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ISHI INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION

SAN ANTONIO, TX | SEPT. 14–17, 2020

May 2020

The ISHI Report

News from the World of DNA Forensics

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Letter from the Editor

What a difference a couple of months make. In February we were lamenting the cold weather and this month we are dealing with the ugly impact of COVID-19 on every facet of our lives! We are proud to share that Promega has been actively assisting in fighting the outbreak through our manufacturing of reagents and supplies being used to support 26 different COVID-19 diagnostic kits worldwide. Since the beginning of the epidemic in January, Promega has provided enough amplification reagents and enzymes to enable testing an estimated 52.5 million samples for SARS-CoV-2 worldwide.

You may be wondering what the plan is for holding this year's 31st International Symposium on Human Identification. The short answer is that at the time of publication we are still monitoring the COVID-19 pandemic to assess the feasibility of holding a physical conference. The health and safety of our ISHI attendees, exhibitors, partners, and staff is our top priority and we will look to the Centers for Disease Control and Prevention (CDC) and the World Health Organization (WHO) for guidance.

Risk-free registration for the in-person event is being offered to all attendees, with the option to receive a full refund for cancellations made up to the date of the conference. You can also reserve a place at ISHI and defer payment until a later date. In the event that ISHI can't be safely held in person, we are exploring the possibility of holding the event in a virtual format for a reduced rate. If this happens, general session talks will be recorded and available on demand. A selection of workshops will also be available.

We know that your lives and work are also being impacted by the virus. It's our hope that this latest ISHI Report will provide you with a welcome diversion as it explores current topics in forensic science and introduces forensic professionals who are influential in the field.

We were thrilled to Zoom with CeCe Moore and Paul Fronczak, our keynote speakers for this year's ISHI to talk about Paul's story and the role that genetic genealogy played in resolving the mystery of his identity. Be sure to check out the interview to get a sneak peek into their keynote address and to learn more about CeCe's new television show!

Our colleague Ken Doyle documents several very cold cases solved through the work of the DNA Doe Project, including a century old mystery. Karra Porter, co-founder of the Idaho Cold Case Coalition describes how she came to organize the group and provides details on how individuals can contribute to its success.

Ronaldo Carneiro da Silva Junior, who will be leading this year's Grupo Cientifico Latino-Americano de Trabajo Sobre Identificacion Humana (GCLAITH) provides an update on forensic practices in the region and invites interested parties to submit abstracts for this year's GCLAITH workshop.

We also interviewed Michael Coble and Jo Bright who will be co-chairing a workshop on presenting probabilistic genotyping data in court at ISHI. They elaborate on the advantages that probabilistic genotyping can offer and provide practical advice for adopting this technology. If you are interested in learning more, consider registering for their workshop.

Dr. Maria Corazon A. De Ungria shares details on The Innocence Project Philippines Network, Inc. (IPPN)'s efforts to free wrongfully convicted persons in the Philippines. She discusses the numerous challenges the dedicated team from law schools, scientific and academic laboratories and non-governmental organizations have experienced since its inception, as well as their plans for the future.

On the lighter side, we feature an interview with Walther Parson in which he describes how he became involved in forensic science. His path to the lab might surprise you. Walther will be presenting at the upcoming ISHI on Otzi the "Ice Man" and his modern-day relatives.

Don't forget to visit the conference website for updates on ISHI including details on submitting abstracts for oral presentation, workshop offerings and more.

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

Rock Your Favorite ISHI Tee for a Good Cause!



Even though we may not be able to come together in the same location right now, we can still come together virtually. Let's unite as one ISHI community and support those in our field and our neighborhoods.

Learn more on Page 15!

Submit an Abstract for ISHI 31

Would you like to share your work at ISHI?

We are now accepting abstracts for oral, interesting case, and poster presentation.

Abstracts will be considered for oral presentation on topics related to advances in the DNA typing process, policy updates and interesting case studies.

All proposals will be reviewed by an outside committee of forensic experts and selected based on perceived interest to the forensic community. Abstract proposals should be non-commercial and focused on educating forensic scientists on topics that will improve their technical, legal or policy knowledge.

Abstracts must be received by June 5 to be considered for oral or interesting case presentation and by July 5 for poster presentation.

Submit Your Abstract



The Innocents Project Philippines Network

Maria Corazon A. De Ungria, Ph.D., DNA Analysis Laboratory, Natural Sciences Research Institute, University of the Philippines

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The issue of wrongful convictions is not new to the Philippines. In 2004, the Philippine Supreme Court recognized in People of the Philippines v Mateo (General Register No. 147678-87) that lower court judges were meting out the death sentence erroneously in 71.77% of capital cases. In 2008, we reported on efforts to find potential cases for post-conviction DNA testing from 2002 to 2006 (De Ungria *et al.*, 2008).

With funding from the European Commission, the DNA Analysis Laboratory, Natural Sciences Research Institute at the University of the Philippines conducted an investigative review of capital cases. They did this by going to the National Penitentiary for Men, the Correctional Institute for Women, the Supreme Court archives and the Public Attorney's Office, and consulting with NGO's including the Free Legal Assistance Group (FLAG), and Philippine Jesuit Prison Service and the Coalition against the Death Penalty.

Because I was still relatively new in my role as Head of the Laboratory, it meant that there were additional challenges brought about by our lack of familiarity with the Philippine criminal justice system.

Out of the 106 cases that were reviewed, we found three cases involving sexual assaults which led to the birth of a child, or as they were known, "criminal paternity cases". These cases were worth re-opening due to the existence of DNA evidence that supported the accused's claim of innocence at a time when the Philippine criminal justice system was not yet prepared to accept post-conviction proceedings because of settled principle on finality of judgments.

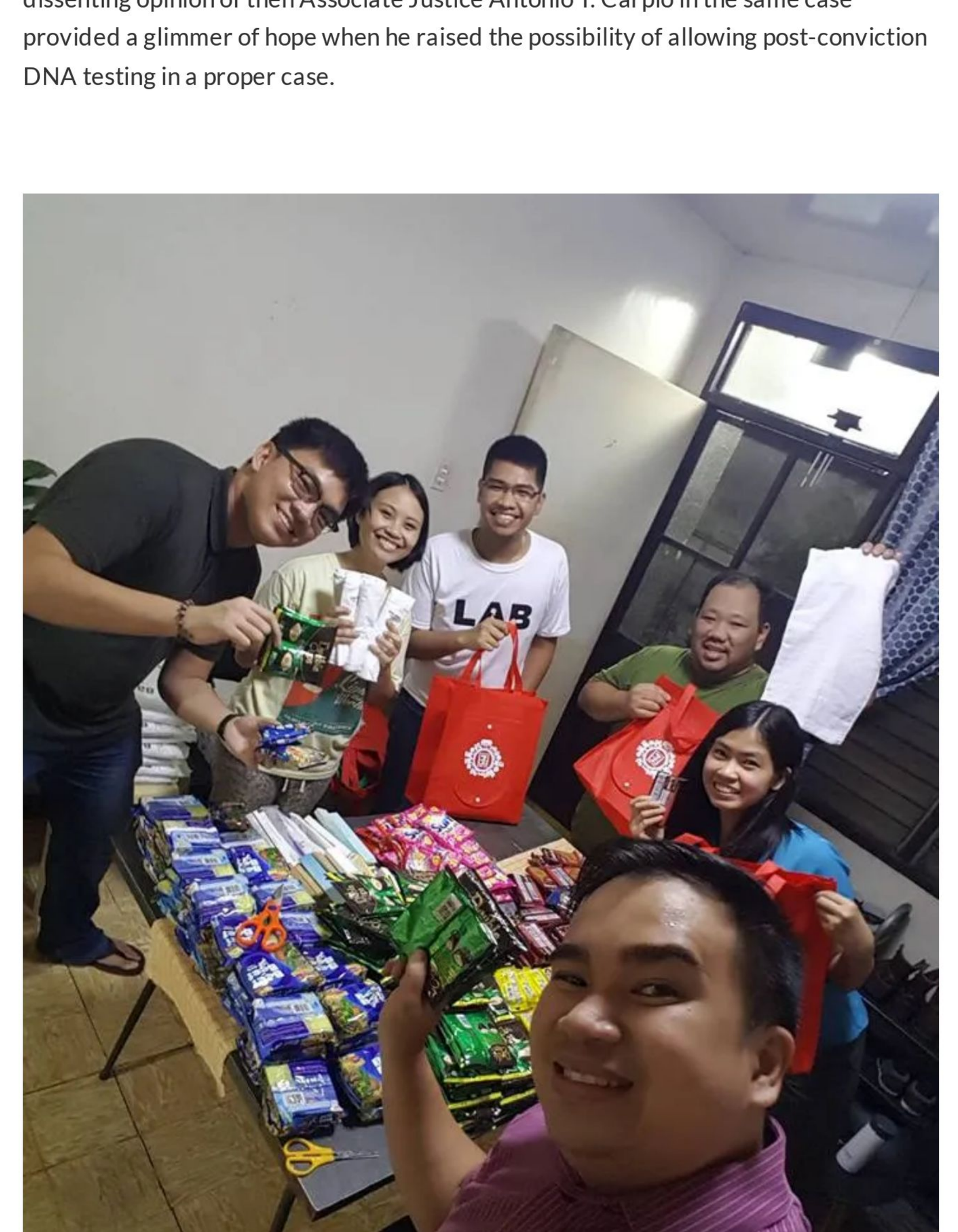


Consultation between a prisoner and members of the Innocents Project Philippines Network

Our 2008 paper reported on the challenges that were encountered while attempting to assist a man whom we believed to have been erroneously convicted. After two years of searches were done to find a way to reopen the case, the Supreme Court denied the habeas corpus petition of the accused in 2004, citing, among other things, the principle that pregnancy was not an element of rape, despite DNA test results having excluded the accused from being the biological father of the child. This was the same child who the victim claimed had been conceived during a sexual encounter with the accused when she was just shy of 13 years old.

Notwithstanding the setback, we continued to work with our partners, especially the lawyers of FLAG, to help the accused in this case. In 2005, the accused was pardoned by then Philippine President Gloria Macapagal-Arroyo and was released after being incarcerated for 11 years. Apparently, the DNA test results that showed non-paternity and the accused's advanced age (he was over 70 years old at the time), were included in the request made to the President for his eventual pardon.

While feeling disillusioned at the Supreme Court's decision not to reopen the case, the dissenting opinion of then Associate Justice Antonio T. Carpio in the same case provided a glimmer of hope when he raised the possibility of allowing post-conviction DNA testing in a proper case.



Volunteers pack supplies for inmates.

