Defeating Opposition Experts Using Science in a Recent Case Example

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Abstract

In 2020, a man was shot following an altercation. He later died from his injuries. Video surveillance linked a suspect to the murder. There were no witnesses to the shooting. Police collected the gun and magazine used in the crime. Was the suspect the killer? Could DNA evidence help?

The local crime lab tested the firearm items for DNA. Their DNA data showed at least two (gun) or three (magazine) contributors to the mixtures. A private DNA lab interpreted the data and compared it with the defendant's DNA profile. By manual inspection, the lab excluded the defendant from the major DNA contributor. However, the lab couldn't draw any conclusions regarding the minor contributors, for either evidence item.

When the suspect's defense attorneys received the inconclusive DNA results, they reached out to Cybergenetics for "probabilistic" genotyping computer interpretation. Objective TrueAllele® Casework analysis statistically excluded the defendant as a DNA contributor. Separated genotype components included a 6% minor contributor (gun), and a 2% minor contributor (magazine). Cybergenetics reported exclusionary likelihood ratio (LR) match statistics, along with exact false exclusion error rates (ER)[1].

The government retained an expert to review the TrueAllele results. The opposition expert's report contained many flawed arguments. A notable flaw was an incorrect description of computed error rates. Relying on this opposition report, the government filed a Daubert motion to challenge TrueAllele admissibility.

The opposition expert argued that TrueAllele had a high binary false exclusion error rate (LR<1 for true contributors). For minor contributors, they described a 60% error rate for the 1-5% mixture range, and an 18% error rate for the 5-10% range. They based their claim on a published validation study[2] from a previous TrueAllele version. (In the version used in the case, these hypothesized error rates would be lower at 35% and 0%, respectively.) Where was the flaw in their argument?

Error rate depends on LR[1]. That mathematical fact is given in the error rate law ER ≤ LR – exclusionary error rate can never exceed the likelihood ratio. The error rate is only meaningful relative to LR, giving the chance that other people would be excluded as strongly. But the opposing expert ignored error rate's dependence on LR.

Cybergenetics calculated[1] and reported relevant error rates in the case. However, the government incorrectly applied a cutoff of 1 for a binary error rate, discarding the LR value. That is not how to determine forensic DNA error rates. The relevant context is how strongly the evidence matches (or doesn't match) the suspect – the actual LR statistical support for the suspect, not some cherry-picked cutoff level.

We revisited the validation paper's LR data. We showed that the opposition's purported "error rates" entailed weak exclusionary LR values near 1 (Figure 6, red crosses) from less informative genotypes. These validation points were not relevant to the case's highly informative genotypes, which gave strong exclusionary LR values (Figure 6, green line) of one in 70 million (gun) or 160 billion (magazine). The prosecution's spurious argument was entirely unrelated to TrueAllele reliability or its results in the case.

Responding to the Daubert challenge, Cybergenetics prepared a 26-page declaration. We detailed the opposition report's flaws, refuting inapplicable arguments with science and facts. We described the TrueAllele technology's error rate, admissibility, and court acceptance. Based just on document submissions alone, without even an admissibility hearing, the judge admitted the TrueAllele results as reliable scientific evidence.

Admissibility Standards

Frye (1920)

- general acceptance standard
- "…while courts will go a long way in admitting expert testimony deduced from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs."

Daubert (1993)

- Whether the technique or theory in question can be, and has been tested;
- Whether it has been subjected to publication and peer review;
- Its known or potential error rate;
- The existence and maintenance of standards controlling its operation; and
- Whether it has attracted widespread acceptance within a relevant scientific community.

