DNA Transfer for Lawyers

Continuing Legal Education
Office of the Allegheny County District Attorney
February, 2019
Pittsburgh, PA

Mark W Perlin, PhD, MD, PhD

JUSTICE THROUGH SCIENCE®

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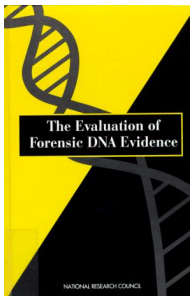
Unexpected DNA

The Cat in the Hat holding an umbrella and speaking to a fish in its bowl from "The Cat in the Hat".

It should not be here
It should not be about
DNA won't appear
When the suspect is out!

Random match probability



Simple match statistic
for
simple DNA evidence

DNA mixture

eye of newt

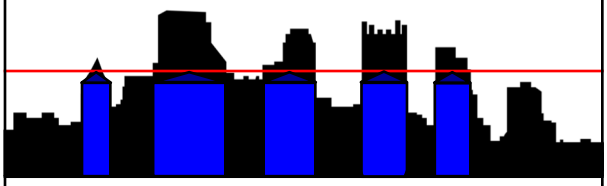
toe of frog

Double, double toil and trouble

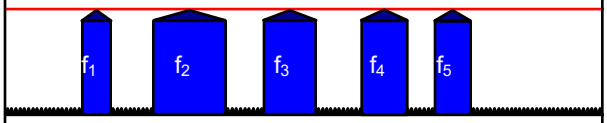
Pittsburgh skyline

Draw a threshold

Same heights & vacant lots



Simplify data to interpret mixture



1. Apply threshold to find “alleles”
2. Add allele frequencies ($f_1 + f_2 + \ldots$)
3. Square sum, take reciprocal
4. Locus “probability of inclusion” (PI)
5. Multiply locus PI values
6. Combined (CPI) **match statistic**

When DNA Is Not a Gold Standard: Failing to Interpret Mixture Evidence

Forensic science connects evidence through shared characteristics. Markings on a bullet can appear to match grooves in the barrel of a gun. Latent fingerprints left at a crime scene may be similar to ridge patterns on a suspect's hand. Tracks in the mud may mirror the treads of a shoe or tire. Police gather forensic evidence to help build a case, and police dramas on television convey the myth of forensic infallibility through the "CSI" effect.[1]

In 2009, the National Academy of Sciences (NAS) published its seminal report titled *Strengthening Forensic Science in the United States*.[2] The NAS report reviewed many forensic modalities and questioned their scientific validity. The interpretation of forensic data is often unreliable. Match statistics are needed to gauge the strength of match between items, relative to coincidence. But forensic statistics are typically absent or incorrect. Human bias can skew answers by unconsciously selecting favorable data, using knowledge about defendant characteristics, or by trying to please stakeholders who have a desired criminal justice outcome.

Deoxyribonucleic acid (DNA) evidence seems immune to such criticism, long serving as a gold standard for other forensic disciplines. Abundant DNA from one person produces pristine data signals. Interpreting these clear signals yields an unambiguous genetic type ("genotype"). Comparing definite genotypes, relative to a random person, yields a reliable match statistic that numerically conveys the probative force of DNA evidence. But most crime scene DNA is now a mixture of two or more people, with good data but less certain interpretation. As the NAS report noted, there may be problems with how the DNA was interpreted, such as when there are mixed samples.

Simplistic interpretation of DNA mixture data often fails to produce an accurate match statistic or give any answer at all. While the limitations and liabilities of unscientific DNA mixture interpretation were recognized early on,[3] only recently has this profound forensic failure come to the fore. Crime laboratories in Austin, Texas, and Washington, D.C., have been shuttered in large part because of failed DNA mixture interpretation.[4] Virginia re-evaluated DNA match statistics for mixture evidence in hundreds of cases.[5] Texas is reviewing 24,000 criminal cases for flawed interpretation of DNA mixture evidence.[6] The New York State Police (NYSP) has suppressed reliable DNA mixture interpretation methods that could expose its crime laboratory's mistakes in thousands of cases.[7] These numbers extrapolate to hundreds of thousands of mixture items throughout the United States, and the national press has taken notice.[8]

This failure of forensic DNA interpretation is of broad concern. Pervasive errors in DNA match statistics undermine public trust in science and erode confidence in government agencies that misuse science to obtain convictions. A failed DNA gold standard portends little hope for fledgling forensic fields. Perhaps the greatest loss is true justice in a free society. Misinterpreting DNA evidence causes injustice for defendants denied potentially exculpa-

BY MARK W. PERLIN, PH.D., M.D., PH.D.