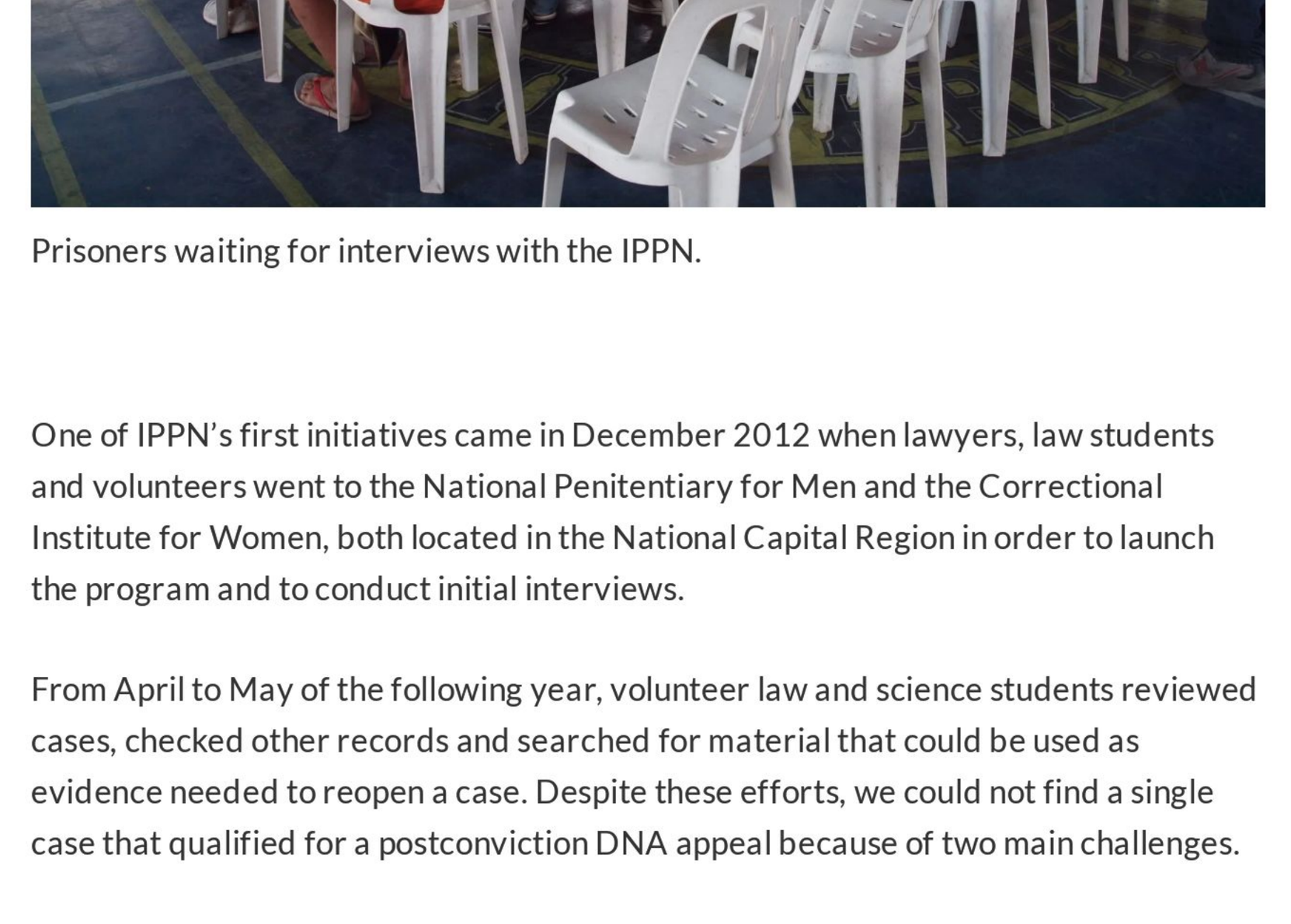
This glimmer of hope became a reality when on October 15, 2007, the Philippine Supreme Court promulgated the Rule on DNA Evidence which included a specific section on post-conviction DNA testing. This set of rules was a product of our work with the Philippine Judicial Academy that recognized the value of objective evidence including DNA evidence in a country that relied mainly, at times solely, on testimonial evidence. To our knowledge, this is the only judicial rule in the world that provides guidelines for the purpose of collecting, handling, storing and presenting DNA evidence at trial.

Five years after the promulgation of the Rule, we decided to form the Innocents Project Philippines Network (IPPN) in 2012. After numerous consultations with our earlier partners, we defined IPPN's mission to be that of assisting persons who claim to have been wrongfully convicted and who are incarcerated in the National Penitentiary for Men, the Correctional Institute for Women or any of the six penal institutions scattered around the Philippine archipelago, provided there is relevant evidence that could potentially lead to a change in the conviction.

IPPN hopes to establish a clearing house which will initially screen cases and distribute these to partner law schools in the regions and provinces where the trial took place. In doing this, we aim to facilitate the access of law students to trial court documents, evidence and witnesses. In addition, IPPN could tap law students who speak the local language and who know the local culture in order to better understand the dynamics of the cases being reviewed.

Unlike human rights organizations such as FLAG which already had an established network of lawyers, some of whom teach in law schools, IPPN became instead a collaborative organization of lawyers, scientists, students of law and/or science, and volunteers that seeks to make justice accessible to wrongfully convicted persons.

The group also aims to advocate reforms in policies, laws, judicial rules, legal education, and criminal investigative procedures and evidence handling to address wrongful convictions in the Philippines; to enhance the capacities of justice stakeholders including judges, prosecutors, lawyers, criminal and forensic investigators, law students, etc.; to eradicate or mitigate wrongful convictions; and to establish an independent and accurate data bank containing all pertinent information on wrongful convictions in the Philippines.



Prisoners waiting for interviews with the IPPN.

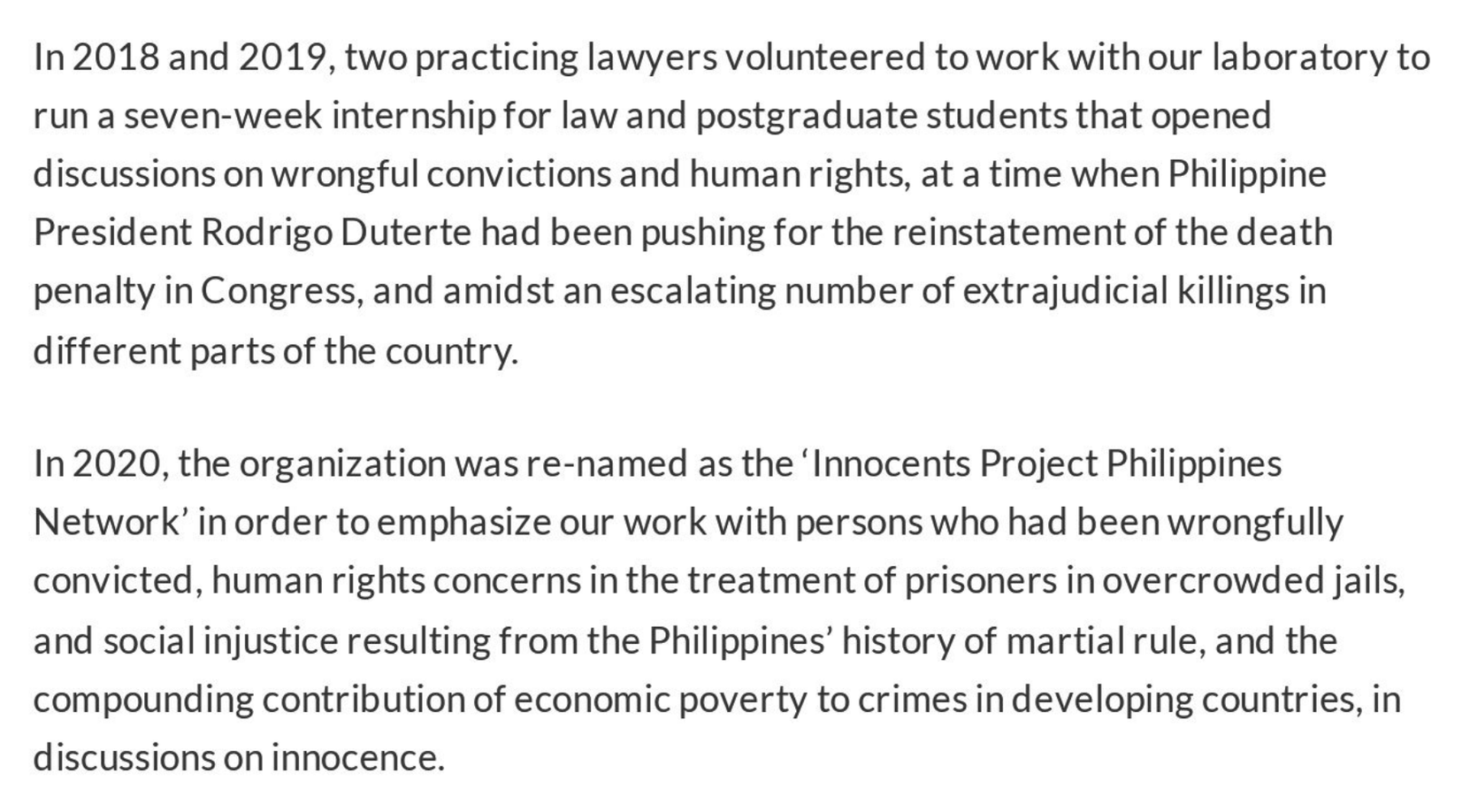
One of IPPN's first initiatives came in December 2012 when lawyers, law students and volunteers went to the National Penitentiary for Men and the Correctional Institute for Women, both located in the National Capital Region in order to launch the program and to conduct initial interviews.

From April to May of the following year, volunteer law and science students reviewed cases, checked other records and searched for material that could be used as evidence needed to reopen a case. Despite these efforts, we could not find a single case that qualified for a postconviction DNA appeal because of two main challenges.

The first and biggest challenge faced by IPPN is that, even though the Rule on DNA Evidence already allows post-conviction DNA testing, there simply were no existing biological samples to work with in the cases that were reviewed.

Unlike in other jurisdictions where physical evidence from crime scenes were routinely collected and stored in designated secure locations, the Philippines has no such physical evidence collection and storage system in place. Thus, there was no crime scene evidence that could be examined using DNA analysis to establish the innocence of an accused.

The second challenge is the insufficiency of funding and infrastructure to run and operate the program on a full-time basis. Without a track record of successful acquittals, IPPN is finding it difficult to secure regular financial support to establish the clearing house. We have not been successful in obtaining seed money to finance the operation of the Network for even one year to work on the IPPN organizational structure and to formalize memoranda of agreements with law schools. To date, we have no personnel working full-time on the program and everything is done on a voluntary basis.



