the quality angle here, because speed, throughput, and time are meaningless if the results aren't truly reflective of the sample. Hamilton and Thermo Fisher Scientific internally validated the ID NIMBUS Presto based on the Scientific Working Group on DNA Analysis Methods (SWGDAM) guidelines. We fully evaluated the performance of the ID NIMBUS Presto so that you can have confidence in system performance right out of the box.

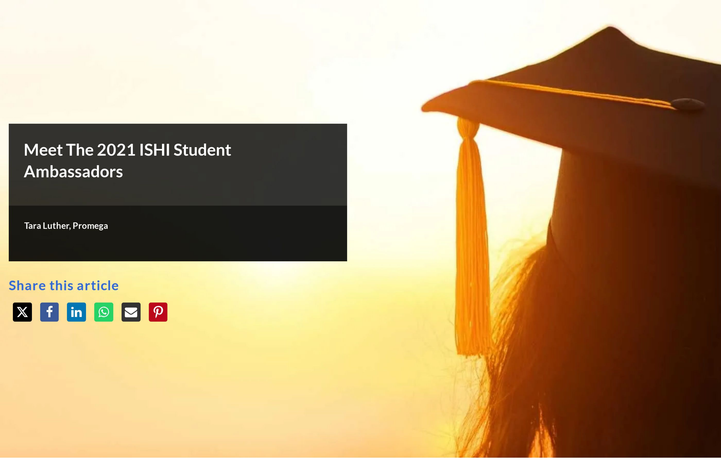
The accuracy of the automated assay using either PrepFiler or PrepFiler BTA chemistry, for example, confirmed that generated reference standard profiles were 100% concordant to expected results, while sensitivity studies confirmed that DNA yield was proportional to sample input. Replicate sample dilutions and concentrations processed over multiple runs in respective automated workflows produced DNA concentrations well within the limits of acceptable and expected variation. And, when compared to a previously validated automated system (with lower throughput), results obtained using the ID NIMBUS Presto results were found to be equivalent or greater than that of the other system.

Finally, in case-type sample studies, we processed a whole bunch of samples typically analyzed in a forensic DNA lab, from routine reference samples to challenging teeth, and swabs from just about anything within reach. The ID NIMBUS Presto yielded results comparable again to that of a previously validated automated system.

Think About Taking the Next Step

It is possible to take small steps along your individual journey to an automated ecosystem. An automated ecosystem with an assay ready workstation that is not only compatible but pre-programmed for use with multiple assay kits. One that can process a wide variety and quantity of forensic DNA samples, put time back on analyst clocks, provide economies of scale and size…all without sacrificing budgets or quality.





Meet The 2021 ISHI Student Ambassadors

Tara Luther, Promega

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We know that it takes a special kind of person to choose forensic science as a career, and this year, we'd like to recognize a few of the students who are making a difference in the field. We're excited to introduce this year's ISHI Ambassadors! These students are all pursuing degrees in the field of forensics. They will be participating in this year's 32nd International Symposium on Human Identification in Orlando. Follow Olivia, Nidhi, Amber, and Haley on social media as they share highlights from the ISHI workshops, presentations, and poster sessions. We'll also hear about the fun moments in between the scientific sessions including the Welcome and Wednesday Night Events. We look forward to seeing the meeting through their eyes, and learning more about their research and career aspirations.



Photo Credit: The University of South Alabama.

Olivia McCarter

Anthropology Major with a focus in Biological Anthropology, University of South Alabama

Like many people my age who are in school for a forensic science career, I grew up watching TV shows that portrayed these characters who were important members of the forensic science community. At the age of thirteen, I decided that I wanted to be a forensic anthropologist, which I am in school for now. When I was eighteen, I got an internship to do forensic investigative genealogy with two pioneers in the fields--Anthony and Lee Redgrave. I was on a team that identified a man that washed up in the Missouri River in 1979 back in April of 2020. I was so taken aback by my emotions about this man whom I had never met and what had happened to him--and I realized that this was one of the greatest things I will ever do in my life. We gave this man back to his awaiting family, who had loved him and had been missing him. The moment that we solved that case , I knew that I was born to work forensic science. After I get my PHD in forensic anthropology, I want to work for law enforcement, either at a state crime lab or the FBI, to help identify the 40,000 unidentified remains in the United States.

Attending ISHI will be a great opportunity for me to learn from different workshops, hear different presentations, and show everyone from my own presentation that I have a place in the forensic science community. I expect that attending ISHI will have a positive impact on my career growth, as I can meet people from all over the world and show them what I can do.

Follow Olivia on Instagram, Twitter, **or connect with her on** LinkedIn.

Nidhi Sheth

Center for Computational and Integrative Biology/ Forensic Science, Rutgers University



At a young age, I decided to pursue a career in criminology after being inspired by my grandfather, a renowned criminal lawyer in Gujarat, India. Hearing stories about his most challenging and convoluted cases captivated me and profoundly influenced my decision to pursue a career in forensic science. To become proficient in the fundamental technological aspects of the field, I pursued a B.S. in Pharmacy from Nirma University, India. Concurrently, I pursued extracurricular social activism, and I was selected as the Gujarat State Representative to present my views on "Preventing Crime Against Women" at the Indian Student Parliament to an audience of over 80,000 people. I opened the event with a discussion on the importance of implementing new educational policies to end the disparity between men and women in the eyes of India's justice system. This experience cemented my commitment to criminal justice, science, and higher education.

