## Slide 1

PLOS | ONE

PUBLISH   ABOUT   BR

OPEN ACCESS   PEER-REVIEWED
RESEARCH ARTICLE

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

Mark W. Perlin, Kiersten Dormer, Jennifer Hornyak, Lisa Schiermeier-Wood, Susan Greenspoon

Published: March 25, 2014 • https://doi.org/10.1371/journal.pone.0092837

"There were 5 genotype comparisons where CPI indicated a match, but the computer found no statistical support (Table 11, TrueAllele <0, CPI >0). Laboratory reexamination of these items agreed with the computer's conclusions."

Slide 2

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

# Labs	Report Conclusions	Reasons given
7	Exclude Suspect C	detailed genotype checks (ID+); TrueAllele negative LR (ID+); assumed major/minor and suspects did not fit (ID+); 4 of 18 labs noted Penta E missing allele 15 (PP16HS)
3	Inconclusive with C only (A & B included)	All these labs used PP16HS
22	Inconclusive for A, B, and C	
76	<u>Include</u> & provide CPI statistics	*All over the road…*

<u>Range of CPI stats for Caucasian population</u>:
FBI allele frequencies: **1 in 9** (Labs 12 & 54) to **1 in 344,000** (Lab 107)

Slide 3

Man Wrongly Convicted of Rape Freed From 25 Years Behind Bars

Prosecutor: "If we took this to trial, we would lose"

By Katie Kim
Published Apr 25, 2016 at 6:06 PM

Cellmark's lab's DNA data had laid dormant for 15 years. The machine's capability surpassed human review .

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 **five** unidentified genotypes
Defendants **not linked** to the crime

Computer transcended human analysis

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.

WWW.NACDL.ORG   THE CHAMPION

5

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.

2

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.

Moving forward

Computer reanalysis of DNA data proved Pinkins innocence

• Exculpatory DNA evidence was available fifteen years ago
• Old 20th century human review couldn't deliver information
• New 21st century computer analysis overcame limitations
• Failed interpretation cost Pinkins 15 extra years in prison

• Thousands of cases with misinterpreted or "inconclusive" DNA
• Other innocents wrongfully imprisoned by old DNA methods
• Revisit "inconclusive" cases with new computer interpretation
• Re-examine old forensic data for new exculpatory evidence

Get *pro bono* DNA help – better science for better justice

Case 2 Gregory Hobbs, convicted of manslaughter, New Mexico Innocence Project

Defense claimed a struggle for the gun preceeded the shooting. Lab tested the ejection port area. Included victim in DNA mixture (match=1 in 14)

The DNA analysts testified about her findings at an evidentiary hearing on March 1, 2017. During her testimony, **the Court asked her if she could specify that there was more than a 50% probability that the victim's DNA was present in the mixtures.** The analysts told the Court that she could not.

The Court denied Mr. Hobbs a new trial noting the DNA "…was from non-biological touch DNA and there was less than a 50% possibility that the DNA was from [the victim]"

TrueAllele Results

- Gun ejection port match to victim was 10,000,000 greater that a random match

Barbara Creel (left) Director of the New Mexico Innocence and Justice Project, Gregory Hobbs, Greg Hampikian, Alex Volner (left) New Mexico Innocence and Justice Project student, Barbara Creel, Director, NM IJP
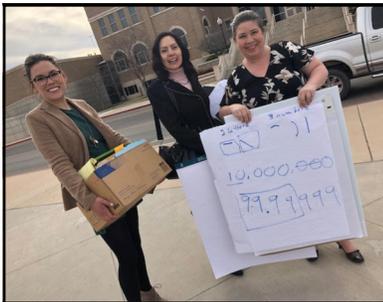
Conviction Overturned May 24, 2018

"The NM lab analyst and Dr. Hampikian testified to the statistical representation provided in the TrueAllele report.

Judge Romero granted a new trial for Mr. Hobbs. He is currently out on release pending the state's appeal. The photo show's the team celebrating after the hearing and successful testimony (but not yet knowing the results)." -B. Creel

Alex Volner (left) New Mexico Innocence and Justice Project student, Barbara Creel, Director, NM IJP, Sara Escobedo, (right) former NM IJP paralegal.

Case 3: Montana Innocence Project 2018: Fred Lawrence and Paul Jenkins

1994 Murder, two men accused.
One admits the crime.
Wife and father in-law testify against the other.
Jailhouse "snitch" testifies against them.

