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A sample from the inside crown area of the balaclava (item JAS/3) was submitted for DNA profiling tests.

A complex mixed DNA results which appeared to have originated from at least four people was obtained from biological material on the crown.

In my opinion, this result is not suitable for meaningful comparison.

DNA lab report: Shoes

The inside heel area and the toe area of the left shoe (item PAC/2) were submitted separately for DNA profiling tests.

Mixed DNA results which appeared to have originated from at least three people were obtained from biological material on each of the sampled areas. In my opinion, Leroy Williams could have contributed DNA to these results in that all of the components that make up his DNA profile are represented in the result;

however, due to the overall complexity of the results and the number of contributors to them, a statistical evaluation is not possible.

DNA lab report: Parka

The left and right cuff areas of the brown parka (item CEG/2) were submitted separately for DNA profiling tests. A complex mixed DNA results which appeared to have originated from at least four people was obtained from biological material on the right cuff. In my opinion, this result is not suitable for meaningful comparison.

A mixed DNA result, which appeared to have originated from at least three people was obtained from biological material recovered from the left cuff of the brown parka (CEG/2). In my opinion Leroy Williams could have contributed DNA to this result; however, the finding is not suitable for statistical evaluation.

The TrueAllele option

Objective, reliable truth-seeking tool

- solves the DNA mixture problem
- relatives & up to six contributors
- handles low-copy and degraded DNA
- provides accurate DNA match statistics
- easy to understand, easy to explain
- automates DNA evidence interpretation

When a report says "a meaningful comparison" or "a statistical evaluation" is not possible, TrueAllele is often highly effective.

Reliable: validation studies

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

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.

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, 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.

Three DNA Match Statistics

Score 13 thousand Method 23 million 189 billion

inclusion with victim TrueAllele

	D					
	Pennsvivania	a Precedent				
3-A10008-11						
	COMMONWEALTH OF RENASYL VANIA	IN THE SUBBRIDE COURT OF				
	Appalian	PENNSYLVANIA				
	KENTN JAMES DOLEV					
	Appellant	No. 2039 WDA 2009				
Appeal from the Judgment of Sentence of June 1, 2009 In the Court of Common Pleas of Indiana County Comma Division in Vario (C:93-2C-4000):179-2007						
BEFORE: PANELLA, SHOGAN, and COLVILLE', JJ.						
OPINION BY PANELLA, J. FILED: FEBRUARY 15, 2012						
Appellant, Kevin James Foley, appeals from the judgment of sentence						
entered on June 1, 2009, by the Honorable William J. Martin, President						
Judge of the Court of Common Pleas of Indiana County, Criminal Division.						
	After careful review, we affirm.					
Because Foley has failed to establish the existence of a legitimate						
dispute over Dr. Perlin's methodology, he has failed to show that Dr. Perlin's						
testimony constituted "novel" scientific evidence. See Betz, 998 A.2d at						
	972. Therefore, we find that the trial court's decision to admit the testimony					
was not an abuse of discretion. Absent a legitimate dispute, there is no						
reason to "impede admissibility of evidence that will aid the trier of fact in						
	the search for truth." Id.					

Penr	nsylvania Cases
	Allegheny Beaver Berks Butler Cambria Columbia Delaware Indiana Luzerne Mercer York

	Alley 19 d	cases, 15 report	s	
	3 tria	als, 1 exoneratio	on	
Crime	Evidence	Defendant	Outcome	Sentence
rape	clothing	Ralph Skundrich	guilty	75 years
murder	gun, hat	Leland Davis	guilty	23 years
rape	clothing	Akaninyene Akan	guilty	32 years
murder	shotgun shells	James Yeckel, Jr.	guilty plea	25 years
murder	fingernail	Anthony Morgan	stipulation	life
weapons	gun	Thomas Doswell	guilty plea	1 year
drugs	gun	Derek McKissick & Steve Morgan	2 guilty pleas	2 1/2 years
murder	door handle, shirt sleeves	Calvin Kane	guilty plea	20 years

TrueAllele today

Invented math & algorithms	20 years
Developed computer systems	15 years
Support users and workflow	10 laboratories
Used routinely in casework	3 labs
Validate system reliability	20 studies
Educate the community	50 talks
Train & certify analysts	200 students
Go to court for admissibility	5 hearings
Testify about LR results	20 trials
Educate lawyers and laymen	1,000 people
Make the ideas understandable	200 reports

- eliminate DNA backlogs
- reduce forensic costs
- solve crimes
 find criminals
- · convict the guilty • free the innocent
- create a safer society

TrueAllele Casework on Virginia DNA Mixture Evidence: Computer and Manual Interpretation in 72 Reported Criminal Cases

Mark W. Perlin¹*, Klersten Dormer¹, Jennifer Hornyak¹, Lisa Schlermeier-Wood², Susan Greenspoon² 10jempendic, Misburgh, Percepturik, Unide States of America, 20opartenet of Formic Scince, Richmond, Veginia, Unide States of America

Abstract

Abstract Motures are a commonly encountered form of biological evidence that contain DNA from two or more contributors. Liabotary analysis of matures produces data signals that usually cannot be separated into distinct contributor genotypes. Comparer modeling can resolve the genotypes up to pobability identifying feeting the usuality interment in the data. Human identification information. Elevated stochastic threshold levels potentially discard more information. This study examines there different mature interpretation methods. In 72 circles data, 111 genotypes comparison were made between 92 documental in DNA match reports that were provided as evidence for each care. Threshold-based Combined Probability of documental in DNA match reports that were provided as evidence for each care. Threshold-based Combined Probability of documental in DNA match reports that were provided as evidence for each care. Threshold-based Schefflacton information. In 01 positive matches was used to assess the relability of its modeling approach. Comparison was made with differences between the DNA interpretation methods. That DNA levels gaves are genomed much statistic of 11 Distino, CDI versage 6.04 million, and in CDI averaged 140. The comparison was made with averaged 6.04 million, and match averaged 140. The comparison was highly weeklift, with a late positive rate used to diversaries 10 documents matching and thread and average for each average for what a late positive rate used counter where the DNA interpretation methods. The DNA level counter was highly specific, with a late positive rate used counter diversaries 0.04 million expecting data averaged based as each counter was highly specific, with a late positive rate used counter diversaries 0.04 million expecting data thread average the data thread and thread average average thread average average thread averaged based averaged based averaged based averaged based averaged averaged based averaged based averaged based averaged averaged based av

define specials was pessis, having a factor is favo within group standard deviation. Too Male security over the dby having uniformly distributed match statistics over the dda set. The comparter could make genotype risons that were impossible or impactical using manual methods. TrueAlele computer interpretation of DMA natures. It can be is kenotive, genotic, precise, accurate and more informative than manual interpretation alternatives. It can the DMA match statistics when threshold-based methods cannot, improved foremic science computation can affect I areas by providing reliable scientific endence.