Receiving recognition for a job well done is not what matters to me: I believe working in this field is about securing justice for the voiceless. While attending the ISHI conference, I will discuss with attendees the incredible potential associated with single-cell pipelines for solving complex DNA mixture problems. This vein of research could eventually help the forensic science community tackle the interpretation and inference of complex mixture samples and the activity-level propositions thereof. Presenting my work and engaging with the forensic science community at ISHI will provide me an incredible platform to collaborate with practitioners and researchers in the field of DNA analysis.

Follow Nidhi on Instagram, Twitter, **or connect with her on** LinkedIn.



Amber Vandepoele

Biochemistry BS and Forensic Science BS, Syracuse University

My interest in forensic science began when I took my first forensic science course in high school. From there, I searched for a university that would allow me to explore my interest in forensic science while also providing me with a rigorous scientific course load. After learning about the groundbreaking research at Syracuse University's Forensic and National Security Sciences Institute and its partnerships with leading companies and agencies in the field, I knew it was where I would be able to grow and develop the skills needed for a career in forensic science. During my first semester at Syracuse, I joined Dr. Marciano's bioforensics lab on campus, the first freshman to do so. Through three years of bioforensics research, I have discovered my passion for forensic science and specifically DNA analysis. Through a career as a DNA Analyst, I will be able to combine my love for science and passion for justice while continuing to learn, teach others, and work through complex problems. I hope to use my knowledge and skills to provide unbiased analysis of evidence which will help seek justice and provide comfort for victims and families. Simultaneously, I hope to foster the interest of women, BIPOC students, and other underrepresented and marginalized groups in STEM and empower them in their pursuit of academic and professional careers in STEM.

Participating in ISHI will be a great opportunity to build on my academic knowledge, further pursue my passion for forensic science, and learn from practicing scientists and professionals in the field. I hope to gain more knowledge of the field by attending workshops and panels, and thus working towards my goal to provide and improve global justice. I expect to gain valuable insight from professionals that can be incorporated into both my research and overall career path. Also, I plan to present my research at ISHI and grow more comfortable with public speaking through a poster presentation of my work. Practicing scientists can provide valuable insight on my research project and discussions can allow new research ideas to emerge.

Follow Amber on Instagram, Twitter, **or connect with her on** LinkedIn.

Haley Falling

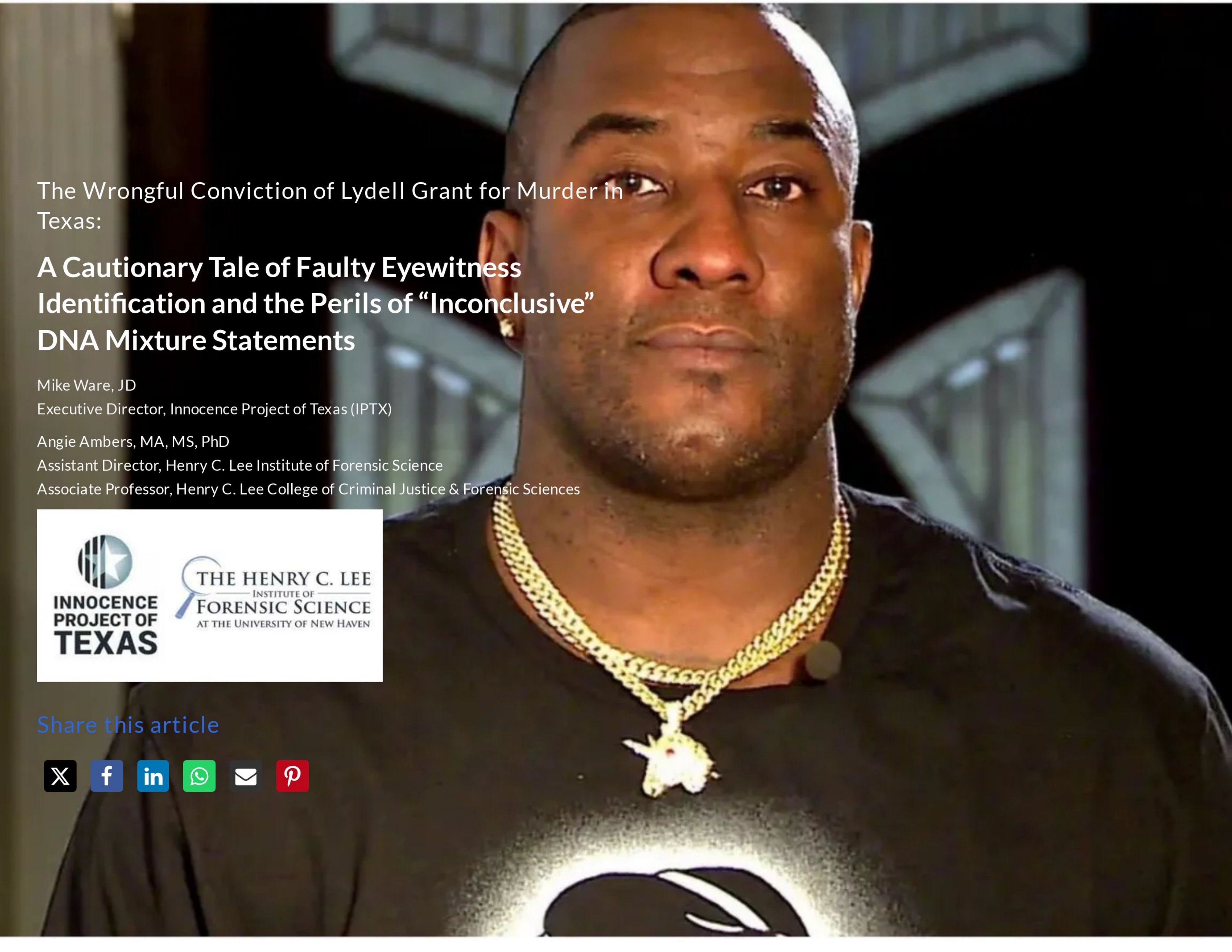
Master of Science in Forensic Science, Towson University