2014 Montana Innocence Project, and Boise State
join post conviction investigation (US Department of Justice grant).

Ligature from scene
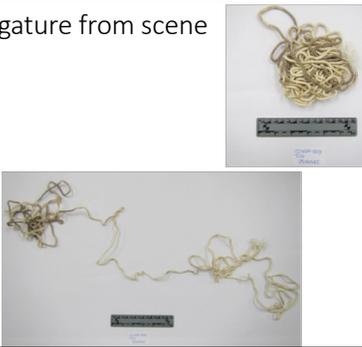
DNA Hit

Nephew had told authorities three times since 1999.

COURT NEWS
FRED NELSON
NEPHEW OF DAVID WAYNE NELSON

On Friday, April 13th, 2018 Lawrence's and Jenkins Freed

Freddie Joe Lawrence, center, walking out of Montana State Prison with his lawyers, Toby Cook, left, and Larry Manuch of the Montana Innocence Project. Photo by Thomas Plank

---

Case 4: 1977, Johnnie Lee Gates admits to murder, and is convicted, sentenced to death.

2016 GA Innocence Project, and Boise State lab with DOJ grant, start working on post conviction.

Post conviction Issues in Gates

- Mental deficiency
- Brought to crime scene for confession, touched items
- Prosecutor struck all black jurors in several capital cases
- DNA never tested (two ligatures)

Muscogee County Capital Cases with Black Defendants
1975-1979

Case	Qualified jurors called	Jurors struck by prosecution	Qualified black jurors called	Black jurors struck by prosecution	Black jurors on jury
Mulligan	42	8	4	4	0
Bowden	45	11	8	8	0
Gates	47	12	4	4	0
Brooks	46	11	4	4	0
Graves	46	11	4	4	0
Lewis	42	10	7	7	0
Hance	37	11	13	10	2

Probabilistic Genotyping: DNA on both ligatures exclude Gates, produce a common major profile

Georgia Innocence Project, Co-Council Southern Center for Human Rights

May 6, 2018
Dr. Mark Perlin
Testifies at hearing.

From Inconclusive to **EXCLUSION** with probabilistic genotyping
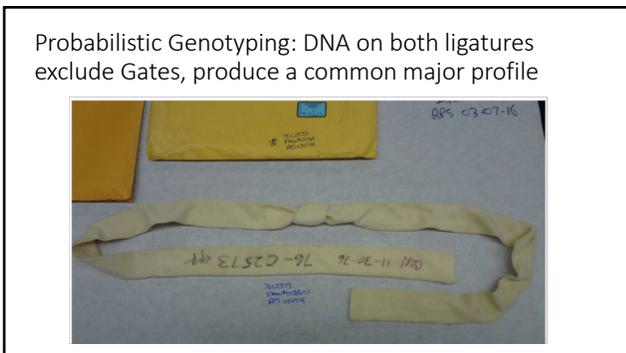
Georgia Innocence Project
May 9 at 1:23pm

For an update on Johnny Lee Gates' Extraordinary Motion For New Trial, check out the Columbus Ledger Enquirer with video at the top and photos at the bottom.

He's been a convicted killer for 40 years. Columbus court will decide if racism put him in prison

Johnny Lee Gates was convicted in the Nov. 30, 1976, rape and murder of Katharina Wright, 19, found bound and shot in the head in the Broadway...

"N" beside potential black jurors

Judge: New DNA evidence means man is entitled to new trial

AP By The Associated Press
January 17, 2019 4:52 pm

Claire Gilbert, GA Innocence Project

Diligence, Dedication, and Devotion

Do we have an ethical duty to perform analyses that could produce new results that might free the wrongfully convicted?

Does your lab have procedures to reexamine old cases with probabilistic genotyping?

To what are we devoted?

Thank you!   Comments? hampikian@yahoo.com

Gianluca Peri, **Karen Rudolph**, **The Idaho Innocence Project volunteer lawyers**
The GA Innocence Project, The Southern Center for Human Rights, The Montana Innocence Project, Frances Watson and The Indiana University Wrongful Conviction Clinic, The New Mexico Innocence Project

The Georgia Bureau of Investigation, The New Mexico Department of Public Safety Forensic Laboratories, The Montana Forensic Science Division Lab
Mark Perlin and Cybergentics,