Volunteers of IPPN in 2019

In 2018 and 2019, two practicing lawyers volunteered to work with our laboratory to run a seven-week internship for law and postgraduate students that opened discussions on wrongful convictions and human rights, at a time when Philippine President Rodrigo Duterte had been pushing for the reinstatement of the death penalty in Congress, and amidst an escalating number of extrajudicial killings in different parts of the country.

In 2020, the organization was re-named as the 'Innocents Project Philippines Network' in order to emphasize our work with persons who had been wrongfully convicted, human rights concerns in the treatment of prisoners in overcrowded jails, and social injustice resulting from the Philippines' history of martial rule, and the compounding contribution of economic poverty to crimes in developing countries, in discussions on innocence.

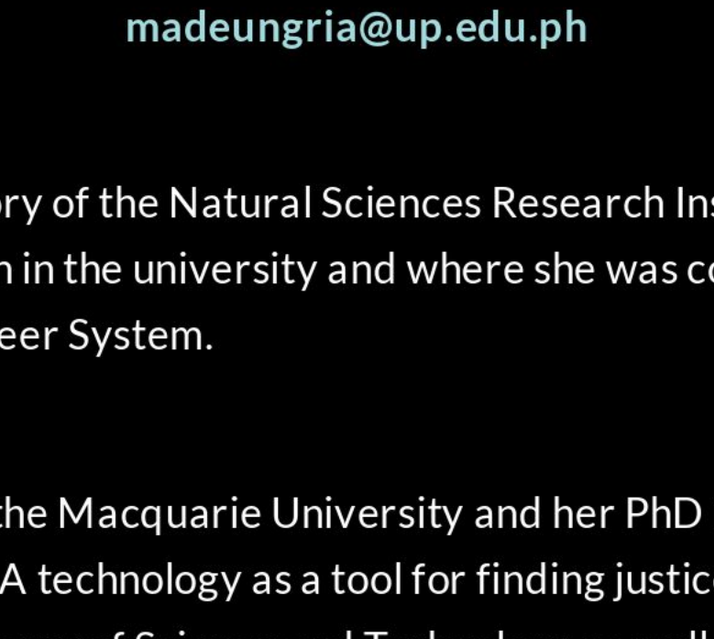
Both internships ended with a visit to the National Penitentiary in order to provide some form of support to elderly prisoners, aged 65 and above, and to expose future lawyers and professionals, some of whom have never visited a jail, to the plight of inmates inside overcrowded prisons in the Philippines.

In the future, we plan to partner with various law schools in order to provide institutional support for IPPN through their legal aid clinics so that we can transition out of its current ad hoc state. We hope to set up a clearing house that can channel inquiries and cases to cooperating law schools and to tap previous IPPN law interns who are now practicing lawyers for assistance in doing this work. Additionally, we are looking at the possibility of advocacy work with the legislature to ensure that the infrastructure for the proper collection and storage of evidence is put in place.

Because of the high rate of erroneous conviction in death penalty cases that was reported by the Supreme Court and the thrust of the present administration to reimpose the death penalty as its most powerful weapon against the war on drugs and other crimes (De Ungria & Jose, 2020), there is a moral imperative for an organization such as the IPPN to be a beacon of hope for wrongfully convicted persons in their quest to obtain justice. We trust that in the future, IPPN would also be able to demonstrate to the Filipino people and the world, how forensic science can touch hearts, inspire minds and embrace humanity.

This article is based on the talk entitled 'Challenges in Establishing an Innocence Project in the Philippines: The Innocents Project Philippines Network Experience' that was delivered by the author during the 72nd Annual Meeting of the American Academy of Forensic Sciences in Anaheim, California on 21 February 2020. The author received the 2018-2019 Henry C. Lee Scholarship awarded by the Forensic Sciences Foundation Inc. during the said conference. The author would also like to acknowledge the many volunteers who through the years have kept helping IPPN in various capacities. Special thanks to our partners from the Free Legal Assistance Group (FLAG), the Coalition Against the Death Penalty (CADP), the Philippine Jesuit Prison Service (PJPS), the University of the Philippines Office of Legal Aid (UPD-OLA), the law schools of the Ateneo de Davao and De La Salle University, and science researchers of the Natural Sciences Research Institute and the Institute of Biology, University of the Philippines Diliman.

More information on IPPN can be found at
https://sites.google.com/site/innocenceprojectphilippines/.



Maria Corazon A. De Ungria, Ph.D.

DNA Analysis Laboratory, Natural Sciences Research Institute, University of the Philippines

madeungria@up.edu.ph

Dr. Maria Corazon A. De Ungria heads the DNA Analysis Laboratory of the Natural Sciences Research Institute, University of the Philippines, Diliman, where she holds the position of University Researcher V, the highest researcher position in the university and where she was conferred a Scientist II rank in the Philippine Civil Service Commission/Department of Science and Technology Scientific Career System.

Dr. De Ungria received her Bachelor of Science with Honors from the Macquarie University and her PhD in Microbiology from the University of New South Wales both in Sydney, Australia. Because of her work in promoting the use of DNA technology as a tool for finding justice. Dr. De Ungria had received prestigious scientific awards such as the Outstanding Young Scientist from the Philippine National Academy of Science and Technology as well as The Science Academy for the Developing World (TWAS).

Dr. De Ungria was named as the first Filipino regional fellow affiliate of TWAS from 2007 to 2011. Her type of leadership was recognized by different sectors that awarded her with The Outstanding Young Men award, The Ten Outstanding Women in the Nation Service award, and the Asia Society Young Leader Award. Dr. De Ungria won the search for the Outstanding Woman Researcher in the Life Sciences organized by the Third World Organization of Women Scientists in Malaysia and was named as a one of the first two National Fellows of the L'Oreal – UNESCO Women in Science Program. In 2014, the National Research Council of the Philippines gave one of the Life-time Achievement Awards to Dr De Ungria.

In 2017, the Philippine Civil Service Commission named her as one of the honorees for the 'Dangal ng Bayan' award for her work in advocating for the use of science to help victims of abuse. In the same year, the Australian Global Alumni Network named her as the Australia Alumni awardee for the Philippines.

After 20 years in government service, Dr. De Ungria continues to advocate for the use of excellent science in nation building, recognizing the power of science in broadening the base from which we can find creative and novel solutions for the problems that afflict society. For Dr. De Ungria, DNA is a powerful catalyst for change and she works to be a change-maker through her dedication to science at the service of society.

Five Leadership Priorities in Times of Distress

John Collins, Critical Victories



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Leadership is easy when times are good. It doesn't require much skill or talent to influence people who aren't confronted by any challenges. But when times become difficult, we get a front-row seat to a leader's true abilities and temperament.

Leading through times of distress is challenging, to say the least. The more intense the distress, the more challenging the leadership effort becomes.

It goes without saying that 2020 has been a year like no other. We have never witnessed nor experienced the kinds of personal and professional disruptions that have overtaken nearly every aspect of our lives.

I recall September 11, 2001 like it was yesterday. I was the director of the DuPage County Crime Laboratory in Wheaton, Illinois and we were in the middle of our five-year accreditation inspection when the attacks happened. That day, as well as the days and weeks and months that followed, were very painful. Life didn't feel the same. Work didn't feel the same either.

But on a national scale, the grip the attacks had on our personal lives went away as quickly as it came. Yes, the horrors we felt and witnessed stayed with us. But we could go to the store. We could go to work. We could visit friends. Heck, with the exception of a short travel ban, we could do whatever we wanted to do and go wherever we wanted to go.

The coronavirus pandemic and the resulting shutdown of our lives are unlike anything that's ever happened in human history. And for those of us tasked with the responsibilities of leadership, we are confronted by the enormous challenge of coping with our own distress while bringing as much comfort and normalcy to our teams as we can.

Leading during times of distress is not easy. But, by the same token, it is also an opportunity to demonstrate competent leadership and earn the long-term trust and confidence of your team. So whether you're dealing with challenging times now or in the future, there are five priorities on which you should focus.



1. Set clear goals and focus on them

Crisis is debilitating because it robs us of our sense of relevance. We become victims of circumstance, left to feel powerless and directionless, like a ship without power in stormy seas. A dear friend and colleague of mine once encouraged me through a very challenging time in my career. He said, "when you're going through hell, keep going." He was right. The promise of a brighter tomorrow is the medicine we need to get through a darker today. When times are most difficult, it is important to rally yourself and your team around a set of goals that bring energy and commitment. Those goals become your beacon of light and distract you from the feelings of doubt and uncertainty that otherwise consume you.

2. Put your team before yourself and others

No individual is more important than the team. Never is this truer than during times of distress. Everything that is said, every decision that is made, and every action that is taken should be for the good of the team. When individuals prioritize their teams, they emotionally distance themselves from the challenges at hand - it is no longer about them because it is about the team. As a leader, resist the temptation to talk about yourself or make yourself the subject of conversation because you are not. Make it about your team and watch how your team rises to meet the challenges before it.

3. Allow your people to see your discomfort

This is not the time to stroke your ego and act like you are unaffected by what is going on. Doing so strips away both your humanity and your credibility. People don't want to be led by a robot. They want to be led by a human being, someone who feels what they are feeling. It's okay to be scared. It's okay to be angry or frustrated. But never allow it to come at the expense of your confidence. Your team should see you as leader who intends to succeed in spite of what's going on and the emotions you are experiencing. People are more likely to follow and support the leader who is struggling than the leader who is putting on a show.

4. Stay visible

During times of distress, it is tempting to want to isolate yourself. Don't do it. Stay visible and close to your people. Keep your door open and make an effort to check in on people to make sure they are ok. And remember, you are still alive and breathing so smile and laugh when you can.

5. Meet more often

In June of last year, I participated in a 430 mile, 7-day bike ride through the Rocky Mountains. Some of the climbs took nearly 3 hours to reach the tops of the passes, during which time every minute felt like an hour as each rider coped with burning leg muscles and oxygen deprivation. A common strategy used by cyclists on long climbs is to pick out small objects up ahead – such as trees, rocks, or road signs - and ride to them, repeating over and over again as you go along. Each object becomes a small victory and breaks the monotony of the climb.

Similarly, meeting with your team more often can break up the monotony of a crisis. No, these meetings should not be a waste of time. They should be fruitful, constructive, focused, and enjoyable (if possible). The more difficult the challenges your team faces, the more often you should be pulling together as a cohesive unit to encourage each other and discuss your goals. Until the major victory of getting through the crisis is achieved, give your team small victories to enjoy along the way.

