B183 Forensic DNA Errors: Lessons From Innocence Network Cases

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The goal of this presentation is to highlight avoidable errors that can result in wrongful convictions.

This presentation will impact the forensic science community by increasing awareness that higher-sensitivity DNA testing, the demand for high-throughput work, and conflicting mixture interpretation methods have created new opportunities for accidental injustice. Simple procedures will be discussed that can be used to reduce common challenges to DNA evidence in court and reduce the chances of wrongful convictions.

One area that was at first insulated from scrutiny by the Innocence Movement was forensic DNA; however, the report by the President's Council of Advisors on Science and Technology (PCAST) in 2016 critically analyzed certain aspects of DNA analysis, including complex mixture analysis. The PCAST report cited several works and criticized the use of some common forensic methods, such as the Combined Probability of Inclusion (CPI) in complex DNA mixtures. "In summary, the interpretation of complex DNA mixtures with the CPI statistic has been an inadequately specified — and thus inappropriately subjective — method. As such, the method is clearly not foundationally valid."[1]

The study cited by PCAST was published in a 2011 peer-reviewed paper.[2] That study demonstrated that DNA analysts using the same data could reach conflicting conclusions. It was reported that 17 analysts at a single crime lab, given the same DNA data from an actual case in another state, came up with all three possible conclusions concerning a suspect (excluded, cannot be excluded, inconclusive). Most striking was that only 1 of the 17 analysts agreed with the original crime lab's conclusion that the suspect was included in the mixture. Several studies since then, including the Mix13 study by the National Institute of Standards and Technology (NIST), have shown that DNA mixtures can be a serious source of erroneous conclusions.[3] The use of probabilistic genotyping in addressing DNA errors will also be demonstrated by case examples.

A new case report concerning a Y-chromosomal Short Tandem Repeat (Y-STR) coincidental match that led to an exoneration will also be discussed.[4] In that case, a man was convicted of participating in a multiple-perpetrator sexual assault, based on a Y-STR mixture inclusion using a 17-locus kit. The conviction was eventually overturned through collaborative work involving the paper's authors from Boise State University, the Taiwan Association for Innocence, National Chiao Tung University School of Law, and the Taiwan Criminal Investigation Bureau.

This presentation will present problems with coincidental DNA matches, DNA contamination, and serology interpretations that can be addressed through proper processing, analysis, and testimony.

Reference(s):

1. President's Council of Advisors on Science and Technology. Report to the president Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods. Washington DC, 2016 (page 78).
2. Itiel Dror and Greg Hampikian. Subjectivity and Bias in Forensic DNA Mixture Interpretation. *Sci Justice.* 2011 Dec;51(4):204-8.
3. See presentation http://strbase.nist.gov/pub_pres/Coble-ABA2014-MIX13.pdf.
4. Greg Hampikian,Gianluca Peri, Shih-Shiang Lo, Mong-Hwa Chin, Kuo-Lan Liu. *Case report: Coincidental inclusion in a 17-locus Y-STR mixture, wrongful conviction and exoneration.* Forensic Sci Int Genet. 2017 Aug 7;31:1-4.

DNA Errors, Wrongful Conviction, Forensic Error

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