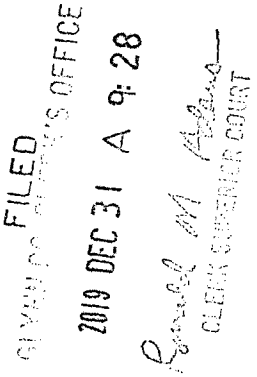
IN THE SUPERIOR COURT OF GLYNN COUNTY
STATE OF GEORGIA

STATE OF GEORGIA,	
v.	Criminal Action No. 87-00763
JIMMY FLETCHER MEDERS,	CAPITAL CASE
Defendant.	

DEFENDANT'S EXTRAORDINARY MOTION FOR A NEW TRIAL AND FOR POST-CONVICTION DNA TESTING PURSUANT TO O.C.G.A. § 5-5-41(c)



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INTRODUCTION

Defendant Jimmy Fletcher Meders, through counsel, moves this Honorable Court for an order directing the performance of deoxyribonucleic acid (DNA) testing of forensic evidence recovered in connection with the murder of Don Anderson and robbery of the Jiffy Mart at which he worked. Meders also moves this Court for an order granting a new trial and sentencing because, as the DNA testing will show, he is not the person who shot and killed Anderson. The motion for new trial is predicated on the anticipated results of the DNA testing sought via this motion. *White v. State*, 346 Ga. App. 448, 451 (2018) ("[A] motion for DNA testing is a preliminary matter and will either precede or accompany any motion for a new trial predicated upon the discovery of exculpatory DNA evidence.") (citing *State v. Clark*, 273 Ga. App. 411, 415 (2005)).

The identity of the perpetrator has been the defining issue of this case. Three individuals—Bill Arnold, James "Greg" Creel, and Meders—were present at the Jiffy Mart when the murder happened. A fourth man, Randy Harris, was with them before and after the crime. At trial, Meders maintained that Arnold was responsible for the murder. The other three men claimed that Meders—a veteran of the National Guard with no prior criminal history—committed the crime. DNA testing of the murder weapon—a Dan Wesson .357 Magnum revolver admitted into evidence at trial as State's Exhibit 9—would resolve this dispute.

If the requested DNA testing were to show that Arnold's DNA is present on the murder weapon, that result would undermine the State's case and create a reasonable probability that Meders would have been acquitted of malice murder. Meders testified at trial that at the time of the crime, Arnold had the weapon and shot the victim. However, Arnold testified that (1) he did not know that Meders had a weapon prior to the shooting, and (2) Meders shot the victim. DNA evidence showing that Arnold had in fact handled the weapon would show that the crux of his testimony—that he did not know of any weapon—was false. It also would provide affirmative support for Meders's defense that Arnold had the weapon and committed the murder.

If the requested testing were to show that Creel's DNA is present on the murder weapon, that result also would shed new light on the case. Like Arnold, Creel testified that (1) he did not know that Meders had a weapon prior to the shooting, and (2) Meders shot the victim. DNA evidence showing that Creel had handled the weapon would show that Creel's testimony was inaccurate and that Meders was not in exclusive control of the weapon.

Finally, if the requested testing were to show that Harris's DNA is present on the murder weapon, that result would show a deliberate attempt by Harris and others to pin the crime on Meders. The police searched Meders's home after his arrest, but they did not find the murder weapon. Two days later, Harris—Arnold's

cousin—suggested to the police that the weapon might be under Meders's waterbed, and the police then found the gun under the waterbed. The only reasonable explanation for the presence of Harris's DNA on the weapon would be that Harris planted the weapon under Meders's waterbed.

The weapon has never been submitted for DNA testing because such testing was not available at the time of Meders's 1989 capital trial, nor has such testing been ordered in a prior proceeding. O.C.G.A. § 5-5-41(c)(4)(B). This motion is not filed for purposes of delay, but rather in an effort to establish what Meders has always maintained: that Arnold possessed the murder weapon and murdered Anderson. O.C.G.A. § 5-5-41(c)(4)(A).

In support of this motion, and as required by O.C.G.A. § 5-5-41(c)(3), Meders sets forth in detail the evidence to be tested, when it was collected, and its present location. Meders also submits in support of this motion the affidavit of Dr. Mark W. Perlin, a preeminent expert who has worked extensively with the Georgia Bureau of Investigation on issues of DNA testing and probabilistic genotyping. *See* App. A (Affidavit of Dr. Mark W. Perlin, with attachments). As Dr. Perlin explains in his affidavit, the DNA testing requested herein is possible and could resolve whether, as the State contended at trial, Meders was the only person among the three who ever possessed the gun.

For the following reasons, it is appropriate and in the interests of justice for this Court to order DNA testing of the physical evidence in this capital case.

FACTUAL BACKGROUND

At approximately 2:35 in the morning on October 14, 1987, Don Anderson was shot and killed while working at a Jiffy Store at Marshes of Mackay on U.S. 17 in Brunswick, Georgia. T.T. 882.[1] A Dan Wesson .357 Magnum revolver was used in the killing, T.T. 795, and $31–$38 was taken from the cash register, T.T. 762. Three men—Bill Arnold, James "Greg" Creel, and Jimmy Meders—were present at the store when the crime occurred, but their accounts of the events surrounding and during the crime differed in several material respects. Most importantly, Meders maintained that Arnold committed the murder, while Arnold and Creel pointed the finger at Meders.

Arnold and Creel were never charged for any crimes arising from the events of that day, leaving only Meders to face charges of malice murder and armed robbery. A jury convicted Meders on both counts, but not before it evinced clear doubts about the State's theory of the case. The competing accounts are presented below.

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[1] "T.T. __" refers to the corresponding page of the trial transcript. "R.H." refers to the evidentiary hearing that occurred during the remand on direct appeal. "S.H." refers to the state habeas proceedings. "Ex." refers to an exhibit introduced at a particular proceeding.

A. The State's Theory

The State presented its case primarily through the testimony of three witnesses—Arnold, Creel, and Harris—who it described as the "major players in this case." T.T. 644. Arnold and Harris were cousins, T.T. 656, while Arnold and Creel were longtime friends, T.T. 719. The three men testified that on the afternoon of October 13, 1987, Creel and Arnold went to Harris's house while Meders and Harris were there working on a car. T.T. 656. The four of them spent much of the day drinking beer and liquor. T.T. 657, 685, 720–21. Later that afternoon, they went to a motel room in a nearby Best Western; Harris had rented it for Sondra Ruggles, an underage teenager with whom he was having an affair. T.T. 658–59. While in the motel room, the four men continued to drink and "smoked a joint or two." T.T. 659.

Harris testified that at 8:30 or 9:00 in the evening, Arnold, Creel, and Meders left the motel room in Harris's Roadrunner. T.T. 660–61. Creel and Arnold told the jury that they left for no particular reason. T.T. 687, 724. They aimlessly drove around Brunswick for the next six hours, "messing around and stuff, no, no particular place." T. 724.[2] They each testified that they never saw Meders with a

[2] Creel and Arnold offered slightly different accounts of their six-hour drive around Brunswick. Creel stated that the three men stopped at bars but did not purchase anything to drink, and instead "just went in there and then walked right back out." T.T. 689. On cross examination, Arnold testified that they stopped at Red Carpet and drank a single beer. T.T. 742.

gun during their long drive. T.T. 689, 725.

At approximately 2:30 in the morning, they stopped at a Jiffy Mart because Creel was hungry. T.T. 690, 728. Arnold and Creel testified that Arnold remained in the car while Creel and Meders went in the store. T.T. 690, 728. Creel stated that while he was standing in the back of the store heating up biscuits, he suddenly heard a gunshot. T.T. 694. As Creel ran out of the store, he heard a second gun shot. T.T. 697. Creel and Meders jumped in the truck, which Arnold drove to Shady Acres Trailer Park. T.T. 700, 731. Arnold testified that he refused money from Meders and instructed Meders to leave. T.T. 731–32.

According to Harris, Meders returned to the motel room at around 3:00 in the morning. T.T. 662. Harris told the jury that Meders confessed to the crime and "dump[ed] all the bullets out on the bed." T.T. 664.[3] Meders then went home. T.T. 675. Harris subsequently picked up Creel and Arnold from the trailer park, brought them to his house, and spoke with them until they all went to sleep. T.T. 676–77.

Three specific aspects of the testimony of Arnold and Creel demonstrate why DNA testing would be probative in this case. First, both denied seeing a weapon that evening. T.T. 701, 725. Second, they denied taking Meders home earlier in the evening, telling the jury that Meders "must have" had the gun on him

[3] There is no testimony regarding what happened to the bullets after Meders allegedly dumped them on the bed. Those bullets have never been found, and police did not conduct a search of the motel room.

the whole day. T.T. 707, 725, 741. And third, both men denied using Meders's gun at any point during the early-morning drive around Brunswick. T.T. 708, 741.

Beyond those three "major players," the State largely relied on investigating officers to present its case. Glynn County Police Officer Charles Byerly testified that he was part of the team that conducted the first search of Meders's home, where he found a torn $1 bill at Meders's residence matching the serial number of bait money taken from the Jiffy Mart. T.T. 827–28.[4] Additionally, Officer Byerly testified that Meders's wallet contained a $1 bill and $5 bill matching the serial numbers of the remaining bait money taken from the store. T.T. 831.

Finally, Sergeant Jack Boyet described his interviews with Meders and his discovery of the murder weapon. Meders initially denied involvement in the crime, T.T. 890, but provided a complete statement to Boyet while in jail over a year after the crime, T.T. 895. In the second statement, Meders told Boyet that Arnold shot the store clerk, and that Arnold had the gun when they separated at Shady Acres Trailer Park. T.T. 898–99. Sergeant Boyet cast doubt on Meders's account:

> PROSECUTOR: At the time you investigated this incident, at the time between that and November of 1988, have you found any evidence whatsoever, any evidence to indicate that Mr. Arnold and Mr. Creel and Mr. Harris ever possessed the gun that killed Don Anderson?

[4] Margaret Clements, the store manager, testified that each Jiffy Store keeps a small amount of "bait money" in the register. T.T. 759. Bait money sets off an alarm when it is removed from the register. T.T. 759.

SGT. BOYET: No, sir, I have not.

PROSECUTOR: Have you found any evidence that would corroborate the statement made by the defendant, anything, that Bill Arnold went in that store, and Greg Creel went in that store, and that Bill Arnold shot Don Anderson?

SGT. BOYET: No, sir, I have not.

T.T. 900.

Sergeant Boyet also described the second search of Meders's home, which occurred two days after Meders's arrest. T.T. 900. Acting on a tip from Harris, T.T. 918, Sergeant Boyet returned to the house to search for the murder weapon under Meders's waterbed, T.T. 901. This time, as Harris predicted, it was there, "under the center of the mattress." T.T. 901.

B. Meders's Account of the Crime

Testifying at trial, Meders agreed with how the day began: after working at Harris's shop for a few hours, Meders and Harris went to Harris's house, where Creel and Arnold eventually joined them. T.T. 1072. Creel and Arnold were broke and in need of money; Creel was trying to sell Meders a gold necklace. T.T. 1072. All four of them drank heavily that day. T.T. 1072.

From there, however, Meders's account of the day substantially differed from Arnold and Creel's story. Meders explained that at around 6:00, Harris left to go pick his wife up from work. T.T. 1079. Creel and Arnold took Meders home,

arriving at around 6:30 or 7:00 in the evening. T.T. 1080. A friend of Meders's, Wayne Martin, was at his house when Meders arrived. T.T. 1080. Because he was intoxicated and knew Harris was having an affair with Sondra Ruggles, Meders convinced Martin to bring him by the motel room so he could "keep [Harris] from having the affair sort of thing." T.T. 1080. Creel and Arnold did not accompany them. T.T. 1080. Meders and Martin only stayed for a few minutes before leaving the motel room and returning to Meders's home. T.T. 1081.[5] Meders stayed at his house—along with several other people—and eventually fell asleep. T.T. 1081.

At around 11:00 or 11:30 that night, Arnold unexpectedly came into Meders's house to wake him up. T.T. 1081–82. Arnold picked Meders up under his arms, "got the .357 Magnum," and walked out. T.T. 1082. From there, the three of them went to the motel room where Harris and Sondra Ruggles were staying. T.T. 1084. Arnold and Harris huddled in the far corner of the room, talking out of earshot, before Arnold left with Creel and Meders. T.T. 1084.

Arnold and Creel drove Meders around, seeking to avenge a fight they had gotten into with a man named Keith Bowen. T.T. 1084–85. Using Meders's .357 Magnum, Arnold shot at Bowen's truck. T.T. 1085. Arnold then drove to a house on Lake Shore Drive, around the corner from where Creel lived. T.T. 1086. The house belonged to a family with whom Creel was feuding, so Arnold shot at the

[5] Martin testified at trial and offered a similar account of the evening. T.T. 952–55.

truck outside the house. T.T. 1086–87. Continuing their drive, they eventually encountered Meders's brother and his wife making a bank deposit. T.T. 1088.[6] While Meders spoke to his brother, Creel "pulled the gun out from under the seat and was waving it around." T.T. 1089. Creel and Arnold also joked about robbing Meders's brother because he had just made a bank deposit. T.T. 1089.

Ultimately, the three of them ended up at the Jiffy Mart where the murder occurred. T.T. 1091.[7] Arnold joined Creel and Meders inside the store. T.T. 1092. While Creel heated up biscuits in the microwave, Meders leaned against the counter. T.T. 1092. Arnold stood in front of the store clerk and suddenly "pulled the gun and shot" Don Anderson. T.T. 1092. Waving the gun around, Arnold told Meders to take money out of the cash register. T.T. 1092.

Arnold drove the three of them to Shady Acres Trailer Park, where Meders told Arnold to keep the gun. T.T. 1093. Arnold and Creel got out of the truck, T.T. 1094, and Meders testified that that was the last time he saw the gun, T.T. 1093.

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[6] Meders's brother, Stacy, testified at trial and confirmed this interaction. T.T. 972–75. Stacy also said that while everyone was talking with each other, all three men in the car held the gun. T.T. 976 ("Well, all three of them handled it."). Stacy's wife, Linda, also testified consistently with this account. T.T. 1022–24.

[7] Meders testified that Arnold first pulled into a different Jiffy Mart near Druid Oaks Trailer Park, which he entered carrying the gun and stating that he intended to rob the store. T.T. 1091. The store was crowded so Arnold left without incident. T.T. 1091. A police report introduced in post-trial proceedings documents an interview with Gordon Spurlock, a store clerk at the Druid Oaks Jiffy Mart, in which Spurlock describes a "suspicious" incident at approximately 1:00 in the morning in which an individual paced around for 20–30 minutes before leaving. R.H. Ex. 1 (Prosecutor's File, Det. Matt Doering Supplemental Report, October 14, 1987).

Meders drove the truck home and was stopped by a city police officer for a brake light violation in front of his house. T.T. 1094.

Finally, Meders did not dispute that the murder weapon was found underneath his mattress, but he vigorously denied placing it there. T.T. 1127. He testified that the "police searched that house thoroughly on October 14th" and did not find the weapon. T.T. 1127. The police only found the weapon at Harris's direction two days after the crime occurred, two days after the original search of the home, and two days after Meders had been booked into the Glynn County Detention Center. T.T. 1127.

C. The Jury Questions the Evidence

Following Meders's testimony, the jury evinced doubt about the State's case. After deliberating for ninety minutes, the jury sent several questions about the evidence to the trial judge, including three that specifically asked for physical evidence:

1. Where fingerprints found on any of the store or any items that was involved in the crime??

2. Where fingerprints look for?

3. During the execution of the first search warrant was the bedroom searched, if so was the waterbed searched?

4. Can fingerprints be taken and if so were they taken on the waterbed mattress??

5. Was there any reports filed on the incident of the truck, on Ga Hwy 303, Reported between the day after or between then and now; being shot at??

6. Was there any item lying on the counter that could have been 49¢ that someone could have put the correct numbers in the machine that would make it look like someone had got something for 49¢??[8]

T.T. 1360 (emphases added; errors in original). In response, the trial court informed the jury that "[t]he Court cannot respond to you in any regard concerning the evidence in this case." T.T. 1261. The Court repeated its instruction to "base all of your findings on the evidence that has been presented to you during the course of this trial." T.T. 1261. Deprived of answers that could have cast doubt on Meders's guilt, the jury convicted Meders on one count of malice murder and one count of armed robbery. T. 1266.

D. Reason to Doubt the State's Witnesses

At trial, the State built its case on the credibility of Harris, Creel, and Arnold.

> You look at their personal credibility, and that involves everything. . . . [Y]ou also look at how their testimony here in Court reflects what they said on October 14th, 1987, because that is an important part of credibility. Have they stuck with their story, have they told the same thing all the way down the line, and if you just decided credibility based on that, if, if that is all you look at, then Randy Harris, Bill Arnold, Greg Creel, the police officers all told the same story all the way down the line from day one.

[8] This question appears to be in response to Margaret Clements's testimony that the last transaction on the register before the homicide was for 49 cents. T.T. 763. Clements testified that a store receipt prints out every time the register was opened. T.T. 764.

T.T. 1182–83. However, pretrial witness statements, police reports, and other law enforcement documents establish that the key witnesses were not, in fact, consistent "from day one."[9]

Creel and Arnold's initial statements to the police contradict their trial testimony in several important respects. Most importantly, Creel told police that he and Arnold both knew that Meders possessed a gun that day. R.H. Ex. 1.[10] Additionally, Creel and Arnold both told police that they dropped Meders off early in the evening before picking him up at around 11:00. R.H. Ex. 1.[11]

There were also police reports documenting two shootings at trucks that Arnold and Creel denied at trial. One report described shots from "an older modle [sic] vehicle posibly [sic] a Dodge white in color with a red stripe along the lower portion." R.H. Ex. 2D.[12] And in the other report, the complainant specifically

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[9] The witnesses' inconsistent statements could have—and should have—been used to undermine their testimony at trial. But they were not.

[10] Prosecutor's File, October 15, 1987 Statement of Greg Creel at 27 ("Creel Statement") (Meders had a gun "[a]ll day long. . . . Bill and Randy said the mother fucker keeps a gun with him . . .").

[11] Creel Statement at 12 (explaining that Arnold and Creel drove around for a couple of hours until "Bill said let's go get [Meders]. So, we went and got him."); Prosecutor's File, October 15, 1987 Statement of Bill Arnold at 1 ("Arnold Statement") ("we'd been riding around all day long and Jimmy went home for a while and then we rode around and picked him up.").

[12] Glynn County Police Department Incident Report, October 14, 1987, 12:40am Shooting at 210 Cypress Mill Road. Harris's Plymouth Road Runner, which Arnold drove that morning, matched this description. T. Ex. S-2 (photograph of Road Runner).

"stated that he feels that the incident was caused by Larry Brockington and Gregg [sic] Creel due to some problems he had with them in the past." R.H. Ex. 2F.[13]

Additionally, Harris's testimony bore little relationship to his police statements. In his first interview at 11:00am on October 14, 1987, he told the police that "he had not seen [Meders] since 6:00pm the previous day." R.H. Ex. 1.[14] Hours later, he provided a second statement to the police about Meders's alleged confession. However, this statement also materially differed from his testimony. First, Harris did not see Meders with a gun. Second, he did not say anything about Meders dropping bullets and money on the bed. Third, he did not know where the victim was shot. And fourth, Harris did not know where the weapon could be found. R.H. Ex. 1.[15]

In its closing argument, the State told the jury that "what is interesting about the State's side of the case . . . [is] the police officers make their case and establish all of the evidence on October 14th, 15th, and 16th, 1987." T.T. 1183. However, if the State's case at trial matched the evidence law enforcement collected on

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[13] Glynn County Police Department Incident Report, October 14, 1987, 1:30am Shooting at 161 Lake Drive. Robert Brown was the complainant in this case. Six weeks after this shooting occurred, Creel was arrested for "threatening to burn Robert Brown's house down and threaten[ing] to kill the said Robert Brown." S.H. Ex. 2. (Creel Criminal History, Case No. 87-11-I06536, Terroristic Threats). According to the incident report, Creel vowed to burn Brown's house down, "went into his residence, returned with a pistol and fired it up into the air." Those charges were pending at the time of Meders's trial.

[14] Prosecutor's File, Sgt. Jack Boyet Supplemental Report.

[15] Prosecutor's File, October 14, 1987 Statement of Randy Harris at 5–7 ("Harris Statement").

October 14th, 15th, and 16th, 1987, it would have looked far more exculpatory for Meders and far more inculpatory for Arnold and Creel:

State's Case at Trial	State's Evidence in October 1987
Arnold, Creel, Meders spent the whole day together.	Arnold, Creel, Meders did not spend the whole day together.
Arnold did not pick Meders up at 11:00pm.	Arnold picked Meders up at 11:00pm.
Arnold and Creel did not know Meders had a gun.	Arnold and Creel knew Meders had a gun.
There is no evidence of any shootings in the area that morning.	There were two documented shootings in the area that morning.
Harris saw Meders with a gun after the crime.	Harris did not see Meders with a gun after the crime.
Sherri Meders told Harris where the gun could be found.	Harris did not know where the murder weapon could be found.

This evidence should have been used at trial. It was not. Even without these statements, the jury's questions indicate that this was a close case. If DNA testing had been available at Meders's trial, there is a reasonable probability that the jury would have reached a different verdict. DNA testing is therefore essential.

PROCEDURAL HISTORY

On April 7th, 1989, a jury convicted Meders of one count of malice murder and one count of armed robbery. T.T. 1266. The sentencing hearing occurred the same day; it lasted one hour and eight minutes, including the preliminary and final

jury instructions. T.T. 1285 (jury receives preliminary instructions at 3:15pm), 1332 (jury retires to deliberate at 4:23pm). Just twenty minutes into their sentencing deliberations, jurors sent the judge a note:

> If the jury recommends that the accused be sentenced to life imprisonment can the jury recommend that the sentence be carried out without parole??

T.T. 1361. The judge instructed the jury that "such matters as you have inquired about are not proper for the jury's consideration in any shape, form or fashion." T.T. 1338. Nearly four hours later, the jury sentenced Meders to death. T.T. 1343.

The Supreme Court of Georgia conditionally affirmed Meders's conviction on direct appeal but remanded the case for an evidentiary hearing on whether Meders received effective assistance of counsel at trial. *Meders v. State*, 260 Ga. 49, 55 (1990). After the superior court found that Meders's trial counsel had not performed ineffectively, the Supreme Court of Georgia affirmed Meders's conviction and sentence. *Meders v. State*, 261 Ga. 806 (1992). The United States Supreme Court denied Meders's petition for writ of certiorari. *Meders v. Georgia*, 506 U.S. 1015 (1992).

On April 2, 1993, Meders filed a petition for habeas corpus in the Superior Court of Butts County. Following an evidentiary hearing, the state habeas court denied relief on several grounds but granted Meders relief on his claims that trial counsel had been ineffective in the guilt phase of Meders's trial. The State

appealed the order and Meders cross-appealed. The Supreme Court of Georgia reversed the grant of relief but otherwise affirmed the trial court's order. *Schofield v. Meders*, 280 Ga. 865 (2006). The United States Supreme Court again denied Meders's petition for writ of certiorari. *Meders v. Schofield*, 549 U.S. 1126 (2007).

Meders filed a federal petition for a writ of habeas corpus on July 24, 2007, which he amended on January 15, 2012.[16] In an unpublished order, the federal habeas court denied Meders's petition. *Meders v. Chatman*, 2014 WL 3973912 (S.D. Ga. 2014). The Eleventh Circuit Court of Appeals affirmed the district court's ruling on January 4, 2019. *Meders v. Warden, Ga. Diag. Prison*, 911 F.3d 1335 (11th Cir. 2019). The United States Supreme Court subsequently denied Meders's petition for writ of certiorari. *Meders v. Ford*, No. 19-5438 (U.S. Oct. 15, 2019).

THE LEGAL STANDARD

The procedures governing post-conviction DNA testing in Georgia are codified in O.C.G.A. § 5-5-41(c). The statute proceeds in two parts. First, a petitioner must make a threshold showing before he is entitled to a hearing. Second, if the petitioner makes that threshold showing and earns a hearing, the

[16] The federal habeas proceedings were stayed pending the disposition of a second state habeas petition. The Superior Court of Butts County denied the petition on December 16, 2009. The Supreme Court of Georgia subsequently denied Meders's application for a certificate of probable cause and the United States Supreme Court denied Meders's petition for writ of certiorari. *Meders v. Hall*, 565 U.S. 965 (2011).

petitioner must satisfy a post-hearing standard in order to obtain DNA testing. The statutory scheme is set out in more detail below.

