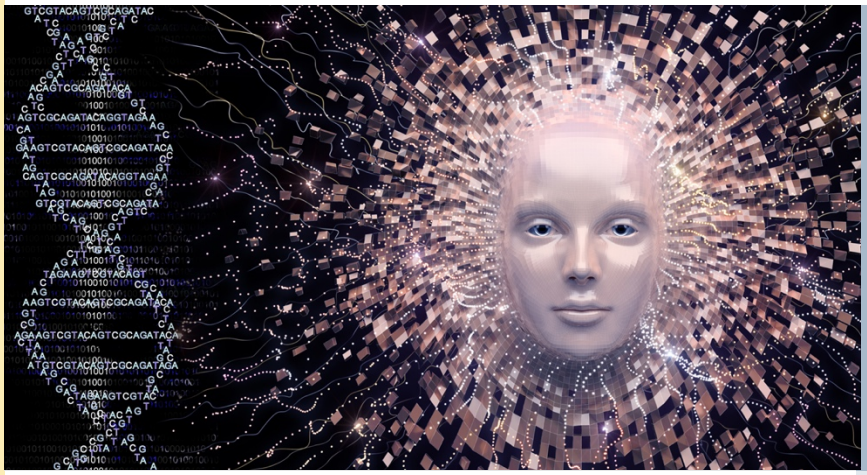
# IN-BRIEF

# Forensic DNA: The Beginning of the SNP Era Webinar Series



"The biggest benefit of this series was learning of the potential of SNPs and microhaplotypes with respect to forensics and identification. The presenters discussed how this could be integrated into the current infrastructure for practitioners."

*—Webinar Attendee*

## Overview

To help the forensic community stay informed about recent advances in technology, the Forensic Technology Center of Excellence (FTCoE) provides educational opportunities for forensic professionals—including practitioners, researchers, and stakeholders—to discuss and cultivate ideas.

The FTCoE, in collaboration with The George Washington University, hosted a five-part webinar series about using SNPs for forensic applications and about recent advances in the forensic sciences field. This in-brief summarizes the content of the webinar series as well as the forensics community's feedback about the webinar series.

Short tandem repeats (STRs) are currently used in all forensic DNA laboratories for human identification; however, single nucleotide polymorphisms (SNPs) have recently emerged as markers of interest. SNPs present several benefits, including their ability to be identified from highly fragmented DNA, the ancestral and phenotypic information they may carry, the power they have to deconvolute complex mixtures, and their utility in distinguishing STRs of the same size. New technologies for genotyping SNPs have been developed in recent years, and such technologies will continue to advance for many years to come.

## Objectives

- Provide an overview of using SNPs for forensic applications and recent advances in the field of forensic DNA analysis.
- Describe how linkage disequilibrium patterns can be used to identify pairs of genetic records.
- Discuss principles, methods, and applications of DNA-based prediction of human phenotypic traits for forensic and anthropological use.
- Highlight the history of SNPs as forensic markers as well as the development of SNP and microhaplotype multiplexes.
- Explain how multiplex assays targeting DNA methylation sites can be used to estimate ages of individuals and identify body fluid types.
- Explore the technical and operational aspects of implementing forensic investigative DNA testing.

***Disclaimer:*** *This project was supported by Award No. 2016-MU-BX-K110, awarded by the National Institute of Justice, Office of Justice Programs, U.S. Department of Justice. The opinions, findings, and conclusions or recommendations expressed in this publication/program/exhibition are those of the author(s) and do not necessarily reflect those of the Department of Justice.*

## Dr. Daniele Podini

Dr. Daniele Podini from The George Washington University served as a key individual for this collaborative webinar series. Dr. Podini is a forensic DNA expert whose current research focuses on microhaplotypes (MHs) and on the use of next-generation technologies for human identification purposes. His forensic experience ranges from processing crime scenes for biological specimens to processing evidence in the laboratory, and from DNA profiling to testifying in court as an expert witness. Dr. Podini has been a faculty member in the Department of Forensic Sciences since 2004. He is also a member the American Academy of Forensic Sciences, the International Society of Forensic Genetics, and the Subcommittee on DNA Analysis of the Organization of Scientific Area Committees. As a member of these organizations, Dr. Podini works to strengthen forensic sciences in the United States.