Accurate, unbiased computing

The Blairsville Slaying and the Dawn of DNA Computing

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5 October 2012

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To appear as a chapter in the forthcoming book:

"Death Needs Answers: The Cold-Blooded Murder of Dr. John Yelenic"
by Andrea Niapas
Grelin Press, New Kensington, PA; 2012

Suspect-centric Bias in DNA Mixture Interpretation

Mark W. Perlin, Ph.D., M.D.

Bias abounds in criminal justice. Predictive policing can bake bias into software, reflecting and reinforcing prior beliefs. Bail-risk computer programs may entrench pre-trial detention disparity. Human judgment pervades the process. Prosecutor and defender alike passionately argue their client's case, drawing opposite conclusions from identical facts.

Science is above the fray. Objective data suggest forensic match between crime scene and suspect. Statistical data analysis yields incontrovertible numbers for the strength of match. Cold DNA facts are presented as confirmed theories in court.

But what if DNA analysts could pick and choose their data? Or adjust software parameters to suit their theories? Changing data and parameters will alter forensic match results. Quantitatively, subjective manipulation can artificially inflate match strength. Qualitatively, some DNA evidence that excludes a suspect may be statistically twisted to include him.

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PAPER

CRIMINALISTICS

Mark W. Perlin,[1] M.D., Ph.D.; Matthew M. Legler,[1] B.S.; Cara E. Spencer,[1] M.S.; Jessica L. Smith,[1] M.S.; William P. Allan,[1] M.S.; Jamie L. Belrose,[2] M.S.; and Barry W. Duceman,[3] Ph.D.

Validating TrueAllele® DNA Mixture Interpretation*,†

ABSTRACT: DNA mixtures with two or more contributors are a prevalent form of biological evidence. Mixture interpretation is complicated by the possibility of different genotype combinations that can explain the short tandem repeat (STR) data. Current human review simplifies this interpretation by applying thresholds to qualitatively treat STR data peaks as all-or-none events and assigning allele pairs equal likelihood. Computer review, however, can work instead with all the quantitative data to preserve more identification information. The present study examined the extent to which quantitative computer interpretation could elicit more identification information than human review from the same adjudicated two-person mixture data. The base 10 logarithm of a DNA match statistic is a standard information measure that permits such a comparison. On eight mixtures having two unknown contributors, we found that quantitative computer interpretation gave an average information increase of 6.24 log units (min = 2.32, max = 10.49) over qualitative human review. On eight other mixtures with a known victim reference and one unknown contributor, quantitative interpretation averaged a 4.67 log factor increase (min = 1.00, max = 11.31) over qualitative review. This study provides a general treatment of DNA interpretation methods (including mixtures) that encompasses both quantitative and qualitative review. Validation methods are introduced that can assess the efficacy and reproducibility of any DNA interpretation method. An in-depth case example highlights 10 reasons (at 10 different loci) why quantitative probability modeling preserves more identification information than qualitative threshold methods. The results validate TrueAllele® DNA mixture interpretation and establish a significant information improvement over human review.

