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ISHI INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION

STARTING SEPTEMBER 13, 2021

November 2020

The ISHI Report

News from the World of DNA Forensics

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The ISHI Report

Letter from the Editor

Greetings from Madison, Wisconsin. We hope this edition of the ISHI Report finds you well.

The latest ISHI Report is packed with updates from the field of forensics. The topic of genetic genealogy is top of mind in large part for its effectiveness in solving cold cases when all else has failed. Andrew Macleod from King's College in London will describe how genetic genealogy is being used to bring justice to victims of sex trafficking. Swathi Kumar will expand on the talk she gave at ISHI to provide an update on the GEDmatch database. The database continues to be one of the best tools available to research genetic pedigrees and is a valuable tool for investigative genetic genealogy.

Dr. Angie Ambers describes how DNA testing using multiple parallel sequencing was done on two sets of adult skeletal remains recovered from the 17th century *La Belle* shipwreck. These remains were from the last expedition of the French explorer La Salle. Sergeant Jarrett Morris and Detective Brice Bruenig of the Santa Barbara Sheriff's Office share how Rapid DNA testing is changing the way that labs process samples and increase their efficiency, and Dr. Ambers shares how the technology was used to resolve a case of mistaken burial.

Also, our colleague Ken Doyle explores population genetics and what examining ancient DNA can tell us about humanity's past, and the latest OSAC for Forensic Science updates are shared.

Many of you joined us for the first virtual International Symposium on Human Identification. We had the largest audience ever participating with more than 2500 people tuning in. A brief recap of ISHI 32 describes what you missed if you didn't attend. If you missed the keynote presentation led by CeCe Moore and Paul Fronczak, you can watch it in its entirety on our YouTube channel. The twists and turns of Paul's story continue to fascinate and we've asked him to provide us with an update.

Finally, we are excited to launch a new video series in collaboration with Othram. This series will launch in the new year and will highlight how a multi-disciplinary approach coupled with the latest DNA technologies and forensic genetic genealogy is closing the coldest of cases.

If you would like to play a part in next year's meeting scheduled for September 14-17 at Disney's Coronado Springs Resort, consider submitting a workshop proposal. The deadline for workshop proposals will be January 10, 2021. In the event that ISHI 32 can't safely be held in person we will again host the symposium in a virtual format.

You can find the latest information on plans for ISHI 32 by visiting the official symposium website, www.ishinews.com Visit often to keep up with the latest news in DNA forensics.

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

Stay well,

The Editorial Board

Contact ISHI

ISHI 31

Our First Foray into the World of Virtual Events

David Hughes Krenzel

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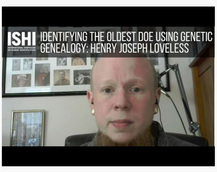
We have all had to learn new things in 2020. Necessity is the mother of invention, and the team in charge of organizing ISHI had to reimagine how to make a virtual symposium valuable for attendees. We learned a new vocabulary and picked up a new set of skills to pivot from an in-person conference to a virtual event. Although there were many angst-producing moments, we are pleased to report that the *31st International Symposium on Human Identification* was a big success. A huge debt of gratitude is owed to the workshop organizers and instructors and session speakers who gamely learned how to record their presentations and appear "in person" to field questions from the audience.

The silver lining to holding ISHI in cyber-space was the expanded reach. A record number of people participated in this year's event. More than 2600 people registered for the symposium representing over 40 countries. More than 30 percent of symposium attendees were from outside of the United States compared to our previous average of 18 percent.

The Symposium included three half days of general session talks. The event started on a high note with a joint keynote presentation by CeCe Moore and Paul Fronczak. Moore is a well-known celebrity in the field of genetic genealogy. She researches and explains family trees for guests on the show, Finding Your Roots with Henry Gates Jr., and recently starred in her own show, the Genetic Detective which featured cold cases solved through use of genetic genealogy. In the keynote, CeCe shared the story of how she assisted Paul Fronczak in the search for his true identity. Paul was kidnapped from a Chicago area hospital hours after birth and found abandoned a few years later before being reunited with his parents. Or was he? A DNA test revealed that Paul was not really his parent's biological child, setting off a search for his true identity and leading to an even deeper mystery. Watch the keynote presentation and learn more about Paul's case on our YouTube channel. **Plus, he's provided an update in** this article!

Additional general session talks covered the use of genetic genealogy to solve cold cases, including *Loveless Lost: the case of the oldest Doe identified using forensic genetic genealogy*, which was co-presented by Anthony Redgrave and Margaret Press. An update on the GEDmatch platform was provided by Swathi Kumar and Colleen Fitzpatrick provided insight on how law enforcement and genealogists might collaborate in future criminal investigations.

Identifying the Oldest Doe Using Forensic Genetic Genealogy: Henry Joseph Loveless

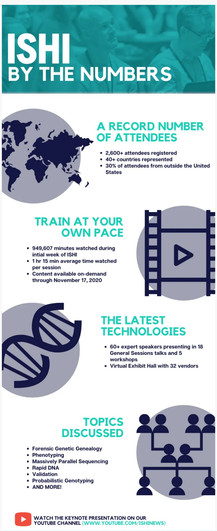


In this interview, we speak with Anthony Redgrave, who led the team that mapped Loveless' family tree to identify him. Anthony describes why the case was so difficult to solve, the steps he takes when working Doe cases, and what he anticipates for the future of the field. Anthony also discusses the work he's doing with the LGBTQ community and in training those interested in learning more about forensic genetic genealogy.

For more genetic genealogy videos, view our playlist on YouTube.

New processes and techniques for DNA analysis were also explored during the conference. We heard updates on the use of Rapid DNA analysis from a policy perspective as well as in an applied setting. Speakers discussed using data from massively parallel sequencing in court and obtaining mitochondrial sequencing results. Walther Parson gave an update on the VISAGE project, organized to learn more about how physical traits can be discerned from DNA. Susan Walsh shared her work on predicting eye color from DNA.

In all eighteen talks were presented over the three-day general session. Talks were pre-recorded with live, moderated question and answer sessions after each talk. Questions which could not be answered in real time due to schedule limitations were collected and forwarded to speakers. We've begun sharing answers to these questions on the ISHI blog and more will follow in the coming weeks.



The Grupo Cientifico Latino-Americano de Trabajo Sobre Identificacion Humana was presented in Spanish and featured twenty separate presentations. The meeting was skillfully chaired by Ronaldo Carneiro da Silva Junior, Custodian of the National DNA Database for the Brazilian Federal Police. More than 500 people registered to attend the two-day session, a huge increase from the customary attendance.

The theme of the GCLAITH meeting was, "*New frontiers of knowledge: building the forensic genetics of the next decade*". Presenters gave talks on policy and process such as using Interpol's DNA network in Latin America, coordination and standardization of laboratory processes, and incorporating Lean Six Sigma into the lab.

New technologies were discussed, including use of mRNA, next generation sequencing and use of touch DNA. Population and ancestry studies were also presented. The speakers did an excellent job of pre-recording their presentations and responding during the live question and answer period.

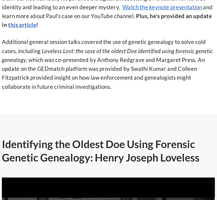
For attendees who wanted more focused information, four workshops were offered on a variety of topics. Doug Hares and Tom Callaghan from the Federal Bureau of Investigation led a workshop on the implementation of Rapid DNA. Workshop speakers addressed the history of Rapid DNA, pilot programs in booking stations throughout the U.S., updates from RDNA task force committees and best practices for Non-CODIS use and courtroom considerations.

Dr. Thomas Kupiec from DNA Solutions coordinated a workshop on use of forensic genealogy to solve criminal cases. This wildly popular workshop attracted more than 800 participants. The workshop covered how genetic genealogy is being used to solve cold cases and the DNA methodology that makes it possible. Additional talks focused on cases solved with genetic genealogy including FBI case studies.

Mike Coble and Jo Bright co-chaired the "Arguing the case for DNA evidence based on probabilistic genotyping" workshop. This workshop was the most popular workshop offering with close to 900 people registered to attend. Jo participated from her home in New Zealand and deserves our utmost thanks for making herself available at 2:00am local time. Presentations focused on courtroom topics such as general acceptance, defense access to software and review of relevant case decisions. Validation topics included independent testing, discriminating between donors and non-donor and inter-laboratory studies.

John Butler and Hari Iyer from NIST, National Institute of Standards and Technology led a workshop on validation principles. This workshop discussed validation principles (the why), practices (the how), parameters (the what), performance evaluations (the when), and protocols (the to what) important to establishing the degree of reliability involved in aspects of forensic DNA-mixture interpretation.

No symposium is complete without exhibitors and this year was no exception. The virtual exhibit hall featured thirty-two companies representing a range of products essential for forensic laboratories. Attendees were able to download product information, watch company videos and interact with company representatives. As an incentive to visit the exhibit hall, attendees could earn a free ISHI t-shirt by visiting three booths.

