When DNA is not enough – exoneration through science

Dr. Greg Hampikian[1], Dr. Mark W. Perlin[2] and Frances Lee Watson[3], Esq.
[1]Boise State University, Boise, ID; [2]Cybergenetics, Pittsburgh, PA; [3]Indiana University Law School, Indianapolis, IN

ABSTRACT

In 1989, five men gang-raped a motorist after bumping her car. Darryl Pinkins and two other innocent men were misidentified as her attackers through stolen clothing. Pinkins was convicted of rape in 1991, and sentenced to 65 years in prison.

In 1995, Pinkins contacted the Innocence Project. In 1999, they in turn contacted Fran Watson, clinical professor at the Indiana University Wrongful Conviction Clinic. Watson and her students represented Pinkins, and codefendant Roosevelt Glenn, through decades of unsuccessful state post-conviction and federal habeas corpus proceedings.

In these proceedings it was shown that the state used false science to convict the men. There was faulty hair comparison testimony, and irrelevant blood typing inclusion evidence. Yet the courts labeled this flawed evidence harmless.

A 2001 DNA analysis of semen on the victim's jacket and sweater showed mixtures of two or more people. Each mixture had a clear 80%–90% major contributor that did not match the accused. But this limited DNA analysis was not enough to exonerate.

In 2007, Greg Hampikian of the Idaho Innocence Project began working with Watson. They showed that the blood typing evidence was incorrectly presented during trial and was irrelevant in light of DNA exclusions, including new post-conviction DNA evidence. But the court ruled that the 2 unidentified major DNA genotypes in the semen, plus the 3 accused, equaled the 5 perpetrators – so post-conviction relief was denied.

In 2014, Dr. Hampikian recruited Mark Perlin of Cybergenetics for *pro bono* assistance. The TrueAllele® system provided the science needed to establish innocence beyond doubt. More complete analysis of existing DNA data revealed the genotypes of all five perpetrators. This convinced the state that the wrong man had been convicted.

TrueAllele compared *evidence with evidence* to calculate *exclusionary match statistics*. It discovered new genotypes from 5%–10% *minor contributors* by *jointly analyzing* DNA mixture data. Kinship analysis showed that three of the perpetrators were *brothers*. These computer capabilities found the victim and 5 unidentified genotypes in the semen and hair evidence. The defendants were not linked to the crime.

Acceding to exculpatory DNA evidence found by science, Lake County Prosecutor Bernard Carter vacated Pinkins' conviction. Instead of hearing newly analyzed DNA evidence, that morning the court released him from prison. Pinkins had spent 24 years in an Indiana prison for a crime he did not commit. Computer reanalysis of old DNA data proved that Pinkins and Glenn were innocent.

Cybergenetics

DNA EVIDENCE

Jacket

Differential extraction of DNA mixture

sperm fraction 90% is J

nonsperm fraction 90% is V

Sweater

Differential extraction of DNA mixture

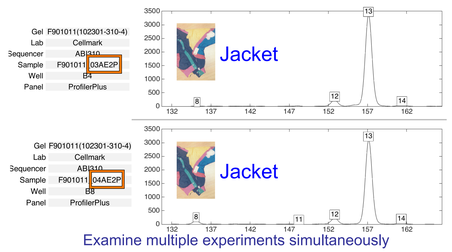
sperm fraction 80% is S

nonsperm fraction

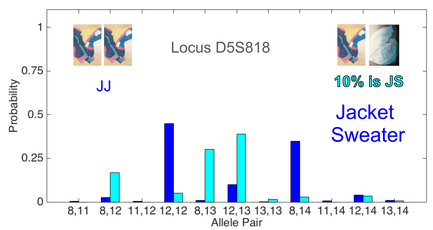
Hair

Roosevelt Glenn case

DNA analysis 100% is H



Examine multiple experiments simultaneously



GENOTYPE

J

S

H

JJ

JS

MATCH TABLE

References

	V	Pinkins
J	-15.39	-18.00

References

	V	P
J	-15.39	-18.00
S	-15.39	-15.17

References

	V	P	Glenn
J	-15.39	-18.00	-15.39
S	-15.39	-15.17	-15.39
H	-15.39	-18.00	-15.39

References

	V	P	G	J	S	H	JJ
J	-15.39	-18.00	-15.39	11.07	1.21	4.15	-6.19
S	-15.39	-15.17	-15.39	1.21	10.22	-2.39	-5.81
H	-15.39	-18.00	-15.39	4.15	-2.39	10.31	-3.52
JJ	-2.78	-8.50	-8.43	-6.19	-5.81	-3.52	7.05

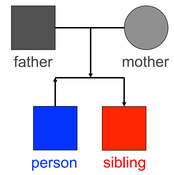
References

	V	P	G	J	S	H	JJ	JS
J	-15.39	-18.00	-15.39	11.07	1.21	4.15	-6.19	-7.66
S	-15.39	-15.17	-15.39	1.21	10.22	-2.39	-5.81	-8.09
H	-15.39	-18.00	-15.39	4.15	-2.39	10.31	-3.52	-5.80
JJ	-2.78	-8.50	-8.43	-6.19	-5.81	-3.52	7.05	-1.49
JS	-10.47	-5.79	-12.60	-7.66	-8.09	-5.80	-1.49	8.06

THREE BROTHERS

The three genotypes J, S and H were similar, having many shared alleles, and showing possible statistical matches. TrueAllele kinship analysis showed these evidence genotypes were brothers. But the defendants were not.

	J	S	H
J	11.07	1.21	4.15
S	1.21	10.22	-2.39
H	4.15	-2.39	10.31



sibling of	J	S	H
J	6.67	4.85	5.08
S	4.70	6.01	3.34
H	5.78	4.18	5.55

XY male genotype, so three brothers

References

	V	P	G	J	S	H
J	-15.39	-18.00	-15.39	11.07	1.21	4.15
S	-15.39	-15.17	-15.39	1.21	10.22	-2.39
H	-15.39	-18.00	-15.39	4.15	-2.39	10.31

MIXTURE FAILURE

Cellmark's 2001 mixture interpretation of the Pinkins crime scene DNA followed the FBI's limited approach. Subjective human data analysis could produce obvious major contributor genotypes. But these simplistic methods failed to find the minor contributors.

- Old methods found 2 unidentified genotypes
- The court required 5 genotypes, one for each of the 5 assailants
- Old methods failed to find the other 3

TRUEALLELE SUCCESS

Cybergenetics' 2015 mixture interpretation of the Pinkins crime scene DNA used TrueAllele. Objective computer data analysis found both major and minor contributor genotypes. This advanced method used techniques previously unavailable to crime laboratories.

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*

- Identified 5 unidentified genotypes
- Showed defendants not linked to crime
- Exonerated Darryl Pinkins

THE TASK AHEAD

DNA mixtures miscalled "inconclusive" by older methods often contain considerable identification information. The older FBI mixture interpretation methods have failed on 100,000's of DNA evidence items. Thus many innocent people have been denied potentially exculpatory DNA evidence; they sit for years in prison for crimes they did not commit. All these cases must be accurately and objectively reanalyzed.

Wrongfully convicted of rape in 1991, Darryl Pinkins (blue shirt) was released from prison. Pinkins' son (orange shirt) was unborn when his father was taken away 24 years ago.