TrueAllele Casework

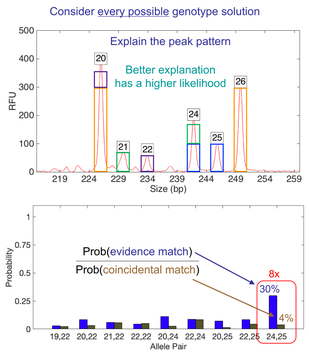

Fig 1a. *Objective inference*

Fig 1b. *Match statistics*

TrueAllele Reliability

- Tested. 42 validation studies, 8 published
- Peer-reviewed. 8 validations, math, & methods
- Error rate. Established through validation and for reported LRs
- Standards. Complies with PG validation standards and guidelines
- Accepted. 46 states, 1,250 cases, 144 trials, 10 user labs
- Transparent. Documents, math, software provided
- Admissible. 41 rulings, 15 states and federal courts

Method Validation

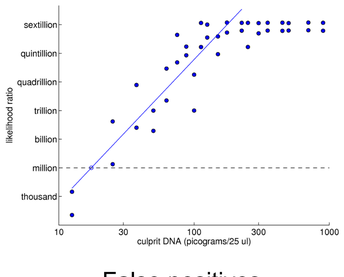

Fig 2. *Contributor DNA amount corresponds to LR making the LR predictable[3].*

Fig 3. *Error rates are established by empirically testing a method on data[4]. Validation error rates can be stratified, counting up observed false inclusions exclusions. Observed data can be limited, not considering the entire sample space.*

False positives

In over 1,000,000 comparisons per group

Tail distribution	Black	Caucasian	Hispanic
0	39	32	29
1	8	11	9
2	2	1	1
3	0	0	1
log(LR) > 0	49	44	40

false positive rate is under 1 in 20,000 (0.005%)
for LR > 100, rate is 1 in 1,000,000 (0.0001)%

Case Results

Lab Results

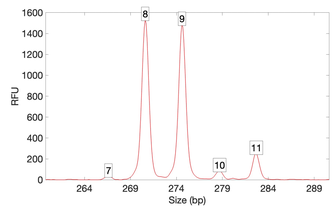

Fig 4. *Evidence items included a gun (data shown at locus D7S820) and magazine.*

Gun conclusion

- At least 2 contributors
- Defendant excluded as major
- "Due to the possibility of allelic drop out, no conclusions can be made on the minor alleles."

Magazine conclusion

- 3 or more contributors
- Defendant excluded as major
- "Due to the limited data obtained, no conclusions can be made on the minor alleles that are not part of the major mixture."

TrueAllele Results

Item	Description	Contributor	Defendant LR
5.1.1	gun	major	one over 36.1 duodecillion
		minor	**one over 72.8 million**
5.2.1	magazine	major	one over 24.3 undecillion
		middle	one over 145 nonillion
		minor	**one over 161 billion**

Table 1*. TrueAllele calculated exclusionary LRs when comparing the evidence genotypes to the defendant's reference for all mixture components.*

LR Error Rate

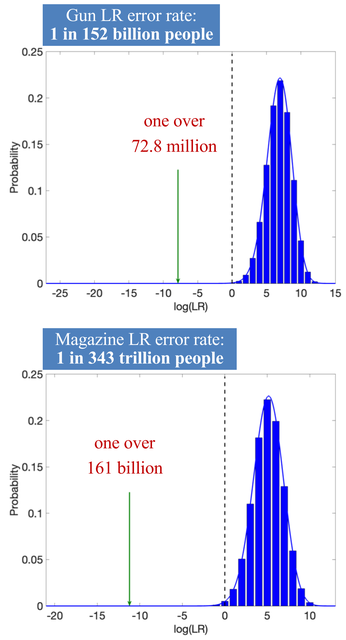

Fig 5. *Exact contributor distributions are shown for the gun 6% and magazine 2% minor contributors. Defendant match statistic is indicated by the green arrow. These distributions were used to calculate the LR error rates for the defendant comparisons.*

Expert Arguments

Opposition Assertions

An opposition expert argued the following:

- TrueAllele has a very high false exclusion rate for minor contributors
- 60% false exclusion rate for 1-5% mixture contributors (magazine)
- 18% false exclusion rate for 5-10% mixture contributors (gun)
- High false exclusion rate applies to the reported minor contributors in this case
- PG report did not note the "unreliable" nature of the evidence

Opposition arguments used only observed binary error rates that do not consider LR strength.

TrueAllele experts responded to each incorrect opposition assertion using science and the data.