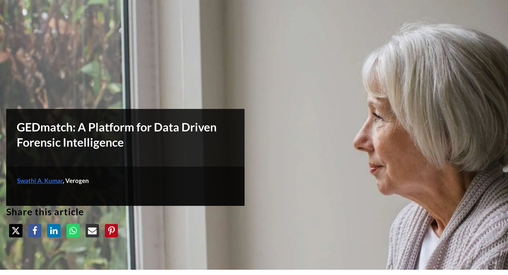


As usual, ISHI provided an opportunity to network with other attendees as well as the chance to compete for prizes. Photo contests were held each day and an ongoing contest was open to all conference goers. Points were awarded for completing talks related to ISHI. Winners of the ISHI Game were: Sandra Avila, Instituto Nacional de Medicina Legal Colombia ($50 gift card), David Fisher, New Jersey Institute of Technology, ($75 gift card) Rebecca Dian, Midwest Regional Forensic Lab ($150 gift card) and Amanda Battaglia, New Jersey State Police who won free ISHI and workshop registration for next year's symposium.

Although we were disappointed to cancel the in-person symposium in San Antonio, Texas this year we hope that many of you were able to attend the virtual event. Would you like to be part of next year's ISHI symposium? We invite you to submit a workshop proposal for consideration. The deadline to submit your proposal is January 10. All proposals should be submitted via the form on www.ishinews.com. Proposals should be non-commercial and contain sufficient detail to allow the review committee to judge its value to the forensic community.

At the time of publication, we are still planning to hold ISHI 32 from September 14-17, 2021 at Disney's Coronado Springs Resort in Orlando, Florida. If circumstances change, updates will be posted on the conference website, www.ishinews.com

On behalf of the ISHI organizing committee, thank you for your continued support of the symposium and patience as we adapt to our new normal.



GEDmatch: A Platform for Data Driven Forensic Intelligence

Swathi A. Kumar, Verogen

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GEDmatch is a genetic genealogy website with over 1.4M users who want to learn more about their genetic roots. It was set up in 2010 with the mission of using science to connect people and has since been used by amateur and professional researchers and genealogists, as well as adoptees looking for their birth parents. GEDmatch users begin this process of discovery by taking a DNA test from direct to consumer (D2C) companies, like Ancestry, 23&me, My Heritage, Family Tree, and others. They upload the results of this test to GEDmatch, which allows them to compare their history with others, irrespective of which vendor they used.

GEDmatch rose to prominence in the public sphere following the arrest and prosecution of the notorious Golden State Killer. Former California police officer Joseph James DeAngelo, who pled guilty to 13 counts of murder and 13 counts of kidnapping with robbery, eluded a statewide hunt that began in the 1970s. After decades of traditional police investigative methods turned up few leads, law enforcement got their first break after comparing DNA collected from the crime scenes with matches in GEDmatch, which helped them narrow down the field of suspects. Falling back on well-established investigative methods for suspect inclusion or exclusion the police were able to bring this investigative odyssey to an end with Joseph DeAngelo's sentencing on August 21st, 2020.

Verogen was founded in August 2017 with the mission of transforming criminal justice and human identification by providing the tools necessary for genetic and biometric linkages. With its acquisition of GEDmatch in 2019, Verogen is driving the adoption of next generation sequencing (NGS) to find answers for cases that were previously unsolvable.

During ISHI 31, Swathi A. Kumar, Ph.D., Director of Product Management at Verogen, in partnership with Kirk Campbell, Lieutenant Supervisor at the Sacramento County District Attorney's (SCDA) Office, discussed the complicated investigation associated with cold cases and how GEDmatch has the enabled SCDA to bring closure to the families affected by these cases. These included the infamous Golden State Killer case, the capture of the NorCal killer, Roy Watkin and the exoneration of Ricky Davis who was wrongly imprisoned for 15 years. Kirk Campbell highlighted the six genealogy tools that his team use in most cases, as well as how they interpret the outcomes from these tools. Dr. Kumar then highlighted various factors that affect outcomes in GEDmatch, such as the underlying genomic technology, assay considerations, input quantity and quality. Finally, the audience was given a preview of the GEDmatch roadmap, including how Verogen has been strengthening the security and privacy of user data in GEDmatch, improving the user experience of the website, adding new genealogy tools, and their plan for delivering a dedicated law enforcement portal for forensic use.

As there was not enough time for Dr. Kumar to answer all the questions that came in during the conference, we have compiled them here. If you have any additional questions about Verogen, their forensic genetic genealogy solutions, the MiSeq FGx Sequencing System or GEDmatch, please reach out to Verogen.

GEDmatch: A Genetic Genealogy Platform Allowing Users and Law Enforcement to Make Important Familial Connections

In this interview, we speak with Swathi Kumar, Director of Product Management at Verogen. We discuss what makes GEDmatch such a valuable and unique tool for solving cold cases and identifying John and Jane Doe remains, how Verogen is diligently working to protect the privacy of its users, and what is in store for the future of the platform.



Several people have had questions about data privacy. Will Verogen sell genetic data to law enforcement or anyone else?

No, Verogen has repeatedly communicated that it will not sell users genetic data to anyone, including law enforcement. Not only do we remain steadfast in our commitment to protecting users' privacy and data rights, we have also made extensive investments in GEDmatch to strengthen its overall privacy position such as limiting exposure to medically relevant SNPs and providing multiple levels of data control privileges within the platform. GEDmatch users have the absolute right to choose whether they want to share their information, with whom that information can be shared and how it is used.

Can you let us know a little bit about the Verogen genetic genealogy assay?

As a human identification company serving the needs of the forensic community, Verogen is acutely aware of the challenges inherent in forensic samples. As stewards of the GEDmatch data, we also understand how the current technologies available to consumers enable less-than-ideal outcomes and fail to address larger concerns about genetic privacy.

These challenges and concerns led us to build our fit-for-forensic-purpose forensic genetic genealogy assay that uses a targeted approach to interrogate parts of the genome that are relevant for forensic use, unlike current solutions that also reveal medically relevant data. We have extensively tested our solution with low quality DNA and degraded or inhibited samples that are commonplace in forensics. The ForenSeq™ DNA Signature Prep Kit currently supports input quantities as low 1ng and we expect our forensic genetic genealogy assay to meet the exacting standards that the forensic community deserves. The assay will run on the Verogen NDIS-approved NGS platform, the MiSeq FGx Sequencing System, that is currently deployed in multiple operational forensic labs around the world. Finally, the data analysis will be supported by solutions that have been designed, engineered, and confirmed with criminalists and forensic analysts. The SNP data can be uploaded to GEDmatch in a way that respects chain-of-custody constraints and requirements that are critical to the handling of forensic samples and data.

Can you tell us a little more about GEDmatch PRO? How will Verogen transition law enforcement users in GEDmatch to GEDmatch PRO?

At ISHI 31, we announced that we will be delivering a dedicated portal for forensic use of GEDmatch. Shortly thereafter, we released additional details, including the name of this portal – GEDmatch PRO. GEDmatch PRO has been designed in partnership with law enforcement users of GEDmatch, as well as with genealogists who work with law enforcement. Differentiating GEDmatch PRO from GEDmatch allows us to meet the unique requirements of law enforcement while preserving the primary purpose of GEDmatch: enabling users to learn more about their roots. More details on the portal will be released closer to launch. We will review law enforcement kits and accounts from GEDmatch to GEDmatch PRO in close communication with the account holders prior to launch, so they will have not have to move their kits themselves.

How will Verogen respond to subpoenas and court orders, or disclose all relevant information regarding GEDmatch PRO to defense attorneys if requested in a relevant case?

Verogen is committed to protecting the choices of our users and strongly believes in their right to control what data is shared and how it is used. Verogen would not voluntarily support requests to disclose information of our users who have not actively opted in for law enforcement matching.

How will Verogen stop law enforcement files from being uploaded to the main database against Terms of Service (ToS)?

With the launch of GEDmatch PRO, law enforcement related kits will no longer be accepted on GEDmatch. The GEDmatch Terms of Service (ToS) will be updated to reflect this, along with the implications for violating these terms. Additionally, new and separate ToS for GEDmatch PRO will clearly outline the proper use of the site.

Are there any differences in privacy options for DNA of deceased persons compared to living?

Yes, quite a bit of difference. In the US, there are no federal laws that specifically extend privacy protection to deceased individuals. In the EU, there are no privacy rights granted to deceased individuals under the General Data Protection Regulation (GDPR).

Do you find that data from minority populations is not as prevalent in GEDmatch? Have there been successful outcomes in law enforcement cases involving minorities?

The GEDmatch database contains more kits from individuals of northern European descent. That said, there have been cases involving minority populations that have been successfully solved using GEDmatch.

What tools within GEDmatch are available to specifically filter out areas that are often imputed for the reports on shared centimorgans?

GEDmatch does not have filters to detect and filter out imputation per se, but it does have filters that detect and block the upload of kits that match too much of the database. In our experience, this is often seen with kits that have been poorly or overly imputed.

Regarding added upload restrictions on bioinformatically engineered data, bioinformatics is often used to enhance degraded DNA from crime scene DNA and Doe kits. How will that affect those kits? Will kits uploaded via GEDmatch PRO not be part of those restrictions?