DNA transfer

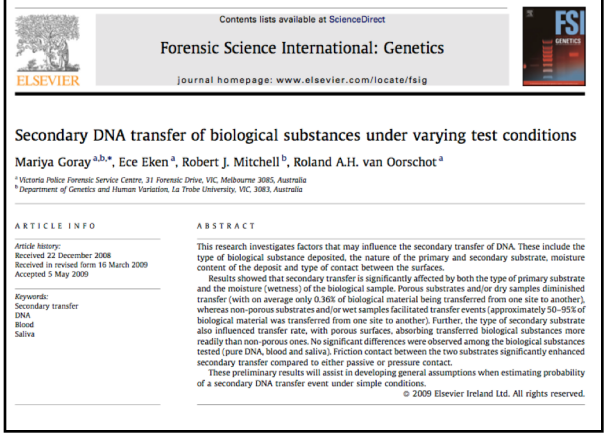
The Cat in the Hat holding a pink-stained shirt in a bathtub from "The Cat in the Hat Comes Back".

Don't fear DNA
Laughed the clever defense
When it transfers we say
That it's not evidence!

DNA transfer

Scientists test

Lawyers argue



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Secondary DNA transfer of biological substances under varying test conditions

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ABSTRACT

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Results showed that secondary transfer is significantly affected by both the type of primary substrate and the moisture (wetness) of the biological sample. Porous substrates and/or dry samples diminished transfer (with on average only 0.36% of biological material being transferred from one site to another), whereas non-porous substrates and/or wet samples facilitated transfer events (approximately 50–95% of biological material was transferred from one site to another). Further, the type of secondary substrate also influenced transfer rate, with porous surfaces, absorbing transferred biological substances more readily than non-porous ones. No significant differences were observed among the biological substances tested (pure DNA, blood and saliva). Friction contact between the two substrates significantly enhanced secondary transfer compared to either passive or pressure contact.

These preliminary results will assist in developing general assumptions when estimating probability of a secondary DNA transfer event under simple conditions.

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Wet DNA transfer

Table 1
Mean % transfer (standard deviation) of DNA under experimental primary and secondary substrate combinations and different types of contact (60 s), with wet pure DNA, blood and saliva.

Primary substrate	Biological source	Secondary substrate								
		Plastic			Cotton			Wool		
		Passive	Pressure	Friction	Passive	Pressure	Friction	Passive	Pressure	Friction
Plastic	DNA	–	–	–	98.6 (1.5)	99.9 (0.05)	100 (0.02)	–	–	–
	Blood	48.6 (27.1)	64.1 (7.71)	44.3 (16.6)	98.2 (1.5)	90.2 (8.75)	97 (2.38)	81.5 (6.63)	87.5 (2.41)	88.1 (3.3)
	Saliva	–	–	–	99.4 (0.2)	96.7 (1.24)	99.6 (0.2)	–	–	–
Cotton	DNA	0.005 (0.009)	0.02 (0.01)	0.04 (0.04)	0.02 (0.03)	0.07 (0.05)	0.23 (0.07)	–	–	–
	Blood	0.425 (0.79)	0.28 (0.38)	3.05 (0.77)	0.23 (0.45)	0.98 (0.59)	1.05 (2.1)	0.15 (0.19)	1.7 (1.91)	18.8 (10.7)
	Saliva	0.03 (0.05)	0.11 (0.17)	0.1 (0.07)	0.05 (0.004)	0.58 (0.4)	4.33 (2.45)	–	–	–
Wool	DNA	–	–	–	–	–	–	–	–	–
	Blood	1.63 (0.78)	1.85 (1.74)	2.55 (0.57)	0.23 (0.29)	1.78 (0.79)	15.5 (5.8)	0 (0)	0.2 (0.22)	7.43 (7.45)
	Saliva	–	–	–	–	–	–	–	–	–

Dry DNA transfer

Table 3
Mean % transfer (standard deviation) of DNA under experimental primary and secondary substrate combinations and different types of contact (60 s), with dry pure DNA, blood and saliva.