As the old saying goes, when the going gets tough the tough get going. But it really isn't about being tough. It's about being smart, creative, and committed to your mission. Leading through times of distress can be very challenging, but it's also an opportunity to test the limits of your leadership abilities.

You and your team will be stronger because of it.

John M. Collins is an executive coach, leadership strategist, and facilitator specializing in high-stakes, high-impact teams and organizations. He is also the creator and facilitator of the Executive Accelerator for Forensic Science Professionals, a 12-week intensive leadership immersion for developing executive leadership skills in forensic science. Visit John at https://www.criticalvictories.com or click here to schedule a call.

The International Frontier in Forensic DNA Sequencing

Interview Written and Condensed by Carol Bingham, Promega

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Charla Kristen Marshall is the Chief of the Emerging Technologies Section at AFMES-AFDIL. She received her B.A. from The Ohio State University, and M.A. and Ph.D. from Indiana University, Bloomington. Her background is in molecular anthropology and ancient DNA.

Dr. Marshall has a keen interest in new DNA sequencing methods. We asked her to comment on some of the more promising new technologies that are being added to laboratories around the world.

Which multiple parallel sequencing (MPS) applications are currently fully validated and implemented in labs?

I am more familiar with the status of MPS in the United States from my SWGDAM involvement on the Next Generation Sequencing (NGS) committee. There are a few laboratories that have MPS applications online right now.

For example, our lab, the Armed Forces Medical Examiner System's Armed Forces DNA Identification Laboratory (AFMES-AFDIL) has two mitogenome sequencing applications in use. The first is a hybridization capture method for degraded samples, and the second is a PCR-based method for reference sample processing. Both methods use the MiSeq or MiSeq FGx for sequencing.

The California Department of Justice also uses MPS for its mtDNA sequencing in the missing persons unit. Their lab validated the Precision ID Identity Panel on the Ion Chef and Ion Torrent.

Then there are many other laboratories in various stages of the validation and implementation process. These include the FBI Laboratory and Ohio Bureau of Criminal Investigation that validated the PowerSeq CRM Nested System using the MiSeq. The DC Laboratory and the California Department of Justice validated the ForenSeq system for STR typing.

Additionally, Verogen led an inter-laboratory study of the ForenSeq system that involved AFMES-AFDIL, DC Laboratory and UNT, to demonstrate its utility for STR typing. UNT has certainly been playing a leading role in MPS validation efforts, and they will soon be implementing the Precision ID panel in their Center for Human Identification. Collectively, this progress has led to NDIS approval of three commercially available MPS kits (Precision ID Whole MtDNA Genome, PowerSeq Control Region MtDNA, and ForenSeq). I imagine that more US laboratories will be adopting MPS officially now that these kits have been given the green light.

The status of the international laboratories is changing rapidly. Some laboratories have MPS applications online already. These include, for example, the Laboratory of Scientific Police of Lyon in France, which is using the ForenSeq system. The Swedish National Board of Forensic Medicine uses the QIAseq Investigator SNP ID Panel and the MiSeq FGx for sequencing. The Institute for Legal Medicine at the Medical University of Innsbruck in Austria has implemented the Precision ID Whole MtDNA Genome Panel as well as and a primer extension capture method for mtDNA sequencing on the S5. The Netherlands Forensic Institute has an internally developed mtDNA control region assay that uses MPS.

Also based in the Netherlands, the International Commission on Missing Persons has developed a trialelic SNP panel for extended kinship analysis. They have been using the QIAseq chemistry with unique molecular indices (UMIs) and the GeneRead sequencing technology to validate their SNP panel for missing persons applications.

What are the hurdles to overcome for a lab hoping to bring MPS applications into practice?

It seems that the biggest hurdles to overcome for labs hoping to bring MPS applications into practice include the associated costs such as the initial investment in the sequencing system, the translational burden of validation and implementation, and the turnaround time since MPS is currently a longer process than CE.

There is also a significant gap in the implementation of MPS for STR typing, specifically, which is the lack of probabilistic genotyping software for MPS. Such software would be needed before many labs could even consider looking into MPS for their casework.

What benefits are offered by MPS compared to "traditional" STR methods?

There are several benefits that MPS offers over traditional CE methods for STR genotyping. These include enhanced discriminatory power because the sequence variation contained within the STR amplicon is revealed. This makes population frequency estimates of STR alleles more precise, in theory. Yet the STR sequence data must be produced from global populations, and practical aspects of STR sequencing have to be worked out, like nomenclature and allele calling guidelines. Many labs, such as NIST and UNT, are coming together to make STR sequence information of use to the forensic community.

Technologically speaking, the detection of STRs by sequencing offers several advantages to detection by size. First of all, size is no longer a limiting factor to the loci that can be multiplexed in a PCR reaction. In CE-based detection, only loci of disparate size can be assigned the same fluorophore for simultaneous electrophoretic separation, and most instruments allow for a maximum of five or six fluorescent signals. This means that a maximum of a few dozen STRs can be multiplexed for current CE technology. In MPS, almost any loci can be included in a multiplex, given compatible PCR primers. This means that autosomal, Y, and X STRs can be combined in the same multiplexed PCR reaction, which can be beneficial when DNA extracts have limited volume or low template DNA.

Another strength of MPS is locus-specific allele detection that is particularly beneficial for challenged samples with low signal intensity. The locus-specific detection of MPS reduces the background noise when compared to the size-based detection of CE, which is aggregated from all the amplicons in the same dye channel.

Do you expect to see MPS replace STRs at some future point? If so, when would you predict this would happen?

This is an interesting question. I do expect to see MPS replace STRs in the future. MPS is especially conducive to SNP genotyping, which has a number of benefits over STRs. I see the community adopting SNPs for forensic use in the near future, perhaps to be used in tandem with STRs for a defined or even a prolonged period. Then I envision the community phasing out STR typing as reference databases become antiquated due to changing population dynamics, or for criminal databases, due to generational turnover. Perhaps 30 years from now, we will only be looking at SNPs.

What are the most promising DNA sequencing methods on the horizon?

The most promising DNA sequencing methods on the horizon, in my opinion, involve hybridization capture and SNP genotyping. These are two methods that are widely used in clinical and medical genetics as well as ancient DNA. Therefore, these methods can be adapted to any sample type, from high quality reference samples to degraded and inhibited DNA. The flexibility of hybridization capture and SNP genotyping to accommodate the broadest range of DNA samples can revolutionize forensic casework. We will overcome the technical problem of having no results or having uninterpretable results, and we will be facing more of the ethical and fiscal problems of having to prioritize which samples to test - because they all will yield usable results.

What are the ethical and legal ramifications to be considered with new marker sets?

The ethical and legal ramifications to be considered with new marker sets are those that relate to genetic privacy and genetic discrimination. In this technological age in which the ascertainment of genetic information is an easy pursuit, it is important that forensic scientists consider what should be assayed. It is possible to perform whole genome sequencing (WGS) on DNA samples, and as sequencing costs decrease, this may be an affordable approach in the future. Yet WGS would reveal an individual's genetic predisposition to disease, creating a genetic privacy issue. In my opinion, the basis for new marker sets should be scientifically driven and should take a targeted approach. Even though it may be more costly in the future to conduct targeted sequencing rather than WGS, we ought to limit ourselves to the analysis of the most critical genetic information that will allow us to solve our cases.

Genetic genealogy has become a powerful tool for solving cold cases. Do you see this expanding to more countries outside of the US?

Yes, genetic genealogy has become a powerful tool in the US and has seen some use in Europe as well. However in my opinion, the US will be unmatched in its use of genetic genealogy, and this tool will not hold the same value in other countries. The reasons are many-fold, ranging from the size of the direct-to-consumer DNA testing market outside of the US, the diversity in DNA testing laws worldwide, cultural views about genetic privacy, etc.

Charla, thank you for talking with us today. We look forward to seeing what the future holds for forensic DNA!



Charla Marshall
Chief, Emerging Technologies Section, AFMES-AFDIL

Charla Kristen Marshall is the Chief of the Emerging Technologies Section at AFMES-AFDIL. She received her B.A. from The Ohio State University, and M.A. and Ph.D. from Indiana University – Bloomington. Charla's background is in molecular anthropology and ancient DNA. Before coming to AFDIL, she was a postdoctoral research associate at the University of Illinois. For fun, she enjoys spending time with her family and going to the beach.

Advertorial

Successful Forensic Lab Automation Starts Here

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

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You might equate automation with increased throughput and reduced hands-on involvement, and you'd be right. What you might not know, however, is that the way that you approach automation is just as important as the robot itself.

What does that mean? In a nutshell, it means that by looking at laboratory operations from multiple angles and applying small, easy-to-implement changes, forensic DNA labs can develop automated workflows that maximize efficiencies and make notable impacts not only to sample backlog and turnaround time reductions, but quality metrics as well. Here, are some insights to ease your successful transition into your very own automated ecosystem.



Bye-Bye Plug & Play, Modular is the Modern Way

Is transitioning a task from manual to automated as simple as your word processing software's find/replace function? Of course not. Although, this does happen when providers restrict their robotic solutions to work exclusively with their assay chemistries.

The "plug & play" or "modular" approach to automating individual workflow steps (e.g. nucleotide extraction) seems straightforward, relatively inexpensive, and easy to validate and implement. Plug & play automation may eliminate task-specific labor, but all the indirect activities, like sample transfers or incubation and mixing steps, are still manual. Moreover, you can't just validate an extraction robot by itself – you need the data that come from downstream processes such as quantification and DNA typing. This means that traditional plug and play solutions are not saving as much time or reducing as many variables as you might expect. So, why stop at a single step? Automate more of your process to realize efficiencies in both validation and casework. Today, modularity is about choosing universal robotic solutions that reduce touch points from one step to the next within a given workflow, while increasing reproducibility. Universal robotic platforms expand the contribution that each instrument makes to the overall workflow, decreasing the number of instruments required. They also share common deck accessories, programming language, and even consumable products, enabling flexibility in assay chemistry choice and workflow direction enhancing the lifespan of your capital purchase.

Take a look at your workflow with a fresh set of eyes, and physically map the process. Having this visual helps to eliminate roadblocks and pain points throughout the process, not just at isolated steps. This will inform your purchasing requirements and immediately let you know how the tools you already have are being (under)utilized.



Process Flows to Efficiency

It's not just workflow or sample flow that matter. Analyst flow through the lab is just as important. Go back to that whole-workflow map we talked about and include detail on how people are physically moving through the lab space over time. Include all the details regarding who, what, where, why, and how. You might be surprised at the labor inefficiencies, quality risks, and other bottlenecks that you uncover that can easily be solved by automation.