GEDmatch and GEDmatch PRO will have the same filters that detect and block kits that match too much of the database. For permission to upload such kits, please reach out to us at gedmatch@verogen.com so we can assess the need individually.

Will GEDmatch be expanded to Latin American countries, or has this not yet been contemplated?

We are constantly evaluating new capabilities that will enable us to better serve our users. Expanding to other geographies is a potential future direction for GEDmatch.

Opening a Window into the Past

Kim Doshe, Promega

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The study of natural variability within human, animal and plant populations has its origins in the work of Darwin; however, understanding the causes of this variability was not possible until the development of Mendelian genetics. Born from the evidence supporting Mendel's work on heredity, the field of population genetics emerged out of attempts to reconcile Darwinian and Mendelian genetic theories. Population genetics is defined as studying "the genetic composition of biological populations, and the changes in genetic composition that result from the operation of various factors, including natural selection."

Advances in DNA analysis technology and bioinformatics have extended the classical methods of population genetics, resulting in the emerging science of population genomics. In a broad sense, population genomics examines the variability at multiple loci across the whole genome. Using statistical analysis, it provides a historical perspective on the origins, relationships, migration patterns and other demographics of populations over time.

Population genomics studies originally relied on the methods that form the backbone of forensic DNA analysis—amplification of short tandem repeats (STRs). However, the introduction of microarray technology and massively parallel sequencing (MPS) have facilitated the use of single-nucleotide polymorphisms (SNPs) as genetic markers. SNP analysis provides additional power of discrimination and is more suitable for analyzing degraded DNA samples, compared to STRs.

Population genomics distinguishes between two types of genetic markers: adaptive and neutral. Adaptive loci or genomic regions are those in which variation occurs in response to natural selection—for example, the mutation responsible for lactase persistence in adults, which confers the ability to digest lactose in dairy products. In contrast, neutral loci are those that are not evolving in response to selective pressures. This type of variation usually results from random genetic drift, immigration or population migration. In general, neutral loci across the genome will be similarly affected by demographic changes and the evolutionary history of populations, while loci under selection will often behave differently and reveal outlier patterns of variation (reviewed by Lukert et al., 2003).

The staggering amount of whole-genome data now available from population genomics studies has demanded more powerful and sophisticated methods of statistical analysis. These methods have enabled a deeper understanding of the changing demographics of human populations over time, going back as far as the Neolithic and Mesolithic eras.

Working with Ancient DNA

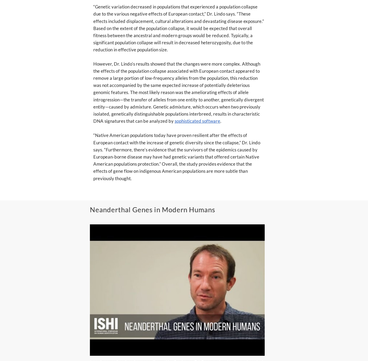
A time machine would provide an irresistible opportunity to study the behavior and characteristics of human populations over centuries and millennia. Lacking such a device, the next best solution is the analysis of ancient DNA, which is often a multidisciplinary effort that brings together DNA analysts, historians and archeologists. When working with ancient specimens, the two sampling options available for DNA analysis are usually bones and teeth. Extracting usable DNA from these samples poses unique challenges.



Dr. John Lindo in his state-of-the-art ancient DNA laboratory. Credit: Stephen Nowland, Emory University

Dr. John Lindo is an Assistant Professor of Anthropology at Emory University in Atlanta, Georgia, and he is intimately familiar with these challenges. Earlier this year, his research group celebrated the opening of a new, state-of-the-art laboratory for ancient DNA analysis, bringing together the molecular and computational aspects of ancient DNA research. "Ancient labs can be costly due to their strict adherence to clean room protocols that aim to prevent contamination," Dr. Lindo says. The laboratory was designed to create positive air pressure in each room so that air flows out, instead of in, when a door is opened, thereby minimizing the risk of contamination. The laboratory is also designed to inactivate DNA that may be free-floating or on surfaces by constantly dosing rooms with UV radiation. Another limitation of working with ancient DNA, Dr. Lindo notes, is that "amplification of DNA cannot be done in the same building in which the ancient DNA lab is located, due to contamination risk."

Dr. Lindo's work with ancient DNA developed from his need to understand evolution and natural selection in human populations by "going back in time". The availability of technologies such as whole-genome sequencing, which is used extensively in the Lindo laboratory, has proved extremely beneficial. "There are many questions about human evolution," Dr. Lindo says, "that we can answer with these relatively new methods, that would otherwise have remained intractable."



Native American Populations

One area of focus for Dr. Lindo's research group is the regional human population history in the Americas, especially examining how colonization impacted Native American populations. These populations suffered extensive declines associated with the impact of European colonization, and these events would presumably impact genetic variation within the surviving populations. Although previous studies have looked at genetic diversity of contemporary Native American populations, no research has examined ancient Native American genetic diversity.

Dr. Lindo's team compared whole-exome sequencing data from an ancient indigenous population (before European contact) to their present-day descendants, the Coast Tsimshian people of Prince Rupert Harbor, British Columbia (Lindo et al., 2018). The Tsimshian suffered dramatic population declines, with a 57% reduction in population size, in response to the effects of European contact and various epidemics in the 1800s.

"Genetic variation decreased in populations that experienced a population collapse due to the various negative effects of European contact," Dr. Lindo says. "These effects included displacement, cultural alterations and devastating disease exposure." Based on the extent of the population collapse, it would be expected that overall fitness between the ancestral and modern groups would be reduced. Typically, a significant population collapse will result in decreased heterozygosity, due to the reduction in effective population size.

However, Dr. Lindo's results showed that the changes were more complex. Although the effects of the population collapse associated with European contact appeared to remove a large portion of low-frequency alleles from the population, this reduction was not accompanied by the same expected increase of potentially deleterious genomic features. The most likely reason was the ameliorating effects of allele introgression—the transfer of alleles from one entity to another, genetically divergent entity—caused by admixture. Genetic admixture, which occurs when two previously isolated, genetically distinguishable populations interbreed, results in characteristic DNA signatures that can be analyzed by sophisticated software.

"Native American populations today have proven resilient after the effects of European contact with the increase of genetic diversity since the collapse," Dr. Lindo says. "Furthermore, there's evidence that the survivors of the epidemics caused by European-borne disease may have had genetic variants that offered certain Native American populations protection." Overall, the study provides evidence that the effects of gene flow on indigenous American populations are more subtle than previously thought.

Neanderthal Genes in Modern Humans

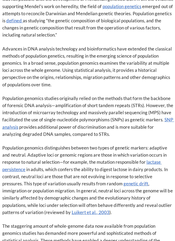


In an international project coordinated by Professor Ed Green, scientists have decoded the DNA of Neanderthals. They discovered that Europeans and Asians share 1 to 4 percent of their genetic material with Neanderthal.

In this video, Professor Ed Green discusses sequencing of the Neanderthal genome and signs that early humans interbred with Neanderthals.

Sardinia

In 1991, the story of "Ötzi the Iceman" captured widespread public attention. The mummified remains of this Copper Age man, dating around 3400–3100 BCE, were discovered in the Ötztal Alps near the Austria-Italy border. Subsequently, whole-genome sequencing in 2012 revealed that Ötzi shared a significant amount of genetic ancestry with the present-day inhabitants of the Mediterranean island of Sardinia (Keller et al., 2012). These results sparked considerable interest in Sardinian population genomics and migration history.



Credit: South Tyrol Archaeology Museum, Eurac and M.Samadelli

A recent study (Marcus et al., 2020) conducted a detailed analysis of the genetic history of Sardinia and examined how the relationships between Sardinian and mainland populations changed over time. Earlier studies using ancient DNA analysis provided the foundation for the current understanding of how early, geographically distinct European mainland populations showed such a high affinity with modern Sardinians. A popular model suggests that early European farmers accounted for much of the initial Sardinian ancestry, but the island remained relatively isolated from subsequent admixture that occurred on mainland Europe. However, no genome-wide studies had previously been conducted to support this model.

The research team—spanning academic institutions across the US, Germany, Italy, France and Spain—extracted DNA samples from the skeletal remains of 70 Sardinian individuals, dating between 4100 BCE and 1500 CE. The researchers sequenced DNA libraries enriched for the complete mitochondrial genome as well as a targeted set of 1.2 million SNPs, and analyzed the ancient DNA sequencing data together with published autosomal data for both ancient and modern humans in and outside Sardinia. The study covered three periods of Sardinian history: the Sardinian Neolithic (~5700–3400 BCE), the Sardinian Chalcolithic or Copper Age (~3400–2300 BCE) to the Sardinian Bronze Age (~2300–1000 BCE), and the post-Bronze Age period. Several patterns emerged from the study.