A. The Threshold Showing

O.C.G.A. § 5-5-41(c) authorizes "a person convicted of a felony [to] file a written motion before the trial court that entered the judgment of conviction in his or her case for the performance of forensic deoxyribonucleic acid (DNA) testing." O.C.G.A. § 5-5-41(c)(1) (alteration added). The statute requires that a petitioner "show or provide" four key facts:

> (A) Evidence that potentially contains deoxyribonucleic acid (DNA) was obtained in relation to the crime and subsequent indictment, which resulted in his or her conviction;
>
> (B) The evidence was not subjected to the requested DNA testing because the existence of the evidence was unknown to the petitioner or to the petitioner's trial attorney prior to trial or because the technology for the testing was not available at the time of trial;
>
> (C) The identity of the perpetrator was, or should have been, a significant issue in the case; [and]
>
> (D) The requested DNA testing would raise a reasonable probability that the petitioner would have been acquitted if the results of DNA testing had been made available at the time of conviction, in light of all the evidence in the case[.]

O.C.G.A. § 5-5-41(c)(3)(A)–(D). Additionally, a petitioner must provide a "description of the evidence to be tested"; the results of any prior DNA testing;

information regarding the entity in possession of the evidence; and the identities of individuals who may testify for the petitioner. O.C.G.A. § 5-5-41(c)(3)(E)–(H).

The Supreme Court of Georgia has recognized that "[r]equiring a petitioner to 'show' a possible DNA testing result and to 'show' the relevance of that hypothetical result is not tantamount to requiring the petitioner to 'prove' the hypothetical result will be obtained through actual testing." *Crawford v. State*, 278 Ga. 95, 97 (2004); *see also White v. State*, 346 Ga. App. 448, 450 (2018) (the results of DNA testing "are assumed to be valid for purposes of the motion"). In other words, in considering this motion, this Court should assume that any DNA result will be favorable to Meders. Bearing that assumption in mind, this Court should then consider whether such a result would "in reasonable probability have led to [the defendant's] acquittal, or to his receiving a sentence less than death, if they had been available at [the defendant's] trial." *Crawford*, 278 Ga. at 99 (citing O.C.G.A. § 5-5-41(c)(3)(D)).

Beyond the requirements of subsection (c)(3), the statute requires a defendant to state that "the motion is not filed for the purpose of delay" and that the issues have not been previously raised in a prior proceeding. O.C.G.A. § 5-5-41(c)(4). Meders has made those statements above and reiterates them here. As the Supreme Court of Georgia has recognized, the "two prerequisites in paragraph (4)

are simple matters that require no detailed explanation in a petitioner's motion." *Crawford*, 278 Ga. at 97.

If a defendant satisfies this pleading standard, "the court shall order a hearing" on whether the defendant is entitled to DNA testing. O.C.G.A. § 5-5-41(c)(6)(A); *White*, 346 Ga. App. at 449–50 ("Assuming the petitioner complies with the filing requirements set forth in O.C.G.A. § 5-5-41(c)(3) and (4), the trial court is required to hold a hearing on the motion.").

B. The Hearing and Post-Hearing Standard

The primary purpose of the hearing is to allow the parties to be heard on the issue of "whether upon consideration of all the evidence there is a reasonable probability that the verdict would have been different if the results of the requested DNA testing had been available at the time of trial . . . ." O.C.G.A. § 5-5-51(c)(6)(E). In addition, the hearing also serves to determine whether the following requirements have been met:

> (A) The evidence to be tested is available and in a condition that would permit the DNA testing requested in the motion;
>
> (B) The evidence to be tested has been subject to a chain of custody sufficient to establish that it has not been substituted, tampered with, replaced, or altered in any material respect;
>
> (C) The evidence was not tested previously, or, if tested previously, the requested DNA test would provide results that are reasonably more discriminating or probative of the identity of the perpetrator than prior test results;

(D) The motion is not made for the purpose of delay;

(E) The identity of the perpetrator was a significant issue in the case;

(F) The testing requested employs a scientific method that has reached a scientific state of verifiable certainty such that the procedure rests upon the laws of nature; and

(G) The petitioner has made a prima facie showing that the evidence sought to be tested is material to the issue of petitioner's identity as the perpetrator, or accomplice to, the crime, aggravating circumstance, or similar transaction that resulted in the conviction.

O.C.G.A. § 5-5-41(c)(7). Both parties may present evidence at the hearing, and the court may receive additional legal memoranda up to thirty days after the hearing. O.C.G.A. § (c)(6)(C)–(D). If the petitioner meets the above requirements, the court "*shall* grant the motion for DNA testing . . . ." O.C.G.A. § 5-5-41(c)(7) (emphasis added).

ARGUMENT

I. MEDERS SATISFIES THE THRESHOLD SHOWING AND IS THEREFORE ENTITLED TO A HEARING.

The DNA testing statute requires Meders to satisfy several preconditions in order to obtain a hearing on this motion. O.C.G.A. § 5-5-41(c)(3)(A)–(H). Meders satisfies those conditions. As a result, this Court "is required to hold a hearing on the motion." *White*, 346 Ga. App. at 450 (citing O.C.G.A. § 5-5-41(c)(6)).

A. The State Collected Evidence that Potentially Contains DNA.

In support of this motion, Meders has attached a sworn affidavit from Dr. Mark W. Perlin, the chief scientist and executive at Cybergenetics, Corp. App. A (Affidavit of Dr. Mark W. Perlin, with attachments). As an expert in DNA collection and analysis, Dr. Perlin developed TrueAllele, a probabilistic genotyping software that allows examiners to analyze and report on DNA mixture evidence not otherwise able to be interpreted by human analysis alone. When the Georgia Bureau of Investigation implemented TrueAllele in 2018, Dr. Perlin trained the bureau on its use of the software.

As Dr. Perlin explains in the attached affidavit, there is reason to believe that the gun potentially contains DNA evidence:

> [A] photograph taken one month ago in the office of the Clerk of Court in Brunswick, Georgia shows the revolver in a clear sealed plastic evidence bag. Nothing seen in the photograph indicates unsuitability for DNA testing. The revolver appears to be dry and well-preserved. Evidence storage under cool and dry conditions should not interfere with successful DNA testing.

App. A at 2. Dr. Perlin also explains that in his experience, "DNA recovered from revolvers is often a mixture of four or more people." App. A at 3. Although that previously posed a barrier to meaningful analysis of the DNA sample, recent developments have made such an analysis possible:

> [M]odern computer analysis of complex DNA mixture data (called "probabilistic genotyping") regularly yields statistical identification information that can either (a) connect a defendant with the evidence

item, or (b) demonstrate that there is no connection between the defendant and the evidence.

App. A at 3. Thus, Dr. Perlin "conclude[s] that the evidence in this case potentially contains DNA that can be used to help determine the identity of the people who handled the revolver." App. A at 5.

The DNA testing statute further requires Meders to recite where the evidence is presently located. O.C.G.A. § 5-5-41(c)(3)(E). State's Exhibit 9 is presently located in the Evidence Locker in the Clerk's Office of the Glynn County Superior Court, as counsel has recently confirmed.[17] A picture of the gun in its present location and condition is reproduced below:

The DNA testing statute also requires Meders to provide "the date, time, and means" of the "original collection" of the evidence. O.C.G.A. § 5-5-41(c)(3)(E). As Meders explained above, Sergeant Jack Boyet found the murder weapon on October 16, 1987, underneath the waterbed in Meders's home at 3113 Prim Place, Brunswick, GA 31520. T.T. 900–01. At present, the Clerk of the Superior Court,

[17] At a hearing, Meders will be able to demonstrate that the gun has not been held other than in the proper chain of custody. O.C.G.A. § 5-5-41(c)(7)(B).

Ronald M. Adams, 701 H Street, Brunswick, GA 31520, is in possession of the evidence. O.C.G.A. § 5-5-41(c)(3)(G).

Meders anticipates calling as a witness Dr. Mark W. Perlin, Cybergenetics, Omega Building, Suite 210, 160 North Craig Street, Pittsburgh, PA 15213, phone: (412) 683-3004. O.C.G.A. § 5-5-41(c)(3)(H). Meders will also call any other witnesses necessary to establish chain of custody and/or other matters required by O.C.G.A. § 5-5-41(c)(7). Finally, Meders will call as a witness his prior counsel: James Jenkins, 1506 Brandt Court, Boulder, CO 80303, phone: (303) 443-9048.

B. The Evidence Has Never Been Subjected to DNA Testing Because DNA Testing Was Not Available at the Time of Meders's 1989 Trial.

To Meders's knowledge, the murder weapon has never been submitted for DNA testing. O.C.G.A. § 5-5-41(c)(3)(F). There is a simple reason that the evidence was not submitted for DNA testing prior to Meders's 1989 trial: at the time, the Georgia Supreme Court had never deemed such evidence admissible. The first case in which the Georgia Supreme Court recognized the scientific validity of DNA evidence in criminal cases occurred in 1990—after Meders's trial occurred. *Caldwell v. State*, 260 Ga. 278 (1990).[18] Moreover, Dr. Perlin explains in his

[18] In post-trial proceedings, Sheriff Wayne Bennett testified that DNA testing was not available in Glynn County at the time of Meders's trial. S.S.H. Tr. 107 ("At that time, sir, no, we did not [have any DNA evidence against Mr. Meders in this case]. DNA was not prevalent and available in the United States of America at that time.").

affidavit that he anticipates the presence of multiple contributors to the DNA evidence found on the gun. App. A at 3. Analysis of such a mixture was impossible until the recent development of probabilistic genotyping software; prosecutors in Georgia did not begin relying on such software until this year. App. A at 3–4.

Neither the State nor the defense has previously requested DNA testing in this case, nor has it ever been ordered in a prior proceeding. O.C.G.A. § 5-5-41-(c)(4)(B).[19]

C. The Identity of the Perpetrator Was the Defining Issue of This Case.

The central dispute in this case was the identity of the shooter. At trial, the State claimed Meders committed the crime alone, and that Arnold and Creel were merely present when Meders—a veteran of the National Guard who had no prior criminal history—suddenly decided to shoot and kill Don Anderson. By contrast, Meders testified that Arnold committed the crime, that Meders did not know Arnold would commit the crime in advance, and that Meders took money from the register only because Arnold directed him to do so after killing Anderson. The years of post-trial litigation have also consistently centered around this dispute. There can be no doubt that the identity of the perpetrator is, was, and always has been a "significant issue" in this case.

[19] The gun was submitted for fingerprint analysis prior to trial, but the results were inconclusive. Dr. Perlin explains that such analysis should not interfere with any DNA analysis. App. A at 2–3.

D. There Is a Reasonable Probability that Meders Would Have Been Acquitted of Malice Murder or Sentenced to Life Imprisonment if DNA Testing Had Been Available.

The DNA testing statute requires Meders to "show or provide" that the "requested DNA testing would raise a reasonable probability that the petitioner would have been acquitted if the results of DNA testing had been available at the time of conviction, in light of all the evidence in the case." O.C.G.A. § 5-5-41(c)(3)(D). The Georgia Supreme Court has clarified that this standard does not require a petitioner to show that it is more likely than not that the result would have been different. *Miller v. State*, 285 Ga. 285, 286 (2009). Instead, it merely requires a petitioner to demonstrate "'a probability sufficient to undermine confidence in the outcome.'" *Id.* (quoting *Strickland v. Washington*, 466 U.S. 668, 694 (1984)). Additionally, in assessing this prong of the DNA testing statute, courts should consider whether such results would "in reasonable probability have led to [petitioner's] acquittal, or to his receiving a sentence less than death, if they had been available at [petitioner's] trial." *Crawford*, 278 Ga. at 99 (citing O.C.G.A. § 5-5-41(c)(3)(D)); *see also Drane v. State*, 291 Ga. 298, 303–04 (2012) (trial court erred when it refused to consider materiality of newly-discovered evidence as to the defendant's sentence).

Meders satisfies this requirement as to the probable outcome of both the guilt and sentencing phases.

1. There Is a Reasonable Probability that the Jury Would Have Acquitted Meders of Malice Murder.

Given the lack of physical evidence, and as the State argued at trial, this case hinged on the credibility of Arnold, Creel, and Harris. T.T. 1183. If DNA testing revealed that any of them handled the weapon, then the State's case would have to be viewed in a completely different light.[20] Specifically, the presence of Arnold's DNA on the gun would have undermined several key aspects of the State's case:

- Arnold's testimony that he never possessed a gun that evening, T.T. 725;

- Sergeant Boyet's testimony that there was "no evidence to indicate that Mr. Arnold and Mr. Creel and Mr. Harris ever possessed the gun that killed Don Anderson," T.T. 900; and

- The prosecution's argument that Arnold was credible because he "admit[ted] things that you would expect some people to try to hide," T.T. 1183.

It would also have supported the testimony of several defense witnesses that Arnold and Creel possessed the gun shortly before the murder:

- Sherry Meders's testimony that "Bill Arnold came up and got me out of bed, start asking to borrow the gun," T.T. 936;

- Stacy Meders's testimony that he saw "all three of them handl[e]" the gun approximately thirty minutes before the murder, T.T. 976; and

[20] Arnold, Creel, and Harris each have multiple convictions, and thus it is possible that their DNA has been uploaded into CODIS, which would render a comparison possible. Even if their DNA has not been uploaded into CODIS, it may be possible to extract their DNA from the latent fingerprint cards they each completed. Those cards are in the possession of the District Attorney and were admitted as evidence during the remand hearing. R.H. Ex. 4.

- Jimmy Meders's testimony that Bill Arnold was using the gun throughout the drive, T.T. 1085–86.

Moreover, the presence of Arnold's DNA would have been directly responsive to the jury's first question about whether there were any fingerprints found on an item used in the crime. T.T. 1360. In short, if the jury saw evidence that Arnold's DNA was on the gun, the trial would have looked completely different.

There would be a similar effect if Creel's DNA is found on the gun. If Creel's DNA is on the gun, then it would significantly undermine his credibility, as well as the credibility of Sergeant Boyet's testimony that there was "no evidence" to indicate Creel had ever possessed the gun. T.T. 900. The presence of Creel's DNA on the gun would also undermine the linchpin of the prosecution's case: that Meders was in exclusive control of the murder weapon that night.

Finally, the presence of Harris's DNA on the gun would show a deliberate attempt by Harris and others to pin the crime on Meders. The police searched Meders's home after his arrest, but they did not find the murder weapon. Two days later, Harris suggested to the police that the weapon might be under Meders's waterbed, and the police then found the gun under the waterbed. The only reasonable explanation for the presence of Harris's DNA on the weapon would be that Harris planted the weapon under Meders's waterbed.

The presence of DNA from Arnold, Creel, and/or Harris would have transformed the trial. Even without any physical evidence tying Arnold, Creel, or

Harris to the gun, this was a close case—as the jury questions indicate. This evidence would have directly undermined the testimony of the State's key witnesses and bolstered Meders's defense. As a result, there is a reasonable probability that the jury would have voted to acquit Meders of malice murder.

2. There Is a Reasonable Probability that the Jury Would Not Have Sentenced Meders to Death.

Alternatively, if this Court determines that Meders cannot show a reasonable probability of a different result in the guilt phase of the trial, then he can satisfy the standard as to his sentence. *Crawford*, 278 Ga. at 99; *Drane*, 291 Ga. at 303–04. This crime was not highly aggravated, and Meders was a National Guard veteran with no criminal history. Moreover, the jury was already divided at sentencing, asking the court if it could recommend a sentence of life imprisonment without the possibility of parole. T.T. 1361. As discussed above, the presence of DNA from Arnold, Creel, and/or Harris on the gun would undermine the State's case in several material respects. If there are multiple contributors to any DNA found on the gun, then that evidence would, at a minimum, create substantial doubt as to who possessed the gun when Anderson was killed. When combined with the other factors weighing in favor of a life sentence, DNA evidence would create a reasonable probability of a sentence less than death.

Meders has demonstrated above that he complies with the filing requirements set forth in O.C.G.A. § 5-5-41(c)(3) and (4). As such, this Court "is

required to hold a hearing on the motion." *White*, 814 S.E.2d at 450 (citing O.C.G.A. § 5-5-41(c)(6)).[21]

CONCLUSION

For the foregoing reasons, as well as any other reason apparent to the Court, Meders respectfully requests that this Court: (1) order an evidentiary hearing as required by statute; (2) order DNA testing as set forth herein and in the attached declaration; (3) grant Meders a new trial and/or sentencing proceeding; and (4) enter any other order(s) required in the interests of justice.

Respectfully submitted,

by special permission
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Southern Center for Human Rights
60 Walton Street NW
Atlanta, GA 30303
Tel: (404) 688-1202
Fax: (404) 688-9440
madmirand@schr.org

Counsel for Mr. Meders

[21] Meders also maintains that, after a hearing, he will be able to satisfy the standard to obtain DNA testing. Several of the post-hearing preconditions to obtaining DNA testing overlap with the initial showing discussed above. O.C.G.A. § 5-5-41(c)(7). Additionally, Meders will be able to show a sufficient chain of custody to establish that the gun has not been altered in any material respect. O.C.G.A. § 5-5-41(c)(7)(B). To counsel's knowledge, the evidence has only been held in proper chain of custody since Meders's trial in 1989. Meders is also in possession of the chain-of-custody documentation that law enforcement created prior to trial.

CERTIFICATE OF SERVICE

I hereby certify that on December 30, 2019, I served the foregoing *Extraordinary Motion for a New Trial and for Post-conviction DNA Testing Pursuant to O.C.G.A. § 5-5-41(c)* on the following individuals via electronic mail:

Ms. Jackie Johnson
District Attorney
Brunswick Judicial Circuit
701 H Street, Box 301
Brunswick, GA 31520

Sabrina Graham
Senior Assistant Attorney General
40 Capitol Square SW
Atlanta, GA 30334

/s/ Michael Admirand
Michael Admirand

VERIFICATION

I am the petitioner in this action and know the content of the above *Extraordinary Motion for a New Trial and for Post-conviction DNA Testing Pursuant to O.C.G.A. § 5-5-41(c)*. I verify that the assertion in this motion are true of my own knowledge, except as to those that are stated in it on my information and belief, and as to those matters I believe them to be true. I swear penalty of perjury that the contents of the foregoing are true.

_____ _____

Jimmy Fletcher Meders Date

Sworn to and subscribed before me this ____ day of _____, 20__.

_____

Notary Public or Other Person Authorized to Administer Oaths

VERIFICATION

I am the petitioner in this action and know the content of the above *Extraordinary Motion for a New Trial and for Post-conviction DNA Testing Pursuant to O.C.G.A. § 5-5-41(c)*. I verify that the assertion in this motion are true of my own knowledge, except as to those that are stated in it on my information and belief, and as to those matters I believe them to be true. I swear penalty of perjury that the contents of the foregoing are true.

Jimmy Fletcher Meders — Date: 9-18-19

Sworn to and subscribed before me this 18 day of Sept, 2019

Notary Public or Other Person Authorized to Administer Oaths — CE 7/5/2020

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APPENDIX A

Affidavit of Dr. Mark W. Perlin

IN THE SUPERIOR COURT OF GLYNN COUNTY
STATE OF GEORGIA

STATE OF GEORGIA	)	
v.	)	Criminal Action No. 87-00763
JIMMY FLETCHER MEDERS,	)	CAPITAL CASE
Defendant.	)	

AFFIDAVIT OF DR. MARK W. PERLIN

I, Dr. Mark W. Perlin, hereby state under oath and on personal knowledge:

1. My name is Dr. Mark W. Perlin. I am over eighteen (18) years of age, and competent and qualified to give the testimony herein. All statements provided for herein are based upon my personal knowledge.
2. I am currently the Chief Scientist and Executive Officer for Cybergenetics, Corp. in Pittsburgh, Pennsylvania ("Cybergenetics"). My curriculum vitae is attached as Exhibit A.
3. At the request of Michael Admirand, Staff Attorney with the Capital Litigation Unit of the Southern Center for Human Rights, Cybergenetics was asked to assess the suitability of DNA testing and TrueAllele® probabilistic genotyping on evidence in the case of State v. Jimmy Meders in the Criminal Court of Glynn County, Georgia.

4. This assessment relates to a Dan Wesson .357 magnum revolver (Serial Number 58642) that was presented in court at Mr. Meders' 1989 trial. I understand that the revolver has remained in the custody of the Clerk of Court in Brunswick, Georgia since that time. I have seen a recent photograph of the revolver.
5. The revolver was subjected to cyanoacrylate fuming (aka, a "superglue bath") to test for latent fingerprints. The fingerprint results were inconclusive.
6. To assess whether the crime-related revolver evidence potentially contains useful DNA information, there are three issues. The first concerns how well DNA was preserved during storage. The second concerns how cyanoacrylate fuming might have affected DNA testing. The third concerns how much identification information can be recovered from DNA on a revolver. I address these issues in turn.
7. Firstly, a photograph taken one month ago in the office of the Clerk of Court in Brunswick, Georgia shows the revolver in a clear sealed plastic evidence bag. Nothing seen in the photograph indicates unsuitability for DNA testing. The revolver appears to be dry and well-preserved. Evidence storage under cool and dry conditions should not interfere with successful DNA testing.
8. Secondly, scientific studies have been recently been conducted on how cyanoacrylate fuming affects modern short tandem repeat ("STR") DNA

testing. The current consensus is that such fuming has no adverse affect, as described in the following two published peer-reviewed articles.

9. Bhoelai et al. found that "cyanoacrylate (CA) fuming ... did not affect subsequent STR typing." See Exhibit B: Bhoelai B, de Jong BJ, de Puit M, Sijen T. "Effect of common fingerprint detection techniques on subsequent STR profiling." *Forensic Sci Int: Genetics Supplement Series.* 2011, 3:e429-e430.

10. Bille et al. found that "cyanoacrylate fuming did not have a measurable effect on the success of the DNA analysis." See Exhibit C: Bille TW, Cromartie C, Farr M. "Effects of cyanoacrylate fuming, time after recovery, and location of biological material on the recovery and analysis of DNA from post-blast pipe bomb fragments." *J Forensic Sci.* 2009, 54(5):1059-1067.

11. Thirdly, DNA recovered from revolvers is often a mixture of four or more people. Ten years ago, such mixtures posed an obstacle for human interpretation of DNA evidence. However, modern computer analysis of complex DNA mixture data (called "probabilistic genotyping") regularly yields statistical identification information that can either (a) connect a defendant with the evidence item, or (b) demonstrate that there is no connection between the defendant and the evidence.

12. Cybergenetics' TrueAllele® Casework is one such probabilistic genotyping computer system. TrueAllele has been used in 43 states, including Georgia.

The Georgia Bureau of Investigation ("GBI") has its own TrueAllele system, and regularly uses it to analyze and report on DNA mixture evidence. Georgia prosecutors and defenders alike use TrueAllele results for accurate and objective analysis of complex DNA evidence in their criminal cases.

13. I have testified in Harper admissibility hearings in State of Georgia v. Thaddus Nundra, South Georgia Circuit, 18-CR-134, January 21, 2019, and in State of Georgia v. Monte Baugh and Thaddeus Howell, Coweta County, 2017 R 618, March 11, 2019. See Exhibit D: Coweta County admissibility ruling.

14. GBI analysts have testified in Harper admissibility hearings in State of Georgia v. Alexander Battle, Ben Hill County, 16-CR-082, May 22, 2019, and in State of Georgia v. Guy Sewell, Floyd County, 17-CR-1675 JFL004, August 7, 2019.

15. I testified about low-level DNA mixtures containing four people for the Georgia Innocence Project in Johnny Lee Gates v. State of Georgia in May of 2018. See Exhibit E: Order on defendant's extraordinary motion for new trial.

16. TrueAllele has been extensively validated, and shown to be reliable in over thirty-five validation studies. GBI conducted two of these validation studies. Eight validation studies have been published in peer-reviewed scientific journals. Two of these published articles specifically demonstrated the reliability of TrueAllele analysis on low-level DNA mixtures containing five or more people, as cited next.

17. Perlin et al demonstrated "the reliability of TrueAllele interpretation on complex DNA mixtures of representative casework composition." See Exhibit F: 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.

18. Bauer et al "found that TrueAllele is a reliable method for analyzing DNA mixtures containing up to ten unknown contributors." See: Bauer DW, Butt N, Hornyak JM, Perlin MW. Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors. *Journal of Forensic Sciences*. (in press)

19. Cybergenetics has consulted on over a hundred criminal cases where it has used its TrueAllele technology to develop DNA identification information from handgun evidence. I have personally reviewed these cases.

20. Based on the aforementioned facts, I would conclude that the evidence in this case potentially contains DNA that can be used to help determine the identity of the people who handled the revolver.

This 20th day of September, 2019.

Dr. Mark W. Perlin

Sworn to and subscribed before me this 20 day of September, 2019.

