B186   The First Five Exonerations Using TrueAllele® Statistical Software: How Labs Can Review and Correct Old Cases

Greg Hampikian, PhD*, Boise State University, Boise, ID 83725-1515; Mark W. Perlin, PhD, MD*, Cybergenetics, Pittsburgh, PA 15213

Learning Overview: The goal of this presentation is to show that reexamination of old DNA samples (or data) with TrueAllele® can produce conclusions in formerly inconclusive cases and can correct interpretation errors in complex mixture analysis. DNA casework that involves complex mixtures, or "below-threshold" alleles can result in analyst misinterpretation or inconclusive results, which can be corrected using fully continuous probabilistic software. After attending this presentation, attendees will know how TrueAllele® software was used to correct five wrongful convictions.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by showing that inconclusive (or disputed) DNA results can be easily reexamined without new wet-lab work using TrueAllele® software analysis. Attendees will see that this software has provided exculpatory evidence in 5 exonerations. Some of these exonerations involve DNA that was previously assessed by manual methods with inconclusive results. The forensic community will be shown how this software can review any STR case where the electronic data is available. In one case presented, the community will see how new DNA evidence freed two men after 23 years of a life sentence and identified a new suspect.

TrueAllele® software was used to analyze STR electronic data from crime scene samples in postconviction claims of innocence. This presentation describes the first 5 exonerations using this software and suggest improvements in crime lab processing that can help prevent and correct wrongful convictions.

It has been established by several studies that complex DNA mixtures and low template samples can result in conflicting interpretations and inconclusive results.[1,2] These problems can result in wrongful convictions. Recently developed statistical approaches have produced several software packages to analyze complex DNA mixture analysis and low template DNA analysis. These software approaches are usually combined with traditional manual review.

This study reviews the use of TrueAllele® software by Cybergenetics to examine postconviction claims of innocence. This is a commercial product that uses Marco chain Monte Carlo based, fully continuous probabilistic genotyping. The presentation will cover 5 exonerations that used TrueAllele® analysis. These cases represent DNA mixtures and low template DNA samples, including cases where traditional methods were inconclusive. Reevaluation of electronic data from traditional STR testing was performed by Cybergenetics using TrueAllele® and was corroborated by manual analyst review at Boise State University.

The results demonstrate that TrueAllele® can be used to examine contemporary and old cases—even cases where only electronic STR data remains and no new DNA testing can be performed. In one case, two men were freed after 23 years in prison on dual life sentences for murder. Freddie Lawrence and Paul Jenkins were freed in Montana in 2018. In that exoneration, TrueAllele® analysis (corroborated by the state crime laboratory) produced a full STR profile that matched a new suspect in CODIS. That person has now been named a suspect in the murder.

The cases described are from a partnership of the Boise State University laboratory of one author (GH), the Montana Innocence Project, the Georgia Innocence Project, the Illinois Innocence Project, and the New Mexico Innocence Project.

Reference(s):
1.   Dror, I. and Hampikian, G., Subjectivity and bias in forensic DNA mixture interpretation, *51 SCI. & JUST*. 204, 205 (2011).
2.   Augustein, Seth, NIST Publishes Landmark Mix13 DNA Study, Forensic Magazine Online, 8.2.18, https://www.forensicmag.com/news/2018/080/nist-publishes-landmark-mix13-dna-study

TrueAllele®, Exoneration, Probabilistic Genotyping