## Webinar Presenters

The presenters were an integral part of this webinar series, helping to accomplish the overall goal of providing an overview about using SNPs for forensic applications and about recent advances in the field of forensic DNA analysis. **Table 1** provides information about the five webinars and the presenters.

## Webinar Archives

The archived webinars are available on the FTCoE website at forensiccoe.org/webinar/snps-webinar-series/.

**Table 1.** A summary of the *Forensic DNA: The Beginning of the SNP Era* webinar series.

| Webinar | Presenter(s) |
|---|---|
| **Record Linkage of CODIS Profiles with SNP Genotypes**<br>September 21, 2017 | **Michael "Doc" Edge, PhD**<br>University of California, Davis |
| **Predict Human Appearance from DNA Focusing on Pigmentation**<br>October 25, 2017 | **Manfred Kayser, PhD**<br>Erasmus University Medical Center<br>**Susan Walsh, PhD**<br>Indiana University–Purdue University Indianapolis |
| **The Evolution of SNPs as a Forensic Marker**<br>November 7, 2017 | **Kenneth Kidd, PhD**<br>Yale University<br>**Chris Phillips, PhD**<br>University of Santiago de Compostela<br>**Tom Parsons, PhD**<br>International Commission on Missing Persons<br>**Daniele Podini, PhD**<br>The George Washington University |
| **DNA Methylation-Based Age Prediction and Body Fluid ID**<br>December 6, 2017 | **Athina Vidaki, PhD**<br>Erasmus University Medical Center<br>**Hwan Young Lee, PhD**<br>Yonsei University |
| **Investigative DNA Testing Implementation**<br>January 16, 2018 | **Katherine Gettings, PhD**<br>National Institute of Standards and Technology<br>**Maretta Chase, MS**<br>Centre of Forensic Sciences, Ministry of Community Safety and Correctional Services (Canada)<br>**Runa Daniel, PhD**<br>Victoria Police Forensic Services Department (Australia) |

## Record Linkage of CODIS Profiles with SNP Genotypes

### Presenter

Michael "Doc" Edge, PhD
Postdoctoral Researcher | University of California, Davis

### Objectives

- Understand population-genetic sources of linkage disequilibrium (LD), or associations between markers at distinct loci.
- Describe a way in which LD patterns can be used to identify pairs of genetic records that closely match or do not match.
- Predict the limits and potential of LD-based record matching as the number of Combined DNA Index System (CODIS) loci increase.

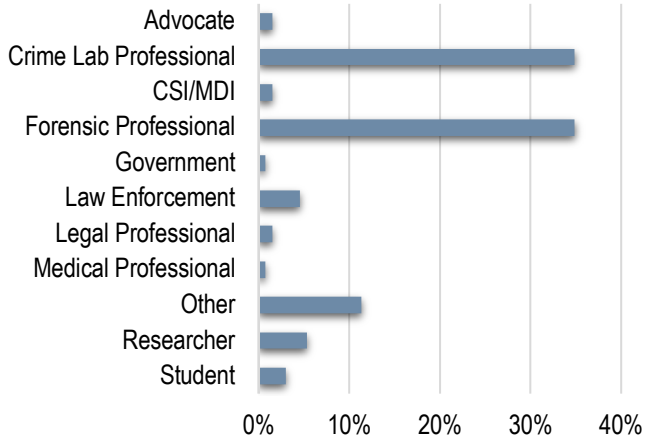
### Summary

In this webinar, Dr. Edge described a method for assessing whether a genotype based on the CODIS microsatellite loci could be associated with a person already genotyped for an array of genome-wide SNPs. He discussed the population-genetic basis of his LD method and described how LD can be leveraged to identify the closeness of a "match" between two sets of genotypes, even when the genotype sets do not have any markers in common. LD refers to the lack of independence in the inheritance of different regions of the genome, and the principle applies between various CODIS loci and SNPs. Dr. Edge also used data from a worldwide sample of humans to discuss some of the method's empirical demonstrations. Finally, he explained the potential and limitations of the method and also outlined some challenges for future work.