Notary Public

My commission expires: 06/20/2021

COMMONWEALTH OF PENNSYLVANIA
NOTARIAL SEAL
Jason Martin, Notary Public
City of Pittsburgh, Allegheny County
My Commission Expires June 20, 2021
MEMBER, PENNSYLVANIA ASSOCIATION OF NOTARIES

Curriculum Vitae

Mark W. Perlin, PhD, MD, PhD
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

Professional Societies

American Academy of Forensic Sciences
American Society of Human Genetics
American Statistical Association
Duquesne University Forensic Science and Law, Scholar in Residence

Honors and Awards

Innovation Award for Forensic Science, Pittsburgh Business Times, 2017
Pittsburgh Smart 50 Impact Award, Smart Business Magazine, 2017
Solution Provider of the Year: Innovative Technology, Pittsburgh Technology Council, 2017
Paul Chapman Justice Award, Foundation for Improvement of Justice, 2017
Keynote Speaker, International Conference on Forensic Inference and Statistics, 2014
Keynote Speaker, International Conference on Forensic Research and Technology, 2012
Keynote Speaker, Duquesne University Summer Research Symposium, 2010
Keynote Speaker, ACM Symposium on Software Reusability, 2001
Keynote Speaker, SRI Biotechnology Conference, 1997
CUNY Alumnus Achievement Award, 1990
Phi Beta Kappa, 1977
Eagle Scout, 1974
Bausch and Lomb Science Award, 1973

Patents

M. W. Perlin, "Method and system for DNA mixture analysis," U.S. Patent #9,708,642, Jul. 2017
M. W. Perlin, "Method and system for DNA mixture analysis," U.S. Patent #8,898,021, Nov. 2014
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Thesis (2)

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Presentations

M. W. Perlin, "Forensic validation, error, and reporting: a unified approach", *American Academy of Forensic Sciences 71th Annual Meeting*, Baltimore, MD, 2019.

G. Hampikian and M. W. Perlin, "The first five exonerations using TrueAllele® statistical software: how labs can review and correct old cases", *American Academy of Forensic Sciences 71th Annual Meeting*, Baltimore, MD, 2019.

J. Donahue* and M. W. Perlin, "Genotype information criteria for forensic DNA databases", *American Academy of Forensic Sciences 71th Annual Meeting*, Baltimore, MD, 2019.

L. Gumbs, E. Kanal, M. W. Perlin, G. Shannon, "CERT Data Science in Cybersecurity Symposium", Panel, *Software Engineering Institute, Carnegie Mellon University*, Arlington, VA, 2018.

M. W. Perlin, "Solving sexual assault cases using DNA mixture evidence", *National Sexual Assault Kit Initiative (SAKI), National Institute of Justice*, Webinar, 2018.

N. Butt*, D. Bauer* and M. W. Perlin, "Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors", *American Academy of Forensic Sciences 70th Annual Meeting*, Seattle, WA, 2018.

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D. Bauer* and M. W. Perlin, "Validating TrueAllele® genotyping on ten contributor DNA mixtures", *Mid-Atlantic Association of Forensic Scientists Annual Meeting*, Pittsburgh, PA, 2017.

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M. W. Perlin, "Transforming DNA evidence into reliable information: computers, science and society", *Pathology Informatics Summit, Association for Pathology Informatics*, Pittsburgh, PA, 2017.

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M. W. Perlin, W. P. Allan and C. Hughes, "On the threshold of injustice: manipulating DNA evidence", *American Academy of Forensic Sciences 69th Annual Meeting*, New Orleans, LA, 2017.

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M. W. Perlin, "Transparency in DNA evidence", *President's Council of Advisors on Science and Technology (PCAST)*, Washington, DC, 2016.

M. W. Perlin, "Justice denied: Mr. Hopkins invisible semen", *Annual Conference, American Investigative Society of Cold Cases*, St. Louis, MO, 2016.

M. W. Perlin, "Forensic stasis in a world of flux", *Quattrone Center Spring Symposium on Technology in Criminal Justice Reform, Penn Law School*, Philadelphia, PA, 2016.

M. W. Perlin, "DNA investigation: across the universe", *Spring Training Conference, Pennsylvania Homicide Investigators Association,* State College, PA, 2016.

M. W. Perlin, "Overcoming bias in DNA mixture interpretation", Presented by Dr. Ria David at the *American Academy of Forensic Sciences 68th Annual Meeting,* Las Vegas, NV, 2016.

M. W. Perlin and G. Sugimoto, "Separating DNA mixtures by computer to identify and convict a serial rapist", Presented by Dr. David Bauer at the *American Academy of Forensic Sciences 68th Annual Meeting,* Las Vegas, NV, 2016.

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M. Bowkley* and M. W. Perlin, "Compute first, ask questions later: an efficient TrueAllele® workflow", *Midwestern Association of Forensic Scientists 43rd Annual Fall Meeting*, St. Paul, MN, 2014.

J. Hornyak*, W. P. Allan and M. W. Perlin, "TrueAllele® Casework validation on PowerPlex® 21 mixture data", *Twenty Second International Symposium on the Forensic Sciences of the Australia and New Zealand Forensic Science Society (ANZFSS)*, Adelaide, Australia, 2014.

M. W. Perlin, "TrueAllele® interpretation of DNA mixture evidence", Keynote talk, *Ninth International Conference on Forensic Statistics and Inference (ICFIS)*, Leiden, The Netherlands, 2014.

M. W. Perlin, "Solving crimes using MCMC to analyze previously unusable DNA evidence", *American Statistical Association, Joint Statistical Meetings (JSM)*, Boston, MA, 2014.

M. W. Perlin, "Preventing rape in the military through effective DNA computing", *Forensic Europe Expo, Forensic Seminar Theatre*, London, UK, 2014.

M. W. Perlin, "Cracking the DNA mixture code – computer analysis of UK crime cases", *Forensic Europe Expo, Forensic Innovation Conference*, London, UK, 2014.

M. W. Perlin and M. M. Legler, "Coding a safer society through computer interpretation of DNA evidence", *MATLAB Virtual Conference*, Europe and North America, 2014.

M. W. Perlin, "Getting past first Bayes with DNA mixtures", *American Academy of Forensic Sciences 66th Annual Meeting*, Seattle, WA, 2014.

M. W. Perlin, "DNA knowledge, DNA power: how computers interpret evidence", *Cybergenetics Webinar*, Pittsburgh, PA, 2013.

M. W. Perlin, "Unleashing forensic DNA through computer intelligence", *Forensic Europe Expo, Forensic Innovation Conference*, London, UK, 2013.

M. W. Perlin, "Finding truth in DNA mixture evidence", *Innocence Network Conference, Advanced DNA*, Charlotte, NC, 2013.

M. W. Perlin, K. Dormer, J. Hornyak, L. Schiermeier-Wood, and S. Greenspoon, "Virginia TrueAllele® validation study: casework comparison", *American Academy of Forensic Sciences 65th Annual Meeting*, Washington, DC, 2013.

M. W. Perlin, K. Dormer, J. Hornyak, T. Meyers, and W. Lorenz, "How inclusion interpretation of DNA mixture evidence reduces identification information", *American Academy of Forensic Sciences 65th Annual Meeting*, Washington, DC, 2013.

M. W. Perlin, "DNA mapping the crime scene: do computers dream of electric peaks?", *Promega's Twenty Third International Symposium on Human Identification*, Nashville, TN, 2012.

M. W. Perlin, "When good DNA goes bad," *International Conference on Forensic Research and Technology*, Chicago, IL, 2012.

M. W. Perlin, "Forensic thinking, fast and slow," *International Conference on Forensic Research and Technology*, Chicago, IL, 2012.

M. W. Perlin, "The Massereene touch DNA evidence", *Twenty First International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Hobart, Tasmania, 2012. (Talk presented by DCI John McVea of the Police Service of Northern Ireland.)

M. W. Perlin, "Combining DNA evidence for greater match information", *American Academy of Forensic Sciences 64th Annual Meeting*, Atlanta, GA, 2012.

M. W. Perlin, "Investigative DNA databases that preserve identification information", *American Academy of Forensic Sciences 64th Annual Meeting*, Atlanta, GA, 2012.

R. David* and M. W. Perlin, "Creating informative DNA libraries using computer reinterpretation of existing data", *Northeastern Association of Forensic Scientists 2011 Annual Meeting*, Newport, RI, 2011.

J. Ballantyne and M. W. Perlin, "DNA mixture deconvolution by binomial sampling of individual cells", *Eighth International Conference on Forensic Inference and Statistics*, Seattle, WA, 2011.

M. W. Perlin, "Computer interpretation of uncertain DNA evidence", *National Institute of Justice (NIJ) Conference*, Arlington, VA, 2011.

M. W. Perlin, "Taming uncertainty in forensic DNA evidence", *European Network of Forensic Science Institutes (ENFSI) DNA Working Group meeting*, Brussels, Belgium, 2011.

M. W. Perlin, "Sherlock Holmes and the DNA likelihood ratio", *American Academy of Forensic Sciences 63rd Annual Meeting*, Chicago, IL, 2011.

M. W. Perlin, "The science of quantitative DNA mixture interpretation", *Scientific Working Group on DNA Analysis Methods (SWGDAM)*, Fredericksburg, VA, 2011.

M. W. Perlin, "Reliable interpretation of stochastic DNA evidence", *Canadian Society of Forensic Sciences 57th Annual Meeting*, Toronto, ON, 2010.

M. W. Perlin, "Overcoming DNA stochastic effects", *Northeastern Association of Forensic Scientists 2010 Annual Meeting*, Manchester, VT, 2010.

M. W. Perlin, "Inclusion probability is a likelihood ratio: implications for DNA mixtures" (poster), *Promega's Twenty First International Symposium on Human Identification*, San Antonio, TX, 2010.

M. W. Perlin, "Explaining the likelihood ratio in DNA mixture interpretation", *Promega's Twenty First International Symposium on Human Identification*, San Antonio, TX, 2010.

R. David* and M. W. Perlin, "More informative DNA identification: computer reinterpretation of existing data", *Midwestern Association of Forensic Scientists*, Kansas City, MO, 2010.

M. W. Perlin and K. E. Williams, "Preserving DNA information", *National Association of Medical Examiners 2010 Annual Meeting*, Cleveland, OH, 2010.

M. W. Perlin and B. W. Duceman, "Profiles in productivity: greater yield at lower cost with computer DNA interpretation", *Twentieth International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Sydney, Australia, 2010.

M. W. Perlin and M. Greenhalgh, "Scientific combination of DNA evidence: a handgun mixture in eight parts", *Twentieth International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Sydney, Australia, 2010.

M. W. Perlin, "DNA identification science: the search for truth", *Duquesne University 2010 Summer Research Symposium Keynote Address*, Pittsburgh, PA, 2010.

M. W. Perlin, "Statistical computation for forensic DNA evidence", *University of Pittsburgh Department of Human Genetics*, Pittsburgh, PA, 2010.

M. W. Perlin and R. W. Cotton, "Three match statistics, one verdict," *American Academy of Forensic Sciences 62nd Annual Meeting*, Seattle, WA, 2010.

M. W. Perlin and B. W. Duceman, "Casework validation of genetic calculator mixture interpretation," *American Academy of Forensic Sciences 62nd Annual Meeting*, Seattle, WA, 2010.

M. W. Perlin, J. B. Kadane and R. W. Cotton, "A match likelihood ratio for DNA comparison," *American Academy of Forensic Sciences 61st Annual Meeting*, Denver, CO, 2009.

M. W. Perlin, A. Sinelnikov, E. Vey, M. Legler and M. Clarke, "Identifying victim remains from uncertain data," *American Academy of Forensic Sciences 61st Annual Meeting*, Denver, CO, 2009.

M. W. Perlin, J. B. Kadane and R. W. Cotton. "Forensic DNA inference," *Seventh International Conference on Forensic Inference and Statistics*, Lausanne, Switzerland, 2008.

M. W. Perlin, "Exploring forensic scenarios with TrueAllele® mixture automation," *American Academy of Forensic Sciences 59th Annual Meeting*, San Antonio, TX, 2007.

M. W. Perlin, "Scientific validation of mixture interpretation methods," *Promega's Seventeenth International Symposium on Human Identification*. Nashville, TN, 2006.

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M. W. Perlin, "Simple reporting of complex DNA evidence: automated computer interpretation," *Promega's Fourteenth International Symposium on Human Identification*. Phoenix, AZ, 2003.

M. W. Perlin, "Expert systems for automated STR analysis," *Scientific Working Group on DNA Analysis Methods (SWGDAM)*, Quantico, VA, 2003.

M. W. Perlin, "Automated interpretation of forensic STR data," *DNA Forensics Conference, Cambridge Healthtech Institute*. Washington, DC, 2002.

M. W. Perlin, "Automated interpretation of forensic DNA data," *Third Annual DNA Grantees' Workshop, National Institute of Justice (NIJ)*, Washington, DC, 2002.

M. W. Perlin, "Automated interpretation of forensic DNA data," *Attorney General's Initiative on DNA Laboratory Backlogs (AGID-LAB), U.S. Department of Justice*, Washingon, DC, 2002.

M. W. Perlin, D. Coffman, C.A. Crouse, F. Konotop, and J.D Ban, "Automated STR data analysis: validation studies," *Promega's Twelfth International Symposium on Human Identification*. Biloxi, MS, 2001.

M. W. Perlin, "Automating STR analysis," *Federal Bureau of Investigation (FBI), Scientific Working Group on DNA Analysis Methods (SWGDAM)*. Quantico, VA, 2001.

M. W. Perlin, "Automated STR analysis for DNA databases," *Second Annual DNA Grantees' Workshop, National Institute of Justice (NIJ)*, Washington, DC, 2001.

M. W. Perlin, "Automating STR analysis," *Sixth CODIS User's Conference, Federal Bureau of Investigation (FBI)*, Washington, DC, 2001.

M. W. Perlin, "Fully automated computer analysis of forensic STR data," *STR Analysis Workshop, 53rd Annual Meeting of the American Association of Forensic Sciences (AAFS)*, Seattle, WA, 2001.

M. W. Perlin, "An expert system for scoring DNA database profiles," *Promega's Eleventh International Symposium on Human Identification*. Biloxi, MS, 2000.

M. W. Perlin, "Computer automation of STR scoring for forensic databases," *First International Conference on Forensic Human Identification in The Millennium*, London, UK, The Forensic Science Service, 1999.

Courses

Legal Education

M.W. Perlin, "Mining the mixture - a DNA analyst explains", *Judicial Summer Seminars, New York State Judicial Institute,* Rye Brook, NY, June, 2019.

M. W. Perlin, "Probabilistic genotyping in theory and practice," *Brooklyn Defender Services*, Brooklyn, NY, April, 2019.

M. W. Perlin, "Bayesian reasoning for complex DNA evidence," *Quantitative Reasoning in the Law, Northwestern Pritzker School of Law*, Chicago, IL, April, 2019.

M. W. Perlin, "DNA mixtures in sexual assault: evidence and admissibility," *Legal Medicine & Forensic Science, Duquesne University Law School*, Pittsburgh, PA, March, 2019.

M. W. Perlin, "DNA transfer for lawyers," *Allegheny County Courthouse - Continuing Legal Education*, Pittsburgh, PA, February, 2019. (Mock trial panel: W. P. Allan, D. W. Bauer, J. M. Hornyak)

M. W. Perlin and M. J. Machen, "DNA evidence and transfer," *CLE at Beaver County Bar Association,* Beaver, PA, December, 2018.

M. W. Perlin and J. Mulholland, "TrueAllele® preparation and testimony for a Daubert/Harper hearing," *Georgia District Attorneys Association, Fall Meeting*, Athens, GA, November, 2018.

M. W. Perlin, "Daubert in practice," Lecture in *Evidence* class, *Penn State University Law School*, State College, PA, November, 2018.

M. W. Perlin, "Probabilistic genotyping: bad, good & ugly," *Minnesota DNA Defenders,* Minneapolis, MN, October, 2018.

M. W. Perlin, "Probabilistic genotyping to the rescue for Pinkins and Glenn," *Wrongful Conviction Day, Indiana University McKinney School of Law,* Indianapolis, IN, October, 2018.

M. W. Perlin, "DNA science, systems and strategy," *Full day CLE for New York City Legal Aid Society public defenders,* New York, NY, August, 2018.

M. W. Perlin, "TrueAllele® science and court," *Half day CLE for Cuyahoga County prosecutors, with crime lab scientists*, Cleveland, OH, July, 2018.

M. W. Perlin, "TrueAllele for DNA mixtures," *Georgia District Attorneys Association, Spring Meeting*, Savannah, GA, May, 2018.

M. W. Perlin, "Getting away with murder: forensic science and society," *Duquesne University Law School*, Pittsburgh, PA, April, 2018.

M. W. Perlin, "Presenting TrueAllele® evidence in the courtroom," *Twelve hour joint workshop for Baltimore City prosecutors and scientists*, Baltimore, MD, February, 2018.

M. W. Perlin, "Detecting and denying DNA evidence: a history of forensic identification", *Pioneers of Forensic Science, Duquesne University*, Pittsburgh, PA, June, 2017.

M. W. Perlin, "DNA: TrueAllele® statistical analysis, probabilistic genotyping", *Indiana Prosecuting Attorneys Council, IPAC Winter Conference*, Indianapolis, IN, December, 2016.

M. W. Perlin and M. J. Machen, "Forensic failures: the ethics of unfounded science in the courtroom", *Duquesne University Ethics and Eats Seminar*, Pittsburgh, PA, December, 2016.

M. W. Perlin, "Fighting for DNA justice: genotyping software in the Hillary acquittal", *Questioning Forensics: Inside the Black Box, Legal Aid Society*, New York, NY, October, 2016.

M. W. Perlin, "Solving serious crime with TrueAllele technology", *DA Roundtable, Annual Summer Meeting, Pennsylvania District Attorneys Association*, Bedford, PA, July, 2016.

M. W. Perlin, "The probative power of DNA mixtures", *The Balancing Act of Justice, 39th Annual Conference, Louisiana District Attorneys Association*, Destin, FL, June, 2016.

M. W. Perlin, "How to defend yourself against DNA mixtures", *National Forensic College, National Association of Criminal Defense Lawyers*, Cardozo School of Law, New York, NY, June, 2016.

M. W. Perlin, "Issues with DNA evidence, past and future", *Washington County Bar Association*, Washington, PA, March, 2016.

M. W. Perlin, "Understanding DNA evidence", *Beaver County Courthouse*, Beaver, PA, March, 2016.

M. W. Perlin, "Understanding complex DNA evidence", *New York Legal Aid Society*, New York, NY, March, 2016.

M. W. Perlin, "Understanding DNA", *Pennsylvania Conference of State Trial Judges*, Philadelphia, PA, February, 2016.

M. W. Perlin, "DNA mixture evidence", *Penn State University Dickinson Law School*, State College, PA, February, 2016.

M. W. Perlin, "Mix & match: getting comfortable with DNA reporting", *Duquesne University Forensic Fridays*, Pittsburgh, PA, October, 2015.

M. W. Perlin. "Cutting edge DNA strategies", *Forensic Science and Criminal Law, Pennsylvania Association of Criminal Defense Lawyers*, Pittsburgh, PA, September, 2015.

M. W. Perlin, "Challenging DNA Evidence", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, February, 2015.

M. W. Perlin, "Shedding light on inconclusive DNA: TrueAllele® computer analysis", *Office of the Onondaga County District Attorney*, Syracuse, NY, November, 2014.

M. W. Perlin, "TrueAllele computing: all the DNA, all the time", *NSW Office of the Director of Public Prosecutions, Continuing Professional Development*, Sydney, Australia, March, 2014.

M. W. Perlin. "TrueAllele® interpretation of Allegheny County DNA mixtures", *Allegheny County Courthouse, Continuing Legal Education,* Pittsburgh, PA, February, 2014.

M. W. Perlin, "No DNA left behind: when 'inconclusive' really means 'informative'", *Office of the Schenectady County District Attorney,* Schenectady, NY, January, 2014.

M. W. Perlin, "Understanding DNA mixtures" & "How to convict an innocent man using DNA mixtures" *DNA in the 21st Century, New Jersey Office of the Public Defender,* Trenton, NJ, October, 2013.

J. Butler, A. Mitchell, M. W. Perlin, A. M. Schubert, J. Friedman and J. Spriggs, "DNA mixture interpretations and statistics – to include or exclude", *Prescription for Criminal Justice Forensics, American Bar Association Criminal Justice Section,* New York, NY, June, 2013.

M. W. Perlin, "DNA mixture statistics", *Virginia Spring Institute, Commonwealth's Attorneys' Services Council,* Richmond, VA, March, 2013.

G. Hampikian, V. Weedn, M. W. Perlin, A. Blumstein, J. Rangos, K. Mains, L. Irwin, A. Adepoju and W. Oliver, "Whose DNA is it anyway?", *Duquesne University Forensic Fridays, Continuing Legal Education Program on DNA Access*, Pittsburgh, PA, March, 2013.

M. W. Perlin, "Reanimating Zombie™ DNA", *Penn State Dickinson Law School*, State College, PA, September, 2012.

M. W. Perlin, "DNA evidence: computer interpretation, case investigation and court presentation", *Kern County District Attorney's Office, Continuing Legal Education*, Bakersfield, CA, April, 2012.

M. W. Perlin, J. Galloway and M. Agnew, "Investigation and trial in the Massereene case", *Police, Public Prosecution and Forensic Services of Northern Ireland, Continuing Professional Development*, Belfast, Northern Ireland, March, 2012.

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Effect of common fingerprint detection techniques on subsequent STR profiling

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ABSTRACT

DNA profiling of latent fingerprints can be compromised by fingerprint detection techniques. We found that cyanoacrylate (CA) fuming and/or vacuum metal deposition (VMD) did not affect subsequent STR typing. Treatments that involved washing steps like basic yellow or safranin staining reduced DNA quantities. Methods that rely on immersion of items like 1,8-diaza-9-fluorenone (DFO) and ninhydrin staining were found to present the risk of introducing DNA contamination from the staining solution even though the fingerprint DNA was not negatively affected. The use of physical developer was deleterious for the DNA results. When items are handled before a fingerprint is placed, contaminating alleles occur at the fingerprint area. The fingerprint DNA can outstand this background, but due to the large variation for DNA quantities in fingerprints this is not certain and cautious interpretation is appropriate.

1. Introduction

Both fingerprints and DNA are used as individualizing evidence. Fingerprints cannot be analyzed when prints are badly smudged or distorted but the DNA present in these prints can provide individualizing information. Latent fingerprints have been reported to contain enough DNA for a genetic analysis [1,2]. In the forensic process, the dactyloscopic methods generally precede DNA typing, and it is relevant to study the effects of fingerprint enhancement methods on subsequent DNA profiling [2]. Since the amount of DNA in a latent fingerprint varies tremendously [1,2] an experimental design that allows comparison of treated and untreated fingerprints is imperative. Furthermore, a distinction between alleles of the fingerprint donor and alleles of other donors is appropriate as DNA contamination may arise from various.

2. Materials and methods

Probands placed fingerprints by pressing fingers of unwashed hands during 60 s on chlorine-free paper or plastic sheets which had been irradiated for 30 min in an UV-crosslinker to remove contaminating DNA. Fingerprint enhancement techniques involved CA fuming (fumed for 10 min at 80% humidity and 120 °C) enhanced by basic yellow or safranin staining, VMD (vacuum $<1 \times 10^{-4}$ mbar), DFO (with evaporation for 30 min at 100 °C) and ninhydrin (with evaporation for 30 min at 70 °C) and physical developer (maleic acid pre-wash, silver nitrate solution, reductant solution).

For QIAamp-based DNA isolation (Qiagen; standard protocol), fingerprint areas are cut into fragments. Standard profiling uses 5 μl of the 100 μl extract. Alternatively, full extracts were concentrated (to 10 μl) by standard ethanol (EtOH) precipitation using 1 μl GlycoBlue™ (Ambion) as coprecipitant. For STR profiling the AmpFlSTR SGM Plus kit (Applied Biosystems) was used. Rfu values complying with donor alleles at all 11 loci were summed, and analyzed with a Grubbs test ($P < 0.05$) to remove significant outliers. A fingerprint detection technique was regarded harmful for subsequent DNA analysis when the average rfu values at D3S1358, D8S1179 and FGA were 50% or less for the treated halves than that for the untreated halves.

3. Results and discussion

For 12 different donors we examined the sampling area of latent hand- and fingerprints that is needed to obtain an informative STR profile. Standard DNA profiling (in which 1/20th of the extract is analyzed) does not yield full donor profiles, even when full handprints are used. However, when the full extract is analyzed (which is achieved by EtOH precipitation of the DNA extract), a single fingerprint suffices to obtain a full or nearly full donor profiles for some donors (Table 1). In these profiles both the number and the peak heights of contaminating non-donor alleles are low (results not shown).

To assay the effects of fingerprint enhancement techniques on subsequent DNA analyses we decided on the following approach: new fingerprints of a donor whose fingerprints constitutively gave positive DNA typing results, were cut in halves after which one half

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Table 1
STR typing results for various fingerprint sampling areas in fingerprints of 12 different donors.

Fingerprint	Procedure	Full profile	Nearly full profile	Partial profile	No profile
1 Finger	Standard	0/12	0/12	6/12	6/12
4 Fingers	Standard	0/12	1/12	7/12	4/12
Full hand	Standard	0/12	3/12	9/12	0/12
1 Finger	EtOH precipitation	2/12	1/12	8/12	1/12

Table 2
Effect of fingerprint detection techniques on subsequent STR profiling.