My undergraduate coursework in forensic science challenged and inspired me as I learned the ropes of drug chemistry, genetics, and crime scene processing. Similarly, the liberal arts education I was receiving challenged and inspired inspired my core beliefs, particularly in regard to my education on human dignity. The understanding that there is intrinsic, undeniable dignity found within each person informed my undergraduate experience, as well as my approach to forensic science; every attempt on a human life was an attempt to disregard the dignity and humanity found within that person. Therefore, I found that forensic science not only served the objectives of criminal justice, it served justice itself. Forensic science confirms the value of a life by simply seeking the truth.

I plan to attend the 2021 ISHI at Disney's Coronado Springs Resort, where I hope to gain further insight into the field of forensic DNA analysis from our nation's leading scholars and professionals. I also hope to gain a larger network of colleagues at ISHI so that I may continue to learn and build relationships with others who are passionate about forensic DNA technologies. I plan to use my participation experience at ISHI as a catalyst for other graduate students to attend forensic science conferences by sharing my experiences with my fellow classmates and with other young professionals and students via social media.

Follow Haley on Instagram **or connect with her on** LinkedIn.



The Wrongful Conviction of Lydell Grant for Murder in Texas:

A Cautionary Tale of Faulty Eyewitness Identification and the Perils of "Inconclusive" DNA Mixture Statements

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Shortly before midnight on December 10, 2010 (a Friday night), patrons of Club Blur (a bar in the Montrose district of Houston, Texas) watched in horror as a young man was beaten and stabbed to death in the parking lot. None of the witnesses knew the victim or the perpetrator, nor were they privy to the events that led up to the brutal murder. The Houston Police were called and, throughout the night and the next day, eyewitnesses provided video-recorded statements to investigators. Accounts from eyewitnesses varied in some ways, but were consistent in other respects. The victim had run into the parking lot and up the steps leading to the front door of the bar. He begged to be permitted to enter and to be protected from someone who was trying to kill him. The victim was a Caucasian male in his 20s. Bar employees failed to understand the seriousness of the situation and refused to let him inside the club for sanctuary. The perpetrator appeared moments later. He was an African-American male described as being 6'0"-6'6" tall, weighing approximately 200-260 lbs, in his late 20's or early 30's, and in athletic condition. He was well-dressed and wearing an orange shirt. The perpetrator and the victim scuffled in the parking lot; at one point during the struggle, the victim broke loose, but was ultimately caught and murdered. The perpetrator walked away into the night.

The following evening -- Saturday, December 11, 2010 -- Lydell Grant was parking his car in the parking lot shared by Club Blur and adjacent establishments as he prepared to meet friends at a neighboring bar. One of the employees of Club Blur who had witnessed the murder the night before saw him and believed he looked similar to the perpetrator. Indeed, Lydell Grant was an African-American male who otherwise fit within the broad and general descriptions provided by eyewitnesses. The bar employee wrote down the vehicle identification number (VIN) of Mr. Grant's car, called Crime Stoppers to report the sighting, and eventually collected a cash reward for the information.

Based on the Crime Stoppers tip, Houston Police investigators assembled a photo lineup of six African-American males, including a photo of Mr. Grant. Over the next day and a half, all six eyewitnesses selected Mr. Grant's photo as that of the perpetrator. The lead detective was allowed to administer the identification process in a non-double blind manner. In other words, he was aware of which photo was the "suspect" as he displayed the spread and observed each eyewitness as they were deciding on a choice. This approach permitted the detective to influence and/or cue the witness during deliberation and to reinforce their decision when they chose the suspect (or, in other words, when they made the "right" choice). Six months later, the Texas legislature would pass a law discouraging such procedures as these procedures have led to hundreds of wrongful convictions of innocent people.

The following week Lydell Grant was arrested on a murder warrant. He professed his innocence and had a solid alibi for the night of the murder. Nevertheless, he was immediately adjudged guilty in the media and through public comments of the Houston Police Department. Two years later, in December 2012, he was convicted of the murder based on the strength of testimony of six eyewitnesses who had identified him in a police photo spread. The jury completely disregarded Mr. Grant's alibi and he was sentenced to life imprisonment.

During trial, a forensic DNA analyst who worked for the Houston Police Department Crime Laboratory testified that she had tested the victim's fingernails collected during autopsy in an effort to obtain the DNA profile of the perpetrator (i.e., from skin cells that may have transferred during the struggle in the parking lot). She testified that there was at least one unknown male donor to the DNA mixture (i.e., there was a DNA profile present in the mixture that was not the victim's profile). She first testified that it was "inconclusive" whether Mr. Grant could be excluded as the "unknown male donor" to the mixture. Upon further prodding by the prosecutor, she testified that this meant that Lydell Grant "could not be excluded" as the unknown male donor to the mixture. This testimony, in conjunction with the eyewitness identification, was obviously damaging to Grant's case and contributed to the guilty verdict.