For example, where can manual handoffs be reduced? This may be as simple as changing labware to a more automation-friendly type. At what points do analysts manually enter data or repetitive information? Worklists are easily, and sometimes automatically, created. How far do analysts transport samples from one step to another? Integrated devices may be less expensive than you think. When are people competing for shared equipment? Scheduling software easily solves this issue. Lastly, consider using everyday laboratory tools like your LIMS, which is commonly underutilized but can provide a beneficial framework for all of your flows.

Understanding this process flow allows you to create smooth, integrated automated workflows that increase throughput, decrease quality issues and unplanned downtime, and reduce turnaround times. On top of that, analysts can spend less time on low value tasks and more time applying their high value expertise where it matters most.



(Deck) Real Estate is King

Sure, throughput is the superstar consideration when selecting a robotic workstation, but the robot's workable deck area is King! The deck's size is what enables your workflow to be truly automated. Pipette tips, consumables, reagents, peripheral devices (i.e. heaters, shakers, on-deck thermal cyclers, plate sealers, and more), and samples must all reside on the instrument's deck.

Need filtered tips for massively parallel sequencing? These don't stack and, unless you have adequate deck real estate for them, you will be tied to a series of endless labware reloads. Assay mix en place, to borrow a cooking term, reduces manual restocking time and helps the robot to be as efficient as possible when moving labware and samples around the deck. Have a thermal cycling step in the middle of a workflow? An on-deck thermal cycler eliminates multiple manual sample interactions. Once you've laid out your process and studied it with colleagues, you can determine how much deck real estate that you need.

Want to really maximize your deck real estate? Opt for a solution with storage for frequently used consumables. Not quite ready yet? That's okay, too. Modularity in automated liquid handling platforms means that deck layouts can be changed and upgraded as your workflow requirements evolve. Thinking "automation ecosystem" yet?



Don't Let Your Samples Control You

Instead, leverage your automated workflow to reign in the chaos. Streamlined automated workflows already exist for the majority of HID sample types – from simple reference samples to tough evidentiary samples that are environmentally or chemically challenged, degraded, embedded in difficult matrices, of very high or low volume, and more – and separate workflows can be combined on the same instrument to maximize the number of different runs that you can conduct each week.

Your instrumentation is modular and universal, right? So modify your deck and script slightly to alternately work property crimes and sexual assault cases. Saliva on paper got you down? Consider automating samples on specialized matrices within a separate branch of your automated workflow. In this case, add liquid handling to your automated punching device to create a complete sample to answer solution.

Now that you are the master of your samples, look around your deck to see how you can fine tune other workflow details.



Approach Transformation from Every Detailed Angle

But wait, there's more! It's not just the sample. Not just the chemistry. Not even the people. Consider all of the other "stuff" that goes into your process. Consumables and labware vessels can be tricky. Robots can't reliably manipulate some consumables like unframed FTA paper, microtubes, special tubes such as those with spin baskets, and unskirted PCR plates.

However, most consumable products have automation-friendly alternatives, such as microtubes that can be capped and uncapped in a hands-free manner, completely automatable spin basket tubes that can be expanded and collapsed, and sturdy PCR plates that can be more easily manipulated. All of these products are easily integrated onto universal robotic platforms. On deck peripheral devices like those that we previously mentioned, can perform a variety of actions on automation-friendly consumables, further increasing walk away time

Small changes to the type of consumables, vessels and devices that you use, if needed, can make a big difference in the long run. Not sure what or how to change some of these items? Contact your local automation representative for expert advice.



Sterile ≠ Clean

While we are on the topic of consumables, think about this. Why would you specify sterile tips if your reagents aren't sterile? Sterile means free from microorganisms, but it doesn't mean free from molecular contaminants like trace nucleic acids, enzymes, and other PCR and DNA typing interferents.

Molecular biology grade assay reagents are tested to be free from molecular contaminants, so it's only natural to expect this from your pipette tips and consumables, too. Tips from some leading automation manufacturers are made completely robotically without any human intervention. Ask about a manufacturer's quality standards and lot testing documentation.

If you are concerned about the risk of aerosol contamination, then consider using filter tips. Choose an enclosed liquid handling platform, and go the extra mile in clean air protection by adding features such as integrated HEPA filtration. Lastly, add ultraviolet lamps to your robot to complete your multi-strategy for nucleotide decontamination.



Act Now to Prevent Problems Later

Much like a car engine tune-up, automation maintenance may seem like an afterthought to some naysayers who scoff at the idea of continuous upkeep. But don't forget overall preventative maintenance measures for your automated workstation. These make sense and keep your workflows running cleanly and smoothly. Your work is a matter of life and death. Literally. Why risk unplanned and disruptive downtime?

Even the seemingly smallest actions, like pre-programmed daily, weekly, and monthly preventative maintenance protocols included in most automated tools help to ensure smooth instrument operation. On top of that, twice yearly automated instrument tune-ups can spot wear-and-tear and correct tiny issues before they grow into major performance deviations that may call into question as much as a full year of data! As an added bonus, integrations such as HEPA filtration, can be rolled into your preventative maintenance plan eliminating the need for a separate benchtop hood and its maintenance plan.

For more information, visit our webpage or email Kevin.W.P.Miller.Ph.D.



A Fresh Take on Cold Cases

The Utah Cold Case Coaltion

Interview Written and Condensed by Carol Bingham, Promega

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There are currently over 400 cold cases throughout the state of Utah. These unsolved crimes include homicides, missing persons, and unidentified deceased individuals. State and private labs do their best to bring closure to these cases, but their resources and budgets are limited.

In 2017, the non-profit Utah Cold Case Coalition was formed under the direction of Salt Lake City attorney, Karra Porter. Their services go beyond reviewing original case files. They interview witnesses and suspects, go undercover, offer rewards, and look for bodies with cadaver dogs, ground penetrating radar, and ground searches.

Late last year, they even opened their own DNA laboratory, which is the first non-profit DNA lab in the United States.

We talked with Karra Porter to learn more about the Utah Cold Case Coalition and the new lab. Among the questions we asked her are what prompted her to organize the coalition, challenges faced, and the difference between operating a non-profit and for-profit lab.



What prompted you to organize the Utah Cold Case Coalition?

In 2017, the family of Rosie Tapia emailed me. I recognized the name – I knew she was a 6-year-old girl who had been raped and murdered. They wanted to know if I could help them. Their daughter's 1995 murder had never been solved, and they were concerned whether local police were still working on the case. I met with a private investigator who was donating his time, and we decided that there were ways we could supplement (not supplant) law enforcement efforts in cold cases. We were proved right at our first press conference in November 2017 – a witness in Rosie's case came forward who had refused to speak with police. That led to a sketch (by a volunteer professional police sketch artist), which led to several tips. We believe this case is on the verge of being solved.

What are the biggest challenges you face when tackling a cold case?

Missing or incomplete files – especially if the case is 30 or more years old. Also, there are a few law enforcement agencies whose policy is not to share information even with family members. That's one reason why families are especially frustrated at those agencies.

How do you decide which cases to accept and work?

We accept and work on all unsolved homicides, disappearances, and unidentified human remains. We started in Utah, but over the past couple of years, we've had cases referred to us from other states. (Some of these cases have been referred by law enforcement and other government agencies that don't have jurisdiction over the suspected crime.) The numbers of unsolved cases are overwhelming, but we have a growing base of qualified volunteers.

Can you speak to the importance of coordinating resources with other agencies?
What other agencies are most helpful to you?

We don't exactly coordinate with agencies, because as a private entity we have more freedom. We try to provide resources that will save law enforcement time. For example, sometimes we get a tip that we are able to eliminate without wasting law enforcement time. For example, one woman told us that her ex-husband had murdered a man and she wanted the reward we were offering on the case. We were able to confirm that her ex-husband was actually in prison at the time.

We're also contacted regularly by people who refuse to speak with the police. Some are afraid that they will be criminally charged for not telling what they knew earlier. Some just don't like cops. One woman called me because, she said, her husband said he would kill her if she called the police. "You're not the police," she figured.

How does operating a non-profit differ from traditional law enforcement agencies?
What is your source of funding? Are there advantages or disadvantages to this model?

There are both advantages and disadvantages to being a nonprofit. One advantage is that we're not constrained by the Fourth Amendment. Because we're not a government agency, information that we learn or evidence that we find is generally not subject to a motion to suppress. Another is that some people feel more comfortable with us than with the police.

One significant disadvantage is that we usually have less information than the investigating agency. We sometimes bark up wrong trees for a while because we don't know that they have already been eliminated.

Also, we have to rely on donors and volunteers. We did receive a significant grant from the federal government (administered by the State of Utah) to help with our nonprofit DNA lab.

Our laboratory – the only nonprofit forensic DNA lab in the country – has state of the art technology and seasoned personnel thanks to the willingness of some believers to make us favorable long-term loans. We will be providing at cost accredited DNA testing for unsolved homicides, rapes, and court-authorized innocence challenges. Our testing will also be available in other cases, including to defense counsel and other laboratories.

Can you talk about the importance of community volunteers?
What services/support can they provide to cold cases?

We could not do what we do without volunteers. Except for our lab personnel, we are all unpaid volunteers. We have dozens of volunteers who just want to help – be it picking up a copy of a court record, or operating a bobcat, or organizing case files, or looking for unmarked graves with ground penetrating radar.

In 2019, we provided evidence to a police department in Utah about a murder case that had been closed by a Henry Lee Lucas confession. The law enforcement agency agreed to reopen it. We then had dozens of volunteers start looking at other Lucas cases throughout the United States that should be reopened.

You are using "cold case playing cards" as a tactic for raising awareness and finding leads for cold cases.
Have you had any success with this effort?

Our cold case playing cards are still new. We donated 1,600 decks to county jails in late 2019. We haven't had any tips yet, but these cards have solved murders in other states, so we are keeping our fingers crossed.



Photo credit: The Salt Lake Tribune

What is Rosie's law?

When we started our Coalition, we quickly realized that there was no centralized location to learn about cold cases. Some jurisdictions had individual websites, but others provided no public information about their unsolved homicides. For example, one of Utah's highest profile murders was not listed on any website. This made it impossible to compare the facts of cases, look for trends, or even just to know how many unsolved murders and disappearances were out there.

We contacted a state senator, who agreed to run a bill to create a state cold case database. For homicides more than three years old, law enforcement is now required to submit information to the database. Some information is public, but most is accessible only to law enforcement.

Can you talk about a case that's been successfully solved through the work of UCCC?

We will be able to shortly. We have nearly a dozen cases that have been reopened, or presented to prosecutors, or similar activity as a result of our investigations. We have agreed not to disclose specific cases until charges are brought or we are informed that they won't be brought.