Method	Reaction to	Application	Surface	*n*	>50% decrease rfu donor alleles	Contaminating alleles in 'no fingerprint' blanks
CA fuming	Eccrine sweat & sebum	Fume	Plastic	9	No	No
VMD	Layers gold & zinc	Under vacuum	Plastic	9	No	No
CA & VMD	Combination	Fume & vacuum	Plastic	9	No	No
CA & safranin	Enhance CA staining	Spray & wash	Plastic	7	Yes	No
CA & basic yellow	Enhance CA staining	Spray & wash	Plastic	10	Yes	No
CA & water washes	–	Wash	Plastic	10	Yes	No
Ninhydrin	Amino acids in eccrine	Immerse, dry & heat	Paper	9	No	Yes
DFO	Amino acids in eccrine	Immerse, dry & heat	Paper	9	No	Yes
Physical developer	Sebum components	Maleic acid, immerse & wash	Paper	9	Yes	No

Table 3
Number and average peak height (PH) of detected donor and non-donor alleles in fingerprints of out selected donor on 20 previously touched items.

Fingerprint	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
# Donor	22	22	22	22	22	22	22	22	22	22	22	22	20	20	19	19	18	18	12	8
# Non-donor	28	18	20	19	9	6	11	11	9	8	23	5	12	4	4	6	6	4	11	9
PH donor	6229	5703	556	374	343	323	319	283	260	226	209	157	152	149	152	111	158	115	103	168
PH non-donor	671	115	210	246	116	70	81	90	198	83	94	80	127	72	64	98	94	106	80	87

was left untreated and the other half was treated with seven different reagents (Table 2). CA fuming and VMD (and the combination of both) did not affect subsequent DNA profiling (Table 2). However, when CA fuming was combined with safranin or basic yellow staining less donor DNA was retrieved. This reduction appears related to the wash step that is used to remove the surplus of stain, as a similar reduction is seen when CA fuming is combined with water washes (Table 2). Ninhydrin or DFO treatment did not affect subsequent DNA profiling. However, blanks (paper sheet immersed in ninhydrin or DFO solution either before or after immersing the series of fingerprints) showed contaminating alleles (10–15 peaks with rfu values up to 150). These alleles did not correspond to the fingerprint donor, which suggests that the staining solutions are susceptible to contamination. Precautions to minimize DNA contamination (*e.g.*, freshly prepared solutions) are recommended when using ninhydrin or DFO to-stain fingerprints that are subjected to DNA analysis. Physical developer was found to be deleterious for DNA profiling (Table 2), which is most likely due to the pre-wash with maleic acid. In many DNA profiles (also from untreated fingerprints halves), non-donor alleles were observed that probably originate from non-donor cell material residing on the hands of the proband as DNA had been cleared from the surfaces by UV-irradiation.

In real casework, surfaces may also contain cell material especially when items have been touched. Therefore, plastic items were touched by several persons after which the proband placed fingerprints at indicated areas. After CA fuming, the full fingerprint areas were collected and subjected to STR typing using the EtOH-precipitated full DNA extract as PCR input. For 12 of the 20 recovered fingerprints full donor profiles were obtained for which the average peak height varied from 6629 to 157 rfu (Table 3). For all 20 fingerprints non-donor alleles were observed, the number varied from 4 to 28. In one profile (Table 3, fingerprint 1) the number of non-donor alleles outnumbered the donor's (even without considering allele sharing). For some profiles non-donor alleles were substantially lower than donor peaks (Table 3, fingerprints 1–3), but for several profiles the non-donor peaks had similar peak heights (Table 3, fingerprints 16, 18 and 19). Our proband was selected because of consistent positive profiling results from his latent fingerprints, but the majority of the donors we tested appeared to leave much less DNA in their fingerprints. Consequently, we infer that caution is needed when STR profiles of fingerprints are interpreted, as contaminating alleles may be difficult to distinguish from donor alleles.

4. Concluding remarks

Full STR profiles can be obtained from a single latent fingerprint also after application of various fingerprint enhancement techniques (*e.g.*, CA fuming, VMD). We did not sensitize STR typing by applying low template techniques, but we did use the full DNA extract in a single amplification. Large variation in fingerprint DNA quantity was observed between donors and more variation can occur depending on length and intensity of the contact, the surface or the presence of body fluids. Non-donor alleles were observed that appear to have several origins like the hands of the donor, the use of a touched surface and fingerprint detection solutions like DFO or ninhydrin. Therefore, STR typing of fingerprints detected by various enhancement techniques is not a guaranteed success and the risks of DNA contamination should be taken into account when interpreting the typing results.

Conflict of interest

None.

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TECHNICAL NOTE

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Effects of Cyanoacrylate Fuming, Time After Recovery, and Location of Biological Material on the Recovery and Analysis of DNA from Post-Blast Pipe Bomb Fragments*

ABSTRACT: This study investigated the effects of time, cyanoacrylate fuming, and location of the biological material on DNA analysis of post-blast pipe bomb fragments. Multiple aliquots of a cell suspension (prepared by soaking buccal swabs in water) were deposited on components of the devices prior to assembly. The pipe bombs were then deflagrated and the fragments recovered. Fragments from half of the devices were cyanoacrylate fumed. The cell spots on the fragments were swabbed and polymerase chain reaction/short tandem repeat analysis was performed 1 week and 3 months after deflagration. A significant decrease in the amount of DNA recovered was observed between samples collected and analyzed within 1 week compared with the samples collected and analyzed 3 months after deflagration. Cyanoacrylate fuming did not have a measurable effect on the success of the DNA analysis at either time point. Greater quantities of DNA were recovered from the pipe nipples than the end caps. Undeflagrated controls showed that the majority (>95%) of the DNA deposited on the devices was not recovered at a week or 3 months.

KEYWORDS: forensic science, DNA typing, polymerase chain reaction, Identifiler®, pipe bomb, cyanoacrylate fuming

A pipe bomb is a fairly simple form of an improvised explosive device. The basic components of the device (pipe nipple, end caps, black powder, and fuse) are readily available at common hardware stores and hobby shops. Approximately 3000 pipe bomb investigations were reported to the Bureau of Alcohol, Tobacco, Firearms and Explosives (ATF) over the last 10 years (ATF database). If the device is detected prior to deflagration, the device can be rendered safe through several means which leave any physical evidence relatively unharmed. In some instances, the only way to render the device safe is to cause the deflagration of it in a controlled manner. After a device is deflagrated, in a controlled or uncontrolled manner, any physical evidence that was on the device has now been subjected to extreme insults including exposure to high temperatures and the products of combustion, in addition to any other environmental insults.

In the past, the investigation of a pipe bomb incident involved several types of examinations within the laboratory, including the latent fingerprint, tool marks, and explosive residue examinations, but typically not DNA analysis. As knowledge and technology have improved in the collection, extraction, amplification, and typing of biological material, the range of evidence potentially suitable for DNA analysis has expanded to include touch evidence (1–3). It was hoped that new DNA technologies would enable the DNA section to aid in the investigation of these cases by potentially identifying the maker of the device through the analysis of the biological material transferred to the components during its assembly. The feasibility of this was demonstrated previously by Esslinger et al. (4). In that study, the pipe bomb components were handled by individuals prior to the deflagration. After deflagration, the fragments were recovered and short tandem repeat (STR) DNA analysis was performed. A full profile and multiple partial profiles were obtained.

Once it was determined that DNA of sufficient quantity and quality survived on post-blast pipe bomb fragments, it was important to investigate several practical aspects of the analysis. In this study, the following factors were investigated: time between the deflagration of the device and DNA analysis, cyanoacrylate fuming of the fragments soon after deflagration, and the location of the biological material on the device.

Most disciplines within the crime laboratory have significant backlogs and the DNA analysis section is typically no different. These backlogs can cause delays in the analysis of evidence for months. For dried blood or other biological evidence, this delay will have little to no effect on the success of the DNA analysis. It is unknown, however, what effect, if any, time has on the DNA analysis of post-blast bomb fragments that have been subjected to a different set of environmental insults. In addition to extreme heat, the DNA is also potentially exposed to the products of combustion which have unknown effects. If it is determined that the DNA is significantly degraded over time, then it may be necessary to prioritize pipe bomb cases to reduce the amount of time between the device deflagration and the DNA analysis of the collected fragments.

Latent print examination and DNA analysis are frequently requested on the same items of evidence. The effects of most of the common latent print chemicals have been investigated and have been found to have little to no detrimental effect on the DNA analysis (5,6). Recently though, cyanoacrylate fuming has been found to decrease the amount of DNA recovered from latent fingerprints (7). However, the differences in these results might be because of

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the different cyanoacrylate fuming methods used in each of the studies. To prevent damage or obliteration of latent fingerprints on items of evidence that may occur during transport or subsequent handling, the ATF Laboratory encourages its agents to cyanoacrylate fume evidence in the field, when practical. For the purposes of this investigation, it was hypothesized that cyanoacrylate fuming may protect the biological material deposited on the post-blast fragments by preventing the biological material from being scraped off and creating a barrier, thus preventing the products of combustion or other substances in the environment from degrading the DNA.

During the manufacture of the device, both of the main components of the device, the pipe nipple and the end caps, potentially may be handled by the individual. At the time of deflagration, the propellant contained within the sealed device burns rapidly and builds up extreme pressure to the point that exceeds the structural limits of one or more components of the device. The pressure built up in the device can be relieved in several ways (see Fig. 1). The end caps may be fragmented, the pipe nipple may rupture, or a combination of both can occur. The heat generated by the burning of the black powder inside the device will be transferred to the components. The "maximum temperature of explosion" for black powder is *c.* 2380°C (8). Similar temperatures would be expected for the powders used in this study. How much of the thermal energy reaches the outer surfaces of the device components is unknown, however. Because the biological material spotted on the sides of the end caps has two layers of metal between the surface and the interior of the device (threaded portion of the pipe nipple and the side wall of the end cap), it was thought that biological material on the outer surface of the pipe nipple would be subjected to greater temperatures because of the conductivity of the metal than material on the sides of the end caps. On the other hand, the end caps may demonstrate greater fragmentation and physical abrasion as a result of the deflagration. The proximity of the biological material to the point of rupture and thus release of the heated gases may affect the DNA more than the heat conducted through the pipe. This study compares the success of DNA typing on biological material deposited on the sides of the end caps and the pipe nipples to determine which components are more likely to be useful for DNA analysis.

Methods

To perform this study, six pipe bombs were assembled. The components (pipe nipple and end caps) for devices were purchased at a local hardware store. A ¼″ hole was drilled in the top of one end cap of each device to insert the fuse. The pipe nipples, 1″ × 8″ galvanized steel, and associated end caps were cleaned with 10% bleach (0.615% sodium hypochlorite) and then rinsed with 70% ethanol.

To deposit cells and thus DNA on the devices, Esslinger et al. (4) attempted to create a real world pipe bomb event by having individuals handle the components. Because a wide variation in the amount of cellular material deposited on an item by a single person or between persons during handling has been observed (9), in this study, a cell suspension was used to ensure a consistent amount of biological material on each of the areas analyzed. This protocol allows for a more direct examination of the effects of the deflagration without the variability in the initial quantity of DNA present. Two buccal swabs were collected from a female individual not involved in the study to create a cell suspension. The swab heads were placed in a 1.5 mL centrifuge tube with 1 mL of nuclease-free water and vortexed for 10 sec. The swab heads were removed and the tube was centrifuged at 12,500 × *g* for 3 min to pellet the cells. The supernatant was removed and the cells were resuspended in 1 mL of nuclease-free water. This process was repeated a second time to wash the cells. Finally, the cells were suspended in 1 mL of nuclease-free water. An approximate cell count was performed by microscopically counting the cells in three 2 µL spots and using the average. The cell concentration was estimated at 1000 cells per 2 µL. Six 10 µL aliquots of the cell suspension (*c.* 30 ng of DNA) were deposited on each of the end caps and pipe nipples in spots circled by an indelible marker to allow for easy post-blast collection of the cell spots. The cell spots were allowed to dry at room temperature overnight. Two control pipe nipples and end caps, not to be deflagrated, were prepared in a similar manner and transported with the rest of the devices. One set of components was to be cyanoacrylate fumed, the other was to be left untreated. Unfortunately, the control components were lost at the explosive range.

The actual assembly of the devices was performed immediately before deflagration by ATF explosive enforcement officers at the National Center for Explosives Training and Research at Fort AP Hill in Virginia. The officers wore latex gloves during the assembly process. Three different black powder substitutes were used in the devices: GOEX Pinnacle Powder™ (GOEX Powder, Dayline, LA) was used in devices 1 and 2; Jim Shockey's Gold Powder™ (American Pioneer Powder, Inc., Boca Raton, FL) was used in devices 4 and 5; and Triple 7 Powder™ (Hodgdon, Shawnee Mission, KS) was used in devices 7 and 8. Devices 3 and 6 were not used for this study. The devices were deflagrated in a manner to maximize the recovery of the pipe bomb fragments while maintaining at least some of the cell spots. In previous attempts, the pipe bombs were buried in sand and then deflagrated, which is the typical method employed to recover fragments for studies involving explosive residue testing. No DNA was recovered from any of the fragments recovered. It was thought that the physical abrasion on the surface of the fragments removed most, if not all, of the

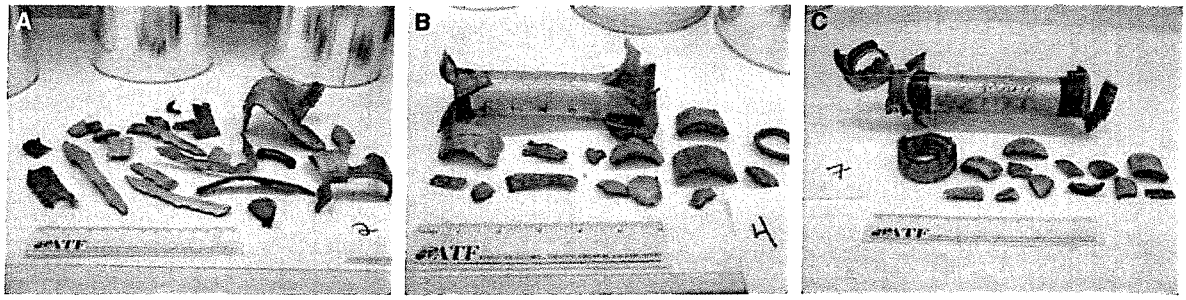

FIG. 1—*Fragments collected from three of the devices post-blast. Different levels of fragmentation were observed depending on the brand of powder used in the device. The circles marking the areas where cell spots were deposited can be seen on some fragments. (A) Device #2, Go Ex Pinnacle, (B) Device #4, Jim Shockey's Gold, and (C) Device #7, Triple 7.*

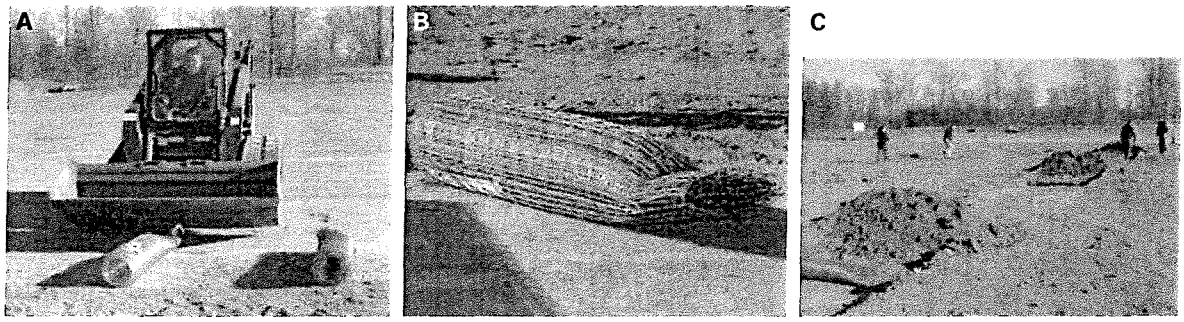

FIG. 2—*Demonstration of how the devices were prepared to prevent cross-contamination of fragments and maximize the number of fragments collected. (A and B) The rolls of wire fencing were crimped on one end and (C) the rolls of wire fencing were placed in 2–3 foot deep trenches.*

biological material. In this study, a roll of wire fencing was crimped on one end (see Fig. 2) and the rolls were placed in individual trenches measuring *c.* 2–3 feet in depth. Each assembled device was then placed in the center of a roll of wire fencing. Pyrotechnic fuses and double primed electric matches were used to initiate the deflagration.

The fragments from each device were then collected by individuals wearing latex gloves and placed in individual metal paint cans. Fragments from the devices were found lying in the trench, embedded in the sides of the trench, and caught in various layers of the roll of wire fencing (see Fig. 3). The fragmentation of the devices varied depending on the type of powder used. For example, devices 1 and 2 resulted in extensive fragmentation of the pipe nipples as well as the end caps. In contrast, essentially only the end caps fragmented for the other devices. While the comparison of the fragmentation of the devices depending on the powder used was not an original intention of the study, the resulting fragmentation may have an effect on the DNA typing success.

The fragments were then transported to the laboratory for examination. The following day, the fragments from devices 2, 5, and 8 were cyanoacrylate fumed following the standard protocol used at the ATF Laboratory. The fragments were placed in a Foster and Freeman (Sterling, VA) MVC 3000 chamber set at 75% relative humidity. The process is comprised of the following steps: a 12-min humidifying cycle, a 10-min step in which the glue is heated at 120°C, and a final purge of 20 min.

The fragments were stored over the weekend at room temperature. The biological material from two cell spots from the fragments of the end caps and the pipe nipples of each device was collected on the tips of cotton swabs using the double swab technique (10) for four pairs of swabs per device for the initial analysis. Cell spots with obvious physical abrasions were avoided as were cell spots within scorched areas. The tips of each pair of swabs were cut into a single 2 mL centrifuge tube. By collecting the biological material on the tips of the swabs and only cutting off the relevant portion of the swabs, the volume of lysis buffer was sufficient to completely cover the swab material. Additionally, this protocol minimized the amount of swab material which may trap the cells, and therefore the DNA, during extraction process. The DNA was extracted and purified utilizing a slightly modified Qiagen QIAamp® DNA Micro Forensic Sample protocol (11). The swabs were incubated in 400 μL of Qiagen Buffer ATL and 20 μL of Proteinase K (20 mg/mL; Invitrogen, Carlsbad, CA) overnight at 56°C in a thermal mixer (Eppendorf, Westbury, NY) rotating at 900 rpm. The following day, 400 μL of Qiagen Buffer AL and 1 μg of carrier RNA (12) were added to the tubes. The tubes were vortexed for 15 sec and then incubated at 70°C in the thermal mixer rotating at 900 rpm for 10 min. The swab tips were then transferred to a SpinEze™ basket (Fitzco, Spring Park, MN) and the basket replaced in the tube. The tubes were centrifuged for 3 min at 12,500 × *g* to collect any lysate remaining in the swab tips. After centrifugation, the basket and swab tips were discarded and the lysate was transferred to the top of a Qiagen QIAamp® DNA Micro column. The lysate was passed through the column's membrane by centrifugation at 6000 × *g* for 1 min. The DNA bound to the membrane was washed with 500 μL of Qiagen Buffer AW1 and then 500 μL of Qiagen Buffer AW2. The membrane was then dried by centrifuging the columns at maximum speed for 3 min. The DNA was eluted with two 50 μL volumes of TE^{-4} (10 mM Tris–HCl, pH 8, and 0.1 mM EDTA) collected by incubation at room temperature for 5 min and then centrifugation at 13,500 × *g* for 1 min. The final elution volume of 100 μL was then concentrated down to *c.* 30 μL using a Microcon 100 filtration unit (Millipore, Billerica, MA). This was accomplished by

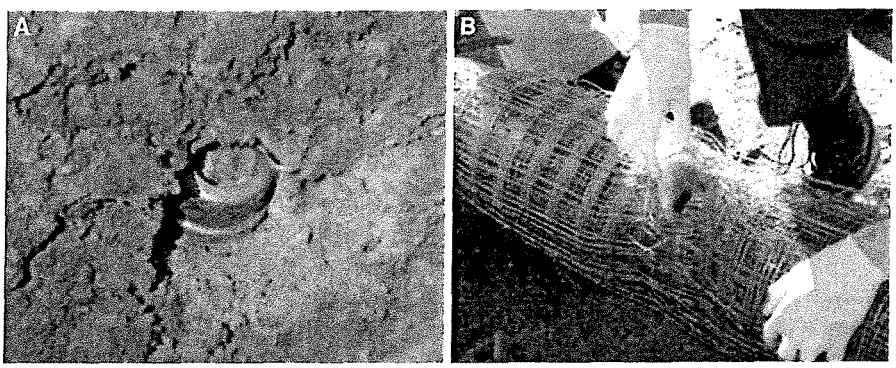

FIG. 3—*Collection of the post-blast fragments. (A) Portion of an end cap embedded in the wall of the trench and (B) portion of the pipe nipple protruding from the roll of fencing.*

transferring the 100 μL elution volume to the top of the Microcon filtration unit and centrifuging the device for *c.* 12 min at 500 × *g*. Prior to inverting the filtration unit into a centrifuge tube, 20 μL of TE^{-4} was added to the top reservoir. The final DNA extract was collected by centrifuging the device at 1000 × *g* for 3 min. The volumes of each sample were measured and then brought up to *c.* 30 μL by adding the necessary volume of TE^{-4}.

The concentration of DNA was determined by using the Applied Biosystems (AB) Quantifiler™ Human DNA Quantification Kit and the AB 7500 Real-Time Polymerase Chain Reaction (PCR) System (Foster City, CA). STR DNA analysis was performed using the AB AmpF/STR® Identifiler® Amplification Kit (AB) and the AB GeneAmp® PCR System 9700 (AB) following manufacturer's recommended cycling parameters: an initial incubation step of 95°C for 11 min; then, 94°C for 1 min, 59°C for 1 min, and 72°C for 1 min (28 cycles); and a final extension incubation at 60°C for 60 min. The following loci are amplified using the Identifiler® Amplification Kit: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA, and the gender determining locus Amelogenin. Fragment analysis was performed on the AB 3130 Genetic Analyzer with GeneMapper™ ID software (AB). The following parameters were used: 1 μL of amplified product mixed with 8.7 μL of Hi-Di™ formamide and 0.3 μL of GeneScan™–500 LIZ™, 3 min denaturation at 95°C, 3 min snap-cooling, and a 3 kV 5 sec injection. The analytical threshold for allele peak height detection is set at 50 RFU.

After the initial analysis, the process was repeated *c.* 3 months later to compare the DNA yield and DNA typing success. The pipe bomb fragments were stored in the paint cans in which they were collected at room temperature during the time interval. A total of 24 DNA samples were analyzed at each time point. Half of these samples were collected from fragments that had been cyanoacrylate fumed.

Results and Discussion

The first objective of this study was to investigate the effect of time on the success of DNA analysis on post-blast pipe bomb fragments. The results of this study indicate that the amount of DNA recovered from post-blast bomb fragments is a fraction of the initial amount of DNA deposited. In addition, the quantity of DNA recovered decreases greatly as time passes (see Tables 1 and 2). Assuming the rough approximation of the cell suspension concentration is close to 5000 cells and therefore 30 ng of DNA, on average only about 10–15% of the DNA from the end caps and 30–35% of the DNA from the pipe nipples was recovered after 1 week. The average concentration of DNA recovered from the end caps and the pipe nipples 3 months after deflagration was roughly an order of magnitude less than the concentration of DNA recovered within a week of the deflagration. In most cases, forensic laboratories do not have a 1 week turnaround time on routine cases. These results demonstrate that cases involving the analysis of post-blast pipe bomb fragments should be prioritized to minimize the loss of DNA.