Forensic-genetic work in the United States relies largely on a set of 20 core CODIS markers. The information that the CODIS loci provide is completely distinct from the information that the larger SNP sets provide. CODIS loci variations are useful for identifying individuals, but unlike SNPs, they have no known connections with individual phenotypes. Moreover, associations between CODIS markers and SNPs are weak, but this could change if pairs of CODIS and SNP genotypes can be linked to the same person.

A recently reported genetic record-linkage method assesses whether a particular set of genotypes from the CODIS markers is likely drawn from the same person (or an identical twin) as a set of genome-wide SNP genotypes.[1] The method identifies matches with high accuracy in the presence of hundreds of false distractor matches, with implications for (1) the plausibility of backward compatibility of an SNP-based forensic database and (2) genetic privacy.

### Attendee Professions




**"Before this webinar, I had never thought it would be possible to compare different markers in a database."**

*—Webinar Attendee*

## Predict Human Appearance from DNA Focusing on Pigmentation

### Presenters

Manfred Kayser, PhD
Professor | Erasmus University Medical Center

Susan Walsh, PhD
Assistant Professor | Indiana University–Purdue University Indianapolis

### Objectives

- Understand the large variation in human appearance and how to find genes for common traits, particularly eye color.
- Provide an overview of genes that determine eye color, beginning with a history of eye color prediction attempts and models.
- Describe the IrisPlex, HIrisPlex, and HIrisPlex-S systems for forensic DNA phenotyping.

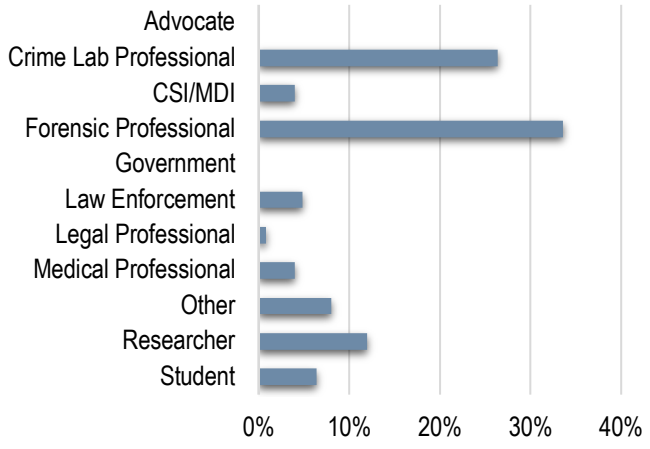
### Summary

This webinar provided an overview of principles, methods, and applications of DNA-based predictions of human appearance traits for forensic and anthropological use. Specifically, the presenters discussed insights into eye, hair, and skin color prediction from DNA.

Conventional forensic DNA analysis based on STRs is an effective approach for individual human identification. However, for cases in which a suspect has not been found, DNA testing aimed at predicting the physical appearance of the unknown sample donor is useful. This testing serves as an unbiased "molecular witness" and can help investigators by prioritizing suspect processing and corroborating eyewitness testimony; additionally, this testing increases the ability to find suspects who cannot be identified through standard forensic DNA profiling. DNA-based prediction of appearance traits is also relevant in missing persons and anthropological cases, augmenting insight into the appearance of deceased persons gained from skeletal remains.

During the past decade, our understanding of the genetics of human appearance has increased significantly, and DNA-based predictions for traits such as pigmentation have been shown to be accurate and useful. In the first part of this webinar, Dr. Kayser summarized existing genetic knowledge about human appearance and where the field of forensic DNA phenotyping, (i.e., predicting appearance traits from crime scene DNA for investigative purposes) currently stands. In the second part of the webinar, Dr. Walsh discussed the DNA-based predictions of eye, hair, and skin color, the only appearance traits that currently can be predicted from DNA with measurable accuracy. SNP-based categorical pigmentation prediction tools were also explained. These tools include the IrisPlex system for eye color; the HIrisPlex system for eye and hair color; and the soon-to-be-released HIrisPlex-S system for eye, hair, and skin color.