The first pattern showed that Sardinian populations in the Middle Neolithic period (4100–3300 BCE) were closely related to the early European farmer populations from mainland Europe. Subsequently, Sardinian genetic ancestry remained stable for an extended period, through the end of the Nuragic period (~900 BCE). The Nuragic period, which began during the Bronze Age around 1800 BCE, is named after the distinctive stone towers, or nuraghe, that can still be seen across Sardinia today. These observations contradict hypotheses that the nuraghe were designed following an influx of people from eastern sources.

Finally, the post-Nuragic period witnessed complex gene flow with both northern and eastern Mediterranean sources. Although the researchers acknowledge that substantial uncertainty exists due to the low-differentiation among plausible source populations, their finding of increased variation in ancestry after the Nuragic period supports other ancient DNA studies in the Mediterranean that have observed fine-scale local heterogeneity in the Iron Age and later.

China

The genetic history of ancient human populations in East Asia is not widely understood, particularly in northern and southern China. Archaeological evidence suggests that East Asian populations were more diverse in the past than they are today, but a lack of sampling makes it difficult to develop a detailed picture of this genetic diversity. A recent study (Yang et al., 2020) provides a fresh look at the genetic history of northern and southern China.

One theory suggests that East Asians have two "layers" of ancestry. The first layer is composed of ancient hunter-gatherers, while the second consists of agricultural populations that spread across East Asia in the Neolithic to the present era. To gain more insight into these populations, the researchers obtained ancient DNA samples from individuals who lived across East Asia between 9,500 to 300 years ago. The team enriched the DNA samples for mitochondrial DNA and for nuclear DNA at 1.2 million SNPs before sequencing.

The genome-wide data from Neolithic humans revealed the closest genetic relationship to present-day East Asians who belong to the "second layer." While more divergent ancestries could be found in Southeast Asia and the Japanese archipelago, Neolithic populations in northern and southern China already displayed genetic features belonging to present-day East Asians. Thus, the results did not support the two-layer model of genetic dispersion in East Asia. A direct comparison of Neolithic East Asians with present-day East Asians and early Asians showed that Neolithic East Asians tend to be more closely related to present-day East Asians than to any early Asian populations.

The researchers also observed that the spread of northern East Asian ancestry led to increased admixture in both directions, such that most of the present-day East Asian population is a mixture of northern- and southern East Asian ancestries. Since this extensive admixture was not observed in the Neolithic, much of the human movement that contributed to present-day East Asian genetic patterns must have occurred after the Neolithic period.

Further, the team observed different coastal connections in Neolithic populations from as far north as coastal Siberia and the Japanese archipelago so far south as coastal Vietnam, implying that gene flow among coastal populations in East Asia is a common trend. They conclude that genetic sampling from the Paleolithic and from populations further inland in central China should help to further clarify the relationships among Paleolithic hunter-gatherers, Neolithic farmers, and present-day populations of East Asia.

In summary, ancient DNA analysis offers new insights into the ancestry and migration of human populations across the globe. Multidisciplinary efforts that combine DNA analysis, historical records and archeological evidence will continue to provide more information about our past and present—and, hopefully, guide the decisions that shape our future.

The Foundling

Updates on Paul Fronczak's Inspiring Story



Interview written and condensed by Tara Luther and Carol Bingham, Promega

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Like most kids before Christmas, 10 year-old Paul Fronczak was eager to learn what presents would be waiting for him under the tree. As he ducked into the crawlspace, he discovered boxes that had been tucked away towards the back. His anticipation grew as he began to peer into the boxes, imagination wild with what he might find. What he uncovered stored in those boxes was a family secret that would change his life forever.

On April 27, 1964, Dora Franczak rested in her hospital room in Chicago next to her newborn son, Paul. A nurse entered the room and informed her that it was time to move the baby to the nursery (commonplace at the time), scooped up the baby, and left. A few hours later, a second nurse visited Dora's room to take baby Paul to the nursery. Confusion turned to horror as a mother's worst fear was realized: her newborn baby had been stolen.

Though the kidnapper had only a few hours to escape, they were never seen again, but authorities never stopped looking for baby Paul. A year later, a small toddler aged boy was found abandoned outside of a store in New Jersey. DNA testing was not yet available, and blood tests were inconclusive. It was the shape of the child's ears that caused authorities to believe the baby could be Paul Fronczak. The toddler was eventually sent to live with the Fronczaks in Chicago, and the case was considered closed.

It was this secret that 10-year-old Paul had uncovered that day in the crawlspace. As he took in the numerous cards, letters, and newspaper clippings displaying his name in large, bold headlines, he knew that he had uncovered something big.

Though Paul moved upwards of 50 times in his life, he kept those newspaper clippings with him, their words needling his curiosity. It wasn't until 2012, when commercial DNA testing became more popular, that Paul had the means to answer the questions that had been swirling in his mind for years.

Paul had been living in Las Vegas when his parents came to visit him. On a whim, he asked them to take a DNA test, and they agreed, though they had second thoughts the moment they returned home to Chicago. They called Paul, begging him not to submit the tests. Though he relented at the time, he did eventually submit the tests and they confirmed his suspicion: he was not his parents' natural born son.

After doing research into her own family, Investigative Genetic Genealogist, CeCe Moore, knew that she could help Paul solve his unique case. She reached out to him on his Facebook page to offer assistance, but at the time, Paul's focus was on working with a local reporter to get his story out to the media. It worked, and he was inundated with messages from people sending tips, information, and potential leads. Unfortunately, CeCe's note slipped through the cracks.



A year later, the television show 20/20 became interested in airing an episode on Paul's case. Having worked with CeCe previously, they asked her if she would be willing to help, which, of course, she was. 20/20's producers told CeCe that they'd already located Paul's second cousin through the databases, so they envisioned the case would be solved quickly, in time to air the following month.

CeCe began researching Paul's second cousin and immediately hit a roadblock. His second cousin had been adopted, and without his family tree, it was impossible to figure out Paul's true identity. Paul's remaining top matches were Ashkenazi Jewish and were not as closely related as they originally appeared. While they looked to be third cousins, CeCe explains they may have been fifth cousins eight times over, which meant starting over.

The first step was to upload Paul's DNA to all three databases that were available at the time (Ancestry DNA, 23andMe, and Family Tree DNA). CeCe points out that the databases were much smaller at the time than they are now, with less than a million people in all three combined. The next step was for Paul to have Y-DNA and mitochondrial DNA testing done. With testing completed, CeCe examined Paul's ancestral origins. She noted that he has a unique combination of ancestral lines containing Jewish, Southern European, and Northern European roots.

Paul's case was one of her most difficult to unravel. After working on her own for several months, CeCe later enlisted a team of volunteers to help, including Carol Rolnick, Michelle Trostler, and Allison Demsky. Altogether, over two years was spent pouring through Paul's family tree.

Paul was at work when he received a text from CeCe that read, "You need to call me. It's important." When the call connected, she said, "Well, the whole team's here. What do you think of the name Jack?"

Paul thought for a moment and then responded, "That's a good name. It's a strong name."

CeCe replied, "That's your name." Before Paul could process this, she continued, "You had a twin sister, but she's missing."



It was Paul's Facebook page that once again played a vital role in propelling his story forward. A tipster wrote about a man in Michigan who could possibly be the real Paul Fronczak. Comparing DNA from one of Paul's cousins to a woman who was potentially the real Paul's daughter allowed CeCe to confirm that they had located him after all these years. He has since been introduced to the mother that he was stolen from, and their relationship continues to grow.

During the keynote presentation at ISHI 31 in September, Paul revealed that he's actively working on solving the mystery of his twin sister. Unfortunately, Paul does not hold out hope that he will find her alive, believing that an accident or something worse claimed her life.

Earlier this year, before the pandemic began, Paul and his team visited a home in New Jersey that once belonged to his Grandmother to search for Jill. Using radar technology, they located a couple of possible gravesites, which Paul had the chance to explore. Upon digging down six feet into the Atlantic City soil, water started to come up from the ground, but before giving up, his shovel made a "tinkling" sound. It had made contact with a bone. Unfortunately, analysis of the bones determined them to be animal bones and not human. Though this search didn't pan out, Paul remains determined that he will one day find his sister.

Paul's story captivated the ISHI 31 audience as it did us, and questions and comments poured in after the presentation concluded. We did not have time to address all of them during the conference, so we have asked Paul to answer them for our readers.

View the Keynote Presentation



How has solving the mystery of your identity affected you personally?

It's had a really big effect on me. I realize now that not knowing who I was affected my behavior and led me to be a kind of wanderer, going from job to job and never feeling like I was rooted anywhere. And when I had my daughter Emma, I knew that had to stop. Finding out my real identity allowed me to feel more secure in who I am, and as a result I feel more grounded, and I feel like I can be a better parent to Emma. I always tell people that living with a lie is a really hard thing to do. You can get away with it, but it's really hard and it takes a toll.

Have you been able to meet many members of your biological family?

Yes I have, though not as many as I would have liked. For instance, I don't have a relationship with either my biological brother or sister. They simply didn't want to deal with the consequences of their family's past. But I did meet a cousin named Lenny who is a really great guy, and also a well known doo-wop singer, and he and I jammed together, and it was the first time I got to know a blood relative who had music in his blood, like I do. It was a thrill.