How important are genetic genealogy databases to the success of your cold cases?

Genetic genealogy databases are incredibly important to solving tens of thousands of unsolved murders in the United States. We feel strongly that people should have the right to submit their own DNA for law enforcement to compare. The first piece of equipment we bought for our nonprofit DNA lab was one that will produce genealogical forensic results suitable for uploading to databases like GEDmatch. Solving these cases is important, not just for the victims in that particular case, but because it is a constant reminder to potential perpetrators that they will be caught.

How can people learn more about your program and provide help/support?

Our general website is at coldcaseconnection.com. We also have an active Facebook page under Utah Cold Case Coalition. Our podcast is Cold Case Talk, available on Apple, Spotify, etc., or at ColdCaseTalk.com.

Forensic Scientist of Note

Dr. Walther Parson

Interview conducted by Martina Vokurkova Chocova, Promega



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One of the most familiar names in forensic genomics is Dr. Walther Parson. An Associate Professor at the Institute of Legal Medicine at the Medical University of Innsbruck, his resume is long and is filled with many notable accomplishments. He supervised the establishment of the Austrian National DNA Database Laboratory in 1997, where he currently oversees the High Through-Put DNA Database Laboratory and the Forensic Genomics research group.

Walther has been instrumental in assisting with the identifications of victims of numerous mass fatality incidents including the 2004 tsunami. In 2014, he wrote a book called Irgendwann Kommt Alles ans Licht (At Some Point Everything Will Come to Light) detailing his work in identifying the missing Romanov children, Wolfgang Amadeus Mozart, Günter Messner, and German poet, Friedrich Schiller.

As engrained into forensic genomics as Walther has become, it's strange to think that it all happened by chance. In a past interview with ISHI, Walther shared that while obtaining his degree in Zoology, he worked as a taxi driver. Upon returning home from vacation in September of 1994, he planned to return to driving taxis when a friend told him of a contract position at the Innsbruck Institute of Legal Medicine. Though the job paid less than he made as a taxi driver, he thought it would be a better investment into his professional future and would buy him time to look for a "proper job." Luckily for all of us, fate intervened, and the short-term position has led to years of advancements for the field of forensic genomics.

Dr. Walther Parson has presented on the ISHI stage many times before. We are honored he is returning for the 31st International Symposium on Human Identification this September, where he will be presenting on locating the relatives of Ötzi the Iceman.

In 1991 the 5,300 year-old mummy, Ötzi the Iceman, was found in a melting glacier in the Alps. Using a sample of hip bone, scientists sequenced his genome to determine how he was related to regional ethnic groups. Later, Walther's team compared DNA on Ötzi's y-chromosome with blood donated by 3,700 people in Western Austria to see how many descendants exist.

Last year, at the 20th European Forensic DNA Working Group Meeting in Hamburg, Germany, our Promega colleague, Martina Vokurkova Chocova had the opportunity to sit down with Walther so that we can get to know him a little better.



You studied biology and then forensic molecular biology in Innsbruck, and right now, you are considered to be one of the leading gurus in the forensic field. Tell me, what was the impulse for you to become a forensic scientist? Was it fate or did you want it from the start?

Well, I should probably say that I really wanted it from the start, because it very much fit my career, but the truth is I was searching for a job after I completed my master's in biology. I did a road trip. I came back and needed to work to get money, and I thought I would do taxi driving. That's what I did during the studies. Three days after I came, this job position opened, and I took it.

Good for us! So, what would be your elevator sentence. Say, you're in the lift and there was someone who doesn't know you, because he or she is from a different field. So, how would you introduce yourself? Who is Walther Parson?

Well, I would say, "Hello, my name is Walther Parson, I am a skier and mountaineer, and for professional, I'm a forensic geneticist."

That's nice! My second question is about your book, because not everyone knows that you wrote a book. Are you considering translating it into English, because it's available only in German. What is the book about?

The idea for the book came from a publishing company. The publisher sort of persuaded me to write a book for the broad community (rather than the scientific community writing that I usually do). I started to like it the more that I was thinking about it. So I thought, if I'm going to write a book in forensic genetics, I don't want to write about the fate of the witness or the brutality of the murderers or the blood. There are enough books that describe this, and I know people like it a lot, but I thought I would like to put an emphasis on the science. So, I tried to take the challenge to translate the science into very simple words to make it understandable for a broader audience. And I think I've partially succeeded with this. I know that it's very much appreciated by students, or by people who have a scientific background or interest. One of my friends said, "You can't read your book on the toilet," which tells me that it's kind of a level too high for this kind of audience, but more or less, I'm very happy with the outcome. And what I hear from colleagues is that they would like to read the book, but they don't understand German. So, it's a consideration, but it's quite, quite difficult to translate a book from German to English. Not the translation per se, but the process of commercializing it. So, I didn't pursue it really strongly, but that's probably something that I would need to do in order to get this done. If time allows, I probably will do it.

Ok, well maybe your next book will be in English?

That would be the best idea.

The third question is a little bit more of a private question. You have a very happy family life, right? You have three daughters, two of which are twins. I know very well how challenging that can be sometimes. So, how do you balance your family life and your work life? You travel quite a bit, so how do you do that?

That's true. Well, first of all, I need to have somebody who is taking care of the family business, and that's my wife. And, second, so I'm trying to constantly refine work time with private time, which means I travel, and I'm gone a lot of the time, but when I'm here, I try to be active in it. Not working, besides being at home or doing emails or whatever. I try to be with the family. That helps a lot, because you generate quality time, and quality time is what counts. The price I have to pay is that I don't have much time for my friends that I used to have when I was at university, so that is something that I need to work on. But what I also want to do very much is be out in nature. I like mountains very much, so I try to combine this with the family. It's a struggle from week to week. So, we always refine this. We make plans for the future, and we have our holidays already worked out for the year, so we know when we can have time together, and I also know when I need to travel for work.

Ok, and it works well I guess.

So far it works good, yeah.

Do you know how many publications you have?

No, I don't know that one.

Ok, well, when did you stop counting?

Oh my, I think I stopped counting very early. My first paper that I wrote as a first author dates back to 1998, and my second paper I wrote not before 2000. So, at this very early stage, I thought, "oh my God, this is going to take ages until I have a very comparable track record to other scientists." But then I figured out how science really works. Science works a lot in networking. You have a couple of different projects in different stages. You start writing a manuscript and you see that you lack some data, so you go back to the laboratory or have people do that work for you. You have PhD students, you have collaborators, you have post-docs. It's like cooking several meals. You need to take care of the different stages of the meals, and you need to know when they are good to put them on the platter and disseminate them. With that, if you like to do that, and if you like networking and collaborating, the publications come automatically. That's the time that I stopped counting them.

Well I found on ResearchGate that you have 554 research items there, 64,531 reads, and 12,487 citations.

I'm impressed!

I know, me too! The last question is a little bit of a tricky one. Just imagine you are in a jungle and you are on a tree. You have one gun with only one bullet inside, and under the tree there is a lion, a pair of pumas, and a jaguar. What will you do? Who will you shoot at?

Good question! I don't like to shoot animals to begin with, but apparently in that story I need to do that.

Well, you need to survive. That's the task.

All three of them can climb the tree, right? So, probably I will wait. They are hungry, right? They are starving. So, I will wait until they kill themselves, and I assume the lion will be the winner, and then I shoot the lion.

Ok, well that's a way to do it! The right answer, or one of the right answers is that you shoot the lion, which you said, then you put on the pumas, which are shoes, and then you drive off in the Jaguar. Thank you very much for your time and for this interview!

Arguing the Case for Probabilistic Genotyping

An Interview with Michael Coble and Jo-Anne Bright

Interview Written and Condensed by Tara Luther, Promega

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Probabilistic genotyping (PG) software is an invaluable tool for forensic analysts working to resolve complex mixtures, allowing analysts to draw conclusions about samples that were typically reported as inconclusive.

With approximately 100 laboratories in the United States currently using some form of PG software, cases that have been processed using this method have begun making their way through the court system, leaving analysts wondering how to best explain these techniques to judges, attorneys, and juries.

Michael Coble, Associate Professor and the Associate Director of the Center for Human Identification at the University of North Texas Health Science Center and Jo-Anne Bright, Senior Science Leader within the Forensic Biology group at the Institute of Environmental Science and Research Limited, are co-chairing a workshop during ISHI 31 to provide analysts with some direction.

In the "Arguing the Case for DNA Evidence Based on Probabilistic Genotyping" workshop, they will focus on drawing upon data, logic, case decisions, and scientific literature to present and defend DNA evidence based on probabilistic genotyping.

We interviewed Mike and Jo to learn more about the hurdles labs may experience when bringing PG software online, the advantages they've seen after implementing PG software, and resources available.

In your experience, how have labs been adapting to the use of probabilistic genotyping software in comparison to previous methods? What hurdles might a lab experience when bringing PG software online?

Someone recently said that labs were jumping into the adoption of probabilistic genotyping. That has not been our experience at all. Labs have taken a very scholarly approach to PG implementation. Some of the challenges labs are facing are how to communicate the resulting likelihood ratios, particularly if they are low level. This is of course not an issue restricted to PG but is new for many labs whose first experience with LRs is with the use of PG software.

Many labs are beginning to feel pressure to come online with PG software. What advice do you have to relieve the pressure that they are facing?

Labs are most likely to be successful with the implementation of PG software if they treat it like a project. By assigning resources, setting milestones, allowing analysts the time to complete the validation work and being realistic about timeframes labs will succeed. There are many labs in the US and internationally who have adopted PG and are using it for casework – over 50 in the US alone. Reach out to these labs as an additional resource. Find out what lessons they learned. As the saying goes, "the early bird gets the worm, but the second mouse gets the cheese." We have found that early adopters of PG software are very open to providing guidance and lessons learned.

What are some of the advantages that labs have experienced after implementing PG software into their workflows?

Labs are getting much more information from their forensic DNA profiles. As an example, one lab director announced at AAFS that they now have 19 to 34% more interpretable profiles since implementing STRmix in their laboratory.

Validating PG software can appear both daunting and cumbersome. There seems to be confusion about how many single source samples should be run during the validation process. Is there a magic number that you would run? Are there additional validation guidelines that you can share?

JB: My experience is mostly with STRmix and therefore my answer will be relating to that particular PG software. We recommend as part of STRmix implementation that labs test 100 single source profiles to model the peak height variability inherent to the lab system. We know from empirical data that things like DNA profiling kit, PCR cycle number, capillary electrophoresis instrument, and possibly even injection parameters have an effect of peak height variability. If you change any of these, you may have to re-tune your settings and that would require a performance check of your software.