Primary substrate	Biological source	Secondary substrate								
		Plastic			Cotton			Wool		
		Passive	Pressure	Friction	Passive	Pressure	Friction	Passive	Pressure	Friction
Plastic	DNA	0	0.84 (0.78)	3.75 (1.83)	0.05 (0.01)	0.02 (0.02)	0.25 (0.14)	–	–	–
	Blood	1.45 (2.9)	0.25 (0.5)	44.5 (16.4)	0	3.4 (6.8)	16.1 (10.1)	0.4 (0.47)	0	16.8 (21.7)
	Saliva	0.005 (0.01)	0	0	0.006 (0.01)	0.002 (0.002)	0.27 (0.32)	–	–	–
Cotton	DNA	0	0.004 (0.005)	0.02 (0.03)	0.03 (0.02)	0.06 (0.04)	0.49 (0.47)	–	–	–
	Blood	0	0	0.05 (0.1)	0	0	0	0.08 (0.05)	0	1.43 (1.25)
	Saliva	0	0	0.006 (0.01)	0.01 (0.02)	0	0.57 (0.18)	–	–	–
Wool	DNA	–	–	–	–	–	–	–	–	–
	Blood	0	0.05 (0.01)	1.35 (1.05)	0.05 (0.1)	0.15 (0.1)	1.15 (0.61)	0	0.13 (0.19)	0.5 (0.49)
	Saliva	–	–	–	–	–	–	–	–	–

END

Justice Denied:
Mr. Hopkins Invisible Semen

American Investigative Society of Cold Cases
AISOCC Annual Conference
June, 2016
St. Louis, MO

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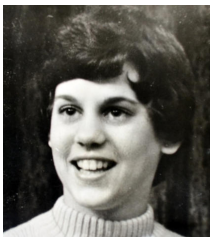
19

1979 murder of Janet Walsh



Janet Walsh

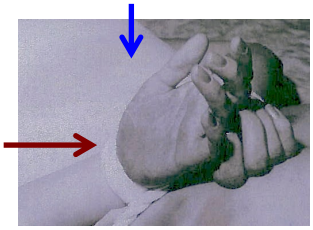
- 23 year old woman
- Monaca, Pennsylvania
- strangled with bandana
- face down in her bed
- nightshirt top only
- bathrobe tie on hands
- divorcing husband
- multiple partners

20

The crime scene

blue nightshirt

bathrobe tie



Viewed as homicide, not sex crime

21

Prosecutor theory

Frank Martocci

- sexual misadventure
- man straddling woman
- bandana asphyxiation
- ejaculates, and hits nightshirt & robe tie
- explains coincidental location on two items

How and when the DNA got there
(unusual expert testimony)

22

Defense theory

Hon. James Ross

- Hopkins wasn't there when Walsh died
- old DNA from before
- no coincidences
- DNA is expected
- no semen on hands
- with prior sexual relations, DNA is not probative

DNA doesn't say how or when it was left (typical expert testimony)

23

DNA transfer

Forensic Science International: Genetics

Secondary DNA transfer of biological substances under varying test conditions

Mariya Goray, Ece Eken, Robert J. Mitchell, Roland A.H. van Oorschot

Increases with:

- moisture
- pressure
- friction
- absorbent cotton material

24

From nightshirt to robe tie

- Walsh struggled, perspired
- back moist, shirt wet
- old semen stain on shirt
- wet shirt moistens robe tie
- pressure and friction from tied hands behind back
- sperm moves from shirt to bathrobe tie
- DNA detected years later

END

25

Computer Interpretation of Quantitative DNA Evidence

Commonwealth of Pennsylvania v. Carlos Harris
August, 2017
Pittsburgh, PA

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Cybergenetics

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26

Curriculum Vitae

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DNA evidence interpretation and the likelihood ratio

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Positions Held

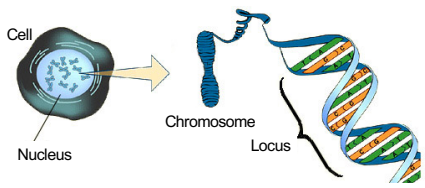
Cybergenetics, Corp.	chief scientist & executive	1996-present	Comput. Bioscience
Carnegie Mellon University	senior research scientist	1995-1996	Computer Science
Carnegie Mellon University	research computer scientist	1992-1995	Computer Science
Carnegie Mellon University	research associate	1988-1992	Computer 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