### Attendee Professions




**"The biggest benefit of attending this event was broadening my horizons towards a very promising investigative DNA tool."**

*—Webinar Attendee*

## The Evolution of SNPs as a Forensic Marker

### Presenters

Kenneth Kidd, PhD
Professor Emeritus | Yale University

Chris Phillips, PhD
Researcher | University of Santiago de Compostela

Tom Parsons, PhD
Director of Forensic Sciences | International Commission on Missing Persons

Daniele Podini, PhD
Professor | The George Washington University

### Objectives

- Describe the evolution of SNPs as forensic markers from restriction fragment length polymorphisms (RFLPs) to microhaplotypes (MHs).
- Highlight ongoing research efforts to develop SNP-based assays for human identification and ancestry prediction.

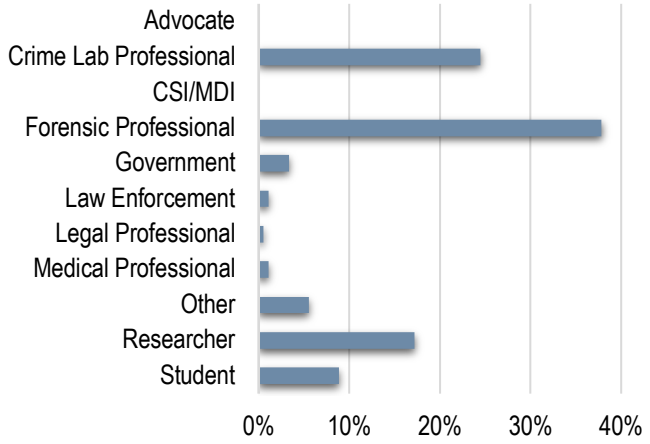
### Summary

Four presenters participated in this webinar. Dr. Kidd discussed the history of SNPs as forensic markers, highlighting some of the resources available to practitioners. Dr. Phillips and Dr. Parsons covered the design and development of large SNP and MH multiplexes for forensic and missing person identification. Lastly, Dr. Podini talked about the performance of MH assays on simulated forensic samples for individual identification and ancestry prediction.

Four major categories of SNP and SNP-related markers useful for human identification have been found: individual identification SNPs (IISNPs), ancestry informative SNPs (AISNPs), phenotype informative SNPs (PISNPs), and MHs. IISNPs are polymorphisms that vary considerably between individuals, and any one multi-locus genotype has a very low probability of being found in another individual. Although these loci differ from the CODIS STRs, they can be more easily recovered from single-source degraded DNA samples due to their smaller size. AISNPs are characterized by having allele frequencies that vary significantly across populations and can be used to infer an individual's population of origin. PISNPs are in the coding or regulating region of proteins that play important roles in determining somatic traits, and thus PISNPs can be used to infer physical appearances. MHs are defined as clusters of at least two SNPs within a short distance of each other, and which have three or more allelic combinations. They can provide information about an individual's identity and their ancestry.

Massively parallel sequencing (MPS) technologies are routinely used in clinical genetics; the sensitivity and reliability of these technologies are consistent with conventional forensic DNA analysis methods. These technologies enable hundreds of DNA markers to be genotyped simultaneously. Thus, large multiplexes targeting SNPs and MHs in very small amplicons can be developed for analyzing degraded DNA samples where STRs might be unsuccessful. Advantages of sequencing MHs compared to STRs are that (1) stutter is eliminated by the absence of short-repeated sequences; (2) alleles are the same size, eliminating length-based preferential amplification of shorter alleles; (3) MHs have a significantly lower mutation rate, which is important in family relationship testing; and (4) MHs allow for individual and ancestry prediction from a single sample using the same analysis methods.

### Attendee Professions




**"The biggest benefit of attending this event was learning about microhaplotypes. Before this webinar, I was only vaguely aware of their use in the forensic sphere."**

*—Webinar Attendee*

## DNA Methylation-Based Age Prediction and Body Fluid ID

### Presenters

Athina Vidaki, PhD
Postdoctoral Researcher | Erasmus University Medical Center

Hwan Young Lee, PhD
Research Associate Professor | Yonsei University

### Objectives

- Provide an overview of epigenetics, specifically DNA methylation, and how epigenetics can be useful in forensics.
- Describe how to build a model for chronological age prediction based on age-associated methylation sites.
- Understand how to perform multiplex assay for body fluid identification.

