

TrueAllele for DNA Mixtures

District Attorney's Association
Spring Meeting
May, 2018
Savannah, GA

Mark W Perlin, PhD, MD, PhD
Pittsburgh, PA



Cybergenetics

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JUSTICE
THROUGH
SCIENCE

Dr. Mark W. Perlin

Curriculum Vitae

Mark W. Perlin, PhD, MD, PhD
DNA evidence interpretation and the likelihood ratio

Cybergenetics, Corp.
160 North Craig Street, Suite 210
Pittsburgh, PA 15213 USA
Phone (412) 683-3004; FAX (412) 683-3005
www.cybgen.com

Positions Held

Cybergenetics, Corp.	chief scientist & executive	1996-present	Comput. Bioscience
Carnegie Mellon University	senior research scientist	1995-1996	Computer Science
Carnegie Mellon University	research computer scientist	1992-1995	Computer Science
Carnegie Mellon University	research associate	1988-1992	Computer Science
Carnegie Mellon University	visiting researcher	1986-1988	Computer Science
Pittsburgh NMR Institute	research scientist	1985-1986	Comput. Radiology
Mercy Hospital, Pittsburgh, PA	transitional resident	1984-1985	Medicine/Radiology
IBM/Watson Research Yorktown, NY	post-doctoral fellow	1984-1984	Mathematics

Education and Training

Carnegie Mellon University, Pittsburgh, PA	Ph.D.	1991	Computer Science
The University of Chicago Pritzker School of Medicine	M.D.	1984	Medicine
City University of New York Graduate School	Ph.D.	1982	Mathematics
Harpur College/SUNY, Binghamton, NY	B.A.	1977	Chemistry

Cybergenetics, Corp

Pittsburgh, Pennsylvania

Victim Remains



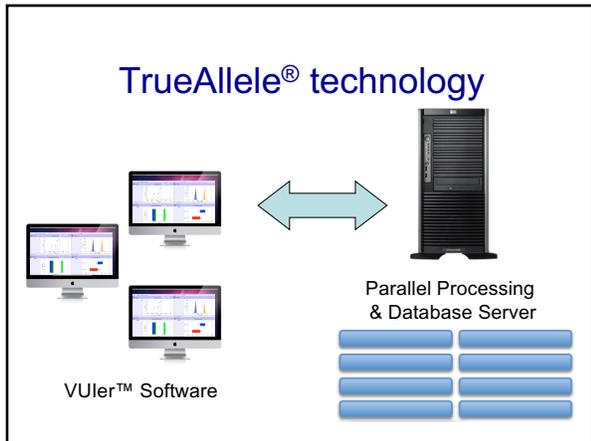
Missing People



Match



September 11, 2001 – New York City



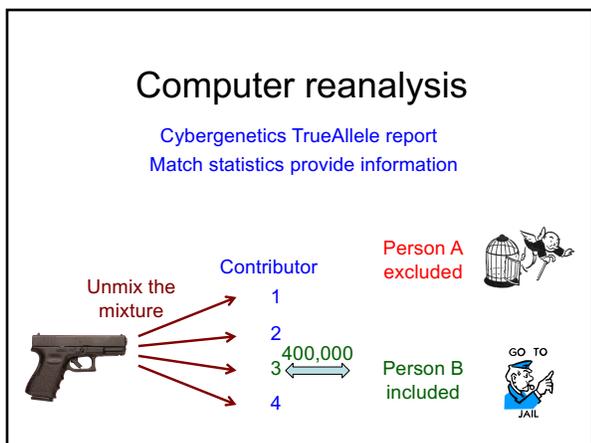
No information from mixture

Crime laboratory DNA report
Crime lab user fee: \$5,000

Conclusions:

Item 1 – Swab of textured areas from a handgun

The data indicates that DNA from four (4) or more contributors was obtained from the swab of the handgun. Due to the complexity of the data, **no conclusions can be made** regarding persons A and B as possible contributors to this mixture.



How is TrueAllele different?

- Computer interpretation
- Fully Bayesian model
- Accurate
- Objective
- Reliable
- Fast
- Automated
- Uses all the data
- Reports all the information
- Advanced DNA database

Unreliable DNA mixture statistics

NIST (Commerce Department) study in 2005
Two contributor mixture data, known victim

Some Differences in Reporting Statistics

LabID	Kits Used	Case1		
		Caucasians	African-Americans	Hispanics
30	ProPlus/Cofiler	1.10E+15	4.13E+14	3.09E+15
34	ProPlus/Cofiler	2.40E+11	7.90E+09	9.60E+10
33	ProPlus/Cofiler	2.94E+08	1.12E+08	1.74E+09
6	ProPlus/Cofiler	40,000,000	3,500,000	200,000,000
9	ProPlus/Cofiler	1.14E+07	1.97E+07	1.54E+08
79	ProPlus/Cofiler	930,000	47,300	1,350,000
16	ProPlus/Cofiler	434,600	31,710	399,100

Remember that these labs are interpreting the same MIX05 electropherograms

When not
"inconclusive":

213 trillion (14)

31 thousand (4)

Forensic DNA labs put on notice 12 years ago

Falsely identify innocent people

MIX13 Case 5 Outcomes with Suspect C
(whose genotypes were not present in the mixture)

# Labs	Report Conclusions	Reasons given
6	Exclude Suspect C	detailed genotype checks (ID+); TrueAllele negative LR (ID+); assumed major/minor and suspects did not fit (ID+); 3 labs noted Penta E missing allele 15 (PP16HS)
3	Inconclusive with C only (A & B included)	All these labs used PP16HS
21	Inconclusive for A, B, and C	
70	Include & provide CPI statistics	All over the road...