Unfortunately, the control pipes for this study were lost. However, the control samples from a subsequent similar study provide valuable additional information (Table 3). Cells were spotted on both PVC and galvanized steel pipe nipples. The control samples were prepared following the same protocol except a smaller amount of cells was spotted. After 1 week, the DNA recovered from the cell spots on the PVC pipe was *c.* 5% of the amount of DNA recovered from the same volume of the cell suspension. The quantity of DNA recovered from the steel pipe cell spots was even lower at 1.7%. At the 3-month time point, the quantity of DNA recovered from the PVC cell spots was approximately the same as the quantity recovered at the 1-week time point. The DNA recovery from the steel pipe nipples at the 3-month time point was *c.* 50% compared with the 1-week time point. The cell spots dried on a different substrate from this study (the adhesive surface of electrical tape) demonstrated little to no loss after 1 week (data not shown). After 3 months, the decrease in recovery ranged from 10% to 50%. This data would suggest that a main factor causing the initial dramatic decrease observed in the amount of DNA recovered from the post-blast fragments is the ability to remove the cells from the surface of the pipe nipple or end cap. Another contributing factor to the loss of DNA could be the efficiency of the recovery of DNA from the swabs during the extraction process. The 90% loss of DNA from the 1-week to 3-month time point in the post-blast samples might be partially because of an increased difficulty in removing the cells from the surface of the components, but there appear to be other factors affecting the amount of DNA recovered also. From the control samples, there is no evidence that normal

TABLE 1—*DNA recovery from pipe bomb fragments 1 week after deflagration.*

	DNA Recovery 1 Week Post-Deflagration					
	Not Cyanoacrylate Fumed			Cyanoacrylate Fumed		
	Device	Sample Name	Quantity* (ng/μL)	Device	Sample Name	Quantity* (ng/μL)
End Cap	1	1E1	0.000	2	2E7	0.290
	1	1E2	0.335	2	2E8	0.309
	4	4E3	0.018	5	5E9	0.101
	4	4E4	0.185	5	5E10	0.000
	7	7E5	0.002	8	8E11	0.000
	7	7E6	0.244	8	8E12	0.230
Average			0.131			0.155
SD			0.144			0.140
Pipe Nipple	1	1P1	0.088	2	2P8	0.279
	1	1P2	0.107	2	2P9	0.285
	4	4P3	0.586	5	5P10	0.433
	4	4P4	0.463	5	5P11	0.394
	7	7P6	0.408	8	8P12	0.261
	7	7P7	0.373	8	8P13	0.229
Average			0.338			0.314
SD			0.200			0.081

*The final volume for all DNA extracts is 30 μL.

TABLE 2—*DNA recovery from pipe bomb fragments 3 months after deflagration.*

	DNA Recovery 3 Months Post-Deflagration					
	Not Cyanoacrylate Fumed			Cyanoacrylate Fumed		
	Device	Sample Name	Quantity* (ng/μL)	Device	Sample Name	Quantity* (ng/μL)
End Cap	1	1E13	0.013	2	2E15	0.000
	1	1E14	0.006	2	2E16	0.000
	4	4E17	0.003	5	5E19	0.034
	4	4E18	0.009	5	5E20	0.052
	7	7E21	0.045	8	8E23	0.000
	7	7E22	0.040	8	8E24	0.000
Average			0.019			0.014
SD			0.018			0.023
Pipe Nipple	1	1P14	0.027	2	2P16	0.043
	1	1P15	0.006	2	2P17	0.042
	4	4P18	0.050	5	5P20	0.041
	4	4P19	0.079	5	5P21	0.044
	7	7P22	0.021	8	8P24	0.031
	7	7P23	0.043	8	8P25	0.077
Average			0.038			0.046
SD			0.026			0.016

*The final volume for all DNA extracts is 30 μL.

TABLE 3—*DNA recovery from undeflagrated control pipes (PVC and steel) 1 week and 3 months after cell deposition.*

Sample Name	1 Week Total DNA (ng)	3 Months Total DNA (ng)
Control pipe-PVC 1	0.174	0.135
Control pipe-PVC 2	0.163	0.280
Control pipe-PVC 3	0.177	0.158
Average-PVC	0.171	0.191
Control pipe-steel 1	0.067	0.023
Control pipe-steel 2	0.018	0.036
Control pipe-steel 3	0.078	0.024
Average-steel	0.055	0.028
Cell suspension-1	3.360	3.680
Cell suspension-2	3.700	3.690
Cell suspension-3	2.350	2.770
Average-cell suspension	3.137	3.380

A different cell suspension with a reduced cell concentration was used in the making of the control samples compared with the test samples. Quantitation results for the DNA extraction from the same volume of the cell suspension are provided, as well.

degradation of the DNA over time accounts for the additional loss of DNA. The electropherograms do not demonstrate the typical downward slope attributed to DNA degradation on either the post-blast fragments or the control samples.

In most cases in which DNA analysis is requested, other forensic examinations are requested as well. In these instances, it is necessary to determine an order of analysis which allows each discipline to conduct its testing without altering the evidence to the point that precludes testing by the remaining disciplines. Because the collection of biological material usually involves the swabbing of the substrate which would obliterate any latent prints, cyanoacrylate fuming is routinely performed prior to DNA analysis. In this study, it was hypothesized that the cyanoacrylate fuming may actually have a beneficial effect on the DNA analysis by protecting the biological material in two ways. First, the cyanoacrylate may prevent the biological material from being scraped off during transport or normal handling of the containers in which the fragments are stored. Second, the cyanoacrylate layer would prevent the products of combustion present on the fragments from reacting with moisture in the air over the course of time during storage. In this case, the fragments were already transported to the laboratory before the cyanoacrylate fuming was performed. There was, however, routine handling of the containers after the fuming occurred. The DNA concentrations recovered from the cyanoacrylate fumed fragments and the untreated fragments of the end caps are similar. This holds true for the fragments of the pipe nipples, as well. It should be noted that the sensitivity limit of the quantitation method used is *c.* 9 pg/μL and the precision is decreased at this concentration of DNA (e.g., 1 SD is approximately half of the target value). Any possible "protective" effect conveyed by the cyanoacrylate fuming would be expected to be most noticeable at the 3-month time point. The average DNA quantitation results again demonstrate similar DNA recoveries for each set of samples (see Tables 1 and 2). Four of the six fumed end cap samples did not yield any detectable DNA while several of the nonfumed samples demonstrated low concentrations of DNA (<10 pg of DNA/μL). Therefore, the cyanoacrylate fuming of the evidence did not demonstrate any protective qualities. A paper published after this study was performed may explain, in part, why no protective qualities were observed. Wargacki et al. (13) demonstrated that the cyanoacrylate layer deposited on the surface can actually be porous. Therefore, water or other molecules in the environment would still have access to the products of combustion and the biological material. There is also no conclusive evidence that cyanoacrylate fuming had a detrimental effect on the success of DNA analysis as has been reported previously (7). Although, as noted earlier, any difference in results when compared with other studies might be because of differences in the cyanoacrylate fuming methods used, which may result in varying amounts of cyanoacrylate deposition. As demonstrated by Pitilertpanya et al. (7), heavier deposition of cyanoacrylate decreased the subsequent DNA typing results. For example, better typing results were obtained from samples fumed for 20–30 min compared with those fumed for 40 min. Other factors, such as the glue heating temperature and the size of the fuming chamber, can significantly affect the amount of cyanoacrylate deposition. Some laboratories (7,14) have investigated replacing water or saline with acetone to moisten the swab used to collect biological material from cyanoacrylate fumed items, because of its

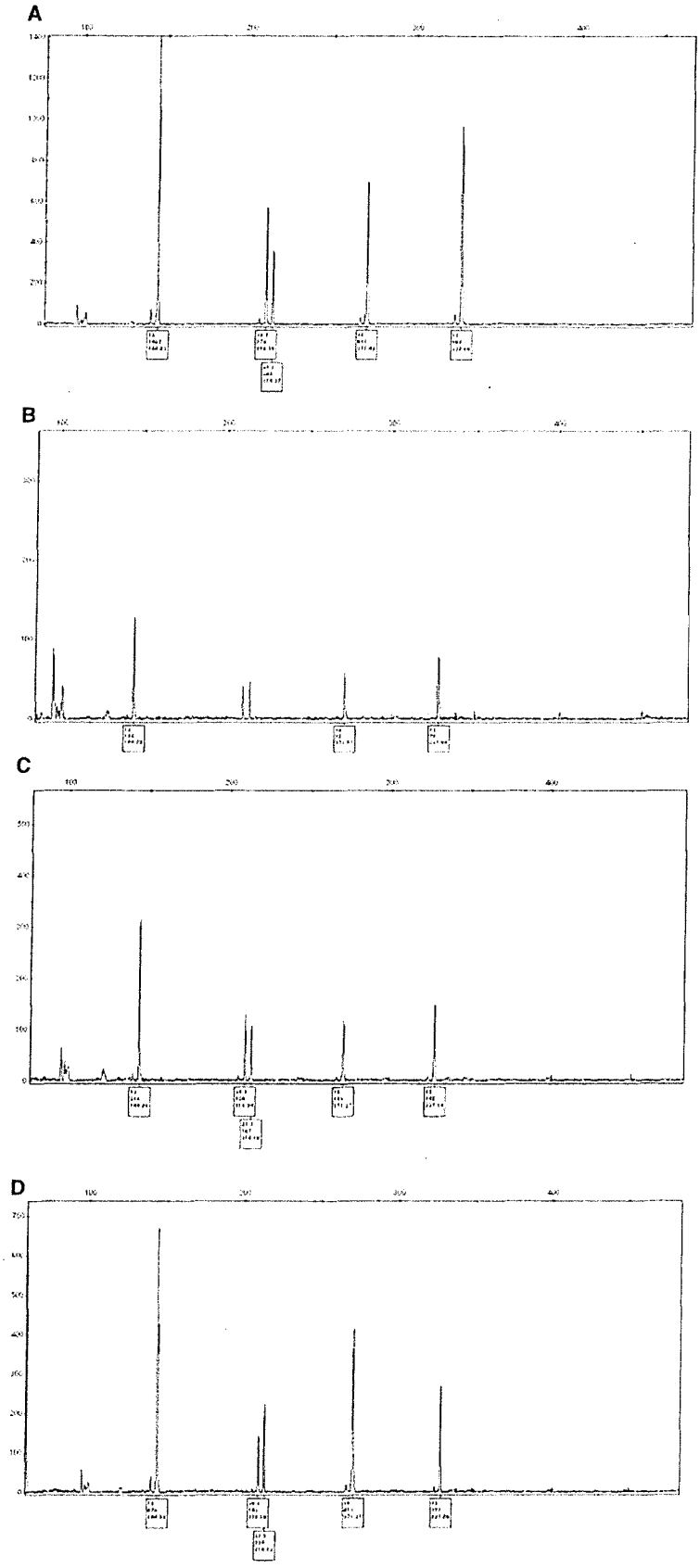

FIG. 4—*Examples of electropherograms from samples analyzed 1 week (A and B) and 3 months (C and D) after deflagration of the devices. The samples were amplified using the AmpFlSTR® Identifiler® Amplification Kit and analyzed on the AB 3130 Genetic Analyzer. Samples (A and D) are from pipe nipples. Samples (B and C) are from end caps.*

ability to dissolve the cyanoacrylate polymer. Initial studies at the ATF Laboratory indicate the use of acetone may increase the amount of biological material collected depending on the surface being swabbed.

As discussed in the Introduction, the location of the biological material on the device may affect its subsequent exposure during deflagration. How it would be affected was unknown. A combined total of 24 cell spots were analyzed from pipe nipple fragments (both time points, fumed and not fumed) which were compared with the 24 cell spots analyzed from end cap fragments (both time points, fumed and not fumed). On average, the quantity of DNA recovered from the pipe nipples demonstrated an approximate twofold increase over the quantity of DNA recovered from the end caps. It was estimated originally that the total quantity of DNA deposited on each spot was 30 ng (5000 cells). While this was a rough estimate calculated by counting the cells in several aliquots of the cell suspension under a microscope, it is a useful number to compare with the actual quantity of DNA recovered from the cell spots. The DNA extraction of the cell spots located on the pipe nipples from the analysis within 1 week post-deflagration yielded *c.* 10 ng of DNA on average, or one-third of the estimated original quantity of DNA. The total DNA recovered from the end caps for the same time point was only about 4 ng. The DNA concentrations recovered at the 3-month time point were *c.* 10% of the concentrations recovered at 1 week. The difference in the DNA recovery observed from the pipe nipples and the end caps may seem insignificant when compared with the total initial DNA. For example, the combined results of recovery of DNA were *c.* 1.7% of the initial DNA spotted on the end caps and 4.2% of the DNA spotted on the pipe nipples. However, five of the 12 DNA extracts from the end caps had concentrations below 50 pg/μL (three had concentrations of 0 pg/μL) while none of the 12 DNA extracts from the pipe nipples had a concentration below 50 pg/μL.

As mentioned in the Methods, it cannot be determined if the variability in the Esslinger et al. (4) results may have been because of the realistic method in which the cells were deposited on the components or the subsequent conditions the samples were exposed to. In this study, a consistent amount of cellular material was spotted on the components, yet there remains a wide range of results from a single component, from a single device, and between devices. This is an indication that exterior surfaces of the fragments are each exposed to unique insults which may affect the biological material present severely or relatively mildly.

Because of the manner in which the pipe bomb fragments were captured, the majority of the fragments had little to no soil contamination. This benefit allows for a more direct comparison of the effects of the deflagration without the extraneous effects of potential external factors such as PCR amplification inhibition because of the presence of soil (15,16). The electropherograms of the amplified product were consistent with expected results for the quantities amplified. Where sufficient DNA was amplified (>300 pg), complete profiles were observed with no indications of degradation (see Fig. 4). At low levels of template DNA, partial profiles were observed with the expected peak height imbalance, allele drop-out and/or locus drop-out. The same was true for the cell spots analyzed at the 3-month time point. A comparison of the DNA concentrations in Tables 1 and 2 to the corresponding number of alleles detected and indicated in Tables 4 and 5 may not always seem consistent. For example, sample 4E3 has a concentration of 18 pg/μL and 14 of the 27 possible alleles were detected. Sample 1E13 has a concentration of 13 pg/μL yet all 27 alleles were detected. This could be the result of two factors. First, as noted previously, the quantitation method used has a decreased precision at the lower end of the standard curve, i.e., for samples with low concentrations of DNA as in this study. In addition, the difference between an allele being "detected" and not "detected" could be a matter of a few RFU. In this instance, most of the alleles observed in sample 4E3 have RFU values between 50 and 100, with many allelic peaks visible below the 50 RFU threshold across the profile. The majority of the allelic peaks for sample 1E13 have values between 50 and 150 RFU. No indication of inhibition was detected by the internal PCR control in the quantitation nor was it indicated in the electropherograms.

One obvious, but still important, point did arise during the course of this study. When collecting items of evidence that potentially contain low levels of biological material, it is critical to take steps to prevent contamination from the individual collecting the items. In this case, the individuals collecting the fragments all wore latex gloves; however, one of the samples analyzed demonstrated the presence of a mixture consistent with the expected profile and the profile of the individual collecting the fragment. Even though gloves are worn, contaminating DNA may still be introduced by

TABLE 4—*DNA typing success of samples from pipe bomb fragments 1 week after the deflagration.*

	Alleles Detected 1 Week Post-Deflagration* (27 alleles possible)					
	Not Cyanoacrylate Fumed			Cyanoacrylate Fumed		
	Device	Sample Name	Alleles Detected	Device	Sample Name	Alleles Detected
End Cap	1	1E1	0	2	2E7	27
	1	1E2	27	2	2E8	27
	4	4E3	14	5	5E9	27
	4	4E4	27	5	5E10	0
	7	7E5	0	8	8E11	0
	7	7E6	27	8	8E12	27
Average			16			18
Pipe Nipple	1	1P1	NA†	2	2P8	27
	1	1P2	27	2	2P9	27
	4	4P3	27	5	5P10	27
	4	4P4	27	5	5P11	27
	7	7P6	27	8	8P12	27
	7	7P7	27	8	8P13	27
Average			27			27

*The target amount of template DNA used for amplification was *c.* 0.5–1 ng if available. All alleles with peak heights greater than 50 RFU were counted.
†This sample demonstrated the presence of a mixture and therefore was not used in this analysis.

TABLE 5—*DNA typing success of samples from pipe bomb fragments 3 months after the deflagration.*

	Alleles Detected After 3 Months* (27 alleles possible)					
	Not Cyanoacrylate Fumed			Cyanoacrylate Fumed		
	Device	Sample Name	Alleles Detected	Device	Sample Name	Alleles Detected
End Cap	1	1E13	27	2	2E15	0
	1	1E14	26	2	2E16	0
	4	4E17	4	5	5E19	27
	4	4E18	5	5	5E20	27
	7	7E21	26	8	8E23	0
	7	7E22	27	8	8E24	0
Average			19			9
Pipe Nipple	1	1P14	27	2	2P16	27
	1	1P15	26	2	2P17	27
	4	4P18	27	5	5P20	27
	4	4P19	27	5	5P21	27
	7	7P22	27	8	8P24	27
	7	7P23	27	8	8P25	27
Average			27			27

*The target amount of template DNA used for amplification was *c.* 0.5–1 ng if available. All alleles with peak heights greater than 50 RFU were counted.

any of a number of routes including sneezing, coughing, and sweating. This situation is similar to the analysis of ancient DNA, severely degraded skeletal remains, or other instances in which a minute amount of pristine DNA introduced by an exogenous source during the collection of the evidence can overwhelm the endogenous DNA. This is a further indication that personnel at a crime scene participating in the collection of handled objects or other items of evidence containing low levels of DNA should take elevated precautions to prevent contamination. These precautions can include changing gloves more frequently, wearing a mask/head covering, or wearing a full Tyvek® suit (Dupont, Wilmington, DE). It also demonstrates the importance of an internal staff DNA index containing the profiles of individuals who may come in contact with the evidence from the crime scene to the laboratory so that the possibility of contamination can be detected and investigated.

In summary, this study again demonstrates that it is possible to successfully perform nuclear DNA testing on biological material recovered from post-blast pipe bomb fragments. However, this study also indicates several factors that may affect the success of the DNA typing. One major factor is the ability to recover DNA from cellular material once it has dried on the surface of the pipe nipple or end cap. One possibility is that the cells become difficult to remove using the typical swabbing method, although there may be other causes. The time between the device deflagration and the collection and analysis of the biological material also had a dramatic effect on the recovery of DNA. On average, a 90% reduction in DNA recovery was observed in a 3-month time period. This data suggests that cases that involve post-blast bomb fragments should be prioritized to increase the chances of successful DNA analysis. The original location of the biological material also affected the amount of DNA recovered subsequently. Roughly double the quantity of DNA was recovered from the pipe nipples compared with the end caps. Finally, cyanoacrylate fuming did not demonstrate a measurable effect on the recovery of DNA or DNA typing success. Further studies should be conducted to determine the cause of the loss of DNA over time from post-blast pipe bomb fragments. If the cause can be determined, then preventative measures can be implemented to reduce this loss and increase the DNA typing success from this type of evidence. Additionally, other methods for collecting biological material from the surface of the pipe bomb components should be researched that will recover a greater quantity of the cells originally deposited through the handling of the objects.

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IN THE SUPERIOR COURT OF COWETA COUNTY

STATE OF GEORGIA

STATE OF GEORGIA

V. CASE NO. 2017-CR-618

MONTE BAUGH,
THADDEUS HOWELL,

DEFENDANTS.

ORDER

This case is before the court regarding the state's intent to present evidence at trial of DNA analysis using TrueAllele® software. The Defendants in the case have moved to exclude this evidence arguing that it does not meet the standard for the admission of scientific evidence set out in *Harper v. State*, 249 Ga. 519 (1982) and subsequent cases. The state has opposed that motion and has moved the court to take judicial notice that this evidence has reached a state of scientific certainty sufficient to admit it under *Harper* without a hearing.

After consideration of the issue, the court denied the state's motion to take judicial notice based on the relative novelty of TrueAllele evidence and the absence of its prior use in this court. The court then held an evidentiary hearing on the admissibility of the TrueAllele DNA evidence on March 11, 2019. After conducting the hearing and considering the evidence presented, the record of the case and arguments of counsel, the court hereby finds that the TrueAllele DNA evidence does meet the *Harper* standard, will be admissible in this case and makes the following findings of fact and conclusions:

DNA Evidence in Georgia

DNA evidence has been routinely admitted in the State of Georgia for decades. As the manner of DNA analysis has evolved over time, Georgia courts have kept up with this evolution by continuously assessing the reliability and validity of any significant advancements in DNA analysis.

DNA evidence's admissibility was first addressed by the Georgia Supreme Court in the landmark decision of *Caldwell v. State*, 260 Ga. 278 (1990). In *Caldwell*, the Georgia Supreme Court first recognized the reliability and admissibility of DNA evidence involving the use of restriction fragment length polymporphism analysis ("RFLP"). Thereafter, advances in DNA analysis led to the development of a new technique of DNA analysis involving the using of polymerase chain reaction ("PCR") as part of the process of extracting, amplifying, and profiling a DNA sample in preparation for making DNA profile comparisons. *Redding v. State*, 219 Ga. App. 182 (1995). Since that time, PCR has continually been recognized as a valid and reliable form of creating DNA profiles for comparison, even as PCR based DNA analysis was applied to different forms of DNA. *Thrasher v. State*, 261 Ga. App. 650 (2003) (holding that PCR based DNA analysis is accepted as valid in Georgia); *Shabazz v. State*, 265 Ga. App. 64 (2004) (affirming the trial court's admission of Y-STR DNA analysis from PCR generated DNA profiles); *Vaughn v. State*, 282 Ga. 99 (2007) (affirming the admission of mitochondrial DNA (mtDNA) analysis results at trial).

The Role of TrueAllele Software in DNA Analysis

Dr. Mark Perlin, the creator of TrueAllele software, provided expert testimony which included an explanation as to how the long-established procedures involving PCR

that have been used in the preparation of DNA profiles for comparison purposes are still used today. TrueAllele does not change in any manner this established and reliable process of generating DNA profiles. Rather, TrueAllele now offers the ability to analyze such DNA profiles using a computer - a task traditionally performed by a human analyst.

Traditionally, PCR generated DNA profiles have been compared by human analysts using the long-standing statistical association technique known as the Random Match Probability ("RMP") based on peak height thresholds. These data thresholds are most suitable for analyzing a simple DNA profile involving a single contributor. Dr. Perlin explained how human analysts are limited in their ability to apply thresholds to a complex DNA profile involving a mixture of DNA formed from multiple contributors.

The threshold-based Combined Probability of Inclusion ("CPI") statistical association analysis of a DNA mixture often results in an "inconclusive" result. This is because humans tend to lack the extraordinary time and mathematical ability needed to analyze the complicated possibilities involved in attempting to unsort the mixture. This is where TrueAllele comes in.

How TrueAllele Software Functions

TrueAllele is a probabilistic genotyping software that analyzes DNA evidence using a mathematical model based on Bayesian statistical analysis and the Markov chain Monte Carlo algorithm. This probabilistic analysis includes a careful consideration of DNA's known biological and PCR properties, and the prevalence of certain DNA variants in the population.

TrueAllele operates by initially analyzing a DNA mixture[1] that was obtained from a piece of *physical evidence*[2]. In analyzing particular locations of DNA in this mixture, TrueAllele considers the overlapping DNA components present from each contributor's DNA. These overlapping components are termed alleles. Alleles may be visualized as peaks of varying heights and locations on an electropherogram. TrueAllele considers, in part, that each individual contributor to the DNA mixture contributes two alleles at any given location. An individual's two alleles at any location is called that individual's genotype.

Deconvolution of a mixture of DNA involves assessing the entire group of alleles present at a particular location of the DNA mixture and considering the likelihood of different possibilities of sorting and pairing the alleles into separated genotypes. Taking certain known biological principles into consideration, TrueAllele is able to determine which proposed configurations of genotypes are more likely. For example, since a genotype is composed of two alleles (one received from the mother and one received from the father), when analyzing a DNA mixture, it is expected that the two alleles forming an individual's genotype will be present in equal amounts represented on the electropherogram. With a number of these biological principles factored in, TrueAllele considers very many possible assortments of pairs of alleles and then determines the probability of each proposed configuration (or genotype). TrueAllele assesses the possible genotypes and assigns a probability that reflects the likelihood the proposed genotype correctly explains the DNA mixture.

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[1] Although TrueAllele's functionality is unique in its ability to analyze DNA mixtures, it's functionality also can apply to non-complex single contributor DNA profiles.

[2] A suspect's DNA is not a part of this initial analysis.

Once every possible genotype has been objectively assigned a probability corresponding to the likelihood that the proposed genotype belongs to one of the contributors, TrueAllele subsequently compares the suspect's genotype to the corresponding genotype which was previously inferred. Where the suspect's genotype corresponds with the inferred genotype, the previously determined probability is obtained.

This probability that is associated with the suspect's genotype is then divided by the probability of a random person in the population having the same genotype. This final consideration of the prevalence of the particular genotype in the population helps provide context for assessing whether it is just a coincidence the suspect's genotype is present or whether it is more likely present because the suspect actually contributed it. The result of this completed analysis is a match statistic referred to as the likelihood ratio ("LR"). The LR reflects the likelihood of a DNA match between the evidence occurring because the suspect actually contributed their DNA to the mixture versus the probability of a match existing by mere coincidence.

The aforementioned procedure is repeated on a number of different locations of the DNA mixture (typically 15 to 25 locations). The LR's determined for each of these locations are then multiplied together to obtain a final LR that reflects the strength of a match with the suspect out of consideration of all of these locations in the DNA mixture. This final LR may be reported, as it was in the instant case, as "A match between the firearm grip (Item 13) and Monte Baugh, Jr. (Item 21) is: 3.02 million times more probable than a coincidental match to an unrelated African American person; 305 million times more probable than a coincidental match to an unrelated Caucasian

person, and 67.6 million times more probable than a coincidental match to an unrelated Hispanic person."