Has your mother been able to meet with the "real Paul"?

Have you met the "real Paul"?

Have there been legal consequences for the person who stole baby Paul from the hospital?

Is the person who posed as the nurse who stole Paul the same person who raised him?

You know, I would love to answer all of these questions, and I will answer them soon, but I just can't right now. This whole process is still unfolding, still happening as we speak. I'm still discovering things about what happened with the real Paul Fronczak, and when the time comes I promise I will share that story with the world.

What advice do you have for people who are in a similar situation (not knowing their real identity)?

I always say that they have to make the decision on their own about whether or not to pursue the matter of their true identity, but before they do, they should understand that either decision has consequences, not all of which are good.

Doing nothing is a definite choice, and I can understand why people make it, because digging up the past can be very disruptive. But doing nothing leaves a lot of unanswered questions that in my experience never really go away.

Then again, deciding to go on this journey of learning your true identity also has serious consequences. It can completely disrupt your life, disrupt your relationships, disrupt your emotions. I mean, my marriage fell apart while I was in the middle of my own journey, and that is a pretty significant consequence to have to live with.

So try to understand what you are getting into, and then make the decision for yourself. I would never advise people outright to do what I did. All I can say is that I felt like I had no choice. I needed to know the truth of who I was.

Where could someone start their search for birth parents?

Well, if they haven't already joined an ancestry website and submitted a DNA test, that's a great place to start. And if that gets confusing, there are a number of online groups that offer support and help for those searching for their biological families.

The first step is the DNA test, and the next step is research. Gather everything you know to be a fact about who you are, or where you came from, because you never know which little detail will lead to a breakthrough. Start a notebook and write everything down. Look for groups that can help you. Find new relatives and reach out to them and ask questions.

There is no one path to doing what I did. But the big thing is taking that first step. Even if you think it's an impossible journey, don't be afraid to get started. If you keep at it, doors will start opening.

What are your future plans?

I want to continue to be a great and loving father to Emma, and I also want to help other people search for their families or their true identities, so I am working on a way where I might be able to do that on a larger scale than just answering emails. Possibly a TV show. But helping others is a big part of this for me. It can be a terribly lonely business, and to know of others out there who have felt like you, or feel like you do, can be enormously helpful.

Advertorial

Solve Cold Cases with DNA from Rootless Hair using Genetic Genealogy

Kelly Harkins Kincaid, PhD, Astrea Forensics

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Rootless hair shafts are often collected at crime scenes. However, the DNA in rootless hair fails in conventional forensic DNA assays.

Astrea Forensics has developed a breakthrough approach for DNA recovery and analysis from rootless hairs. This approach enables forensic genetic genealogy, yielding actionable leads.

Highlights

- Astrea Forensics has adapted paleogenetic methods (technology for recovering and sequencing DNA from remains that are often tens of thousands of years old) for DNA based forensics. These methods are ideal for extracting and sequencing the ultrashort DNA fragments in rootless hair and other degraded samples
- Rootless hair contains billions of nuclear and mitochondrial DNA fragments that are mostly less than 75 base pairs in length – too short for amplifying CODIS markers, including miniSTRs
- With our approach, these billions of ultrashort DNA fragments can be recovered with nextgeneration sequencing (NGS) to reconstruct the full mitochondrial genome and generate nuclear genome data suitable for forensic genetic genealogy.
- From a single hair, Astrea Forensics can often produce a genotype file ready for upload to genealogy databases like GEDmatch or FamilyTreeDNA.

In just a few short years, forensic genetic genealogy has proven to be a revolutionary approach to human identification. From the Golden State Killer to the victims of the Bear Brook murders, law enforcement agencies can access an entirely new path towards solving violent crime cases and unidentified remains. This powerful new genotyping approach requires tens to hundreds of nanograms of high-quality DNA. Until now.

Many forensic samples lack enough recoverable, high-quality DNA to use in traditional genotyping assays, like genotype arrays, even when STR amplification is successful. This limitation is especially pronounced for samples with highly fragmented DNA, like rootless hair. A single rootless hair yields only picograms of ultrashort DNA. These samples often fail traditional forensic testing because the DNA fragments are mostly less than 75 base pairs long. These DNA fragments are too short to amplify using the widely used CODIS markers (Figure 1), resulting in profiles that are hopeless for solving crimes.

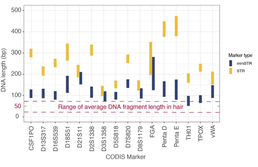


Figure 1: Amplicon size ranges for CODIS STR and miniSTR markers[1]. In red, the average range of DNA fragment lengths in hair.

Fear not! A sample containing only 100 picograms of short DNA still contains over 1 billion unique DNA fragments! How then to recover these data for use in genetic genealogy?

First, our paleogenetic-inspired methods are designed to recover and sequence as many unique fragments as possible, even when the DNA fragments are damaged, e.g. nicked, single-stranded, jagged ends. Second, we sequence all recovered DNA fragments to generate a comprehensive view of the DNA from the sample using whole genome sequencing. Finally, we use a specially developed algorithm to convert this raw sequence data into a genotype file suitable for forensic genetic genealogy. This workflow is shown in Figure 2.

Because we can observe or impute sites across the entire human genome, we can choose from hundreds of millions of informative markers to include in the genotype file.

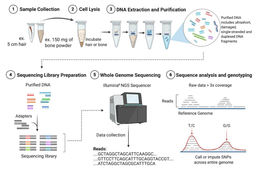


Figure 2: Astrea Forensics general laboratory workflow†

Advantages of hair for genetic genealogy

Rootless hair has unique advantages in forensic contexts. Hair is insoluble, preserving DNA over centuries (Figure 3). Because its exterior can be decontaminated with mild bleach, the extracted DNA is less susceptible to microbial contamination, unlike bone and tooth samples. Importantly, each single hair is a discrete biological unit that necessarily derives from a single individual. Thus, sample mixtures – a common obstacle in DNA-based forensics assays – in not an issue
for DNA derived from single hairs.

Many investigations have collected hair samples with little luck in human identification. Our methods use rootless hairs 5 cm in length but have had success with smaller strands.

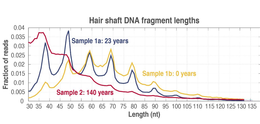


Figure 3: DNA fragment lengths observed in three rootless hairs samples from two individuals collected at different time points. Samples 1a and 1b derive from the same individual, collected 23 years and 0 years ago (i.e. present day), respectively. Sample 2 is from a second individual, approximately 140 years old. Hairs were processed following laboratory methods described above.

Our service

Phase I deliverable

With as little as 100 mg of bone powder or a few centimeters of hair, our paleogenetic-trained scientists prepare samples for whole genome sequencing[2,3]. After shallow NGS sequencing for quality-control analysis, we measure the amount of usable human DNA present in each sample. If enough DNA fragments are observed, we report the chromosomal sex estimation and mitochondrial haplotype of each sample. Because each cell contains many mitochondrial genome copies, we can often reconstruct the entire mitochondrial genome for a sample, even when very few autosomal DNA fragments are observed.

The quality-control sequencing also allows us to estimate the amount of sequencing necessary to achieve a high quality genotype/SNP profile. This Phase I quality-control analysis allows us to determine the feasibility and cost of generating the SNP profile.

Phase II deliverable

Based on quality-control analysis, we deeply sequence approximately 300-400 million read pairs. The Astrea Forensics pipeline works by analyzing DNA sequence data to generate a genotype file in a format suitable for upload to GEDmatch, FamilyTreeDNA, or other databases used for forensic genetic genealogy.

Once the genotype file is delivered, we are committed to supporting the work of law enforcement and forensic genetic genealogists until the case is solved. To see examples where Astrea Forensics' technology was used to solve cold cases, visit https://www.astreaforensics.com/in-the-news.

Company summary

Astrea Forensics, LLC is a biotechnology company focused on applying the most advanced DNA technology to forensics casework. Using the company's unparalleled expertise in ancient DNA research and next-generation-sequencing, Astrea uses proprietary methods for improving the recovery of DNA data from the most degraded of samples, including rootless hair. Astrea offers services to law enforcement and related agencies for recovering, sequencing, and genotyping DNA from samples that fail conventional testing. Astrea has both laboratory and computational innovations that directly address this problem. The product provides a genomewide solution for investigative genetic genealogy.

For more information email clientservices@astreaforensics.com. To speak with our team and submit a case inquiry, visit: requests.astreaforensics.com

Read more:

The NYTimes on our Founder, Ed Green: "Why This Scientist Keeps Receiving Packages of Serial Killers' Hair"

The Bear Brook Murders on ABC's 2020

Precious Jane Doe identified after 43 years

Citations:

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3. Troll, Christopher J., et al. "A ligation-based single-stranded library preparation method to analyze cell/ree DNA and synthetic oligos." BMC genomics 20.1 (2019): 1-14

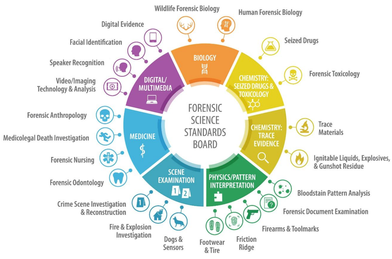
† figure created with BioRender.com

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

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The Organization of Scientific Area Committees (OSAC) for Forensic Science recently launched changes to its structure and processes to speed the drafting and review of high-quality, technically sound forensic science standards.