Range of CPI stats for Caucasian population:
FBI allele frequencies: **1 in 9** to **1 in 344,000**

Biased DNA workflow

(1)
Choose data



(3)
Person decides



(2)
Calculate statistic





- Put people in the process
- To overcome software limits
- And introduce human bias



Statistics lack scientific basis

Misled courts for 15 years on countless DNA mixtures



Editor-in-Chief: **Andriy Peticola**, Pittsburgh, PA, USA

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HTML format

Research Article

Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information

Mark William Perlin¹

¹Cybergenetics, Pittsburgh, USA
E-mail: Mr. Mark William Perlin - perlin@cybgen.com
^{*}Corresponding author

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Human mixture interpretation

- Inaccurate. Disagrees with true information
- Subjective. Workflow introduces human bias
- Widespread. Hundreds of thousands of cases
- Opaque. Choices use only some of the data
- Biased. Can only include – or give no answer

Inconclusive

Peer-reviewed validation

Perlin MW, Sinehnikov 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):103-114.

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;60(4):857-868.

Greenspoon SA, Schiermeier-Wood L, Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;60(5):1263-1276.

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):1430-1447.

Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele® Casework validation study. *Journal of Forensic Sciences*. 2013;58(6):1458-1466.

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):e92837.

TrueAllele® computer technology

- Accurate. 35 validation studies, 7 published
- Objective. Workflow removes human bias
- Accepted. Reported in 42 states, used by labs
- Transparent. Give math, software (4GB DVD)
- Neutral. Can statistically include or exclude

Informative

How is TrueAllele used?

- Prosecution
- Defense
- Investigation
- Post-conviction
- Mass disaster
- Touch DNA
- Complex mixtures
- Kinship, paternity
- DNA database
- Preventing crime

Pennsylvania v. Kevin Foley

Apr 2006: Blairsville Dentist John Yelenic murdered

Nov 2007: Trooper Kevin Foley charged with crime



February 2008: Defense questions 13,000 DNA match score

March 2009: Jury hears 189,000,000,000 TrueAllele statistic

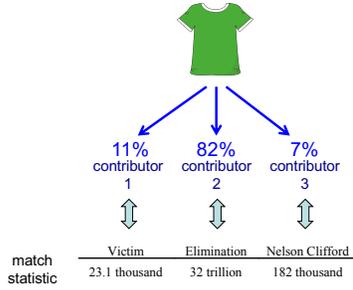
Pennsylvania v. Joshua Huber

Item	Description	Melissa Zuk	Derek Schindler	Joshua Huber
13E	Living room wall bloodstain	1 in 160 million	1 in 36 thousand	11.6 quintillion
29A	Schindler's right hand fingernails		1.37 quintillion	53.8 thousand
1603461-13A	Left hand fingernails of Melissa Zuk	17.4 billion		3.35 thousand

Virginia v. David Black

Item	Description	David Black	Bonnie Black	BettyAnn Armstrong	Craig Black	Eleanora Black
08	Baseball hat velcro strap	32.5 quintillion	16.1 billion		1/1.83 thousand	1/62.6
94	Master bedroom light switch	364 million	8.14 million			
95	Master bathroom light switch	1/19.5	554 million			3.63 million

Maryland v. Nelson Clifford



California v. Billy Ray Johnson

8 mixture items vs. 5 victims + 1 suspect

Description	Item	C0428X	C0459X	C0460X	C0475X	C0820X	C1147X
Purse strap	C0431X	18.73	5.91				1.63
Phone cord	C0432X						4.53
Phone	C0984X	18.74	2.06				4.62
Stain on pants	C0801S				16.39		6.24
Stain from pants	C0802S				17.42		6.73
Back of shirt	C0806S			6.69	17.43		8.86
Bathtub handle	C0929X					5.80	2.74
Zip tie	C0937X					4.55	20.32

DNA match statistics
corroborate victim statements

BRJ

Wolfe sisters homicide



On February 6, 2014, Susan Wolfe (44)
and her younger sister Sarah (38, left)
were killed in their East Liberty home in Pittsburgh.