TrueAllele is Reliable

There is no genuine controversy as to the validity and reliability of TrueAllele's method of analysis. To the contrary, computer analysis of uncertain data using probability modeling is the scientific norm. The reliability of the mathematical concepts TrueAllele uses are not at issue. Bayesian Statistics have been used since the 1700's, and the Markov Chain Monte Carlo algorithm is a well-established algorithm used since the 1950's. The PCR generated DNA profiles TrueAllele analyzes are the same profiles analyzed by other methods of admissible DNA analysis that have existed for decades.

Cybergenetics thoroughly tests its software before it is released. Over thirty five validation studies have been conducted by Cybergenetics and other groups to establish the reliability of the TrueAllele method and software. Seven of these studies have been published in peer-reviewed scientific journals, for both laboratory-generated and casework DNA samples.

In the "peer-review" process, scientists describe their research methods, results and conclusions in a scientific paper, which they submit to a journal for publication. An editor at the journal has, at a minimum, two independent and anonymous scientists in the field read the paper, assess its merits, and advise on the suitability of the manuscript for publication. The paper is then accepted, rejected, or sent back to the authors for revision and another round of review.

A "laboratory-generated" validation study uses data that has been synthesized in a DNA laboratory, and is of known genotype composition. The State provided four published TrueAllele papers of this type for this Court to consider.[3]

A "casework" validation study uses DNA data exhibiting real-world issues developed by a crime laboratory in the course of their usual casework activity. The State provided three published TrueAllele papers of this type.[4]

Conducting such validations is consistent with the FBI's 2010 Scientific Working Group on DNA Analysis Methods (SWGDAM) interpretation guidelines. TrueAllele complies with the 2015 SWGDAM validation guidelines for probabilistic genotyping systems. Regulatory bodies in New York and Virginia have had independent scientists review validation studies before they granted approval for their state crime laboratories to use TrueAllele for casework.

Validation studies concerning TrueAllele assessed and recognized its reliability in the areas of reproducibility, specificity, and sensitivity. (State's Exhibits 7 and 11).

Reproducibility speaks to the consistency of the results of the analysis. As Dr. Perlin explained, and as was demonstrated by the validations studies, the LR's produced

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[3] (1)Perlin, MW. Sinelnikov, A. **An information gap in DNA evidence interpretation.** PLOS ONE. 2009;4(12): e8327; (2) 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;52(2): 103-14; (3) 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; (4) Greenspoon SA, Schiermeier-Wood L, and Jenkins BC. **Establishing the limits of TrueAllele Casework: a validation study.** Journal of Forensic Sciences. 2015 ;60(5): 1263-1276.

[4] (1) 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; (2) Perlin MW, Belrose JL, Duceman BW. **New York State TrueAllele Casework validation study.** Journal of Forensic Sciences. 2013 ;5 8(6): 1458-66; (3) Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, and Greenspoon S. **Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases.** PLOS ONE. 2014:9(3): e92837.

from successive runs of TrueAllele tend to all be within a factor of 100, a reasonable margin given that TrueAllele's match statistics can range into numbers upwards of sextillion (1 followed by 21 zeroes).

Sensitivity measures the extent to which a mixture interpretation method identifies the correct person as a contributor, and Specificity measures the extent to which a mixture interpretation method does not misidentify someone as a contributor. In this context, the validation studies demonstrated how the LR for a known non-contributor is nearly never greater than 999. Thus, great reliability exists in LR's which are greater.

TrueAllele analysis also results in a predictable LR. As the amount of a contributor's DNA in a mixture increases, so does the LR in a predictable manner. (State's exhibits 8 and 9).

TrueAllele's Widespread Acceptance

TrueAllele has been used in approximately 688 criminal cases, with Cybergenetics expert witness testimony given in approximately 85 trials. TrueAllele results have been reported in 43 of the 50 states.

Courts accepting TrueAllele evidence include California, Florida, Indiana, Louisiana, Maryland, Massachusetts, Michigan, Nebraska, New Hampshire, New York, Ohio, Pennsylvania, South Carolina, Tennessee, Texas, Virginia, Washington, the United States Federal Courts (Eastern District of Virginia), United States Marine Corps, Northern Ireland, and Australia.

Over 10 crime laboratories have purchased the TrueAllele system for their own in-house use, and 8 labs are on-line with their validated systems, including the GBI Crime

Lab. These crime laboratories issue their own TrueAllele reports, and give expert witness testimony at trial about their TrueAllele results.

TrueAllele was used to identify human remains in the World Trade Center disaster, comparing 18,000 victim remains with 2,700 missing people. Both prosecutors and defenders use TrueAllele for determining DNA match statistics. TrueAllele is also used by innocence projects and for post-conviction relief. TrueAllele's reliability has been confirmed in appellate precedent in Pennsylvania.[5]

TrueAllele has been admitted into evidence after opposition challenges in nineteen courts in multiple states, including recently in Georgia after a Harper hearing. Jurisdictions that have admitted TrueAllele results after analyzing its reliability include California, Florida, Georgia, Indiana, Louisiana, Massachusetts, Nebraska, New York, Ohio, Pennsylvania, South Carolina, Tennessee, Virginia, Washington, Northern Ireland and Australia.

Nineteen admissibility decisions in the United States are: People of California v. Dupree Langston, Kern County (Kelly-Frye), BF139247B, January 10, 2013; State of Florida v. Lajayvian Daniels, Palm Beach County (Frye), 2015CF009320AMB, October 31, 2018; State of Indiana v. Randal Coulter, Perry County (Daubert), 62C01-1703-MR-192, August 2, 2017; State of Indiana v. Dionisio Forest, Vanderburgh County (Daubert), 82D03-1501-F2-566, June 3, 2016; State of Indiana v. Daylen Glazebrook, Monroe County (Daubert), 53C02-1411 -F 1-1066, February 16, 2018; State of Indiana v. Malcolm Wade, Monroe County (Daubert), 53C02-1411-F3-1042, August 3, 2016; State of Louisiana v. Chattel Chesterfield and Samuel Nicolas, East Baton Rouge Parish

[5] See Commonwealth v. Foley, 47 A.3d 882 (Pa. Super. 2012).

(Daubert), 01 13-0316 (II), November 6, 2014; State of Louisiana v. Harold Houston, Jefferson Parish (Daubert), 16-3682, May 19, 2017; Commonwealth of Massachusetts v. Heidi Bartlett, Plymouth County (Daubert), PLCR2012-00157, May 25, 2016; State of Nebraska v. Charles Simmer, Douglas County (Daubert), CR16-1634, February 2, 2018; People of New York v. John Wakefield, Schenectady County (Frye), A-812-29, February 11, 2015; State of Ohio v. Maurice Shaw, Cuyahoga County (Daubert), CR-13-575691, October 10, 2014; State of Ohio v. David Mathis, Cuyahoga County (Daubert), CR-16-61 1539-A, April 13, 2018; Commonwealth of Pennsylvania v. Kevin Foley, Indiana County (Frye), 2012 PA Super 31, No. 2039 WDA 2009, Superior Court affirmed February 15, 2012; State of South Carolina v. Jaquard Aiken, Beaufort County (Jones), 20121212-683, October 27, 2015; State of Tennessee v. Demontez Watkins, Davidson County (Daubert), 2017-C-1811, December 17, 2018; Commonwealth of Virginia v. Matthew Brady, Colonial Heights County (Spencer-Frye), CR11000494, July 26, 2013; State of Washington v. Emanuel Fair, King County (Frye), 10-109274-5 SEA, January 12, 2017; State of Georgia v. Thaddus Nundra, Ronnie McFadden, and Louis Ousley (Harper), 18-CR-134, January 29, 2019.

DR. PERLIN IS CREDIBLE

Dr. Perlin testified or has been called to court as an expert witness more than fifty times in fifteen state courts as well as military and federal courts. Dr. Perlin reviewed his credentials, summarized in his curriculum vitae admitted as State's Exhibit 1, and the Court declared him an expert in DNA evidence interpretation, TrueAllele, and the field of software engineering. Dr. Perlin first walked the court through the science of DNA analysis and the processes TrueAllele uses to calculate LRs, using slide shows, which is included in the record as State's Exhibit 3. Dr. Perlin then testified about how

TrueAllele had been tested and used a second slide presentation as he described the validation process and explained the sensitivity, specificity, and reproducibility of TrueAllele also included on State's Exhibit 4.

Availability to Test the Reliability of the TrueAllele Method

Cybergenetics provides opposing experts the opportunity to review the TrueAllele process, examine results, and ask questions. This review can be done in Cybernetics's Pittsburgh office, or through an Internet Skype-like meeting. Cybergenetics regularly explains the system, and the results obtained in a case, to both prosecution and defense.

This introduction to the TrueAllele method, the case data, and the application of the method to the data, is a logical first step. The TrueAllele method is inherently objective, since the computer determines evidence genotypes without any knowledge of the comparison reference genotypes. Hence, there is no possibility of examination bias when determining genotypes from the DNA data. Match statistics, whether inclusionary or exclusionary, are calculated only afterwards by comparing evidence genotypes with reference genotypes. TrueAllele's reliability was established on the evidence in this case. The report and its supporting case packet admitted by the State of Georgia in this case described the system's sensitivity, specificity and reproducibility on the DNA evidence. The case packet gives the data and parameter inputs used in running the program in the case. The packet also includes a case-specific mini-validation study of reported TrueAllele match statistics, measuring match specificity by comparison with non-contributor genotypes. (State's Exhibit 5)

Dr. Perlin testified thirty-seven validation studies have been conducted on TrueAllele either by Cybergenetics, independent crime labs, or collaboration of both; studies, twenty-three are internal validation studies. (State's Exhibits 7 and 11)

Seven of thirty-seven studies have been published in peer-reviewed journals—the first published in 2009. Six of the seven published studies were authored or co-authored by Dr. Perlin. The 2016 PCAST Report states, "it is completely appropriate for method developers to evaluate their own methods", while noting that "establishing scientific validity also requires scientific evaluation by other scientific groups that did not develop the method.[6] Here, although the majority of the publications have been by Cybergenetics, other entities have also reviewed TrueAllele's method.[7]

Dr. Perlin further testified TrueAllele abides by quality assurance standards established by the FBI, as well as guidelines issued by the Scientific Working Group on DNA Analysis Methods (herein "SWGDAM"). In 2015, SWGDAM issued guidelines specifically for validation of probabilistic genotyping systems like TrueAllele abides by today.[8]

Dr. Perlin testified sophisticated computer programs solve problems with a hundred dimensions, and TrueAllele uses Markov chain Monte Carlo (MCMC) computing, one of the oldest and well-adopted methods, dating back to the 1950s.[9] Dr. Perlin testified the MCMC algorithm is considered one of the ten most widely used in computer science.

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[6] 2016 Report on Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods, President's Council of Advisors on Science and Technology (PSCAT) Report, at 93.

[7] [7] See S. Greenspoon, L. Schiermeir-Wood & B. Jenkins, Establishing the Limits of TrueAllele Casework: A Validation Study, 60 Journal of Forensic Science, 1263 (2015).

[8] See also State's Exhibit 15 binder titled "Method Reports"

[9] See also State's Exhibit 20 binder titled "Other Papers"

TrueAllele's Visual User Interface (VUIer™) tool uses MATLAB programming language, which Dr. Perlin described as a standard, and widely relied upon and accepted programming language.

Bayesian methods update belief (i.e., probability) based on evidence. Before seeing evidence (e.g., scientific data), one begins with initial beliefs about hypotheses. Informative evidence changes those beliefs. Bayes wrote his mathematical rule 250 years ago, and modern computing has broadly applied it to the natural and social sciences. A forensic hypothesis is that someone was at a crime scene; Bayes rule weighs DNA evidence to assess that hypothesis.[10]

To permit any interested expert witnesses to take a closer look at how TrueAllele software is coded to implement its analysis, Dr. Perlin explained that approximately two years ago he agreed to disclose TrueAllele's source code under specific conditions. (State's Exhibit 12). Dr. Perlin testified the defense in this case did not accept the offer nor has anyone else. Moreover, Cybergenetics offers free cloud-based TrueAllele testing to defense experts.

Dr. Perlin testified the mathematics underlying TrueAllele comply with the SWGDAM guidelines and recommendations. He provided a document that described the TrueAllele methods with both statistical equations and plain English. (State's Exhibit 20). Dr. Perlin further testified TrueAllele has a known error rate under a

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[10] Dale J. Poirier, The Growth of Bayesian Methods in Statistics and Economics Since 1970, Bayesian Analysis (2006), which is included in the binder admitted into evidence as State's Exhibit 20; Matthew Richey, The Evolution of Markov Chain Monte Carlo Methods, Math. Assoc. of America. (May 2010), which is also included in the binder admitted into evidence as State's Exhibit 20; See, e.g. Sho Manab, et al., Development and validation of open-source software for DNA mixture interpretation based on a quantitative continuous model, PLOS One (Nov. 2017) (printout included in the binder admitted into evidence as State's Exhibit 20.

fraction of 1%, and the calculation for a false positive in this case was included on the Cybergenetics Report. He explained false-positive error rates are stratified by the strength of the match statistic; he demonstrated with data on the slides, that when a match statistic, or LR, is up to a hundred, the error rate is one in a million, but by the time TrueAllele gets a match statistic of a thousand, no false positives were seen in the study. In comparison to other genotyping methods used and admitted before, such as the Modified Combined Probability of Inclusion (CPI), TrueAllele has a far lower error rate.

Conclusion

The Court finds TrueAllele software satisfies the *Harper* standard. The procedure or technique in question, TrueAllele's method of probabilistic genotyping and DNA analysis, has reached a scientific stage of verifiable certainty and "rests upon the laws of nature". There has been substantial peer review of the subject matter. Validation studies have been conducted that recognize TrueAllele's reliability. The error rate for TrueAllele's manner of probabilistic genotyping is much less than that of other genotyping methods the Courts have already deemed scientifically reliable, such as CPI and modified CPI.

The trial court makes this determination from evidence presented to it at hearing in the form of expert testimony from Dr. Perlin. The Trial Court also bases its determination on all the exhibits and treatises submitted on behalf of the State as shown in the record, including the rationales of other jurisdictions and in Decatur County, Georgia. (State's Exhibits 1 – 27A).

Based on all the evidence presented, this Court finds the TrueAllele analysis was performed in an acceptable manner in this case, that TrueAllele software is capable of

producing reliable results, and the testimony of either Dr. Perlin or Jennifer Hornyak concerning these results would substantially assist the trier of fact in understanding the evidence. The criticisms raised by the defense go towards the weight of the evidence, not admissibility.

For the reasons set forth above, the Court finds the TrueAllele analysis scientifically reliable, and the testimony concerning the TrueAllele's results are admissible at trial. The Trial Court finds that the State has met its burden under Harper. This matter remains scheduled for trial on April 29, 2019.

IT IS SO ORDERED.

Emory L. Palmer
for Court Judge
Judicial Circuit

IN THE SUPERIOR COURT OF MUSCOGEE COUNTY
STATE OF GEORGIA

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.

STATEMENT OF FACTS

In January 1977, Gates, a black man, was charged with the murder, rape, and armed robbery of Katharina Wright, a white woman. The trial began on August 30, 1977. In the span of three days, Gates was tried, convicted, and sentenced to death by an all-white jury. The trial prosecutors were Assistant District Attorneys from the Chattahoochee Circuit. The Supreme Court of Georgia affirmed Gates's conviction and sentence on direct appeal, *Gates v. State*, 244 Ga. 587, 261 S.E.2d 349 (1979), cert. denied *Gates v. Georgia*, 455 U.S. 938 (1980), and Gates sought habeas corpus relief unsuccessfully in state and federal courts, *Gates v. Zant*, 863

F.2d 1492 (11th Cir. 1989), rehearing denied *Gates v. Zant*, 880 F.2d 293 (11th Cir. 1989), cert. denied *Gates v. Zant*, 493 U.S. 945 (1989).

In 1992, following a subsequent habeas petition, the state habeas court found that Gates was entitled to a trial to determine whether he is intellectually disabled and therefore ineligible for the death penalty. That habeas court specifically advised defendant that his claim of discrimination in jury selection was not being decided at that hearing but could possibly be brought after his mental hearing in a proper habeas court. In 2003, the Court conducted an intellectual disability trial. On the seventh day of the intellectual disability trial, the Court declared a mistrial. Later the same day, the State and Gates agreed to remove the possibility of a death sentence, and Gates was sentenced to life in prison without the possibility of parole.

After he was resentenced, Gates filed a series of pro se motions challenging his conviction. In 2015, attorneys from the Georgia Innocence Project entered the case on Gates's behalf and filed an Extraordinary Motion for Post-Conviction DNA Testing and For New Trial. Gates sought DNA testing on two items of physical evidence that were found at the crime scene. The State's files contained documentation indicating that the two items had been destroyed in 1979; however, the items were discovered in the District Attorney's Office in 2015 by Georgia Innocence Project interns. The Court ordered testing pursuant to the Extraordinary Motion for New Trial statute, O.C.G.A. § 5-5-41(c) (2010). *See* Consent Order

Granting Defendant's Motion for Post-Conviction DNA Testing (Dec. 16, 2015); Supplemental Consent Order (Feb. 1, 2017); Second Supplemental Consent Order (Jul. 6, 2017).

On November 27, 2017, Gates amended his Extraordinary Motion for New Trial to include claims concerning: 1) jury discrimination, 2) destruction of evidence, and 3) suppression of evidence. Gates also sought discovery of the prosecution's jury selection notes from the trial.

At a hearing on January 31, 2018, the Court ordered the District Attorney's Office to locate and produce to the defense all of its materials and information concerning jury selection in six capital cases involving black defendants in Muscogee County in the late 1970s. *See* Order Regarding Rulings Made at the January 31, 2018 Hearing (filed Feb. 8, 2018). Pursuant to the Order, the State disclosed its jury selection notes to Gates for the first time on March 2, 2018. Gates then supplemented his Amended Extraordinary Motion for New Trial, and the Court held an evidentiary hearing on May 7 and 8, 2018.

At the evidentiary hearing, Gates called five witnesses and presented thirty-five exhibits. R. 3-4, 218-19.[1] The State called two witnesses and presented seven

[1] "R. __" refers to the designated page of the reporter's transcript from the May 2018 evidentiary hearing transcript; "T. __" refers to the designated page of the transcript from Gates's 1977 trial.

exhibits. *Id.*

The evidence of systematic race discrimination during jury selection in this case is undeniable.

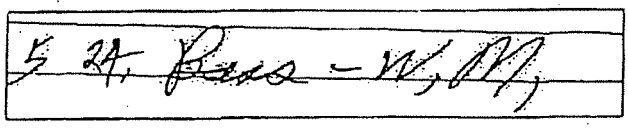
Because Gates's trial took place in 1977, prior to *Batson v. Kentucky*, 476 U.S. 79 (1986), Gates's jury discrimination claim is governed by *Swain v. Alabama*, 380 U.S. 202 (1965). *Swain* requires Gates to show that the State used its peremptory strikes to systematically discriminate based on race *in a pattern of cases*. *Id.* at 223. The ultimate question in a *Swain* inquiry is whether the prosecutors intended to engage in systematic race discrimination. *See Horton v. Zant*, 941 F.2d 1449, 1454-60 (11th Cir. 1991) (finding a *Swain* violation and explaining that "the defendant's goal in demonstrating that the prosecutor struck all or most of the blacks from criminal juries is to enable the court to infer the prosecutor's intent"). When a court is deciding a jury discrimination issue, all of the circumstances that bear upon the issue of racial animosity must be considered. *See id.* at 1459 (approaching a *Swain* analysis with a "broad interpretation of relevance"); *Batson*, 476 U.S. at 93-94 ("Moreover, since *Swain*, we have recognized that a black defendant . . . may make out a prima facie case of purposeful discrimination by showing that the totality of the relevant facts gives rise to an inference of discriminatory purpose.") (citing *Washington v. Davis*, 426 U.S. 229, 239-42 (1976)); *see also Snyder v. Louisiana*, 552 U.S. 472, 478 (2008) (citing *Miller-El v. Dretke*, 545 U.S. 231, 239 (2005)).

The prosecutors clearly engaged in systematic exclusion of blacks during jury selection in this case. They identified the black prospective jurors by race in their jury selection notes, singled them out for peremptory strikes, and struck them to try Gates before an all-white jury. The same prosecutors engaged in the same acts of discrimination in all death penalty trials of black males in Chattahoochee Circuit for the years 1975-1979. The prosecutors then made racially charged arguments to the all-white juries they secured. Based on the evidence presented at the hearing, as detailed below, the discrimination in this case during jury selection was patent. *See Swain v. Alabama*, 380 U.S. 202 (1965); *Horton v. Zant*, 941 F.2d 1449 (11th Cir. 1991); *Timberlake v. Georgia*, 246 Ga. 488, 271 S.E.2d 792 (1980).

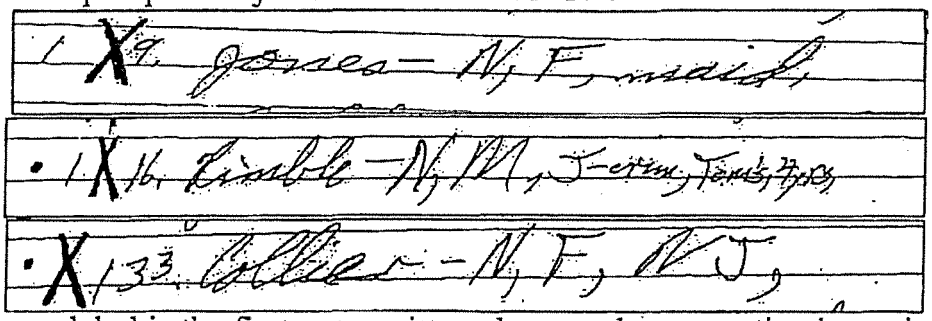
On March 2, 2018, the State turned over to the defense its jury selection notes from Gates's trial, as well as from other capital trials involving black defendants in Muscogee County in the late 1970s. It is uncontested that the Muscogee County District Attorney's Office has been in possession of these notes since the 1970s, with no obligation to give to any defendant absent a proper motion.

The notes support the inference of the prosecutors' practices of race discrimination in jury selection in death penalty cases with Black Defendants in the late 1970s. The notes reflect the following:

First, in Gates's case, the prosecutors labeled the prospective jurors by race. The white prospective jurors are labeled as "W":

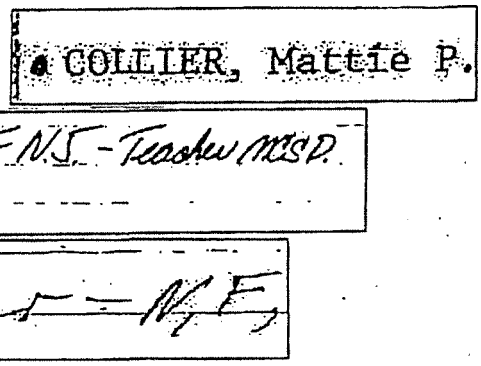


The black prospective jurors are labeled as "N":



This race label is the first note written about each prospective juror, immediately to the right of the jurors' names. In the other cases for which the State produced notes, the prosecutors similarly labeled black prospective jurors with either "N" or "B". These labels were used across multiple cases.

Second, the prosecutors singled out the black prospective jurors by marking dots in the margins next to their names:

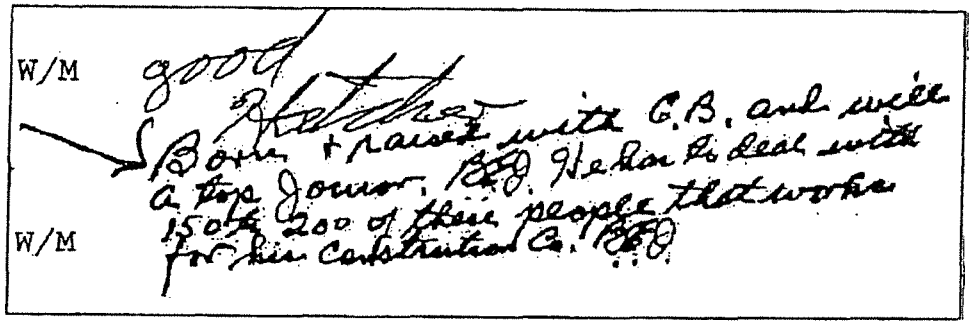


The prosecutors marked dots only for black prospective jurors. As with the "N" and "B" notations, this practice was used across multiple cases, including in Gates's case.

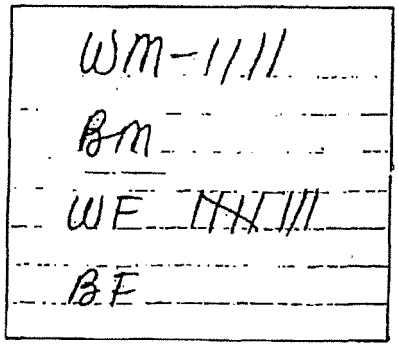
Third, the prosecutors described black prospective jurors as "slow," "old + ignorant," "cocky," "con artist," "hostile," and "fat."