Among OSAC's structural changes, the former Biological Methods Subcommittee and Biological Data Interpretation & Reporting Subcommittee have been combined into the Human Forensic Biology Subcommittee. This group will draft standards focusing on human DNA analysis methods as well as serological techniques. The Human Forensic Biology Subcommittee, along with the Wildlife Forensic Biology Subcommittee, make up the two subcommittees in OSAC's Biology Scientific Area Committee (SAC).



The OSAC Registry approval process has also been changed to make it more efficient, require the technical review and the public comment period to happen earlier, and allow both published and OSAC proposed standards to be placed on the Registry. The OSAC Registry currently contains five DNA-related standards. These standards, initially drafted by OSAC's Human Forensic Biology and Wildlife Forensic Biology subcommittees, then further developed and published by the Academy Standards Board (ASB) include:

- ANSI/ASB Standard 020, *Standard for Validation Studies of DNA Mixtures, and Development and Verification of a Laboratory's Mixture Interpretation Protocol*, First Edition, 2018.
- ANSI/ASB Standard 022, *Standard for Forensic DNA Analysis Training Programs*, First Edition, 2019.
- ANSI/ASB Standard 028, *Wildlife Forensics Morphology Standards*, First Edition, 2019.
- ANSI/ASB Standard 040, *Standard for Forensic DNA Interpretation and Comparison Protocols*, First Edition, 2019.
- ANSI/ASB Standard 047, *Wildlife Forensics Validation Standard – Validating New Primers for Sequencing*, First Edition, 2019.

In addition to the Registry standards, OSAC's Human Forensic Biology Subcommittee drafted several other standards that have been published by ASB. These documents will be moving through the OSAC Registry approval process and include:

- ANSI/ASB Standard 018, *Standard for Validation of Probabilistic Genotyping Systems*, First Edition, 2020.
- ANSI/ASB Standard 023, *Standard for Training in Forensic DNA Isolation and Purification Methods*, First Edition, 2020.
- ANSI/ASB Standard 038, *Standard for Internal Validation of Forensic DNA Analysis Methods*, First Edition, 2020.
- ANSI/ASB Standard 077, *Standard for the Developmental and Internal Validation of Forensic Serological Methods*, First Edition, 2020.
- ANSI/ASB Standard 110, *Standards for Training in Forensic Serological Methods*, First Edition, 2020.
- ANSI/ASB Standard 115, *Standard for Training in Forensic Short Tandem Repeat Typing Methods Using Amplification, DNA Separation, and Allele Detection*, First Edition, 2020.
- ANSI/ASB Standard 116, *Standard for Training in Forensic DNA Quantification Methods*, First Edition, 2020.

OSAC's Wildlife Forensics Subcommittee also have the following ASB published standards in the OSAC Registry approval process:

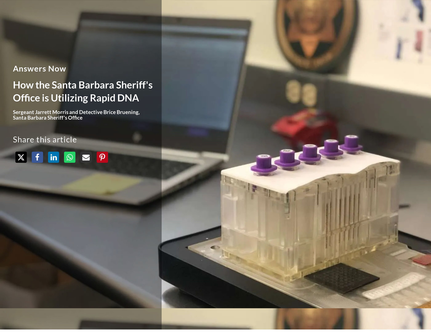
- ANSI/ASB Standard 019, *Wildlife Forensics General Standards*, First Edition, 2019.
- ANSI/ASB Standard 029, *Report Writing in Wildlife Forensics: Morphology and Genetics*, First Edition, 2019.
- ANSI/ASB Standard 046, *Wildlife Forensics Validation Standards – STR Analysis*, First Edition, 2019.
- ANSI/ASB Standard 048, *Wildlife Forensic DNA Standard Procedures*, First Edition, 2019.
- ANSI/ASB Standard 106, *Wildlife Forensics – Protein Serology Method for Taxonomic Identification*, First Edition, 2020.
- ANSI/ASB Standard 111, *Standard for Training in Mitochondrial DNA (mtDNA) Analysis for Taxonomic Identification*, First Edition, 2020.

The Human Forensic Biology Subcommittee is currently drafting standards or best practice documents related to familial searching, elimination databases, statistical analysis, determination of thresholds, interpreting data with contamination and failed controls, testimony regarding DNA activity level propositions as well as next generation sequencing/massively parallel sequencing. Additionally, the Wildlife Forensics Subcommittee is working on items addressing a variety of topics including statistical and in-house databases, building new panels for species identification, curation of reference samples, as well as geographic assignment.

For a monthly update on the forensic science standards moving through the OSAC Registry approval process and standards development process at SDOs, check out the OSAC Standards Bulletin.

To stay informed about and get involved with OSAC:

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



Answers Now

How the Santa Barbara Sheriff's Office is Utilizing Rapid DNA

Sergeant Jarrett Morris and Detective Brice Broening, Santa Barbara Sheriff's Office

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Santa Barbara, California, is often described as the "American Riviera". With 157 miles of beautiful coastlines, the pristine Channel Islands, rugged mountain ranges, award winning vineyards, and micro-breweries. Often sought by the elite as a place to live and play, Santa Barbara is home to Hollywood celebrities such as Oprah Winfrey, Ellen DeGeneres, Kevin Costner and Ashton Kutcher. Its newest celebrities, The Duke and Duchess of Sussex Harry and Meghan now call Santa Barbara home.

Despite its lavish reputation, mild climate and desirable destinations, Santa Barbara is not immune from the ills of neither nature or mankind. Santa Barbara is the location of the worst mass murder ever committed by a female, a deadly shooting rampage on a college campus, devastating wildfires and deadly mudslides. Santa Barbara also has the distinction of having the deadliest maritime disaster on the west coast of the United States in modern times.



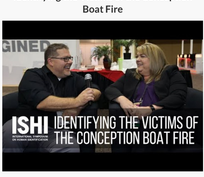
The Santa Barbara County Sheriff's Office is the largest law enforcement agency in Santa Barbara County. The Sheriff's Office is responsible for providing front line law enforcement services for all of the unincorporated areas in the county and four of the seven cities within the county. The Santa Barbara County Sheriff is also the County Coroner. The Coroner's Office is responsible for determining the cause and manner of death for any unattended or unnatural death occurring in the county. These include all homicides, accidents and suicides occurring in the county. In addition to determining the cause and manner of death, the Coroner's Office must also positively identify all persons falling within the Coroner's jurisdiction.

Santa Barbara County was introduced to Rapid DNA technology only recently, due to an incident that no one could have anticipated. On September 2, 2019, the 75 Foot dive boat, Conception, was anchored off the coast of Santa Cruz Island within Santa Barbara Channel. An early morning fire in the galley area trapped 34 souls who were sleeping in the bunkroom below deck. The smoke from the fire filled the bunkroom, and tragically all 34 perished. The fire onboard continued to burn despite efforts to extinguish the blaze. The Conception was burned to the waterline and ultimately sank in 60 feet of water. Dive teams and recovery experts spent the next two weeks recovering the victims of the fire and evidence related to the incident.



As victims were recovered from the water, it became apparent that the usual identification techniques of fingerprints and photographs would not be plausible. Nearly all of the victims suffered significant thermal burns. Often, coroner investigations which require additional identification methods beyond fingerprint analysis, would require the use of forensic odontology, forensic anthropology, prosthetic identification, and conventional DNA analysis. Early in the investigation on September 2nd, the Santa Barbara Sheriff Coroner's Bureau received a phone call that would change the course of the investigation, even before it started. Sacramento County Coroner, Kim Gin, reached out to the Santa Barbara County Coroner's Office, and offered to assist with a piece of technology that helped her office identify many of the 88 victims in the deadly *Camp Fire*, which occurred in Butte County in 2018, Rapid DNA. Sacramento County Coroner investigator's traveled to Santa Barbara with the ANDE Corporation, Rapid DNA instrument.

Identifying the Victims of the Conception Boat Fire



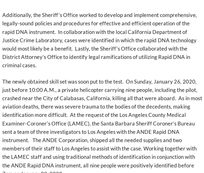
On Labor Day, 2019, The Conception caught fire on the last day of a 3-day diving trip off of the coast of California. Tragically, all 33 passengers and 1 crew member perished in the fire.

In this interview, Kimberly Gin, Coroner at the Sacramento County Coroner's Office shares how she and a Deputy Coroner assisted Santa Barbara in identifying all of the victims in under 8 days using an ANDE Rapid DNA instrument.

Learn More on Our Blog

Within the first 24 hours, investigators set up a protocol and system to collect DNA samples from victims, and run comparative analysis with samples collected from family members. Once familial DNA samples were collected and processed, victim DNA could be matched within a matter of hours with the ANDE Rapid DNA technology. Conventional DNA analyses processed by the Department of Justice could take months. Through this tragedy, the Santa Barbara Sheriff Coroner's Office discovered that Rapid DNA could truly change the way victim identification and death investigation happens. This technology can also have positive impacts on the direction of criminal investigations. The ability to quickly confirm victim identity and confirm or rule out suspect identification, can allow investigative resources to be quickly redirected.