27

DNA biology



28

Short tandem repeat

23 volumes in
cell's
DNA encyclopedia

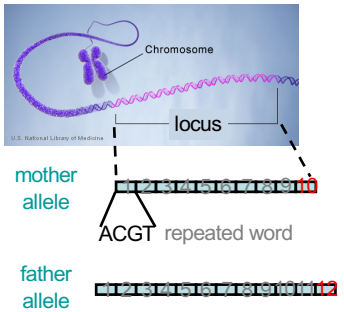
DNA locus paragraph

Take me out to the ball game
take me out with the crowd
buy me some peanuts and Cracker Jack
I don't care if I never get back
let me
root root root root root root root root root root
for the home team,
if they don't win, it's a shame for it's one, two,
three strikes, you're out
at the old ball game

"root" repeated 10 times, so
allele length is 10 repeats

29

DNA genotype



A genetic locus has
two DNA sentences,
one from each parent.

An allele is the number
of repeated words.

A genotype at a locus
is a pair of alleles.

10, 12

Many alleles allow for
many many allele pairs.
A person's genotype
is relatively unique.

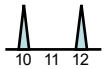
30

DNA evidence interpretation

Evidence item → Lab → Evidence data → Infer → Evidence genotype

10, 12

DNA from
one person

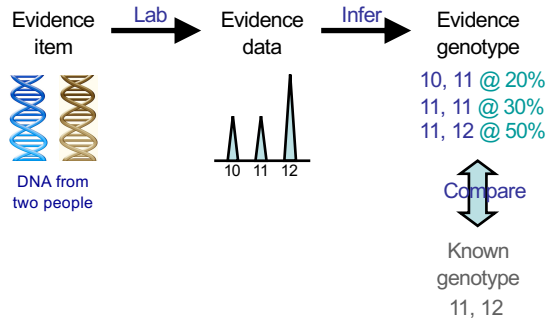


Compare

Known
genotype
10, 12

31

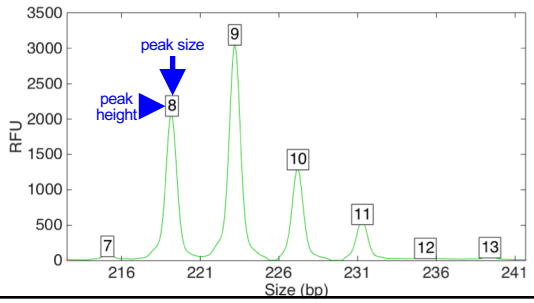
DNA mixture interpretation



32

Computers can use all the data

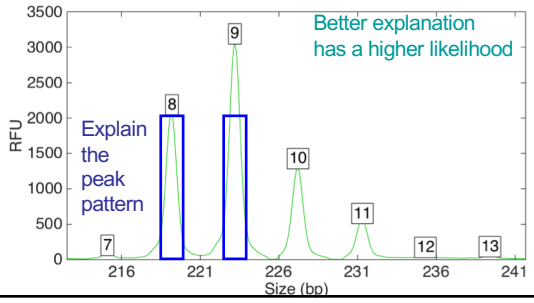
Quantitative peak heights at locus D7S820



33

How the computer thinks

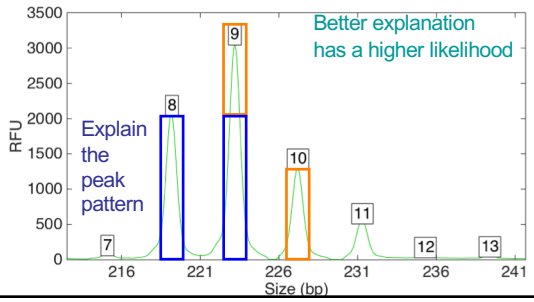
Consider every possible genotype solution