LR-dependent Error Rates

Source	MW %	Exclusionary LR Statistic	log(LR)	Computed Exact LR Error Rate	log(PME)
Magazine	2.40	1 over 161 billion	-11.21	1 in 343 trillion	-14.54
Gun	5.89	1 over 72.8 million	-7.86	1 in 152 billion	-11.18
Validation	1.63	1 over 3,126	-3.49	1 in 1.21 million	-6.08
	1.08	1 over 412	-2.61	1 in 6.97 thousand	-3.84
	1.70	1 over 292	-2.47	1 in 23.3 thousand	-4.37
	1.32	1 over 25	-1.40	1 in 1.39 thousand	-3.14
	2.26	1 over 4	-0.60	1 in 490	-2.69
	1.65	1 over 3.5	-0.54	1 in 234	-2.37
	1.40	1 over 1.4	-0.15	1 in 341	-2.53

Table 2*. Exact error rates were calculated using the relevant software version for the validation study[2] false exclusions. The error rate is dependent on LR.*

LR Validation Comparison

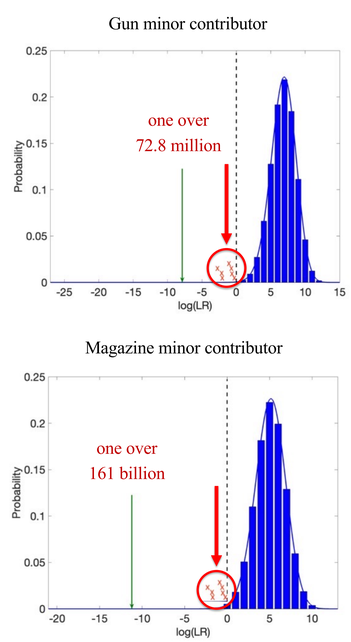

Fig 6. *Exact contributor distributions are shown for the gun 6% and magazine 2% minor contributors. Defendant match statistic is indicated by the green arrow. Validation study[2] "false exclusion" match statistics are shown as red crosses.*

Declaration Conclusion

Cybergenetics TrueAllele report in this case provides strong nonmatch statistics, and commensurately low error rates. These LR error rates were computed using the most complete technology available for complex DNA evidence, accounting for over a trillion trillion reference genotypes. The error rate method has been published in a peer reviewed journal[1]. The TrueAllele technique, both as a method and as applied in this case, clearly meets the Daubert prong for error rates, since "there is a known or potential rate of error."

The government's opposition motion fails to convince. The strong TrueAllele LR statistics in this case are clearly distinguished from the weak LR values in their cited validation paper (Figure 6). Since error rate is bounded by likelihood ratio, their irrelevant LR values are concomitantly irrelevant to the correct error rates given in our case report. Ignoring science is not an argument.

The "Opposition Motion" subsections above describe the major flaws in the government's motion. The government and their expert relied on a study that used the wrong software version (pre-2014) for this case, applied the wrong cutoff of one (instead of the LR value) for determining a false negative error rate, made misleading comparisons of the strong case LR values with irrelevant weak LR values, glossed over a more applicable validation study that used relevant LR software (post-2014) for this case, considered too few comparisons relative to modern error rate determination methods, and didn't disclose the well-known limitations of the other interpretation methods used in this case. The opposition motion is irrelevant, confusing, has no scientific merit, and is not applicable to the TrueAllele results and error rates reported this case. Their motion should be denied.

In conclusion, TrueAllele satisfies the Daubert prongs for the DNA mixture evidence in this case. The method clearly satisfies the error rate prong, with explicit reporting of low error rates for each reported LR statistic, using the best available error rate determination methods. There is no merit to the government's motion to preclude. TrueAllele should be admitted under the Daubert standard.

Admissibility Outcome

The science was clear. No hearing was needed. The judge ruled: "The Court denies the government's motion to preclude evidence of a defense analysis that excluded the defendant as a contributor to the minor components of DNA obtained from a firearm and a magazine. The government's objections go to weight, not admissibility."

References

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[2] Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *J Forensic Sci*. 2015;60(4):857-868.

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

[4] 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.

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