Fourth, the prosecutors routinely ranked black prospective jurors as "1" on a scale of 1 to 5 without any further explanation. In Gates's case, the prosecutors ranked all four black prospective jurors as "1". In contrast, they ranked only one of the 43 white prospective jurors as "1", and they provided a specific explanation for that ranking: the prospective juror was opposed to the death penalty.

Fifth, in the notes from a case involving a 16-year-old black defendant accused of killing a white victim, one prosecutor wrote that a white prospective juror would be a "top juror" because he "has to deal with 150 to 200 of these people that works for his construction co.":



Sixth, in one case, the prosecutors tallied the race of the final jurors selected to serve, with twelve marks in the white column and no marks in the black column:



Taken together, the notes demonstrate a purposeful and deliberate strategy to exclude black citizens and obtain all-white juries. And significantly, both prosecutors from Gates's case wrote notes that reflect intentional discrimination.[2]

The Prosecutors' Strikes Across Cases Confirm the Discriminatory Intent Reflected in the Jury Notes.

The notes do not stand alone. The prosecutors' strikes across the cases confirm the discrimination. Records indicate that from 1975 to 1979, the State brought seven capital cases against black defendants in Muscogee County and struck a total of 41 black prospective jurors. In six of the seven cases, including in Gates's case, the prosecutors removed every black prospective juror to secure all-white juries. In the seventh case, an all-white jury was impossible because the pool of prospective jurors had more black citizens than the prosecutors had strikes.

One ADA was involved in five of the seven cases. In those five cases, the prosecution struck 27 of the 27 black prospective jurors who were qualified to serve. The following chart reflects the strikes in the cases involving this ADA:

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[2] At the May 2018 hearing, Gates presented the testimony of Steven Drexler, a handwriting expert, at the evidentiary hearing. Drexler testified that both ADA authored notes in Gates's case, as well as in each of the other cases for which they were counsel of record matched. R. 195-97.

Case	Qualified jurors called	Jurors struck by prosecution	Qualified black jurors called	Black jurors struck by prosecution	Black jurors on jury
Joseph Mulligan	42	8	4	4	0
Jerome Bowden	45	11	8	8	0
Johnny Lee Gates	47	12	4	4	0
Jimmy Lee Gates	46	11	4	4	0
William Spicer Lewis	42	10	7	7	0

ADA #2 was involved in four of the seven cases. The following chart reflects the prosecution's strikes in the cases involving this ADA:

Case	Qualified jurors called	Jurors struck by prosecution	Qualified black jurors called	Black jurors struck by prosecution	Black jurors on jury
Johnny Lee Gates	47	12	4	4	0
William Brooks	46	11	4	4	0
William Spicer Lewis	42	10	7	7	0
William Henry Hance	37	11	13	10	2

Together, the prosecutors struck 41 black prospective jurors across the seven cases.

The prosecutors' discriminatory intent is further reflected in the closing arguments they made across multiple cases. After securing all-white juries, the prosecutors made racially charged closing arguments. The racially charged arguments spanned across multiple cases, including Gates's case. For example, in the closing argument in *State of Georgia v. Jerome Bowden*, the prosecutor referred to Bowden as a "wild beast" and told the all-white jury, "It took more courage to build this great nation and it will take courage to preserve it, from this man and his like." R. Ex. 18 (Bowden Closing). In several closings, the prosecution employed "us" versus "them" language, R. Ex. 18-21 (Closing Arguments), which is also echoed in the prosecution's own jury selection note stating that a white prospective juror would be a "top juror" because he "has to deal with 150 to 200 of these people that works for his construction co.," R. Ex. 13. In Gates's case, the prosecutor inquired of the all-white jury, "Do you feel as free as you did ten years ago?," referencing the period from 1967 to 1977. T. 591. Accordingly, the closing arguments demonstrate the racial overtones that infected the prosecutions of these black defendants.

The factual matters described above are largely unrebutted. The State offered no rebuttal evidence.

The State argued that Gates should have shown a pattern across more than seven cases. R. 392. The Court rejects that argument. The seven cases addressed

at the hearing represent all of the capital cases tried against black defendants in Muscogee County from 1975 through 1979. That period covers the year of Gates's trial, which was 1977, as well as the two years before Gates's trial and the two years after it. The cases included in this period establish that the prosecution's race discrimination was pervasive and systematic.

Moreover, the ultimate focus of a *Swain* inquiry is the intent of the prosecutors. *See Horton v. Zant*, 941 F.2d 1449, 1454-60 (11th Cir. 1991). Each of the six other cases were tried by one or both of the same prosecutors who tried Gates. Accordingly, these seven cases are pointedly probative as to the prosecutors' practices at the time of Gates's trial. In addition, the evidence of discriminatory intent is overwhelming. Both prosecutors made notes that reflect racial animus in jury selection.

The preceding analysis and Findings of discriminatory intent are necessary to provide Defendant the relief he seeks, but such Finding is not sufficient. Defendant must also satisfy the six prongs required by *Timberlake v. State*, 246 Ga. 488 (1980).

"[T]he procedural requirements for ... [extraordinary motions properly brought before the courts] are the product of caselaw." *Dick v. State*, 248 Ga. 898,899 (1982). The long-standing requirements, pursuant to case law, for granting an extraordinary motion for new trial are set forth in *Timberlake v. State*, 246 Ga. 488 (1980). Under *Timberlake*, Defendant must prove:

> (1) that the evidence has come to his knowledge since the trial; (2) that it was not owing to the want of due diligence that he did not acquire it sooner; (3) that it is so material that it would probably produce a different verdict; (4) that it is not cumulative only; (5) that the affidavit of the witness himself should be procured or its absence accounted for; and (6) that a new trial will not be granted if the only effect of the evidence will be to impeach the credit of a witness.

Id. at 491. "[O]ne who seeks to overturn his conviction for murder many years later bears a heavy burden to bring forward convincing and detailed proof." *Davis*, 283 Ga. at 446. Defendant's failure to meet even one of the requirements under *Timberlake* is grounds for a denial of relief. *See Dick*, 248 Ga. at 900; *see also Timberlake*, 246 Ga. at 491. Application of the rigorous *Timberlake* standard presented during the hearings conducted in this Court, in context of the evidence presented at Defendant's trial and in light of the lengthy post-conviction process pursued by Defendant, demonstrate that Defendant has failed to meet the prong of *Timberlake* requiring due diligence.

Defendant fails to reasonably account for the delay in bringing forth his motion sooner. His "litigation must come to an end." *See Drane v. State*, 291 Ga. 298, 304 (2012). Relief for this Jury Discrimination Issue is Denied.

Evidence of an alleged walk-through prior to Defendant's videotaped confession is not newly discovered.

Under *Timberlake*, to obtain the grant of an extraordinary motion for new trial, Defendant must show that "the evidence has come to his knowledge since the trial."

Timberlake, 246 Ga. at 491. Defendant's current counsel claim that they have recently discovered that Defendant was walked through the crime scene by the Columbus Police Department before he gave his confession that was videotaped there.

The most important witness to both the videotaped confession and any alleged, prior walk-through is Defendant. Evidence of an alleged walk-through, in the nature of things, must have been known to Defendant at trial. *See Ogelsby v. Cason*, 65 Ga. App. 813, 816 (1941) ("Evidence which in the nature of things must have been known to the accused before his trial was ended, cannot after verdict be treated as newly discovered."); *see also Bissell v. State*, 157 Ga. App. 711, 714 (1981) (holding that a ground of a motion for new trial is without merit when it appears from the ground that such evidence must have been known to the defendant before his trial).

"A part of the evidence called newly discovered is not so ... [if the defendant knew of it], and should have informed counsel." *Cobb v. State*, 219 Ga. 388, 391 (1963). "No valid excuse is offered for [Defendant's] failure to disclose his alleged knowledge." *Id.* "There is not attached to the extraordinary motion for new trial any affidavit by the movant, or any affidavit by counsel representing him on his trial, to the effect that they did not know of the matters ... at the time he was tried." *See Hall*, 215 Ga. at 376.

"Such affidavits are essential to an extraordinary motion for new trial where newly discovered evidence is relied on." *See Id.* During his state habeas evidentiary hearing held on September 16, 1980, Defendant testified that he informed trial counsel that Mr. Hicks walked him through the crime scene three times before his videotaped confession. Thus, Defendant fails to show that the facts set forth in this claim "were unknown to [Defendant or trial counsel] before trial." *Ogelsby*, 65 Ga. App. at 816.

The Georgia Supreme Court has repeatedly held that defendants who wait years to bring to the Court's attention evidence either that was known or could have been discovered by reasonable diligence were not entitled to relief. *See Bharadia*, 297 Ga. at 573; *Drane*, 291 Ga. at 304; *Davis*, 283 Ga. at 445; *Llewellyn v. State*, 252 Ga. 426, 428-29 (1984).

On February 10, 2018, almost 41 years after his trial, Defendant procured an affidavit from Mr. Hicks which allegedly reveals that Defendant was walked through the crime scene before his videotaped confession at the same crime scene. "[T]he record reflects no evidence showing that [Defendant] was unable to obtain this evidence prior to trial." *See Bharadia*, 297 Ga. at 573. Mr. Hicks was still employed by the Columbus Police Department at the time of Defendant's trial. (State's Response in Opposition to Defendant's Second Supplement to his Amended Extraordinary Motion for New Trial at Attachment K) He was clearly available to

be called as a witness by Defendant. *See Davis*, 283 Ga. at 445. "[Defendant] has failed to show that he has exercised due diligence in obtaining this new testimony, which was obtained from a witness who was readily identifiable pre-trial." *See Id.* at 446.

"[I]n considering due diligence under *Timberlake*, [the courts] look to the action and inaction of the defendant, including his counsel and defense team." *Bharadia*, 297 Ga. at 543 n.9. This evidence was at least discoverable during Defendant's first state habeas proceedings in 1980. In 2002, during his intellectual disability proceedings, defense counsel alleged that "it's quite possible that when [members of the Columbus Police Department] took [Defendant to Mrs. Wright's apartment] to give his confession, they had put his hand on that heater and that's how his handprint got there." (10-8-2002 Hearing at 49).

Defendant has failed to show any reason for his failure to exercise due diligence in coming forward with this affidavit sooner. This Court finds that Defendant cannot meet the second requirement of *Timberlake*, "that it was not owing to the want of due diligence that he did not acquire it sooner." *Timberlake*, 246 Ga. at 491.

Defendant fails to show that Mr. Hicks's affidavit is not merely impeaching.

Under *Timberlake*, Defendant must also show that his alleged new evidence is not merely impeaching. Defendant fails to satisfy these requirements.

Defendant's trial counsel thoroughly cross-examined Detective Hillhouse and Officer Lawrence regarding a walk-through of the crime scene with Defendant by members of the Columbus Police Department, including Mr. Hicks, prior to Defendant's videotaped confession. Both officers denied the allegation. TT 428-36. Importantly, the focus of the cross-examination was the existence of a prior walk-through during which Defendant's fingerprints were allegedly planted at the crime scene by police. TT 429-36. Therefore, Mr. Hicks's testimony about the existence of the alleged walk-through would merely serve to impeach the credibility of Detective Hillhouse and Officer Lawrence.

The State did not suppress favorable information in violation of *Brady v. Maryland*, 373 U.S. 83 (1963). *supra.* Hicks was known to defendant at the time of trial but not called as a witness. Besides, issues of credibility are not within the province of this Court.

Accordingly, Gates is not entitled to a new trial based on the suppression of evidence claim.

The Newly Available DNA Evidence Is Exculpatory and Entitles Gates to a New Trial.

Gates presented DNA evidence at the May 2018 hearing that demonstrates that he is excluded as a contributor to the DNA on two key items of physical evidence used by the perpetrator to bind the victim's hands – a white bathrobe belt

and a black necktie. The State did not contest the defense's DNA test results. The exclusion of Gates's profile to the DNA on the two items is material and may be considered exculpatory. Therefore, Gates is entitled to a new trial.

The Experts for the State and Defense Agreed that Gates's DNA Is Not on the Bathrobe Belt or the Necktie, used to bind the victim.

At the hearing, Gates presented the expert testimony of Dr. Mark Perlin, the chief executive and scientific officer at Cybergenetics. R. 225-305. Dr. Perlin has a medical degree, a Ph.D in mathematics, and a Ph.D in computer science. R. 225-26. He was qualified, without objection, as an expert in the field of DNA interpretation and probabilistic genotyping. R. 226, 233. Dr. Perlin is the creator of a new DNA interpretation technology called TrueAllele. R. 227-29. TrueAllele is a computer program that uses probabilistic genotyping to objectively interpret degraded, low level, and complex mixtures of DNA. R. Ex. 26 (Cybergenetics Report). TrueAllele deconvolutes complex mixtures and can produce a statistic that indicates the likelihood that a given person's DNA profile is present or is not present in a DNA sample. R. 227-28. It is uncontested that TrueAllele was implemented by the Georgia Bureau of Investigations (GBI) in January 2018. R. 231, 316-17. Dr. Perlin trained the GBI staff in how to use TrueAllele. R. 231, 332. Dr. Perlin's testimony was credible. Dr. Perlin testified that the TrueAllele software determined

that Gates is excluded as a contributor to the DNA on the two items of evidence collected from the crime scene. R. 247-48.

The State called two witnesses at the evidentiary hearing, Ms. Kristen Pfisterer and Mr. James Sebestyen. They testified that human interpretation of the DNA, which was done prior to interpretation with TrueAllele, yielded inconclusive results. R. 311. The inconclusive human interpretation results are relevant insofar as they demonstrate the ability of TrueAllele to interpret what human interpretation methods could not (and the reason the GBI purchased it for use in its casework). R. 327-28, 339-40. Dr. Perlin testified that TrueAllele is designed to interpret complex, low level DNA mixtures, such as the mixtures in this case, where human interpretation cannot. R. 282 ("Human review methods don't separate out genotypes, so, [human interpretation methods] wouldn't have been able to [interpret the DNA]."); R. 290-91 ("The older human review systems would have difficulty getting interpretable results, whereas the more modern . . . computers don't have the same issue."). The State did not contest the accuracy of the TrueAllele results, and the State's witnesses testified that TrueAllele is "scientifically valid" in its approach to using data that falls below the human interpretation threshold. R. 317, 333-35.

It is noteworthy that, largely, Ms. Pfisterer and Mr. Sebestyen's testimony did not contradict, but instead supported, Dr. Perlin's testimony. This was the rare hearing in which the scientist who trained the GBI scientists testified on behalf of

the defense. R. 231, 332. Dr. Perlin presented well, answered questions in a direct and unbiased manner, and was the most qualified and credible of the three DNA experts who testified.

In light of the unified opinion of the experts that Gates is excluded as a contributor to the DNA on the two items taken from the crime scene, the State argued that (1) it stored the belt and necktie in such a way that Gates's DNA degraded, and is no longer on the items; and (2) Gates's DNA could have fallen off of or otherwise been lost from the items over time. R. 312-14, 325-28. The Court should reject these theories for the reasons provided below.

The evidence presented at the May 2018 hearing established that the perpetrator's DNA would be embedded in the bathrobe belt and necktie because of the way in which the crime occurred. At trial, the District Attorney's investigator testified for the State that the perpetrator tied the bathrobe belt "very, very tightly" around the victim's hands, "bound her wrists," and double knotted the belt. T. 276; *see also* R. Ex. 27 (GBI photographs depicting the knots). The necktie also was tied around the victim's hands, with knots binding it together. *Id.*

Citing a peer reviewed study, Dr. Perlin explained that manipulation of the belt and necktie in this manner would transfer a significant amount of DNA from the perpetrator's hands onto the items. R. 267-72; R. Ex. 28 (Goray Study) (discussing variables affecting DNA transfer onto cloth, including friction, pressure, and length

of time engaging with the material). Furthermore, Dr. Perlin testified that even if the perpetrator washed his hands prior to touching the bathrobe belt and necktie, he still would have transferred DNA to the items. R. 273.

The evidence presented at the May 2018 hearing established that TrueAllele yielded informative results, notwithstanding the possibility of degradation of the DNA over time. The State suggested that it stored the evidence in conditions so extreme that the conditions caused extensive bacterial growth resulting in the total degradation of the DNA on the items. R. 313-14, 326-27. There is no indication that the DNA on the items had completely degraded due to bacterial growth or any other reason. Instead, Dr. Perlin testified that while the DNA on the bindings had indeed degraded over time, the samples still uniformly yielded informative results that could be and were interpreted reliably by TrueAllele. R. 289-91, R. 298 ("[T]he data are really dispositive here. We see there's degradation. We see it's not complete degradation."); R. 302 ("We don't see a complete elimination of the data, we see a degradation pattern that shows longer sentences are producing less signal while shorter sentences are producing quite a good signal."). Dr. Perlin credibly explained the several ways that TrueAllele is able to accommodate for and interpret degraded DNA. R. 255.

In addition, the State suggested that the GBI's "inconclusive" findings following human interpretation attempts were due to the extent of DNA degradation

on the bindings. R. 311-13. However, Dr. Perlin explained that the inconclusive findings were not due to an inability of the degraded DNA to yield informative results, but rather due to an inability of the GBI to interpret the degraded, low level complex mixture using human interpretation methods. R. 290-91.

The evidence presented at the May 2018 hearing established that the perpetrator's DNA would not have transferred off of the items simply because other individuals touched the items. The State argued that Gates's DNA could have fallen off of the items because the items were handled by several people over the years and taken in and out of a manila envelope. R. 293, 340. The State's expert was unable to cite any studies to support the State's proposition. R. 316. In support of its theory, the State observes that only three or four DNA profiles were located by TrueAllele on each item, yet the State asserts that many more individuals handled the items.[3]

Dr. Perlin testified that once deposited, fabrics such as a cloth bathrobe belt or necktie would retain the DNA. R. 271 ("DNA sticks around for a long time . . . If it's in the weave of a fabric, it's going to stay there."). Dr. Perlin testified that if additional individuals touched the cloth bindings, their DNA could be added, creating a more complex mixture, but the touching would not remove the perpetrator's DNA. R. 274-76. Dr. Perlin explained that one reason that the items

[3] Although the State's counsel suggested that "dozens" of people handled the items, R. 326, there is no evidence to support that assertion.

may include fewer DNA profiles is because casual or brief touching of the items would result in less DNA, or possibly no DNA, being deposited. R. 298-99; R. Ex. 28 (Goray Study) (explaining the less friction, pressure, and time spent manipulating material, the less DNA deposited).

Gates has met the six elements of *Timberlake* with respect to the DNA issue and therefore is entitled to a new trial.

First, the exculpatory DNA evidence in this case has come to Gates's knowledge since the trial.

Second, Gates was diligent in obtaining the exculpatory DNA evidence. The DNA in Gates's case consists of a low level, degraded, complex mixture. The State and defense experts agreed that the DNA on the two items could be meaningfully interpreted through TrueAllele's probabilistic genotyping, whereas it could not be meaningfully interpreted by traditional human analysis. *See* R. 290-91 (Perlin) (testifying that "[t]he older human review systems would have difficulty getting interpretable results, whereas the more modern . . . computers don't have the same issue"); R. 316-17 (Pfisterer) (testifying that the GBI implemented TrueAllele so that it could analyze low level complex DNA mixtures, like the mixture in Gates's case); R. 333-35 (Sebestyen) (testifying that TrueAllele is a "scientifically valid" method that is able to interpret information below the analytical threshold).

Furthermore, the State and defense agreed that TrueAllele was adopted by the GBI in January 2018. R. 231, 316-17.

The State argued that Gates should have secured DNA testing when contact DNA testing first became available in the 1990s. The State's argument is flawed. According to O.C.G.A. § 5-5-41(c)(7)(C), the Court must grant DNA testing when "it would provide results that are reasonably more discriminating or probative of the identity of the perpetrator than prior results." The evidence at the hearing demonstrated that TrueAllele's results are more discriminating and probative of the identity of the perpetrator than the prior results obtained by human interpretation of complex mixtures. Therefore, Gates satisfies the diligence requirement.

Alternatively, independent from the grounds above, Gates was diligent in his request for DNA testing because he requested the testing immediately after Georgia Innocence Project interns located the two items of evidence in the District Attorney's Office in 2015.[4] At a hearing in November 2017, an Assistant District Attorney

[4] While the State contends that the two items of evidence may have been present in court at a hearing held in October 2002, the State subsequently represented, in November 2002, that the two items of evidence at issue were destroyed in 1979. *See* Transcript of Hearing at 64-65 (Nov. 8, 2002) (indicating that the belt and necktie were among the items destroyed by the crime laboratory in 1979); GBI Record of Evidence Received by Crime Laboratory at 1, item 3 (attached as Ex. B to State's Supplement filed Apr. 9, 2018, indicating the same).

acknowledged that the items were "new evidence located in 2015." *See* Transcript of Status Hearing at 12 (Nov. 7, 2017).

Finally, the State did not raise a due diligence argument when Gates initially requested DNA testing in 2015.[5] And in 2017—after the State had secured the GBI's inconclusive human interpretation results, but before receiving the exculpatory TrueAllele results—the State explicitly conceded that the DNA testing was appropriate and proper. *See* Transcript of Status Hearing at 25 (Nov. 7, 2017) (Assistant District Attorney Bickerstaff) ("[W]e thought it proper that DNA should be tested on those items . . ."); *id.* ("[The items] were there and available and they decided they wanted to test them and we thought that was proper."); *id.* ("[T]he DNA testing would be proper based on the statute."); *id.* at 36 (Assistant District Attorney Lewis) (stating that it is "the State's position" that Gates is entitled to a statutory right to DNA testing); R. 224 (Lewis) ("There is no challenge here as to the testing that took place.").

Third, the exculpatory DNA evidence is material. For the reasons described above, the DNA evidence is meaningful and exculpatory because it demonstrates that Gates was not the person who bound the victim's hands.

Fourth, the exculpatory DNA evidence is not cumulative.

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[5] The State initially opposed DNA testing in 2015 on materiality grounds. *See* Transcript of Hearing at 41, 70-74 (Dec. 16, 2015).

Fifth, Gates submitted affidavits from expert witnesses prior to the evidentiary hearing, including affidavits and reports from Dr. Greg Hampikian and Dr. Mark Perlin. *See* Gates's Supplement to Amended Extraordinary Motion for New Trial Explaining DNA Test Results that Exclude Gates as a Contributor to the DNA on the Physical Evidence (filed Jan. 29, 2018); Notice of Additional Witnesses (filed Apr. 18, 2018). Accordingly, Gates satisfied the affidavit requirement.

Sixth, the evidence presented does not impeach the credibility of a witness. Instead, it provides substantive evidence that Gates did not commit the offense for which he was convicted.

The DNA evidence discussed above is even more concerning given the State's history of destruction of evidence in this case.[6] The State argues that the DNA test results are not sufficient to warrant a new trial for Gates, yet the State itself destroyed the bulk of the remaining evidence that could have been subjected to testing. The State destroyed most of the remaining evidence in 1979, less than two years after Gates's trial and before the Georgia Supreme Court affirmed Gates's conviction and sentence in this death penalty case. *See* GBI Record of Evidence Received by Crime Laboratory (attached as Ex. B to State's Supplement filed Apr. 9, 2018, indicating

[6] During the Extraordinary Motion for New Trial proceedings, the Court repeatedly requested that the State produce a list of evidence taken from the crime scene, the tests that were conducted on that evidence, and the test results. *See* Court Order (filed Feb. 23, 2018). To date, the State has not complied with the Court's request.

that all but five items of physical evidence in Gates's case were destroyed on May 2, 1979).

Some of the evidence destroyed by the State was material and exculpatory evidence. *See Arizona v. Youngblood*, 488 U.S. 51 (1988). One piece of material and exculpatory evidence included Type B blood found on a door next to the deceased victim at the crime scene. *See* GBI Crime Lab Supplementary Report at 1-2 (Feb. 3, 1977) (attached as Ex. B to State's Supplement filed Apr. 9, 2018, indicating that item 29—the red brown stains on the door—is positive for blood of human origin that is Type B). GBI records indicate that the blood was among the items destroyed in 1979.[7] *See* GBI Record of Evidence Received by Crime Laboratory at 1-2 (attached as Ex. B to State's Supplement filed Apr. 9, 2018). The Type B blood was material and exculpatory evidence because it placed a third party on the scene, as Gates and the decedent each had Type O blood. *See* T. 290 (noting the victim had O positive blood type). The State's destruction of evidence, when considered in conjunction with the new DNA evidence described above, provides further reason why Gates is entitled to a new trial.

[7] Additional evidence destroyed by the State includes, in part, (1) two semen slides collected from the victim's cervix and vagina during a sexual assault examination; (2) the bathrobe the victim was wearing, which contained seminal stains; and (3) numerous Caucasian hairs collected from the victim and the crime scene.

Defendant is Granted a new trial on the DNA findings pursuant to O.C.G.A. § 5-5-41(C) (2010).

Defendant is Denied relief on all other grounds alleged in his Extraordinary Motion for New Trial.

SO ORDERED this 10th day of January, 2019.