Post-conviction, Mr. Grant lost all of his appeals and he eventually contacted the *Innocence Project of Texas (IPTX)* for help. Mike Ware is the Executive Director of the *Innocence Project of Texas*, a non-profit committed to identifying and exonerating innocent individuals who have been wrongfully convicted and imprisoned for criminal offenses they had nothing to do with. IPTX receives 50-100 letters per month from incarcerated individuals claiming innocence and requesting assistance with their case. Mr. Ware also teaches an experiential law school class (clinic) at the Texas A&M School of Law in which students assist in identification of cases in which the convicted defendant may have a viable post-conviction claim of actual innocence. The phrase "actual innocence" means either: 1) a person was convicted of a crime that occurred much as the police, witnesses, and prosecutors claim it occurred, but it was committed by a completely different person (e.g., cases of mistaken eye-witness identity); or 2) a person was convicted of a crime that never occurred at all (e.g., the conviction was for arson, but it turns out the fire in question was the result of legitimate electrical problems in the building infrastructure).

In 2018, IPTX and Texas A&M Law School Clinic began reviewing Mr. Grant's case. There were many proverbial "red flags" indicating a possible wrongful conviction, beginning with the manner in which pre-trial identification procedures (i.e., the police photo lineups) were conducted. Moreover, Mr. Grant had a corroborated narrative of innocence in his alibi. These factors alone supported that the case merited further review, study, and investigation. Fairly quickly, law student Jason Tiplitz noticed something was off with the DNA evidence. Mr. Grant appeared to be clearly excluded from the DNA mixture recovered from the victim's fingernails. When compared to the actual trial testimony in which the State's forensic DNA analyst testified that Grant could not be excluded, another red flag was raised. The significance of foreign DNA found under the victim's fingernails in this kind of case was not lost on the police, even before DNA testing was performed. An early investigative report noted that the victim's fingernails should be collected and analyzed for DNA, and that any results obtained should be compared to known suspects and searched against the CODIS database.

Post-conviction review of the DNA evidence

In January 2019, Ware contacted Dr. Angie Ambers, a forensic DNA expert and Assistant Director of the *Henry C. Lee Institute of Forensic Science* in West Haven, Connecticut. Ware requested that Dr. Ambers review the DNA mixture recovered from the victim's fingernails during autopsy and preliminarily assess if Grant's DNA was potentially present in the mixture. After studying the DNA mixture for a short period of time (less than 30 minutes), it became obvious that an unknown (foreign) male profile was present – that is, an autosomal STR profile from a male who was not the victim or Lydell Grant.

This finding is unfortunate because the discovery and confirmation of an unknown male contributor in the DNA mixture could have guided the investigation to find the true perpetrator, and likely could have prevented the wrongful conviction of Mr. Grant. Post-conviction review of the DNA evidence also elucidates issues surrounding the quality of defense sometimes provided to defendants. During trial, Mr. Grant's defense counsel did not hire an independent forensic expert to review the DNA evidence and did not cross-examine the State's expert on the DNA data interpretation.

In terms of post-conviction review of the DNA mixture, it should be noted that the original testing conducted in 2011 involved typing of 15 autosomal STR loci (including the 13 core CODIS loci) plus amelogenin, for a total of 16 loci tested. The formal case report issued by the crime laboratory stated that "a mixture of DNA from at least two (2) individuals, at least one of whom is male, was obtained from this item. The victim cannot be excluded as the contributor to the major component of this DNA mixture. No conclusions will be made regarding Lydell Grant as a possible contributor to this mixture." Although inconclusive statements in DNA laboratory reports are often viewed as a conservative approach to avoid making erroneous inclusions or exclusions (which could lead to wrongful convictions or false acquittals, respectively), this case illustrates the need to further consider the implications of "inconclusive" statements regarding DNA mixtures. In this case, it was not difficult (for a trained eye) to recognize the presence of a foreign male contributor. Given that, as a matter of practice, DNA case reports are shuffled through several internal technical reviews prior to finalization and release, it's concerning that none of these review steps elicited discussion about the apparent exclusion of Mr. Grant from the mixture.

For simple presentation purposes (and not intended as a formal analysis), **Figure 1** displays the DNA mixture data obtained from the murder victim's fingernails and identifies the foreign alleles present in the mixture that do not belong to the victim or to Lydell Grant. In total, there were twenty-six (26) alleles present in the DNA mixture that are not consistent with the STR profiles of the victim or Mr. Grant.

			Alleles present in DNA mixture recovered from victim's fingernails				
Locus	Lydell Grant	Victim	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5
AMEL	XY	XY	X	Y			
CSF1PO	9,11	12,13	10	11	12	13	
D13S317	11,12	8,11	8	11	12	14	
D16S539	9,11	10,12	8	9	10	11	12
D18S51	14,17	11,16	11	15	16	18	
D19S433	14,15	14,15	12	13	14	15	
D21S11	28,32.2	30,32.2	28	29	30	31.2	
D2S1338	19,25	17,24	16	17	25		
D3S1358	15,15	15,18	14	15	16	17	18
D5S818	12,13	12,12	9	11	12	13	
D7S820	10,11	11,12	10	11			
D8S1179	12,15	13,14	12	13	14	15	
FGA	22,25	22,22	20	21	22	23	24
TH01	6,9	7,9.3	5	6	7	8	9.3
TPOX	6,11	10,11	8	9	10	11	
vWA	16,16	16,19	15	16	17	18	

red = foreign alleles not consistent with either the victim or Lydell Grant

Figure 1. Mixed DNA results from autosomal STR typing of fingernail scrapings from the 2010 murder victim. Twenty-six (26) foreign alleles are present in the DNA mixture; the alleles highlighted in yellow and in red font do not match the profile of the victim or the defendant in this case.