34

How the computer thinks

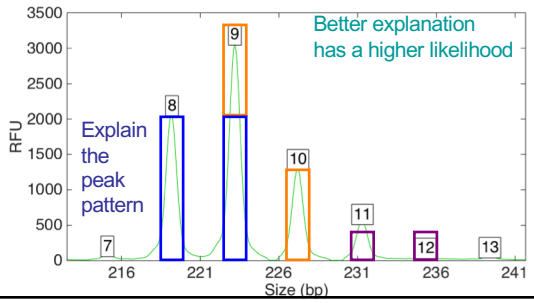
Consider every possible genotype solution



35

How the computer thinks

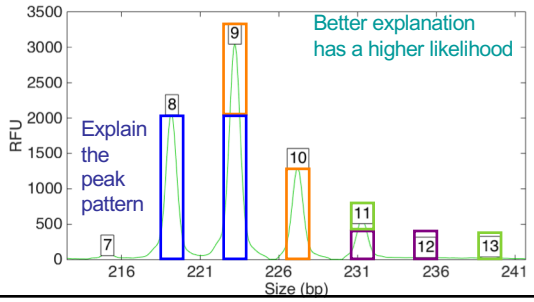
Consider every possible genotype solution



36

How the computer thinks

Consider every possible genotype solution



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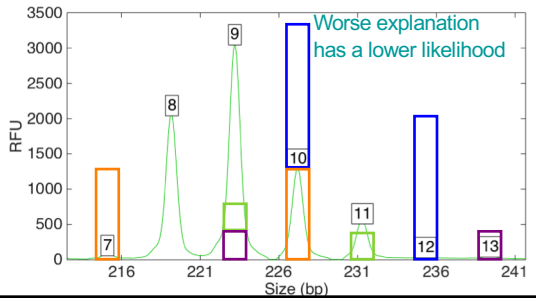
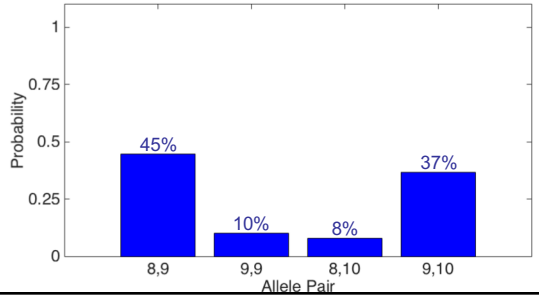


38

Evidence genotype

Objective genotype determined solely from the DNA data.

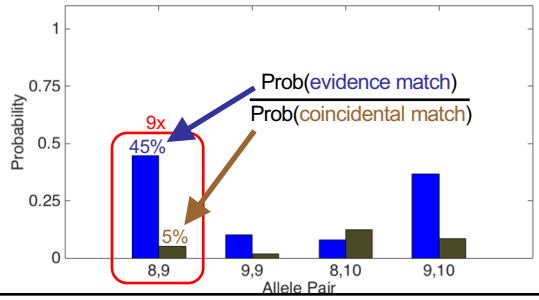
Never sees a comparison reference.



39

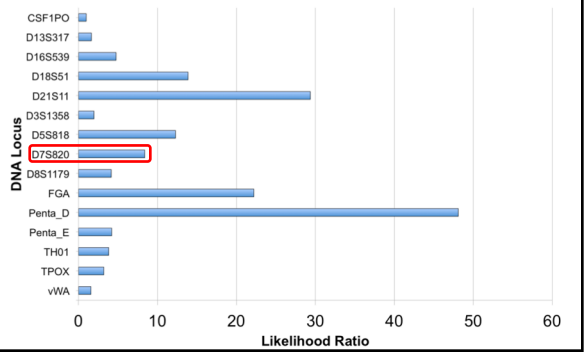
DNA match information

How much more does the suspect match the evidence than a random person?



40

Match information at 15 loci



41

Is the suspect in the evidence?