The Santa Barbara Sheriff 's Office made a commitment to bring the ANDE Corporation's Rapid DNA technology in house. During a contractual trial period, two trainers from the ANDE Corporation conducted a 3-day training at the Santa Barbara County Sheriff Coroner's Bureau for key personnel from the Coroner's Bureau and Forensics Bureau. During the course of the training, staff utilized real samples, learning to process blood, bone and "touch" DNA from items handled by their colleagues in the class. At the conclusion of the training, the staff were feeling confident with their newly learned skill set and they were eager to begin using their new instrument on death investigation identification and criminal casework.



Additionally, the Sheriff 's Office worked to develop and implement comprehensive, legally-sound policies and procedures for effective and efficient operation of the rapid DNA instrument. In collaboration with the local California Department of Justice Crime Laboratory, cases were identified in which the rapid DNA technology would most likely be a benefit. Lastly, the Sheriff's Office collaborated with the District Attorney's Office to identify legal ramifications of utilizing Rapid DNA in criminal cases.

The newly obtained skill set was soon put to the test. On Sunday, January 26, 2020, just before 10:00 A.M., a private helicopter carrying nine people, including the pilot, crashed near the City of Calabasas, California, killing all that were aboard. As in most aviation deaths, there was severe trauma to the bodies of the decedents, making identification more difficult. At the request of the Los Angeles County Medical Examiner-Coroner's Office (LAMEC), the Santa Barbara Sheriff Coroner's Bureau sent a team of three investigators to Los Angeles with the ANDE Rapid DNA instrument. The ANDE Corporation, shipped all the needed supplies and two members of their staff to Los Angeles to assist with the case. Working together with the LAMEC staff and using traditional methods of identification in conjunction with the ANDE Rapid DNA instrument, all nine people were positively identified before 7pm on January 29, 2020.



Over the next several months, the ANDE Rapid DNA Instrument, proved to be invaluable in several more cases. Two additional aviation related accidents required DNA comparison for victim identification, and the identification of a human foot, found on the side of the road in rural San Luis Obispo County to the north. The foot had been exposed to the elements, was partially burned and began to decay. It was believed to belong to the victim of a vehicle collision that had occurred several days prior and several miles away from where it was found. The victim was inaccessible to law enforcement; however, detectives from the San Luis Obispo Sheriff Coroner's Office were able to collect reference samples from the victim's mother. Within 24-hours of receiving the foot and reference samples, the Santa Barbara Sheriff Coroner's Office was able to generate a kinship DNA match and confirm the foot belonged to the victim of the car accident. The ANDE Rapid DNA technology was able to save San Luis Obispo Coroner investigator's valuable time and resources.

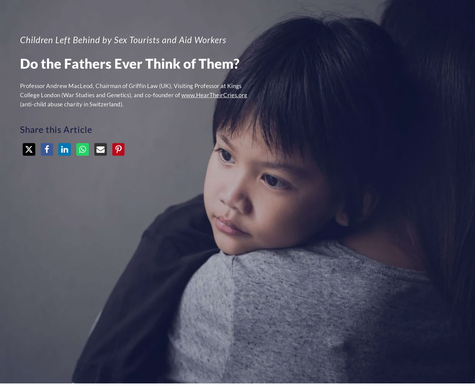
In just over a year's time, the ANDE Rapid DNA instrument has been used to positively identify 12 human remains in death investigations. It has also proven useful in several criminal investigations. As investigators and prosecutors become more familiar and comfortable with the technology, its use in criminal investigations is sure to expand. Sound policies and protocols, acknowledged and approved by all stakeholders in criminal investigations, will expand its purpose and use. Access to DNA analysis and the speed in which analysis is performed are the most important benefits of the instrument, allowing investigators to quickly identify decedents, helping to bring closure to the families of the deceased.

Children Left Behind by Sex Tourists and Aid Workers

Do the Fathers Ever Think of Them?

Professor Andrew MacLeod, Chairman of Griffin Law (UK), Visiting Professor at Kings College London (War Studies and Genetics), and co-founder of www.HearTheCries.org (anti-child abuse charity in Switzerland).

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In December 2019 Susan Bartels at Queens University and Sabine Lee at Birmingham University released to the world a report identifying 265 children born of United Nations Peacekeepers in Haiti and since abandoned[1]. While this number may seem shocking there are two points that will shock the reader more.

Firstly, this huge number of children were identified following interviews with just 2,500 women. Given there are more than 2.5 million women of childbearing age in Haiti, some 1,000 times more than those interviewed, one would hate to think just how many children have been fathered by UN peacekeepers and abandoned.

The second additional shock is the statement from UN Secretary General Antonio Guterres made at the 2017 High Level Panel on Sexual Exploitation and Abuse.

"First, sexual exploitation and abuse is not a problem of peacekeeping, it is a problem of the entire United Nations. Contrary to the information spreading that this is a question related to our peacekeeping operations, it is necessary to say that the majority of the cases of sexual exploitation and abuse are done by the civilian organizations of the United Nations, and not in peacekeeping operations"[2]

The 265 children identified in Haiti from only 2,500 interviews, were fathered by peacekeeping soldiers of the UN. The UN Secretary General says that the problem of sexual abuse is bigger on the civilian side of the UN. So how big is the problem?

The truth is we just don't know how big the problem is as the data available is so sparse.

The numbers quote above are a small proportion of the sex and child rape crimes committed by UN staff and peacekeepers over at least the last two decades. Neither the sex scandals of the UN in the Bosnian War dramatized in the 2010 film Whistleblower[3] nor the long running 'Food for Sex' scandals of the early 2000s[4] are covered in these figures. These figures are just for Haiti and just for UN peacekeeping soldiers, not the rest of the aid world.

We know from the Oxfam scandal of 2017 that Aid staff feel such a level of impunity to abuse that they even order their drivers to home deliver women, as happened in the Oxfam Haiti case.

What do we do about this mountain of sex abuse and the children left behind by impoverished women impregnated by men who are sent to conflict and disaster settings to do good? Surely these children deserve more justice than the empty statements of 'zero tolerance' given by the UN for nearly 20 years?

The sad truth is the problem of peacekeepers and aid workers abusing women and children overseas is a larger problem than the Catholic Church. That statement may be provocative, but think of it this way: There are more aid workers than Catholic priests, in more countries than the Catholic Church is present in, with better access to women and children while controlling food, water and shelter. What makes you think the average aid worker is ethically any better than the average Catholic Church priest?

It is important to note that this is not a question of 'secret conspiracies', rather a huge vulnerability to which there is no adequate preventive measures stopping abuse. It is inaction, not conspiracy, that is causing this problem.

Indeed in 2018 the British House of Commons Committee on International Development handed down a report into sexual exploitation by aid workers saying that the entire industry was 'complacent verging on complicit' and put the reputation of agencies before the protection of children.

Technology may offer a new way to at least find the men that have left children behind and to hold them to account through courts of law.



In 2017 in California the 'Golden State Killer' was captured by taking DNA he left behind at the crime scene and comparing it to extended family members on public data bases. By mapping the extended family members, it is then possible to triangulate the family relationships and often identify the father.

In the case where a man has impregnated a woman or child in cases like aid worker sex abuse or sex tourist abuse, the child they leave behind has half of the father's DNA.

We are evolving the Genetic Genealogy technology used in the 'Golden State Killer' case in California to track sex tourists, abusive aid workers and peacekeepers who have procreated children in the developing world. On behalf of the children we can find their fathers and allow the children to know their heritage, their extended family and seek appropriate child support.

Our secondary aim is to stamp out these abuses by tracking fathers, holding them to account and sending a signal to future potential abusers that one day abusers will face justice.

We have run six test cases in the Philippines with women who have been impregnated by either sex tourists or aid workers to prove both the technology and the legal procedures. Of the first six cases we have found five fathers: One is British, one American, one Canadian, two Australian and the sixth is likely Australian but we are unsure.

In these cases we have:

- M & M, 19 year old twin girls: The father consented to paternity confirmed with a court order. The father is now getting his daughters their UK passports and providing support. The children have come to learn that they have six siblings across three countries.
- S, a 12 year old boy. The father was ecstatic to learn he had a son. The child will be fully supported and is being accepted into the broader family.
- M2, an 11 year old girl: The father is identified but he denies paternity. The father's brother (with whom we got the DNA match as an uncle) accepts the result as does the father's mother. We are giving the family an opportunity to convince the brother before possibly escalating to legal action.
- J, a 19 year old boy: The father is one of two brothers (Australian) who are almost impossible to track. The child's aunt, half aunt, and grandmother have all been identified however they do not wish to be involved and are not helping.
- B, a 13 year old girl: The father has been identified and is Canadian. He originally consented and agreed but has since retracted his agreement and we are now seeking court orders.