Based on Dr. Ambers' initial assessment that there was an obvious foreign male contributor present in the mixture, Ware and IPTX contacted the Harris County District Attorney Office's *Conviction Integrity Unit* to request the raw data (.fsa) files from the original DNA testing that was conducted in 2011 for analysis using probabilistic genotyping. Years after Mr. Grant's conviction, there was widespread adoption of probabilistic genotyping as an improved methodology for DNA mixture deconvolution. Probabilistic genotyping greatly reduces subjectivity in interpretation and is considered superior over the manual CPI/CPE calculations conducted previously by forensic DNA laboratories across the U.S. After receiving the files from the *Conviction Integrity Unit*, the raw data was submitted to Cybergenetics in Pittsburgh, Pennsylvania for analysis using TrueAllele®, one of two commonly implemented probabilistic genotyping software programs (along with STRmix™) for forensic DNA mixture interpretation. TrueAllele® analysis of the DNA mixture recovered from the murder victim's fingernails definitively excluded Mr. Grant as a contributor to the mixture and confirmed the presence of an unknown male profile. Further exploratory processing with TrueAllele® generated an allele list for the unknown contributor that met the criteria for searching in CODIS. In June 2019, with the assistance of a CODIS administrator from the Sherriff's Office in Beaufort County, South Carolina, a CODIS search was conducted and resulted in a hit.

The CODIS hit was to a man who fit the description of the murderer given by the six eyewitnesses (**Figure 2**). His name was Jermarico Carter and he lived in Houston, Texas at the time of the murder. He had previously been arrested on a drug-related charge within feet of where the murder took place. More importantly, he had a violent criminal history and, although he had previously spent time in prison, he was not incarcerated at the time of the murder and he left Houston shortly after the crime was committed (relocating to Atlanta, Georgia). It was Jermarico Carter's DNA recovered from the murder victim's fingernails.

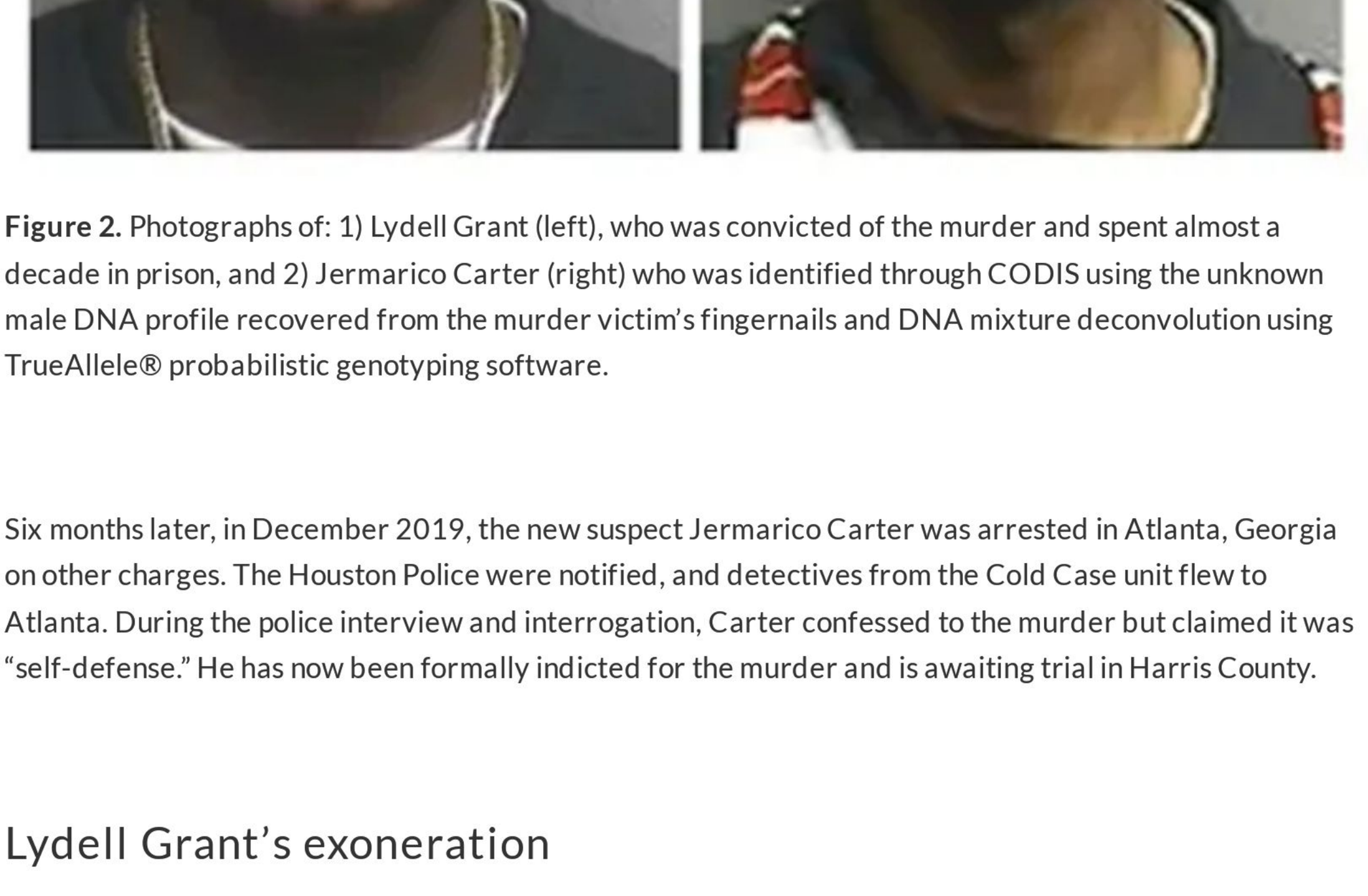

Figure 2. Photographs of: 1) Lydell Grant (left), who was convicted of the murder and spent almost a decade in prison, and 2) Jermarico Carter (right) who was identified through CODIS using the unknown male DNA profile recovered from the murder victim's fingernails and DNA mixture deconvolution using TrueAllele® probabilistic genotyping software.