### Summary

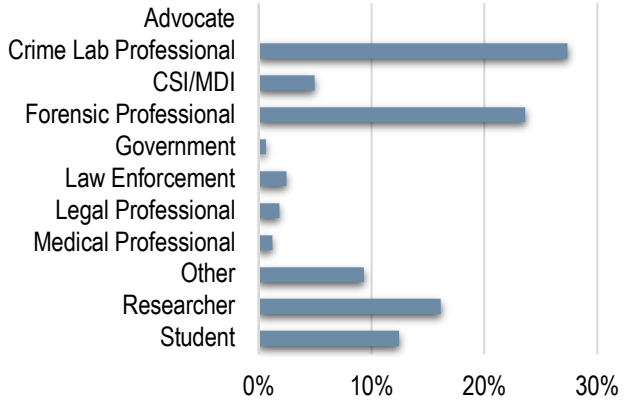
The study of heritable traits caused by molecular mechanisms outside of the DNA sequence, especially those controlling gene regulation, is called epigenetics. DNA methylation is one such modification, and it is primarily associated with the silencing of gene expression. During DNA methylation, a methyl-group ($-CH_3$) is added to a specific carbon atom in a cytosine, and it is especially common for cytosines found in "CpG islands" (regions of the genome where the sequence pair CG is common).

In this webinar, Dr. Vidaki and Dr. Young Lee discussed how multiplex assays targeting CpG methylation sites can be used to predict an individual's age and determine a sample's body fluid of origin.

The ability to estimate a donor's age based on recovered biological material from a crime scene can be valuable to forensic investigations, because this information helps narrow suspect pools. Age-associated DNA methylation patterns can be used for this purpose. Dr. Vidaki and Dr. Young Lee provided an overview of how age-associated DNA methylation profiles can be formed and which genetic or environmental factors are expected to influence these profiles. The presenters also discussed how suitable statistical and computational models can be built based on only a handful of CpG methylation sites that allow for the accurate age prediction of individuals across a wide age range. Additionally, various epigenetic techniques were discussed, including MPS, which can be used to analyze age-associated DNA methylation profiles in forensic-type material.

Methylation patterns can also help identify forensically relevant body fluids, such as blood, saliva, semen, vaginal secretions, and menstrual blood. Body fluid identification (BFID), which refers to the determination of the type and origin of body fluids from molecular profiles of crime scene samples, has important implications in forensics. BFID enables experts to draw conclusions about what led to the deposition of the cellular material at a crime scene, thereby potentially linking sample donors and criminal acts. Compared to RNA-based assays, the other main nucleotide-based fluid-identification method currently being researched, DNA methylation-based assays can be used for older cases, which usually only have DNA available. Additionally, these assays can be easily incorporated into the routine forensic laboratory workflow. Dr. Vidaki and Dr. Young Lee described how to select candidate markers from the Illumina's BeadChip array, how to set up a multiplex assay for the simultaneous detection of multiple markers, and how to interpret the assay's profile. Additionally, several test examples were shown; these examples were performed in actual casework samples.

### Attendee Professions




**"I enjoyed learning new approaches to forensics using unique biochemical advances."**

*—Webinar Attendee*

## Investigative DNA Testing Implementation

### Presenters

Katherine Gettings, PhD
Research Biologist | National Institute of Standards and Technology

Maretta Chase, MS
Senior Technologist | Centre of Forensic Sciences, Ministry of Community Safety and Correctional Services

Runa Daniel, PhD
Forensic Officer | Victoria Police Forensic Services Department

### Objectives

- Describe the validation of an ancestry panel for use in forensic casework.
- Provide an overview of, and considerations for, gathering information from DNA for investigative purposes.

### Summary

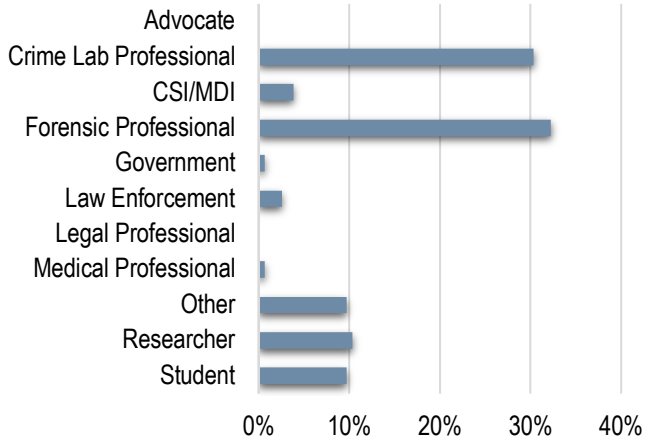
In this webinar, Dr. Gettings, Ms. Chase, and Dr. Daniel discussed technical and operational considerations for implementing the tools and protocols needed to gather information from DNA for investigative purposes. This is especially focused on DNA-based predictions of physical appearance, which can provide investigators with useful leads when a DNA profile does not generate a hit.