A match between the Glock pistol slide serrations and Carlos Harris is:

221 billion times more probable than a coincidental match to an unrelated African-American person

62.9 billion times more probable than a coincidental match to an unrelated Caucasian person

133 billion times more probable than a coincidental match to an unrelated Hispanic person

42

Match statistics

		28	35	36	37
Item	Description	Daren Scott	Carlos Harris	Michael Shipps-Smith	Jaron Satterwhite
18A1	Glock pistol frame		6.51 million		
18B1	Opening and follower of the magazine				
20A	Glock pistol slide serrations		62.9 billion		

43

Match statistics

Item	Description	28 Daren Scott	35 Carlos Harris	36 Michael Shipps-Smith	37 Jaron Satterwhite
18A1	Glock pistol frame		6.81		
18B1	Opening and follower of the magazine				
20A	Glock pistol slide serrations		10.80		

END

44

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45

Wet DNA transfer

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Primary substrate	Biological source	Secondary substrate								
		Plastic			Cotton			Wool		
		Passive	Pressure	Friction	Passive	Pressure	Friction	Passive	Pressure	Friction
Plastic	DNA	–	–	–	98.6 (1.5)	99.9 (0.05)	100 (0.02)	–	–	–
	Blood	48.6 (27.1)	64.1 (7.71)	44.3 (16.6)	98.2 (1.5)	90.2 (8.75)	97 (2.38)	81.5 (6.63)	87.5 (2.41)	88.1 (3.3)
	Saliva	–	–	–	99.4 (0.2)	96.7 (1.24)	99.6 (0.2)	–	–	–
Cotton	DNA	0.005 (0.009)	0.02 (0.01)	0.04 (0.04)	0.02 (0.03)	0.07 (0.05)	0.23 (0.07)	–	–	–
	Blood	0.425 (0.79)	0.28 (0.38)	3.05 (0.77)	0.23 (0.45)	0.98 (0.59)	1.05 (2.1)	0.15 (0.19)	1.7 (1.91)	18.8 (10.7)
	Saliva	0.03 (0.05)	0.11 (0.17)	0.1 (0.07)	0.05 (0.004)	0.58 (0.4)	4.33 (2.45)	–	–	–
Wool	DNA	–	–	–	–	–	–	–	–	–
	Blood	1.63 (0.78)	1.85 (1.74)	2.55 (0.57)	0.23 (0.29)	1.78 (0.79)	15.5 (5.8)	0 (0)	0.2 (0.22)	7.43 (7.45)
	Saliva	–	–	–	–	–	–	–	–	–

END

46

Computer Interpretation of Quantitative DNA Evidence

Commonwealth of Pennsylvania v. Defendant
April, 2018
Pittsburgh, PA

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

Cybergenetics

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47

Match statistics

Item	Description	K1 Victim	K2 Defendant	K3 Elimination
Q3M	Underwear, sperm fraction	2.21 quadrillion	9.29 thousand	

48

THE RETENTION AND TRANSFER OF SPERMATOZOA IN CLOTHING BY MACHINE WASHING[1]

E. KAFAROWSKI[2,3], A.M. LYON[2] AND M.M. SLOAN[2]

ABSTRACT

The interpretation of trace findings on spermatozoa on clothing is often problematic, as the manner of deposition may not be readily determined. Particularly troublesome are cases involving complainants who are unable to relate a complete history. Small numbers of spermatozoa may be a result of some type of sexual activity or may be due to an unrelated, innocuous incident. Transfer of spermatozoa between items during machine washing has been theorized as one possible method of indirect deposition. This research was undertaken to determine the likelihood of such transfer. A normal machine wash was simulated in three independent experiments. Pristine items of clothing were washed together with one pair of semen-stained panties. After washing, random samples (n=162) from nine unstained items were examined microscopically. Some spermatozoa were detected on all nine previously pristine items included in the wash loads. Three to eight spermatozoa were identified in 16% of the samples. One or two spermatozoa were identified in a further 38% of the samples. The original semen-stained panties were also examined following washing. Although there was no visible staining or acid phosphatase activity, significant numbers of spermatozoa were retained in the original stain areas. The analysis and interpretation of these findings is discussed with reference to current DNA methods.