MC: In addition to the single source samples, the laboratory must also run an appropriate number of mixtures to validate their software. Organizations like SWGDAM, the ISFG, and the UK Forensic Science Regulator have published guidance documents that laboratories may find useful in addition to several recent papers in the peer-reviewed literature.

Can you provide any guidelines on when labs should consider re-validating their PG software? For instance, what kinds of changes may occur in a lab that would warrant retesting? Or, if chemistries change, to what extent would re-validations need to be completed?

A new kit or new type of CE instrument would definitely require retesting of the PG software. Changes to kit chemistries would depend on whether peak height variances changed. It may be that a simple performance check could be undertaken to confirm that the changes are not material.

While some analysts are able to attend in-depth training on PG software, they are often asked to train others in the lab. Do any online training or refresher resources exist for analysts to refer to?

In 2019, the FBI partnered with the NIJ FTCOE to create a series of online webinars on PG. There were 8 modules in the series which was pitched to pitched at DNA analysts and legal professionals. We encourage people to check it out at: https://forensiccoe.org/webinar/online-workshop-series-probabilistic-genotyping-of-evidentiary-dna-typing-results/

Let's switch gears a little bit and discuss testifying on PG methods. What are some of the challenges that analysts are bringing forward? Are there any success stories that you've heard that you'd be able to share?

JB: In a 2019 survey of STRmix users, North American labs had reported over 65,000 cases. Analysts for these labs had given evidence in over 1300 court cases. There are literally 1000s of cases where the STRmix evidence has been successfully presented in court. In just one example, in 2018 DNA Labs International used STRmix to interpret mixed DNA profiles in a triple homicide in Jupiter, Florida.

MC: See our answer above regarding how to communicate low LR results. The movement away from CPI and RMP to LRs can be a challenge for laboratories at first. Other recent successes of PG include the exoneration of two men (one in Texas and one in Georgia) who served a combined 27 years in prison for crimes they did not commit.

How would you recommend analysts answer questions about switching from old mixture interpretation methods versus using PG software, such as reworking old cases? Do you have any guidelines for how to address this in court?

PG software provides substantial advantages for interpreting low-level, complex DNA mixtures over older methods. The software makes better use of the data by accounting for dropout rather than excluding the locus which was a common approach using manual methods. Our older methods were not necessarily wrong… they just didn't make the best use of all the data. Using PG, we now obtain higher LRs for true contributors and lower LRs for non-contributors.

What would you say to some of the smaller labs who are worrying about the possibility of Frye/Daubert hearings? Are there resources available to assist them?

There are a lot of resources available to help. We encourage analysts to reach out to the developers and other experts. There are many transcripts of other admissibility hearings that are available online. No laboratory should feel that they are alone in this process. Many analysts working in the field of forensic DNA testing may have never had to prepare for or endure an admissibility hearing. There is help out there!

You're both hosting a workshop called "Arguing the Case for DNA Evidence Based on Probabilistic Genotyping" at ISHI 31 this year. What can attendees expect to learn from this workshop? Who would benefit most from attending? Are there any pre-requisites for attendance?

No prerequisites! Everyone is invited. There has been a LOT of information relating to PG appearing recently either in scientific journals, personal blogs, the courts, and the press. We aim to cut through the noise and give the facts. The goal of the workshop is to highlight the key perceived issues with PG and to point attendees in the direction of the best resources so they can determine the facts for themselves.

Are there any other topics related to PG that you'd like to address in this interview or any words of advice for our readers?

Remember that you are not alone in adopting Probabilistic Genotyping and Likelihood Ratios. Yes, it takes time to purchase, validate, write SOPs, train, and implement new software. However, the benefits of PG far outweigh our previous methods that tend to throw away data.

To learn more about and register for the "Arguing the Case for DNA Evidence Based on Probabilistic Genotyping" workshop, visit our website.

Learn More



Michael Coble

Michael Coble, PhD, is an Associate Professor and the Associate Director of the Center for Human Identification at the University of North Texas Health Science Center in Fort Worth, Texas. Dr. Coble received his Master's Degree in Forensic Science and his PhD in Genetics from The George Washington University. He is a Fellow of the American Academy of Forensic Sciences and a member of the International Society for Forensic Genetics. He serves as a member of the OSAC Biological Data Interpretation and Reporting Committee and is an invited guest at the Scientific Working Group on DNA Analysis Methods (SWGDAM). He is a co-editor of the Forensic Biology subject area of WIREs Forensic Science journal and is a member of the editorial board of Forensic Science International: Genetics.



Jo-Anne Bright

Jo-Anne Bright is a Senior Science Leader at the Institute of Environmental Science and Research Limited (ESR) New Zealand, where she has worked since 1999. She completed her Bachelor of Science degree at Victoria University of Wellington in 1998 and Master of Science degree in Forensic Science at the University of Auckland in 2000. In 2015, Jo was awarded her PhD after studying advanced DNA profile interpretation topics. Jo has co-authored numerous papers and presented at a number workshops in this area, including in the US, UK, Asia, and Europe. Jo is one of the co-developers of STRmix™, expert software for the interpretation of forensic DNA profiles.

An Update from The Organization of Scientific Area Committees (OSAC)

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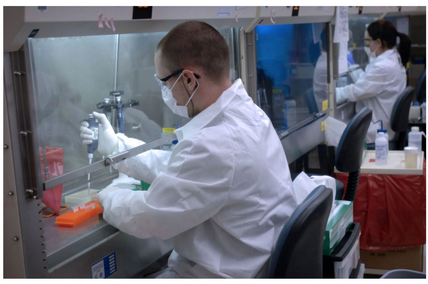
Two New Forensic DNA Standards Added to the OSAC Registry

The Organization of Scientific Area Committees (OSAC) for Forensic Science has placed two new standards covering the interpretation of DNA evidence on its registry of approved standards. This stamp of approval from OSAC, which is administered by the National Institute of Standards and Technology (NIST), indicates that these standards are technically sound and will help forensic laboratories improve their processes and methods.

OSAC is a professional organization whose 550-plus members have expertise in 25 forensic disciplines as well as scientific research, measurement science, statistics, law and policy. OSAC works to strengthen the practice of forensic science by facilitating the development and promoting the use of high-quality, science-based standards.



A forensic DNA analyst prepares a sample for analysis. (Credit: Fred W. Baker/Department of Defense)

This milestone is the culmination of an effort that began in 2015. The two new standards were initially drafted by OSAC, then further developed and published by the Academy Standards Board (ASB) of the American Academy of Forensic Sciences, and finally reviewed by OSAC for placement on the registry. The new standards are:

- ANSI/ASB Standard 020, *Standard for Validation Studies of DNA Mixtures, and Development and Verification of a Laboratory's Mixture Interpretation Protocol.*
- ANSI/ASB Standard 040, *Standard for Forensic DNA Interpretation and Comparison Protocols.*

Before laboratories can use a method to analyze crime scene evidence, they must perform validation studies and use the results of those studies to develop a protocol. These new standards include detailed requirements for conducting validation studies, developing protocols from them and verifying that those protocols work correctly.

> "Every forensic laboratory wants to put out the highest-quality data possible and the most accurate and reliable information and results. These standards will help them do that."
>
> —Robyn Ragsdale, senior crime laboratory analyst at the Florida Department of Law Enforcement and chair of OSAC's Biology/DNA Committee

In addition, the new standards are the first to focus on DNA mixtures, which occur when evidence contains DNA from multiple individuals. DNA mixtures can be more difficult to interpret than evidence that contains DNA from only one individual. Past studies have shown that different labs, or different analysts within a lab, sometimes produce different conclusions when evaluating the same DNA mixture. The new standards are aimed in part at helping labs achieve consistent and reproducible conclusions.

"Every forensic laboratory wants to put out the highest-quality data possible and the most accurate and reliable information and results," said Robyn Ragsdale, a senior crime laboratory analyst at the Florida Department of Law Enforcement and chair of OSAC's Biology/DNA Committee. "These standards will help them do that."

Two aspects of the new standards in particular will help with this. First, the verification step must demonstrate that a laboratory's protocols produce consistent and reliable conclusions with DNA samples different from the ones used in the initial validation studies. Second, the new standards require that labs not interpret DNA mixtures that go beyond what they have validated and verified. For example, if a lab has tested its protocol for up to three-person DNA mixtures, it should not interpret casework that contains DNA from four or more people.

These new standards complement the FBI's DNA Quality Assurance Standards. Those standards mainly apply to laboratories that upload data to the FBI's national DNA database, and they do not address how to develop and verify protocols for interpreting DNA mixtures.

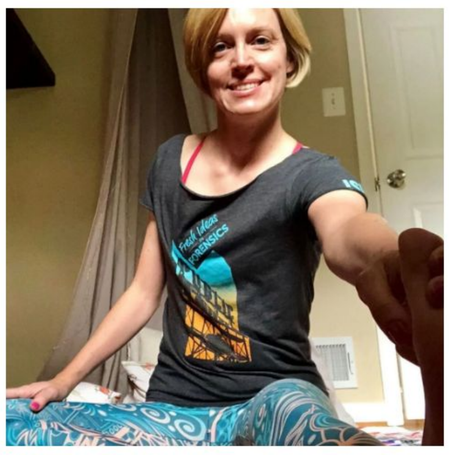
The new standards also build upon guidelines published by the Scientific Working Group on DNA Analysis Methods, or SWGDAM. Guidelines are looser than standards in that they suggest best practices that laboratories should follow, while standards list requirements that labs must follow to be considered in compliance by an accrediting body.

Compliance with these new standards, as with almost all forensic science standards in the United States, is voluntary. However, some labs are already meeting or close to meeting these new standards. In addition, by adopting these standards, forensic labs can improve their processes and demonstrate their commitment to quality.

Additional standards are in the pipeline. For instance, the ASB is finalizing standards, also initially drafted by OSAC, for validating the probabilistic genotyping software that many laboratories use for interpreting DNA mixtures. The American National Standards Institute (ANSI) accredited standards development process at ASB together with the drafting and approval processes at OSAC involve multiple layers of technical review and ensure that standards are developed via a consensus process that invites input from all stakeholders prior to placement on the OSAC registry.

For more information on OSAC, please visit our website at https://www.nist.gov/topics/organization-scientific-area-committees-forensic-science.

If you are interested in applying to join OSAC, please see https://www.nist.gov/topics/organization-scientific-area-committees-forensic-science/apply-join-osac.



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Even though we may not be able to come together in the same location right now, we can still come together virtually. Let's unite as one ISHI community and support those in our field and our neighborhoods.