Six months later, in December 2019, the new suspect Jermarico Carter was arrested in Atlanta, Georgia on other charges. The Houston Police were notified, and detectives from the Cold Case unit flew to Atlanta. During the police interview and interrogation, Carter confessed to the murder but claimed it was "self-defense." He has now been formally indicted for the murder and is awaiting trial in Harris County.

Lydell Grant's exoneration

Legal professionals and forensic DNA experts from four different U.S. states (Texas, Connecticut, Pennsylvania, South Carolina) worked on this case, on behalf of Mr. Grant to prove his innocence and to promote justice for the victim and his family. Subsequent to Mr. Carter's arrest and confession, Lydell Grant's post-conviction appeal filed by the *Innocence Project of Texas* was supported by both the Harris County District Attorney's Office and the District Judge. It has been pending in front of the Texas Court of Criminal Appeals (TCCA) for 16 months, still with no decision by the Court. In mid-2020, the TCCA asked that the case be remanded back to District Court, that the District Court and the DA's office ask the six eyewitnesses at Grant's trial to formally respond to Grant's innocence claims, and that the District Court provide the TCCA with a photo of Jermarico Carter, the confessed murderer now in jail, dated circa 2010 (when the murder was committed). In recently released court documents, one of the six eyewitnesses has stated on record that, at the time of the original investigation, he told police that he didn't see the suspect in the photo lineup. According to the court documents, the eyewitness stated that he was then told to "look again" and eventually chose Grant as a suspect. As of the date of this article, the TCCA still has not made a decision regarding Lydell Grant's request for exoneration.

Lydell Grant, using the stage name, "Dello", rapped about his experience after he was released from prison in November 2019 in his song "I'm Actually Innocent."

Further reading:

Texas man released on DNA evidence still not exonerated after new suspect confesses to murder. https://www.nbcnews.com/news/us-news/texas-man-released-dna-evidence-still-not-exonerated-after-new-n1231621

Editorial: DNA freed Lydell Grant. Why won't Texas' highest court let him go? https://www.houstonchronicle.com/opinion/editorials/article/Editorial-DNA-freed-Lydell-Grant-Why-won-t-15384030.php

"Like I'm still locked up:" Man not yet exonerated even though authorities say he's innocent of murder. https://lawandcrime.com/crazy/like-im-still-locked-up-man-not-yet-exonerated-even-though-authorities-say-hes-innocent-of-murder/

Six eyewitnesses misidentified a murderer: Here's what went wrong in the lineup. https://theconversation.com/six-eyewitnesses-misidentified-a-murderer-heres-what-went-wrong-in-the-lineup-134767

The Lydell Grant case: Here's what went wrong with the eyewitness lineup. https://www.forensicmag.com/566149-The-Lydell-Grant-Case-Here-s-What-Went-Wrong-in-the-Eyewitness-Lineup/

Court docs: Witness wasn't sure Lydell Grant was actual suspect in stabbing death. https://www.khou.com/article/news/crime/lydell-grant-witness-update/285-08073b85-c0a2-425e-bf59-a2c10fcd505d

"It's the most outrageous thing I've ever seen. It makes no sense." https://www.texasmonthly.com/news-politics/dna-evidence-proved-lydell-grants-innocence/

Despite DNA evidence, Texas court asks for more evidence before exonerating Lydell Grant from 2010 murder. https://www.click2houston.com/news/local/2020/07/03/despite-dna-evidence-texas-court-asks-for-more-evidence-before-exonerating-lydell-grant-from-2010-murder/

Lydell Grant waits for exoneration after DNA proves he didn't commit murder. https://abc13.com/lydell-grant-houston-man-wrongfully-convicted-of-murder-dna-proves-didnt-commit-aaron-scheerhorn/8150787/

The police, DA, and judge all agree he's innocent. https://innocencetexas.org/news/the-police-district-attorney-and-judge-all-agree-hes-innocent-why-is-lydell-grant-still-a-convicted-murderer

Lydell Grant, convicted in 2010 Montrose slaying, freed from prison as case is reinvestigated. https://www.chron.com/news/houston-texas/houston/article/Lydell-Grant-who-attorneys-say-was-wrongfully-14863704.php

DNA test frees Texas man from life sentence and leads to confession of a new murder suspect. https://www.usatoday.com/story/news/nation/2019/12/21/dna-test-texas-murder-frees-lydell-grant-leads-arrest/2721810001/

Harris County District Attorney's office supports bail for Lydell Grant based on new DNA evidence. https://www.harriscountyda.com/harris-county-district-attorneys-office-supports-bail-lydell-grant-based-new-dna-evidence

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 has not let a pandemic slow them down! The subcommittee currently has 17 documents at the AAFS American Standards Board (ASB), several of which may be published shortly. Additionally, they have posted OSAC 2020-N-0007, Best Practice Recommendations for the Management and Use of Quality Assurance DNA Elimination Databases in Forensic DNA Analysis as a Proposed Standard on the OSAC Registry (added April 6, 2021). This document has also been sent to ASB for further development and publication. The most recent addition to the Registry, ANSI/ASB Standard 018, Standard for the Validation of Probabilistic Genotyping Systems, First Edition 2020, was added May 4, 2021 and joins three other Registry approved human DNA standards. Furthermore, six ASB published standards are being considered for the Registry. These six standards are all related to training and validation.

