

"Inconclusive" three-person mixture yields guilty plea: TrueAllele genotype revival

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ABSTRACT

In May of 2011, a Kern County prison guard saw inmate Anthony Ford throw a shiv (i.e., homemade weapon) down onto the ground. The shiv was a screw attached to a handle, bound with elastic string. Mr. Ford was charged with possession of a manufactured weapon in prison.

In November of that year, the police sent the shiv to the Kern Regional Crime Laboratory (KRCL) for DNA analysis. In March of 2012, a KRCL analyst advised the Deputy District Attorney that touch items do not produce good DNA results, and are often inconclusive. So in May the unanalyzed shiv was returned to the police.

To pursue this potentially exculpatory evidence, Ford's defense attorney sent the shiv to an outside private laboratory for DNA testing. The private lab sampled three areas of the shiv: screw, handle and elastic string. That August, the lab reported that each sampled area produced a mixture of at least three individuals. One clear major profile was present on all three samples; the rest were low-level minor contributors. While Ford was excluded from the screw and elastic string, he could not be excluded as a minor contributor to the handle.

The private lab calculated combined probability of inclusion (CPI) statistics. 1 of 4 Caucasians could not be excluded from the handle mixture, 1 of 8 African-American could not be excluded, and 1 of 6 Hispanic persons. The defense attorney elected to not use these relatively uninformative CPI results.

In 2013, the KRCL prepared to interpret DNA mixtures using its new TrueAllele® Casework system. Their TrueAllele validation study examined up to five unknown contributors on laboratory-prepared mixed samples. Forensic analysts were trained and certified on how to use the probabilistic genotyping system. On October 10, 2013, the KRCL deployed TrueAllele in-house for automated computer interpretation of forensic DNA evidence. By year's end, the KRCL was poised for computer analysis of complex DNA mixtures.

On February 7, 2014, KRCL received the private lab's .fsa electronic data files, and entered them into TrueAllele. The computer's genotype modeling excluded Ford from the screw and the string. However, TrueAllele found that a match between a minor contributor to the handle and Anthony Ford was 1.4 million times more probable than coincidence, relative to a Caucasian population. The statistic was 2.4 million for African-Americans, and 1.6 million for Hispanics.

Following defense discovery on the KRCL's TrueAllele DNA match results, Mr. Ford pleaded guilty to the charges. Since TrueAllele separated the DNA mixture data into three genotypes (one for each unknown contributor), the computer had also inferred the shiv's major profile. Upon entry into CODIS, this TrueAllele-derived profile yielded an offender hit from the Cal DOJ DNA data bank.

In this touch DNA case, a government lab's TrueAllele computer analysis solved a low-level three-person mixture that human CPI analysis could not. The major contributor produced a CODIS hit, while a minor contributor provided inculpatory DNA evidence that led to a guilty plea.

TIMELINE

May of 2011

A Kern County prison guard saw inmate Anthony Ford throw a shiv (i.e., homemade weapon) down onto the ground.

Mr. Ford was charged with possession of a manufactured weapon in prison.

November of 2011

The police sent the shiv to the Kern Regional Crime Laboratory (KRCL) for DNA analysis.

March of 2012

A KRCL analyst advised the Deputy District Attorney that touch items do not produce good DNA results, and are often inconclusive.

May of 2012

The unanalyzed shiv was returned to the police.

August of 2012

A private lab reported that each sampled area (screw, handle and elastic string) produced a mixture of at least three individuals.

October 10, 2013

The KRCL deployed TrueAllele in-house for automated computer interpretation of forensic DNA evidence. It became the first crime laboratory in the United States to deploy TrueAllele Casework.

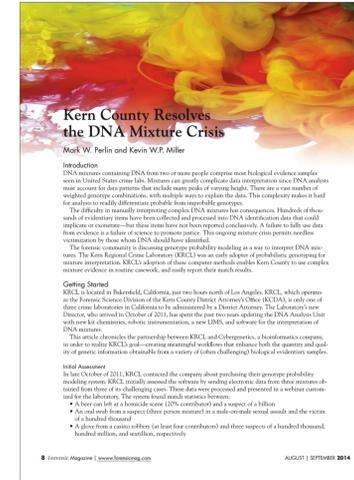
February 7, 2014

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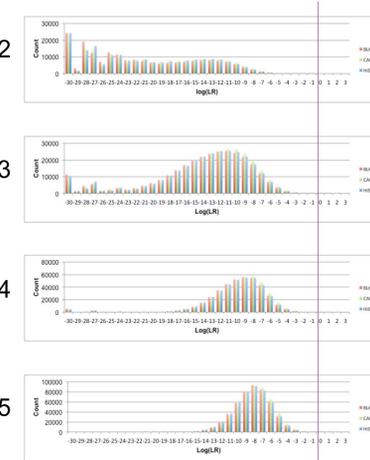
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NONCONTRIBUTOR DISTRIBUTION

How well does TrueAllele exclude genotypes that have not contributed to a low-template DNA mixture?

Very well, since the LR values almost always exclude, and very rarely include, a non-contributor.

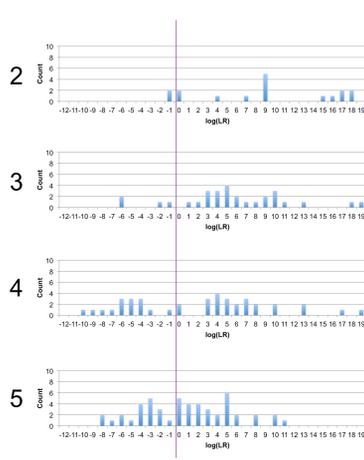


Specificity (200 pg). The log(LR) specificity distribution for mixtures having 2, 3, 4 and 5 contributors. The LRs were computed relative to 10,000 randomly generated profiles across the FBI African-American (BLK, red), Caucasian (CAU, green) and Hispanic (HIS, blue) populations.

CONTRIBUTOR DISTRIBUTION

How well does TrueAllele include genotypes that have contributed to a low-template DNA mixture?

Very well, since the LR values usually include, and less often exclude, a true contributor.



Sensitivity (200 pg). Histograms of the log(LR) distribution for mixtures having 2, 3, 4 and 5 contributors. Average replicated log(LR) scores were used.

VALIDATION PAPERS

Samples of known composition

Perlin MW, Sinelnikov A. An information gap in DNA evidence interpretation. *PLoS ONE*. 2009;4(12):e8327.

Ballantyne J, Hanson EK, Perlin MW. DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: Combining quantitative data for greater identification information. *Science & Justice*. 2013;53(2):103-14.

Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *Journal of Forensic Sciences*. 2015;*in press*.

Greenspoon SA, Schiermeier-Wood L, Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;*in press*.

Samples from actual casework

Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. *Journal of Forensic Sciences*. 2011;56(6):1430-47.

Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele® Casework validation study. *Journal of Forensic Sciences*. 2013;58(6):1458-66.

Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, Greenspoon S. TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLOS ONE*. 2014;(9)3:e92837.

OUTCOME

- A match between a minor contributor to the handle and Anthony Ford was 1.4 million times more probable than coincidence.
- Following KRCL's TrueAllele DNA match results, Mr. Ford pleaded guilty to the charges.
- TrueAllele separated the DNA mixture data into three genotypes, inferring shiv's major profile.
- Upon entry into CODIS, the TrueAllele-derived major profile yielded an offender hit from the Cal DOJ DNA data bank to another person.