Currently, forensic DNA profiling is focused on precisely identifying the donor of biological evidence that has been retrieved from a crime scene. This largely depends on obtaining a standard DNA profile that can be matched to one in a database or to a reference profile. Dr. Daniel suggests that when a match is not found, laboratories often stop using biological evidence in the investigation.

However, current methodologies enable broader investigative information to be extracted from DNA. Forensic DNA intelligence (i.e., forensic DNA phenotyping in this context) enables the prediction of the biogeographical ancestry and the externally visible characteristics of the donor of biological evidence; these predictions are based on analyses of ancestry informative markers (AIMs) and phenotype informative markers (PIMs), primarily SNPs. Additionally, MPS technologies have supported the advancement of DNA intelligence gathering by enabling hundreds of DNA markers to be analyzed simultaneously. The ability to provide such information enables investigators to focus valuable police and forensic resources in an investigation. There are two main challenges in this process: one is technical and has to do with the analytical processes that need to be optimized and validated to effectively type and interpret an AIMs/PIMs profile. The second is related to the ways in which a laboratory reports results and how investigators understand and apply those results.

The presenters discussed the MPS-based ancestry prediction assays suitable for the analysis of forensic samples that are currently available. Additionally, they explored the technical and operational challenges of implementing DNA intelligence, such as processing casework samples (e.g., mixed, degraded, and inhibited samples) and effective and unbiased reporting of the results. Potential guidelines for reporting ancestry results to clients were also discussed, along with the results from a DNA intelligence exercise that involved the application of ancestry and phenotype inference by a senior police intelligence analyst in a mock case scenario.

### Attendee Professions




**"The biggest benefit of attending this webinar was learning about the topic and how other agencies are implementing SNPs for predicting appearance."**

*—Webinar Attendee*

## About the FTCoE

The FTCoE, led by RTI International (RTI), is supported by a cooperative agreement with the National Institute of Justice (NIJ), award 2016-MU-BX-K110. The FTCoE is committed to improving the practice and strengthening the impact of forensic science through effective knowledge transfer and education. One way in which the FTCoE accomplishes its mission is through hosting virtual educational opportunities that provide a setting for practitioners, researchers, stakeholders, and other professionals to discuss and cultivate ideas. The RTI International team includes Ms. Donia Slack, Ms. Sarah Norsworthy, and Mr. Josh Vickers. Ms. Slack is a Research Forensic Scientist with more than 14 years of experience in the forensic DNA research community. Ms. Norsworthy is a Forensic Scientist and supports the FTCoE's human DNA analysis efforts. Mr. Vickers is a Project Management Specialist and is responsible for the coordination of all FTCoE webinars.

## Resource

[1] Edge, M., Algee-Hewitt, B., Pemberton, T., Li, J., & Rosenberg, N. (2017). Linkage disequilibrium matches forensic genetic records to disjoint genomic marker sets. *Proceedings of the National Academy of Sciences of the United States of America*, 114(22), 5671–5676.

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STRENGTHEN SCIENCE. ADVANCE JUSTICE.