END

49

Computer Interpretation of Quantitative DNA Evidence

State of Georgia v. Johnny Lee Gates
May, 2018
Columbus, GA

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50

Match statistics

		76C2573-004
Item	Description	Johnny Lee Gates
76C2573-032	robe belt side 1 swab	one in 1.5 million
76C2573-033	robe belt side 2 swab	one in 134 thousand
76C2573-034	front of black tie swab	one in 4.33 million
76C2573-035	back of black tie swab	one in 963 million
76C2573-042	robe belt M-vac filter	one in 902 trillion
76C2573-044	black tie M-vac filter	one in 825 billion

51

IN THE SUPERIOR COURT OF MUSCOGEE COUNTY
STATE OF GEORGIA

JAN 10 2019 4:21p
DEPUTY CLERK

STATE OF GEORGIA,)
)
v.) Case No. SU-75-CR-38335
)
JOHNNY LEE GATES,)
Defendant.)
)

ORDER ON DEFENDANT'S

EXTRAORDINARY MOTION FOR NEW TRIAL

The facts, absent editorials from each side, are the same from each party. The facts are extracted from trial testimony and subsequent hearings and briefs by both sides in this hearing of May 2018.

END

52

Computer Interpretation of Quantitative DNA Evidence

Commonwealth of Virginia v. Bernard Duse, Jr.
August, 2018
Warrenton, VA

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

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53

Match statistics

		19	65
Item	Description	Rex Olsen	Bernard Duse, Jr.
13	Pants pocket	227 octillion	40.6 quintillion

54

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Secondary DNA transfer of biological substances under varying test conditions

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ABSTRACT

This research investigates factors that may influence the secondary transfer of DNA. These include the type of biological substance deposited, the nature of the primary and secondary substrate, moisture content of the deposit and type of contact between the surfaces.

Results showed that secondary transfer is significantly affected by both the type of primary substrate and the moisture (wetness) of the biological sample. Porous substrates and/or dry samples diminished transfer (with on average only 0.36% of biological material being transferred from one site to another), whereas non-porous substrates and/or wet samples facilitated transfer events (approximately 50–95% of biological material was transferred from one site to another). Further, the type of secondary substrate also influenced transfer rate, with porous surfaces, absorbing transferred biological substances more readily than non-porous ones. No significant differences were observed among the biological substances tested (pure DNA, blood and saliva). Friction contact between the two substrates significantly enhanced secondary transfer compared to either passive or pressure contact.

These preliminary results will assist in developing general assumptions when estimating probability of a secondary DNA transfer event under simple conditions.

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END

55

Computer Interpretation of Quantitative DNA Evidence

People of California v. John Doe
March, 2019

Mark W Perlin, PhD, MD, PhD
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56

Are the references in the evidence?

Based on the TrueAllele results, comparing all evidence with all references produced exclusionary match statistics.

57

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DNA within cars: prevalence of DNA from driver, passenger and others on steering wheels

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[a]School of Molecular Sciences, La Trobe University, Bundoora, Australia; [b]Victoria Police Forensic Services Department, Office of the Chief Forensic Scientist, Macleod, Australia

ABSTRACT

Cars are frequently involved in criminal activities and sampled for DNA to assist investigations. To improve our awareness of DNA transfer, persistence, prevalence and recovery (DNA-TPPR) within cars we studied DNA profiles from samples collected from several sites in the front compartment of cars with known histories and occupancies. Here findings relating to steering wheels are reported. Each of the four quarters of the rim as well as the centre column, of four cars, provided good quantities of DNA for profiling. The driver was observed as the sole, major or co-major in 19/20 profiles, and as a minor in the remaining profile generated from these samples. Known close associates, including co-resident partners and passengers/friends, as well as other unknown individuals, who had not driven the car, are also detected on many of the sampled steering wheel sites. More studies are required to improve our awareness of DNA-TPPR and to generate data to help determine probabilities for different profile types and levels of specific contributions given specific circumstances relating to steering wheels, as well as several other relevant areas within cars, to assist sample targeting and activity level assessments.

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KEYWORDS
DNA prevalence; DNA recovery; DNA transfer; DNA persistence; car; steering wheel

END

58

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