Assessing the Implementation of Forensic Genealogy

Forensic Genealogy (FG) is a powerful tool that can provide investigative leads in long-unsolved crimes. Paired with traditional forensic science, with sufficient DNA these techniques can be used to reliably identify victims and suspects in previously unsolvable cases. Although stringent genealogical standards have existed for decades and genetic evidence standards have evolved and been published since 2015, varied approaches by stakeholders suggest that controls, regulations, and documented best practices must be developed to ensure that this is effectively implemented within the criminal justice process.

Concerns persist about the lack of data review and studies assessing the reliability of forensic genealogy. By establishing the capabilities and limitations of FG, the community will be able to address eventual court challenges and more effectively protect the integrity of cases and the evidence being tested. As a community, we must be careful not to lose this incredibly promising investigative tool. This presentation will explore areas where best practices should be established, from case review and submission to laboratory testing, and ultimately through the genealogical investigative process.

FG starts with an evaluation of the evidence and the case. Every case is different, and each piece of evidence presents individual challenges. SNP microarray analysis or Whole Genome Sequencing (WGS) are the foundations of subsequent downstream genealogical investigation, but when evaluating how to best process evidence, sample quantity is not the only factor in determining the best approach.

Bode Technology has conducted studies to validate the process, examining how variables in forensic evidence may affect the accuracy and quality of the genome-wide SNP data or DNA sequence, as well as relational matches in the direct-to-consumer (DTC) genetic databases. Studies included sensitivity, reliability, and accuracy of FG using varying amounts of intact and degraded DNA from blood, semen, and forensically challenged samples. The effect of varying templates and DNA quality was evaluated by call rate, concordance within and between micro-array platforms, concordance with generated sequence data, and matches with the DTC databases.

While many laboratories performing SNP testing or WGS hold clinically-related accreditations, they may lack experience in managing and handling limited forensic evidence. The accreditations held serve as a benchmark for quality control systems and proper documentation; however, most testing laboratory's experiences come from processing large quantity single-source samples. Understanding the additional variables that can impact test results can preserve valuable evidence. When unreliable test results are generated, investigators may experience false negatives in their database searches. Properly evaluating and understanding testing limitations allows service providers to preserve evidence and save considerable time and money for their clients.

It is important to implement best practices in genealogical research. Successful genealogists possess the experience to identify an individual for a family tree; however, an identification for an unsolved homicide or sexual assault presents additional challenges. Proper confidentiality must be maintained, whether or not volunteers are part of the investigation. Investigative leads must be closely monitored and clearly explained to law enforcement. Finally, like all other forensic evidence, results must be documented properly and captured in case files so they can withstand inevitable court challenges.

Individuals attending this will learn how to work with law enforcement and genealogical stakeholders to provide recommendations on implementation and use of this technology. From identification of the

sample to identification of the genealogical test taker, and finally to the pinpointing of the sample's origin, process and effective techniques will be covered.