While for decades the Aid industry has looked at 'procedures and practices' to try and reduce sexual abuse by their staff, these actions have failed. There are thousands if not tens of thousands of children around the world who have been fathered by UN peacekeepers, UN civilian aid workers and NGO aid workers.

Each of these children has the right to know who their father is, who their extended family is and each has the right to support. Today we have the technology to move beyond words and get real solutions for some of the world's most vulnerable people.

We have proved now that the technology works and now have the technical ability to hold sex tourist fathers to account to a lesser or greater degree. During 2021 we will expand the test program we did in the Philippines to West and Central Africa. While we are not yet at the day when we can stamp out sexual abuse in the aid sector, we are getting closer. In the process though we will be able to get justice for many children whose only question is "Daddy, do you ever think of me?

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Professor Andrew MacLeod, BA/LLB, LLM, GAICD

Andrew is a recognised global leader, negotiator and communicator in the business, diplomatic and humanitarian field. He has a track record of leading organisations through challenge, crisis and change.

Andrew's foundation training was as a lawyer and Army Officer (Australian Infantry). His specialisations included International Shipping, War Crimes, Crimes Against Humanity and Genocide. For the International Committee of the Red Cross, Andrew set up and ran Law of Armed Conflict training with military units in Rwanda and former Yugoslavia during the 1990's that saw a measurable decrease in civilian casualties.

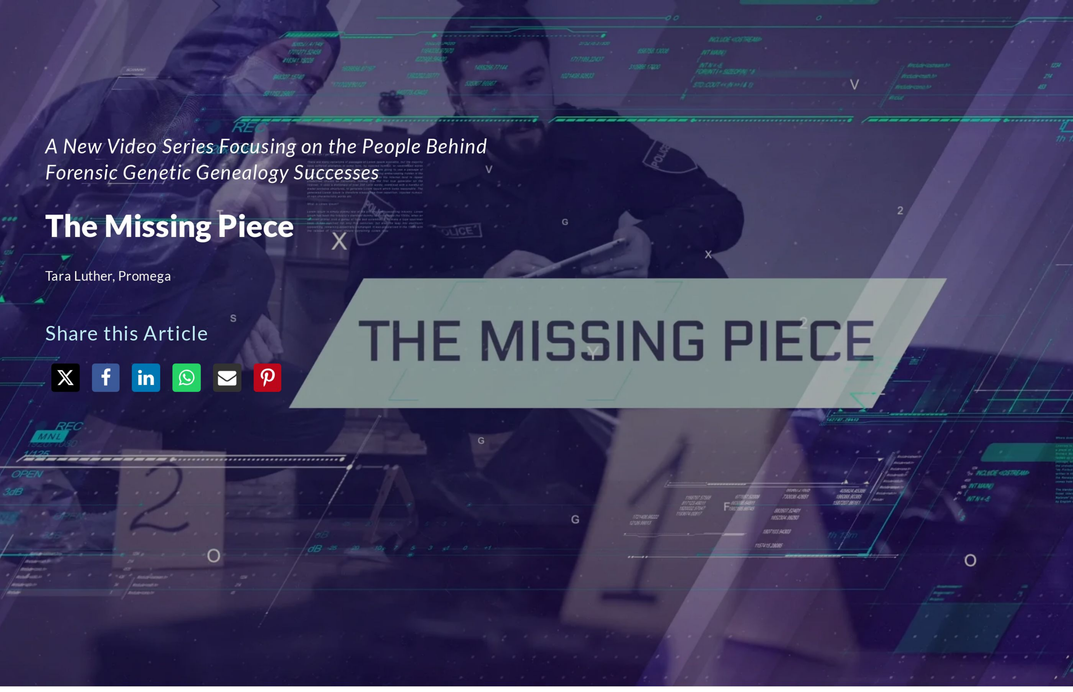
Andrew holds a Bachelor of Arts and Bachelor of Laws from Tasmania University, a Master of Laws from Southampton University, a Graduate Diploma in International Law from Melbourne University and is a Graduate of the Australian Institute of Company Directors.

Andrew is also a Visiting Professor at Kings College London, an Affiliate Senior Associate to the Center for Strategic International Studies in Washington DC. He served on the Advisory Boards of the World Economic Forum's Future of Civil Society Project Advisory Board, Kings College Humanitarian Futures Project, the UN Expert Group on Responsible Business and Investment in High-Risk Areas and is a Non-Executive Director at Cornerstone Capital where he has been part of the team overseeing growth from start-up to stability.

He has been published in journals and newspapers internationally on areas of corporate reform and profitability, stakeholder management, leadership, negotiations, global affairs, security and terrorism. He is the Author of the book A Life Half Lived (New Holland Press) and he is a sought after corporate speaker internationally.

Andrew received the Humanitarian Overseas Service Medal by Australia for work in the Balkans and was awarded a second time for work in Rwanda. He received the Australian Defence Medal for service as an officer in the Australian Infantry. He was awarded the Silver Medal for Humanity from the Montenegrin Red Cross and was recognised by the Australian Government for his work in East Timor. Andrew was awarded as a Vice Chancellor's Distinguished Fellow at Deakin University in 2016, the 2014 University of Tasmania Foundation distinguished Graduate Award, the 2013 Young Britons Foundation Global Leadership for Freedom Award and the 2008 Australian Davos Connection Leadership Award, amongst others.

Andrew was also a world-class swimmer having won a silver medal for the 200 meters Butterfly at the 2002 World Masters Games. He regularly volunteered to help national swimming teams in the developing countries.



A New Video Series Focusing on the People Behind Forensic Genetic Genealogy Successes

The Missing Piece

Tara Luther, Promega

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

To generate leads in criminal cases investigators traditionally upload DNA profiles found at crime scenes to CODIS, a DNA databased maintained by the FBI. As of September 2020, CODIS has produced more than 533,268 hits assisting in more than 521,562 investigations. Yet, CODIS has its limitations. In order for a hit to a known identity to occur, the offender profile must already exist within the DNA database. For the families of Carla, Christine, and Siobhan, no such matches were found.

In 2018, a new tool for crime solving rose to prominence as the notorious Golden State Killer was finally unmasked. For years, Joseph James DeAngelo remained under the radar until investigators in the case partnered with genealogist Barbara Rae-Venter. Using genome-wide testing to generate a comprehensive DNA profile, the team turned to a genetic genealogy website where users came to learn more about their roots - GEDmatch.

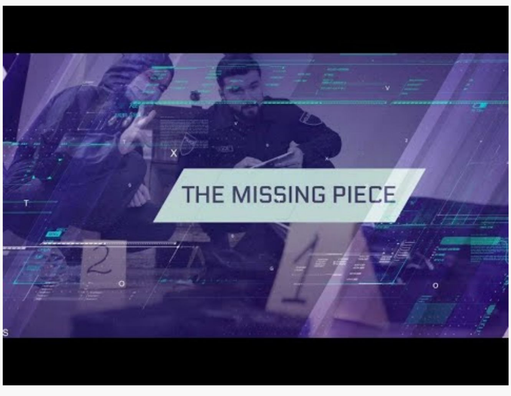
GEDmatch contains DNA profiles from users who had taken tests from direct-to-consumer companies like Ancestry and 23&me. The platform serves as a place where users can upload their DNA data files to compare their genetic relationships with others to build their family trees. It's also been an invaluable resource for a new technique called forensic genetic genealogy.

Forensic genetic genealogy relies on genetic relationships between a DNA profile for an unknown person and profiles of known people in genealogy databases, such as GEDmatch, FamilyTreeDNA, or DNASolves. To begin, investigators upload their unknown DNA profile to the site, which generates a list of the closest genetic matches, based on how many centimorgans (cM) of DNA are shared with the unknown person. Next, investigators will begin to build back the unknown person's family tree until a common ancestor is uncovered. Then, they will build the family trees forward, identifying every descendent possible, using traditional genealogy techniques. Once the trees have been fully built out, investigators look to identify candidate persons that might match the unknown person. Once a person of interest has been identified, new DNA can be collected to compare to the original forensic sample.

After 46 years, through a combination of advanced DNA testing, forensic genetic genealogy and traditional detective work, the Fort Worth Police Department was able to indict Glen Samuel McCurley for the 1974 death of Carla Walker. Using similar methods, Christine Jessop's killer, Calvin Hoover, was identified. Christine was 9 years old when her life was cut short in the small town of Queensville, Ontario. It took 36 years to close the case. In Missoula, MT, investigators were able to determine that it was Richard William Davis who killed 5-year-old Siobhan McGuinness.

This case took 46 years to close and it now appears that the killer of Siobhan may also have been involved in other unsolved crimes.

ISHI is excited to announce our new video series in collaboration with Othram that will showcase the important work being done behind the scenes to solve these cases. We'll meet the analysts performing the DNA work, investigators, victim advocates, and may even speak to family members of some of the victims to hear how forensic genetic genealogy is transforming how cold cases are investigated. For years, these killers escaped justice; maybe forensic genetic genealogy really was the missing piece.



***The Missing Piece* launches on the ISHI YouTube channel in early 2021.**

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