Put on your favorite ISHI tee from a past meeting and take a picture of yourself at home, on a walk in your neighborhood, or with your loved ones or pets and upload it below. We'll share your photos on our social media channels to connect us during this challenging time. For each photo uploaded, we'll donate $10 to your choice of either Feeding America or Doctors Without Borders up to $5,000 total.

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June 5, 2020

Interesting Case Abstracts Due

July 5, 2020

Poster Abstracts Due

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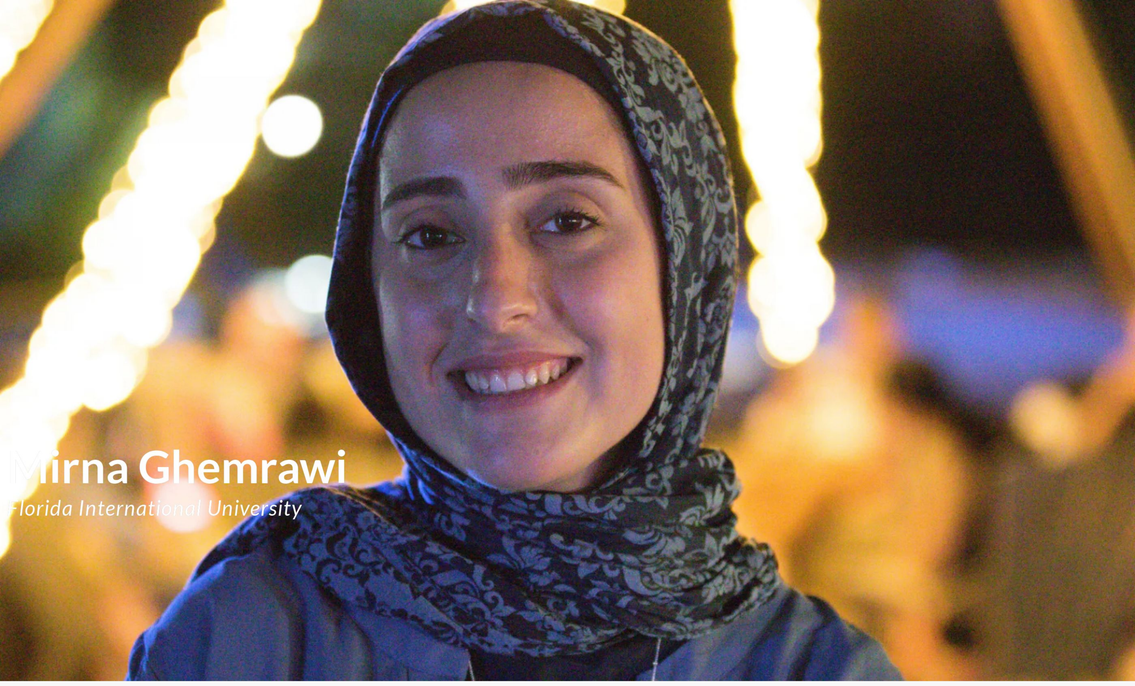

Mirna Ghemrawi

Florida International University

What were your first impressions of the conference?

Attending ISHI was always on my list. As a student, I had to work hard on my project so I can submit an abstract. Little did I know, I was honored not only to attend ISHI or to present at ISHI but also to be an ambassador as well. The moment I arrived to check-in, I knew that it will be once in a lifetime experience (that hopefully would be repeated every year). I was impressed by the organization of each and every details you can think of: time management, logistics, speakers, activities, interviews, exhibits, banners, theme, food, reception …

How does ISHI compare to other meetings that you've been to?

I have been to other conferences in the forensic field, but most of them include more than one concentration: forensic chemistry, biology, csi, impressions … What I liked the most about ISHI is that it focuses on forensic DNA which gave me a satisfaction in the knowledge I got in this area that is by itself huge. Yes, it is important to know about other fields in forensics but also it is very important to get an in-depth focus on your area of research, which I found at ISHI. I also liked the fact that you don't miss a talk because of parallel sessions as each slot has one speaker/panel going on at a time.

What was your favorite part of the conference?

My favorite part of the conference were the interviews I did. I got the chance to be part of #womeninstem as well as interviewing one of my favorite scientists, Dr. John Butler. This opportunity actually made me discover my love to combine science, mass media and communication.

Did you make any new connections with attendees that will assist in your research?

During my poster presentation, I met DNA analysts who were interested in my research. I was happy to discuss opportunities for collaborative studies with crime labs. It was through ISHI that I spoke to speakers in my area of research and had the chance to benefit from their knowledge.

What is one thing that you learned while at the conference?

It is hard to confine all my days at ISHI in just one thing that I learned as each moment was a learning experience by itself. But I would say that the main thing I learned is that as a student, I am on the right track as I loved each and every story I heard. I was thrilled to hear how throughout the years, forensic DNA has developed and that I was only 1 year old when CODIS was established.

What are your biggest takeaways?

My biggest takeaways are that there is no limit to how much we can learn or how much we can serve. Because each family/person deserves to have a closure, we have to constantly work on advancing this field. Last but not least, it is true that forensic science is exponentially growing but we can still make it better.

Do you have any advice for other students or attendees considering attending ISHI?

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 caseworks. 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.



Rachel Kieser

University of North Texas Health Science Center

What were your first impressions of the conference?

I was excited to learn that ISHI 30 was to be hosted in Palm Springs. I had never experienced the California desert and I must say, it did NOT disappoint! The resort atmosphere was perfect to actively facilitate collaboration, networking, and the making of new friends within the field of forensic genetics.

How does ISHI compare to other meetings that you've been to?

Many conferences attempt to merge all things forensic into a short period of time, which often results in attendees missing presentations and opportunities. ISHI is an impressive, well-balanced conference where oral presenters, poster presentations, and exhibits are showcased in a way to best highlight the emerging technology and research within the field.

What was your favorite part of the conference?

My favorite aspect of ISHI is witnessing the progression of research, whether this is a student's thesis project where I get to learn more of what they have discovered year-to-year or something new and novel that it just beginning to move the field forward. Additionally, I enjoy seeing old friends (often with ISHI being the only time I get to see them each year), networking with local organizations or industry, and most certainly, being able to actively engage in scientific "think tanks."

Did you make any new connections with attendees that will assist in your research?

Absolutely! My research focuses on the development of novel methods for typing highly degraded DNA. Accompanying the use of these new molecular methods for challenged remains are numerous applications that have the potential to translate to various other areas within the field of forensic genetics. I greatly enjoyed actively talking with all attendees about my research and its impact across the field.

What is one thing that you learned while at the conference?

Although I had the opportunity to learn so much at this year's ISHI conference, one presentation that really stuck in my mind was the use of isotope analysis to develop a biological profile and determine the place of origin in missing persons cases. This form of investigation has the potential to provide a considerable amount of information in cases that are often limited or where there are no longer any investigative leads. Isotope analysis serves as a bridge to the past identifying an individual's region of birth (based on certain isotopes) as well as what environment that individual was around prior to their death. This research is fascinating and holds the ability to cross a variety of applications.

What are your biggest takeaways?

Currently, there is a considerable push toward using genetic genealogy to solve crimes. Prior to attending ISHI 30, I was unaware of the major policies coming into place concerning the use of databases for this approach to gaining investigative leads. I was pleasantly surprised by the community's proactive attitude to fund such actions and establish policies to protect the individual's genetic information and privacy.

Do you have any advice for other students or attendees considering attending ISHI?

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.



Allison Sherier

University of North Texas Health Science Center

What were your first impressions of the conference?

Palm Springs was an absolutely gorgeous location for this year's ISHI conference and the theme stayed in line with all things Palm Springs. The set up for check-in was fantastic and the staff were absolutely amazing. The glimpse back into forensic genetics history was fun and I was in shock that there were materials from the O.J. Simpson trial out for people to handle. It was absolutely crazy to get to touch things from that case. I am so honored I was able to attend this year.

How does ISHI compare to other meetings that you've been to?

ISHI has a great mix of researchers and analysts. It's the perfect set up for me to learn about the current research going on in forensic genetics, but also talk to analysts about what they think about the research that I am doing. ISHI also has a great balance of time spent listening to speakers and time to network. I feel like most other conferences I have been to have a hard time balancing this. It is either too much and you get bored, or it is too little and you feel rushed. ISHI has a fun and relaxed vibe while also being a very informative conference.

What was your favorite part of the conference?

Networking and visiting with people I have met in previous years is my favorite part. We cannot move forward as an industry if we do not communicate and make friends with other people doing the same work. The forensic genetics community has a special dynamic, we will go farther and improve faster if we all work together and not compete with each other.

Did you make any new connections with attendees that will assist in your research?

My topic area being so narrow, sadly this year I did not meet anyone that was interested in collaborating, but I am sure as the area of human identification using the microbiome expands there will be more people to collaborate with in order to help improve MPS kits.

What is one thing that you learned while at the conference?

Only one thing?? Surely everyone who went to ISHI learned more than one thing. What I found the most interesting and exciting was the work that the DNA DOE Project is doing to help identify individuals using genetic genealogy. It is amazing how much good genetic genealogy has done for families that have missing loved ones.

What are your biggest takeaways?

The forensic genetics industry is changing and with that change, there is a lot to do in crime labs and in the court systems to make sure we are using the most informative genetic information available while also keeping people's personal information safe.

Do you have any advice for other students or attendees considering attending ISHI?

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.



Fabiana Taglia

Florida International University

What were your first impressions of the conference?

The conference was mind-blowing, I am so grateful I had the chance to participate as student ambassador. I met so many researchers and even those experienced and in the field for many years showed excitement to be there. It was amazing.

How does ISHI compare to other meetings that you've been to?

This was my first conference therefore I cannot compare with others, but according to the program and talks offered form ISHI and other conferences, I can say this is the only one focused entirely on forensic DNA offering a whole week of workshops and talks.

What was your favorite part of the conference?

I found all the topics of the conference very interesting but the talks and workshop about genealogy really surprised me. The workshops with the material and the practical exercise also was a section I really loved.

Did you make any new connections with attendees that will assist in your research?

Some researchers stopped by my poster session, and were curious about my research. Although only a few of them are working on my same topic, they asked me to keep them updated on my experiments.

What is one thing that you learned while at the conference?

Listening to all the great talks, I learned how collaboration between researchers is fundamental to coordinate steps of investigations, for example, or solving critical criminal cases.

What are your biggest takeaways?

The determination; the strong will to never give up.

The stories I got from the speakers and their talks gave me an extra boost, a greater awareness of what I am doing and why, increasing my level of optimism.

Do you have any advice for other students or attendees considering attending ISHI?

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.