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CENTER OF EXCELLENCE

RTI INTERNATIONAL

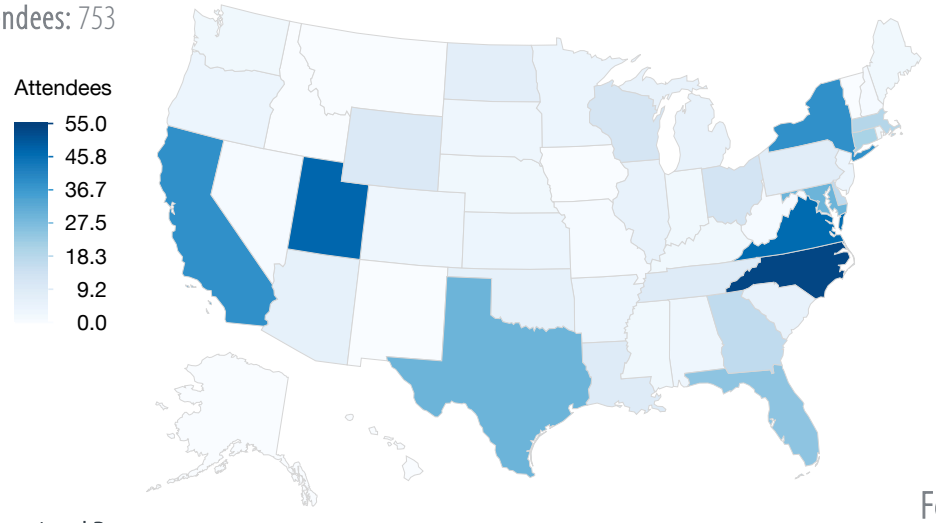
Forensic Technology Center of Excellence
A program of the National Institute of Justice

# Forensic DNA: The Beginning of the SNP Era Webinar Series

A Live Online Event Hosted by the Forensic Technology Center of Excellence
September 2017– January 2018 | 5 Webinars | 12 Subject Matter Experts

## Attendance Profile

Attendees: 753



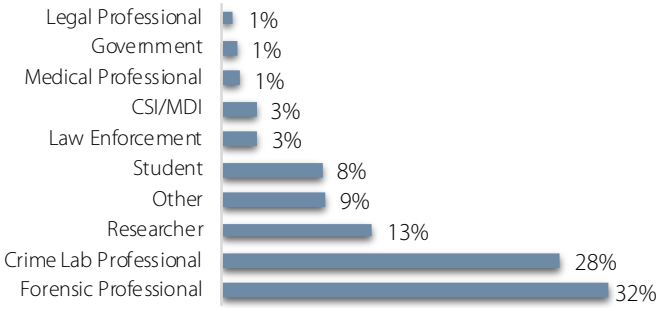

## Speakers

Michael "Doc" Edge, PhD
Manfred Kayser, PhD
Susan Walsh, PhD
Kenneth Kidd, PhD
Chris Phillips, PhD
Tom Parsons, PhD
Daniele Podini, PhD
Athina Vidaki, PhD
Hwan Young Lee, PhD
Katherine Gettings, PhD
Maretta Chase, MS
Runa Daniel, PhD

**International Presence:**

Albania 2 • Australia 4 • Belgium 1 • Bosnia and Herzegovina 4 • Brazil 4 • Canada 29 • Cayman Islands 2 • Chile 1 • Colombia 10 • Costa Rica 9 • Denmark 3 • Finland 1 • France 3 • Germany 9 • Greece 3 • India 4 • Italy 15 • Lebanon 1 • Lithuania 2 • Mexico 2 • The Netherlands 8 • Norway 1 • Pakistan 2 • Poland 1 • Portugal 1 • Puerto Rico 3 • Romania 1 • Serbia 2 •Singapore 1 • Spain 7 • Sweden 5 • Switzerland 2 • Thailand 20 • Turkey 4 • United Kingdom 23 • United Arab Emirates 2

## Professions

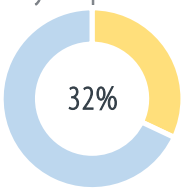



## Feedback

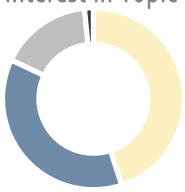
"The biggest benefit of this series was learning of the potential of SNPs and microhaplotypes with respect to forensics and identification. The presenters discussed how this could be integrated into the current infrastructure for practitioners."

"This webinar series provided me the opportunity to learn about and stay abreast of the latest DNA SNP tools available for casework."

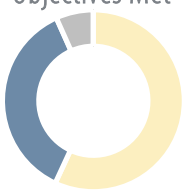
## Survey Response Rate



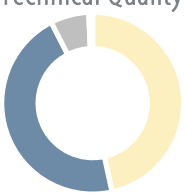

## Interest in Topic



## Objectives Met



## Technical Quality




Access the archived content at forensicCOE.org

Event Performance Statement