Several documents, including ***Standard for Interpreting and Reporting DNA Test Results Associated with Failed Controls or Contamination Events*** and ***Standard for Setting Analytical and Stochastic Thresholds for Application to Forensic Casework Using Electrophoretic Systems***, have been written and are currently going through OSAC's review process. 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.

Please visit the OSAC website 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).

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.

There is No Navel of the World

Looking Beyond Borders to Interpret Y-STR Evidence

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The reporting of Y-STR results with meaningful statistics requires a look beyond the borders, borders of the standard forensic mathematics practiced for decades and political borders. To substantiate this view, let us consult some recently published regulations on forensic Y chromosome testing and statistical interpretation of Y-STR results, for example of Germany [1], Poland [2], the Philippines [3] and the United Kingdom [4] (Table 1). In the United States, the Y-STR interpretation guidelines traditionally provided by the Scientific Working Group on DNA Analysis Methods (SWGDAM) are nearly finalized. Other countries follow the ISFG recommendations published recently [5]. A closer look at these documents reveals the different use of reference data and statistical methods. In this brief correspondence, we want to touch on the challenging problem of how global data resources and statistical methods based on an evolutionary genetic model, which are specifically designed for Y-STR interpretation can be incorporated in a workable approach that forensic experts in a country can follow in their daily routine.

Table 1. Overview on currently published Y-STR guidelines

	Germany	Poland	Philippines	United Kingdom	ISFG recommendation
Year of publication	2018	2020	2021	2021	2020
Primary data resource	YHRD	YHRD	YHRD	YHRD	YHRD
Default reference database	Western Europe	Poland	Austronesian	Western Europe	Listed MP's
Default statistics	Discrete Laplace	Kappa	Discrete Laplace	n+2/N+2	Discrete Laplace
Reference	[1]	[2]	[3]	[4]	[5]

The expert panels on Y-STR testing convened in different countries agree to recommend the global YHRD database (https://yhrd.org) as the primary source of reference data, however they disagree on the best statistical model to calculate haplotype frequencies. The result is a heterogeneous picture of methods. While the ***Discrete Laplace (DL) calculation*** [6], endorsed by the ISFG [5], is recommended as the default method for example in Germany and the Philippines, other countries consider different modifications of the counting method more appropriate. Poland recommends the ***Kappa method*** [7] and the United Kingdom the ***augmented count estimate n+2/N+2*** [8]. In addition, the recommendations on the choice of the default reference databases within the YHRD differ remarkably. Some countries (Germany, United Kingdom, Philippines) prefer metapopulations i.e. groups of population samples shown to have characteristic common features (e.g. language, demography, phylogenetic SNPs) while others prefer national databases (in Poland).

No doubt, all these methods and databases have limitations. The limitation of different counting methods is the direct relationship between the evidentiary weight and the size of the database [2]. On the other hand, the count estimates are easy to defend at court and are seen as "conservative". This is not the case for the extrapolation (Discrete Laplace, DL) method, which requires a number of assumptions on the composition of the reference population(s) and the evolution of haplotypes by mutation. The method is much more independent from the database size and "realistic". The DL method has its limitations in the calculation of partial profiles or profiles bearing non-consensus alleles. The calculation for larger STR panels requires considerable computer power. In addition, calculations are prone to errors if a database consists of subpopulations. Currently the DL method is enabled at YHRD and provides metapopulation-based calculations for core haplotypes (17 loci) included in widely used commercial kits.

The DL method using the full global YHRD dataset extracts important information from a haplotype match, which must be given special consideration by the forensic expert. Let's demonstrate this with an example:

In a forensic investigation a Y-STR haplotype is found identical in a trace and a suspect. The haplotype is observed Zero times in a national Y chromosome reference database (N = 15,000). This database is composed of five defined subpopulations each of which has N = 3000. The observed frequency using the augmented counting method (n+1/N+1) would be 1/15,001 in the general database and 1/3,001 in all five subpopulation databases. If guidelines stipulate the reporting of count results, the qualitative statement "non-exclusion of the suspect as the donor of the trace" would be further specified using these five frequency values, which describe the likelihood that the matching haplotype occurs by chance in any of the subpopulations. The higher the frequency of the haplotype in the reference database, the more it relieves the defendant. In our example, the value of the Y-STR evidence is extremely low. And this is not because of the incapability of the method, but due to the small numbers of reference samples on the one hand and the inadequacy of the estimation method on the other. Forensic genetic research recently succeeded to show, that another grouping principle for reference populations and a statistical method that can analyze haplotype distributions, could significantly increase the evidential value of a trace/person match based exclusively on Y-STRs.

The YHRD is structured in a way, that new categories of **metapopulation** (MP) databases (larger than national) are built on basis of ancestry groups defined by geography, demography, language and phylogenetic Y-SNP information [9]. These MP's include population samples that are related and distributed globally. Names for these new categories have been found which differ from national census schemes that often follow historical conventions. A good example for such a historical name is "Caucasian". In the YHRD samples categorized as US Caucasians belong to the European MP. The YHRD further provides a number of statistical methods built upon haplotype distributions in populations, among these the Discrete Laplace method [9]. This method is able to analyze the connectivity of haplotypes in a metapopulation if it is built on basis of common ancestry and represents the prevailing deep-rooting male lineages. The probability of occurrence of a haplotype, whether it is observed or not in this and any other MP, can then be estimated.