Pennsylvania v. Allen Wade

Thresholds failed to interpret most DNA mixtures

Hat	No conclusions
Cup	Insufficient data
Fingernails	Contamination, insufficient data
Gear shift	Insufficient data
Seat lever	Cannot be excluded
Knit hat	Insufficient data
Sock	Too complex, no conclusions

Pennsylvania v. Allen Wade

The crime lab reported 5 DNA mixture matches
TrueAllele found 17 matches on the same data

Hat	65.3 thousand	Allen Wade
Cup	20.5 thousand	Susan Wolfe
Fingernails	6.06 trillion	Allen Wade
Gear shift	9.37 million	Sarah Wolfe
Seat lever	385 billion	Sarah Wolfe
Knit hat	25.7 thousand	Allen Wade
Sock	300	Sarah Wolfe

Reported DNA match statistics

A match between the right fingernails
and Allen Wade is:

6.06 trillion times more probable than
a coincidental match to an unrelated Black person

32.5 trillion times more probable than
a coincidental match to an unrelated Caucasian person

8 trillion times more probable than
a coincidental match to an unrelated Hispanic person

Allen Wade Found Guilty On All Counts In East Liberty Sisters' Slaying

CBS News, May 23, 2016

PITTSBURGH (KDKA/AP)

- A man accused of killing two sisters who lived next door to him in East Liberty has been found guilty on all counts.
- Allen Wade was accused of shooting Sarah and Susan Wolfe after they returned from work on Feb. 6, 2014, apparently to steal a bank card.
- On Monday morning, a jury found Wade guilty of first-degree murder, robbery, burglary and theft by unlawful taking.

Pennsylvania v. Allen Wade

Thresholds failed to interpret DNA mixture
TrueAllele succeeded on the same data

A hat left from a burglary of the Wolfe sister's home
six weeks before the murder matched
Allen Wade with a 65.3 thousand statistic



Preventable Crime

Darryl Pinkins imprisoned

1989 – 5 men raped an Indiana woman
Darryl Pinkins and 2 others misidentified
1991 – wrongfully convicted, 65 year sentence

2001 – DNA mixture evidence
2 contributors found, not the accused
but 5 were needed, post-conviction relief denied

TrueAllele Pinkins findings

1. compared *evidence with evidence*
2. calculated *exclusionary match statistics*
3. revealed 5% *minor mixture contributor*
4. *jointly analyzed DNA mixture data*
5. showed three perpetrators were *brothers*

found 5 unidentified genotypes,
defendants not linked to the crime

Pinkins exonerated



TrueAllele report



Cybergenetics

160 North Craig Street, Suite 210
Pittsburgh, PA 15219
Tel: (412) 483-3000
Fax: (412) 483-3000

March 6, 2016

TO: JAMES SMITH
LAW OFFICE
PITTSBURGH, PA 15213

REPORT
Cybergenetics: CY16-001
Lab: CY16-001

Victim: THOMAS, Ramona

Suspect: JONES, Richard

Evidence Items:

Item: T721916 Cutting from a blood-stained area of running shoes
Item: T750722 Trace sample from Ramona Thomas
Item: T750616 Blood sample from Richard Jones

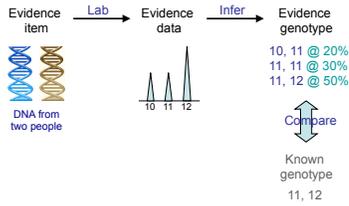
METHODS:

- The DNA Identifier® data profiles referenced in this report were previously developed and addressed in a lab report issued by the Crime Lab.
- The TrueAllele® Casework system processed each evidence item in independent replicate computer runs to infer possible DNA contributor genotypes from the samples.
- The United States Federal Bureau of Investigation generated the population allele frequencies.
- The DNA match statistics herein were calculated using VUE™ version 3.3.926.1 (13-Jan-2016) at a theta value (co-ancestry coefficient) of 0.01.
- All evidence genotypes were compared with all reference genotypes to compute likelihood ratio (LR) DNA match statistics.

RESULTS:

Trial preparation

DNA mixture interpretation



Disclosure materials

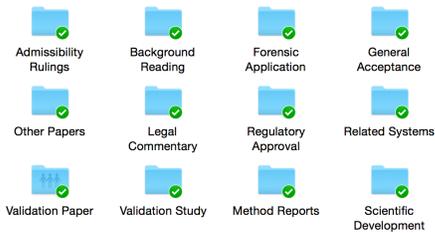
Case Packet

Commonwealth v. Richard Jones
April 13, 2016



- Case**
Notes
- Data**
Table
EPG
- Request**
Listing
Timing
- Genotype**
Evidence
Reference
Population
- Match**
Table
Locus Table
Non-contributor Analysis

Daubert hearing



Trial presentation

A match between the running shoes
and Ramona Thomas is:

850 quintillion times more probable than
a coincidental match to an unrelated African-American person

136 quintillion times more probable than
a coincidental match to an unrelated Caucasian person

387 quintillion times more probable than
a coincidental match to an unrelated Hispanic person

Cybergenetics resource



More information

<http://www.cybgen.com/information>



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<http://www.youtube.com/user/TrueAllele>
TrueAllele YouTube channel



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