Now, if the frequency of the haplotype of our example is calculated using DL in different MP's, there will be a number of highly diverging estimates. This means, by chance the haplotype was not sampled in the five rather small national databases, but is nonetheless rather frequent in one or more worldwide populations and rare in others. Among these populations is probably the one, which represents the ancestors of the trace donor.

Regardless of an intriguing result like this, the true donor of the trace remains unknown, because the Y-STR method does not disclose the individuality of the DNA. However, a naïve counting in the five example databases resulting in equal values dismissed the information, which is built-in in the haplotype structure and accessible via the DL method and global databases. The judgement of the count and the DL outcome is the exclusive responsibility of the court, but the available information (if requested) should not be withheld. The availability and scrutiny of representative reference data placing the evidence in a context is a strong argument for the applicability of the Y-STR method in casework.

To summarize: We think that with sufficient empirical data, well structured databases and a suitable statistics the court-going forensic experts can prove their expertise on Y-STR interpretation, with defensive methods like counting (naive, augmented, kappa inflated) their expertise for using Y-STRs can be severely contested.

In Table 2 we compare different statistical values (reanalyzed using current YHRD release 63) for a trace/person match in a homicide case from Germany, which is described in detail in [10]. In accordance with the German Y-STR guidelines the DL value for the Western European metapopulation was used by default for reporting the results. The suspect was sentenced to life imprisonment and the ruling was confirmed by the highest appellate court in Germany.

Table 2. Frequency estimates for a trace profile using the YHRD reference database (Release 63, queried 2021/04/26) and different calculation methods

Calculation Method	Estimate	Reference Database
Augmented count (n+1/N+1)	1/27,064	n=0, N=27,063 (Western European MetaPopulation)
Augmented count (n+2/N+2)	1/13,532	n=0, N=27,063 (Western European MP)
Kappa database inflation	1/70,882	n=0, N=27,063, κ=0.618 (Western European MP)
Discrete Laplace (Yfiler)	1/51,824*	n=0, N=27,063 (Western European MP)
Discrete Laplace (Yfiler)	1/415,247	n=0, N=5,226 (Southeastern European MP)
Discrete Laplace (Yfiler)	1/1,867,449	n=0, N=8,730 (Eastern European MP)
Discrete Laplace (Yfiler)	1/14,307,872	n=0, N=84,265 (Chinese Han MP)
Discrete Laplace (Yfiler)	1/193,865,105	n=0, N=7,647 (Indian MP)

n = database count, N = database size
*Value used by default according to the German Y-STR guidelines for LR calculation and reporting

The new guidelines mentioned earlier will help forensic practitioners in their daily life. But the evaluation of Y-STRs remains challenging and often the results are not very meaningful. However, with the understanding that ancestry is key for the interpretation of a Y match, it is possible to restructure databases and apply methods based on an evolutionary genetic model. So equipped, we expect growing acceptance of the Y-STR method within the forensic community, law enforcement and justice.

Fill out the form below to receive a copy of the YHRD Instruction Manual

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Announcing ISHI 32

Attend In Person or Virtually

Carol Bingham, Promega

Share this article

The 32nd International Symposium on Human Identification (ISHI 32) will be held this September at Disney's Coronado Springs Resort in Orlando, Florida. Long time conference attendees might remember that Coronado Springs Resort played host to ISHI 10 in the way back year of 1999.

A raft of innovations has transformed forensic science since our last meeting in Orlando. This year's symposium will be exploring many technologies that were not even on the distant horizon decades ago. The general session will open with a look back on the twentieth anniversary of the 9/11 attack. A panel discussion later in the week will uncover how techniques born from the tragedy of that day have impacted the field. New methods for working with severely compromised remains, protocols for mass fatality events and advances in kinship analysis were the result of dedicated teams of forensic scientists who worked to identify victims of the attacks.

Additional general session talks will cover updates on use of genetic genealogy, including updates from the FBI, the latest innovations in forensic science, practical applications of Bayes Theory and much more.

Are you interested in presenting a scientific talk or interesting case? ISHI is still currently accepting oral abstract proposals for the general session. (**deadline June 14**). Two poster sessions will also be scheduled during the meeting in Orlando. **Poster abstracts are due July 12**. All abstracts will be reviewed by an outside panel of experts and selected for presentation based on perceived interest to the forensic community.

Learn more about all things ISHI including the roster of workshops offered before and after the general session on the official conference website, www.ishinews.com. That's also where you'll find the links to register for the symposium and workshops, book your hotel room and see updates on speakers as they are confirmed.

Attendance at the conference will be limited to 550 people. Safety protocols will be in place including mandatory masking and social distancing in all meeting spaces. For the comfort and well-being of all participants we are requiring that attendees be vaccinated against COVID.

Benefits of in person attendance include networking opportunities, social events like the welcome reception and an off-site event at Disney, exhibitor presentations, focused lunch topics and workshops that are only offered in person.

If you would like to participate in the symposium but are unable to travel. we will offer a virtual symposium option. The general session talks and **select** workshops will be available for a reduced fee following ISHI. Don't worry about missing out on the ISHI t-shirt. Attendees at the virtual ISHI meeting will qualify to have a t-shirt mailed right to their door!

Join us either in person or in cyber space as we celebrate 32 years of supporting the forensic science community! Visit www.ishinews.com for the details.



Calendar of Events

Deadlines

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

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