John D. Allen

Honorable John D. Allen
Superior Court Judge
Chattahoochee Judicial Circuit

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PAPER

CRIMINALISTICS

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TrueAllele® Genotype Identification on DNA Mixtures Containing up to Five Unknown Contributors*

ABSTRACT: Computer methods have been developed for mathematically interpreting mixed and low-template DNA. The genotype modeling approach computationally separates out the contributors to a mixture, with uncertainty represented through probability. Comparison of inferred genotypes calculates a likelihood ratio (LR), which measures identification information. This study statistically examined the genotype modeling performance of Cybergenetics TrueAllele® computer system. High- and low-template DNA mixtures of known randomized composition containing 2, 3, 4, and 5 contributors were tested. Sensitivity, specificity, and reproducibility were established through LR quantification in each of these eight groups. Covariance analysis found LR behavior to be relatively invariant to DNA amount or contributor number. Analysis of variance found that consistent solutions were produced, once a sufficient number of contributors were considered. This study demonstrates the reliability of TrueAllele interpretation on complex DNA mixtures of representative casework composition. The results can help predict an information outcome for a DNA mixture analysis.

KEYWORDS: forensic science, DNA mixture, genotype modeling, validation study, likelihood ratio, probabilistic genotyping

Deoxyribonucleic acid (DNA) evidence is the forensic gold standard (1). Millions of short tandem repeat (STR) (2) genotypes have been assayed for forensic comparison. The principles of STR interpretation are clearest on pristine, single source items containing abundant DNA (typically about 1 ng). A definite genotype can first be inferred, and then compared with another definite genotype, in order to compute a random match probability (RMP) statistic relative to a "random" population genotype. This is certainly the situation when comparing the pristine DNA of individual reference items.

However, crime laboratories today process DNA evidence that is far less pristine. The biological evidence can be mixed (containing two or more contributors), lower level (having under 200 pg of DNA [3]), or degraded. In some forensic DNA laboratories, the majority of evidence items are mixtures, possibly low level, that often contain three or more contributors. The manual "threshold-based" data interpretation procedures (4), originally developed for pristine samples, are not as effective on mixed DNA data (5).

Computer interpretation methods that use more of the quantitative STR peak height data (rather than thresholds) have been used for twenty years (6). Basic "mixture deconvolution" of forensic DNA mixture data into possible contributor genotypes is performed by other software applications such as Applied Biosystems' Genemapper® ID-X and NicheVision Forensics' ArmedXpert™. Qualitative allele "dropout" methods put a probability to unobserved peak data, as in David Balding's likeLTD (7) and Adele Mitchell's FST (8) software programs.

The "genotype modeling" method goes further and strives to preserve DNA identification information by explaining the observed STR data in terms of adding together contributor genotypes (9,10). This method develops Bayesian probability model equations that can explain the data and (when the solution space becomes vast) uses statistical search methods to solve the equations. Such computer systems include DNAmixtures (11) and related efforts (12), MixSep (13), STRmix (14), and TrueAllele® Casework (15,16).

Cybergenetics TrueAllele Casework system separates complex mixture data into its component genotypes. For each contributor, at each locus, a genotype and its uncertainty is described by a probability distribution over allele pair possibilities. This genotype summarizes the data's identification information and imparts to DNA mixtures the original simplicity of single source interpretation. For example, the match statistic resembles RMP, as inferred genotypes are compared with one another.

Previous TrueAllele validation studies have been published. Two-person mixtures of known composition have been examined for their information response, with varying amounts of template DNA (17) and on small quantities using joint interpretation (18). Over 150 casework mixture items containing 2, 3, or 4 contributors have been analyzed for match information across a broad range of mixture weights and quantities, with comparison made to human review methods (15,16,19). However, there has not yet been a study of known mixtures with up to five unknown contributors, where the mixture weights reflected realistic casework instead of simple integer ratios.

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*Presented the 66th Annual Meeting of the American Academy of Forensic Sciences, February 17-22, 2014, in Seattle, WA.

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TABLE 1—*Study design. Five known references were used to randomly create ten mixture samples having 2, 3, 4, and 5 contributors. The mixture weights are shown.*

Reference	Sample	Two	Three	Four	Five	Sample	Two	Three	Four	Five
1	1	0.4674	0.5568	0.1628	0.0346	6	0.0891		0.0489	0.4786
2			0.3064	0.0274	0.0150				0.0475	0.0720
3		0.5326			0.4852			0.3106	0.8976	0.1236
4			0.1368	0.0876	0.2238		0.9109	0.4711	0.0060	0.0782
5				0.7222	0.2413			0.2184		0.2477
1	2		0.2322	0.5367	0.6423	7			0.4350	0.4159
2				0.3430	0.0530		0.5650		0.2087	0.0392
3		0.1770			0.0498			0.5224		0.2900
4			0.2731	0.0746	0.0730			0.2162	0.3385	0.0751
5		0.8230	0.4948	0.0457	0.1820		0.4350	0.2614	0.0179	0.1798
1	3	0.0989	0.4115		0.0930	8	0.1116	0.5774	0.0077	0.4932
2				0.4382	0.0085		0.8884	0.0728	0.0869	0.0400
3				0.1322	0.0586			0.3498	0.5230	0.0655
4			0.2702	0.3969	0.3854				0.3824	0.0876
5		0.9011	0.3182	0.0327	0.4545					0.3136
1	4			0.0271	0.2781	9				0.1197
2					0.2149		0.0585	0.6270	0.0043	0.0802
3		0.3855	0.9438	0.4956	0.2442				0.7007	0.4272
4		0.6145	0.0515	0.4117	0.1468		0.9415	0.0619	0.1750	0.2290
5			0.0047	0.0656	0.1159			0.3111	0.1201	0.1438
1	5				0.0444	10	0.6840		0.3718	0.4555
2		0.8866	0.2749	0.0397	0.3963		0.3160	0.1522	0.2480	0.1777
3			0.1044	0.3229	0.0009			0.3252		0.0197
4		0.1134		0.3603	0.1278				0.1198	0.0317
5			0.6208	0.2771	0.4306			0.5227	0.2604	0.3154

TABLE 2—*Mixture weight variation. The average standard deviation is shown for three concordant methods of computing mixture weight.*

Contributors	*N*=	Human Scoring	Genotype Unknown	Genotype Known
2	20	0.03285	0.02859	0.01944
3	30		0.07699	0.02390
4	40		0.11543	0.01894
5	50		0.15075	0.02221

This study explores the strengths and limitations of DNA interpretation using the TrueAllele Casework system on laboratory-synthesized mixtures of known composition. Mixtures having 2, 3, 4, and 5 contributors are tested, having both high and low DNA amounts. A randomized study design ensures realistic simulation of real-world casework evidence. DNA match information is used throughout to assess interpretation results.

Materials

Randomized Design

A validation study helps establish the reliability of a method, and its suitability for forensic application. DNA mixture evidence contains contributions from two or more individuals in random, unknown proportions. Most mixture studies use integer mixture ratios, providing a convenient simplification for laboratory sample assembly. While these integral ratios may suffice for manual interpretation, computer modeling can extract more information from quantitative data. Therefore, randomized mixture ratios were used in this study to more realistically represent actual casework evidence.

There were four mixture groups, corresponding to 2, 3, 4, or 5 contributors. Within each group, ten mixtures were constructed from five known reference samples. The contributors included in each mixture were determined by randomly selecting DNA references. The mixture weights of the contributors in each mixture item were randomly drawn from a uniform distribution, computed by Dirichlet sampling. The four mixture groups, each containing ten items, yielded a total of 40 randomized DNA mixture items (Table 1).

STR Data

STR mixture data were developed from the known DNA samples according to the experimental design (Table 1). DNA templates were amplified using an Applied Biosystems (Foster City, CA) Identifiler® Plus STR panel at two different DNA concentrations (1 ng and 200 pg). The PCR products were detected on an Applied Biosystems 3130xl Genetic Analyzer, with the higher concentration injected for 5 sec, and the lower amount for 10 sec. (The lower amount was also injected for just 5 sec, but the 10 sec data were more informative.)

Methods

Genotype Inference

TrueAllele Casework has a hierarchical probability model that describes STR data (17). In this Bayesian model (20), the prior genotype probability comes from population allele prevalence, while the likelihood function compares linear combinations of contributor genotypes (with experimental distortion) to observed STR data patterns. The computer uses Markov chain Monte Carlo (MCMC) statistical search (21) to sample from the joint posterior probability distribution. The posterior genotype probability is reported for each contributor at every locus. To eliminate examination bias, where conclusions can be affected by knowledge of a comparison reference (22),

TrueAllele objectively infers genotypes solely from the evidence data.

Electronic data (.fsa) files were processed through the TrueAllele Casework system, and interpretation requests were formed that assumed 1, 2, 3, 4, 5, or 6 contributors. One, two, and three contributor requests were processed with a burn in time of 100,000 MCMC cycles, and sampled from the joint posterior distribution for 100,000 cycles. Requests having four or more contributors were burned in and sampled for twice as many cycles. All requests were run in duplicate, and further replicated as needed, possibly with longer run times.

Match Statistic

Comparing two genotypes relative to a population produces a likelihood ratio (LR) (23). The LR is unaffected by prior beliefs about guilt or innocence and focuses on how well the evidence data support an identification hypothesis. A better mathematical model can elicit more identification information from the same data and (through an inferred evidence genotype) produce a more accurate LR (24). The LR is a Bayes factor that considers the effect of evidence on changing the odds of an identification, commonly used in forensic science to assess the probative force of a DNA match (25). The base

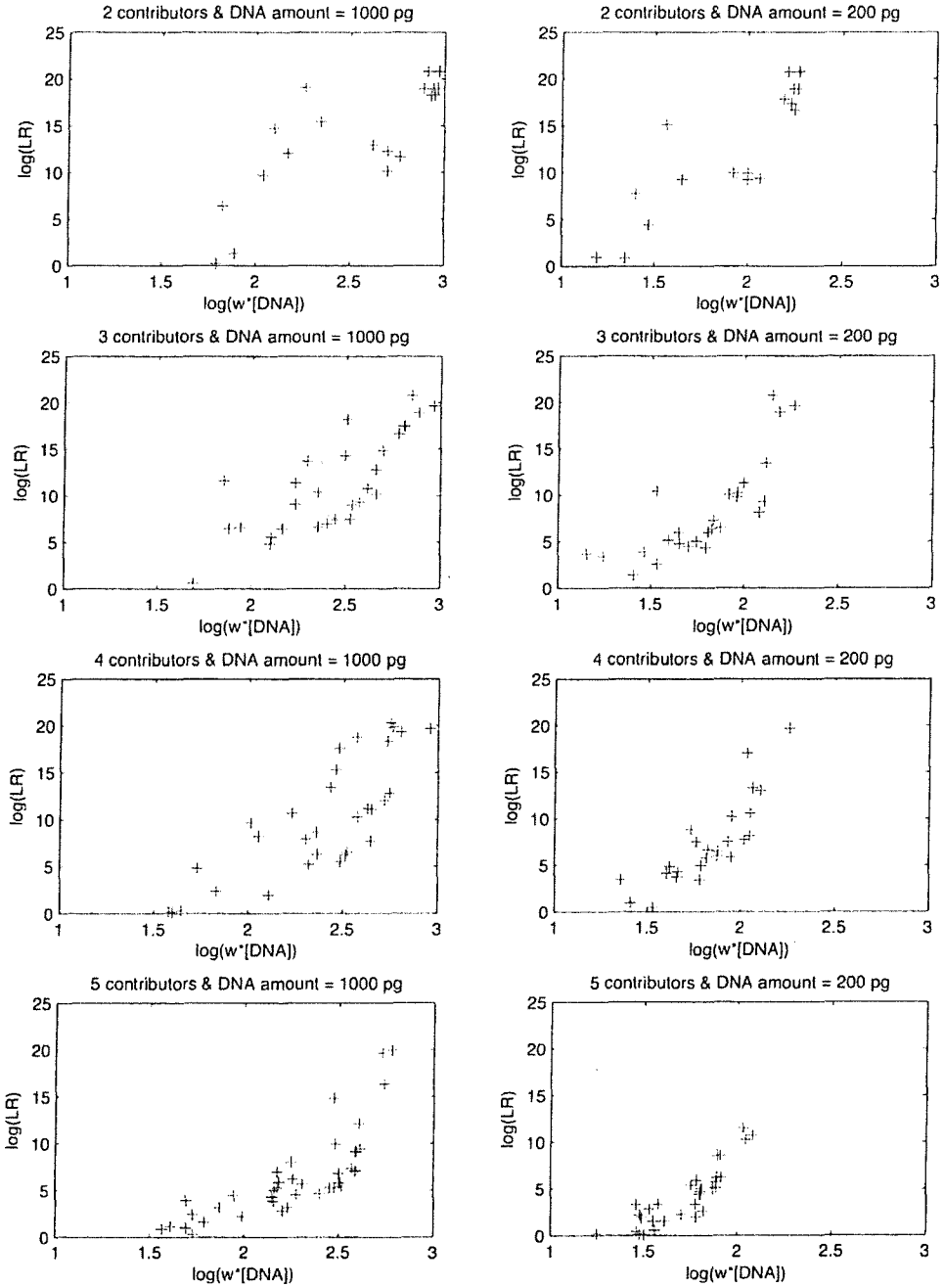

FIG. 1—*DNA information vs. amount. Scatterplots of TrueAllele-inferred log(LR) versus known DNA contributor amount shown for different numbers of contributors (2, 3, 4, and 5 individuals) and DNA amounts (1 ng and 200 pg). Only match results having positive log(LR) are displayed.*

TABLE 3—*Regression coefficient estimates. Log–log scatterplot regression line parameters of LR versus DNA contributor amount (pg). The x-intercept log(w·[DNA]) value is calculated as "−y-intercept/slope".*

Contributors	DNA (pg)	*N*=	Slope	y-intercept	x-intercept
2	1000	20	11.4148	−14.8765	1.3033
3	1000	29	11.9879	−17.8749	1.4911
4	1000	31	12.9912	−20.7610	1.5981
5	1000	41	10.3856	−17.1034	1.6468
2	200	18	15.4039	−16.8288	1.0925
3	200	26	14.0801	−17.0204	1.2088
4	200	25	17.1104	−23.9083	1.3973
5	200	31	13.2820	−18.6383	1.4033

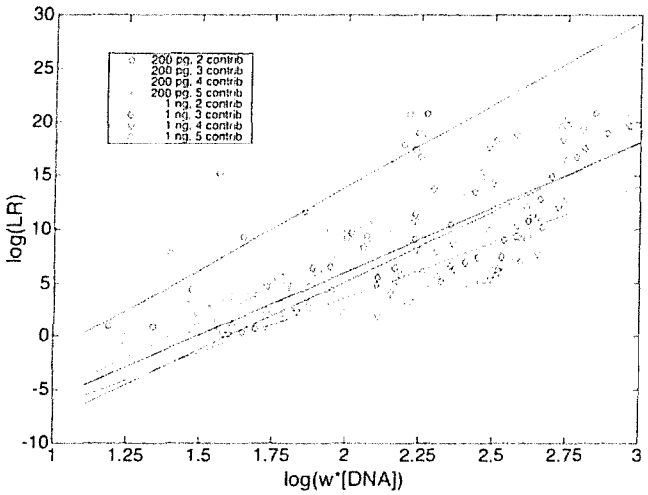

FIG. 2—*Information change regression slopes. Scatterplots of log(LR) vs. DNA amount are shown for eight different groups: 2, 3, 4, or 5 contributors, and either 1 ng or 200 pg of DNA. The scatterplots and regression lines are overlain to show their similar slope behavior.*

TABLE 4—*Analysis of covariance for regression slope. The last column in the ANCOVA gives the statistical significance of the interaction term "ncon*DNA".*

Source	d.f.	Sum Sq	Mean Sq	*F*	*p* > *F*
ncon	7	1731.33	247.33	24.99	
DNA	1	3647.95	3647.95	368.57	
ncon*DNA	7	78.03	11.15	1.13	0.3478
Error	205	2029.02	9.90		

ten logarithm of the LR. "log(LR)" or "weight of evidence", is a standard additive measure of information change, expressed in "ban" units (26).

A competent TrueAllele user reviewed the computer-inferred genotype and match results. Because of genotype uncertainty, a contributor may match more than one reference. Using the study design information, each contributor genotype inferred from a mixture item was paired with a unique known reference. Other useful pairing information included the expected contributor genotype LR value (Kullback–Leibler divergence, or "KL") (27), LR match statistics, and the mixture weights.

Match statistics were calculated relative to the United States Federal Bureau of Investigation allele databases for African American, Caucasian, and Hispanic populations (28). The most conservative LR value among these populations was used. The

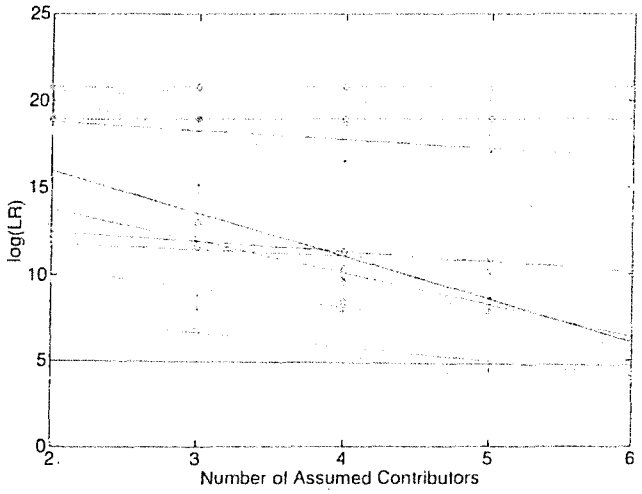

FIG. 3—*Information with excess contributors (two-person mixtures). In separate computer runs, TrueAllele assumed 2, 3, 4, 5, or 6 unknown contributors and inferred log(LR) match statistics. For each mixture component, the regression line and data points are shown under these five different contributor assumptions.*

reported log(LR) was the average of two independent computer runs, where all contributor match values were within one ban and the genotypes were concordant. On average, 3.1 computer runs were conducted per sample. The co-ancestry coefficient (theta value) was set to 1% (29).

Results

Mixture Weight

The mixture weight (w) of each item's contributor had a predetermined design value (Table 1), but was subject to laboratory variation (e.g., pipetting, volumes, quantification). As the study relates other variables to w, it was important to obtain an accurate mixture weight estimate. Therefore, empirical methods based on observed data, rather than expected design values, were used to estimate w for the items.

First, TrueAllele estimated mixture weights in the usual casework manner, without making any genotype assumptions. That is, all variables (including w and the genotypes) were estimated solely from the quantitative STR peak height data (15).

Next, the TrueAllele system used the known contributor genotypes as provided input when estimating mixture weight. That is, the genotypes were assumed, but the other variables (including w) were estimated based on the data and that genotype knowledge (10). As this approach starts with more information, it can produce more precise results.

Finally, mixture weights were manually calculated for all the two contributor items. Within each item, loci were identified where the two contributors had nonoverlapping alleles. The allele peak heights from these loci were entered into an Excel® (Microsoft®, Redmond, WA) spreadsheet that found each contributor's mixture weight mean and standard deviation.

There was a strong pairwise association (r^2 = 0.999) between all three data-derived contributor w values for an item, whether calculated by TrueAllele or a person. However, less association (r^2 = 0.907) was found between the data-derived mixture weights and the experimental design values. The TrueAllele

TABLE 5—*Contributor sufficiency. How TrueAllele behaves when assuming more than the known number of contributors. For each mixture sample having a known number of contributors (known), TrueAllele processed the data assuming up to six total contributors. This produced a group of log(LR) values for each sample's contributor. A linear model* $y = (\alpha + \alpha i) + (\beta + \beta i)\, x + \varepsilon$ *was fitted to the data, where x is the assumed number of contributors, y is the log(LR) information obtained, there are average α and group αi y-intercepts, average β and group βi slopes, and ε is the error. The table shows the average β slope values for each number of known contributors.*

Known	Slope β	SE	*p*-value
2	−0.6653	0.1120	1.5401×10^{-7}
3	−0.8501	0.1151	6.6154×10^{-10}
4	−1.3025	0.2930	1.2587×10^{-4}
5	−0.2598	N/A*	N/A*

*Five contributors provided only two points per line (assuming 5 or 6), which was insufficient for some statistical estimates.

calculations that used both the observed data and known genotypes gave the most precise mixture weights (Table 2). With two contributors, for example, the average mixture weight standard deviation was 0.0194. These minimum variance mixture weight values, inferred by TrueAllele with all genotypes known, were used in this study.

Information Response

TrueAllele's inferred identification information varies with contributor DNA amount in a predictable way (17). A scatterplot of log(LR) information (*y*-axis) as a function of a contributor's log(*w*·[DNA]) quantity (*x*-axis) is roughly linear. Linear regression of a scatterplot permits examination of many match results within a single analysis, and lets each contributor in a group of mixture items be considered separately.

There are expected deviations from linearity in some situations. First, when mixture weights are equal, peak height data do not help uniquely assign alleles to a particular genotype. This inherent genotype ambiguity impedes contributor separation, diffusing probability across multiple allele pair possibilities. Such genotype probability diffusion at equal mixture weights reduces the LR, as seen in Figure 10 of (15). Second, once there is sufficient contributor DNA to achieve the RMP maximum value, additional DNA cannot further increase the LR beyond this limit. Thus, at high DNA amounts there is an information saturation, where the LR plateaus instead of continuing to linearly increase, as seen in Figure 7 of (17).

Scatterplots of log(LR) information versus log(*w*·[DNA]) contributor quantity were developed from the mixture contributors

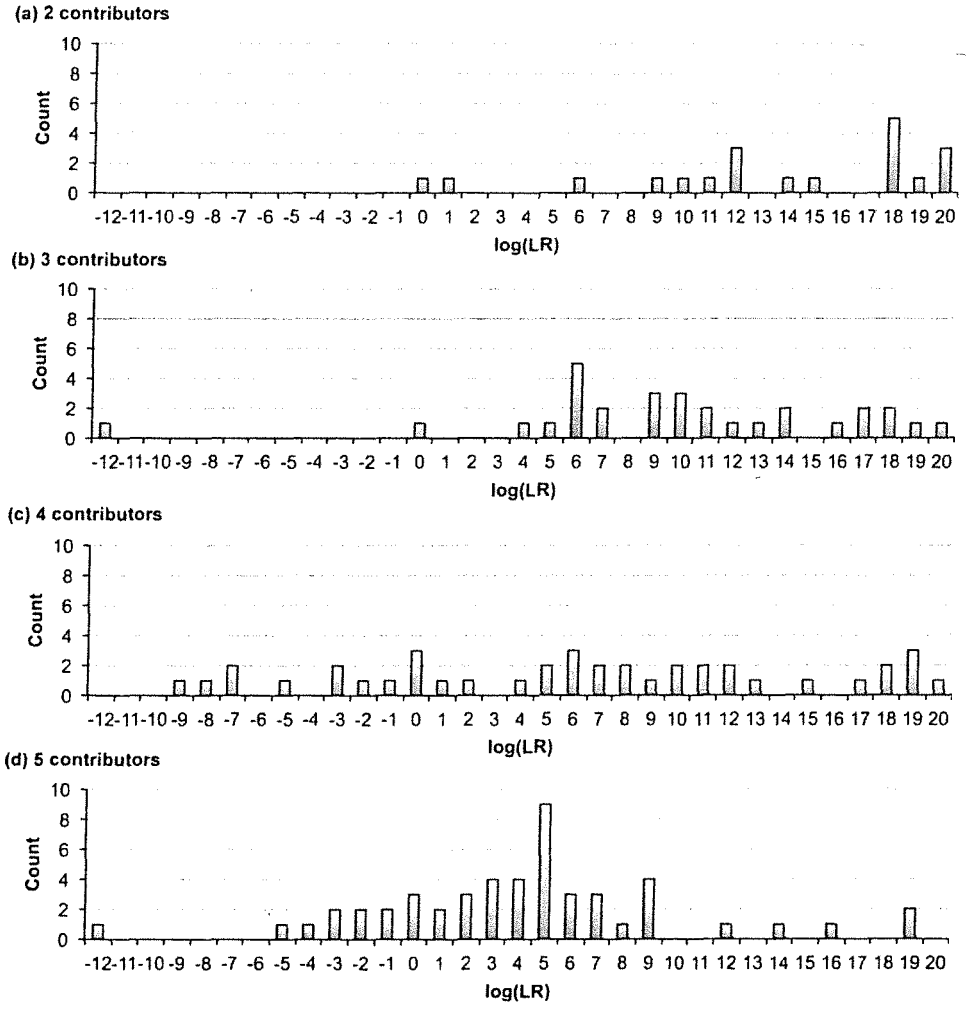

FIG. 4—*Sensitivity (1 ng). Histograms of the log(LR) distribution for mixtures having (a) 2, (b) 3, (c) 4, and (d) 5 contributors. Average replicate log(LR) scores were used.*

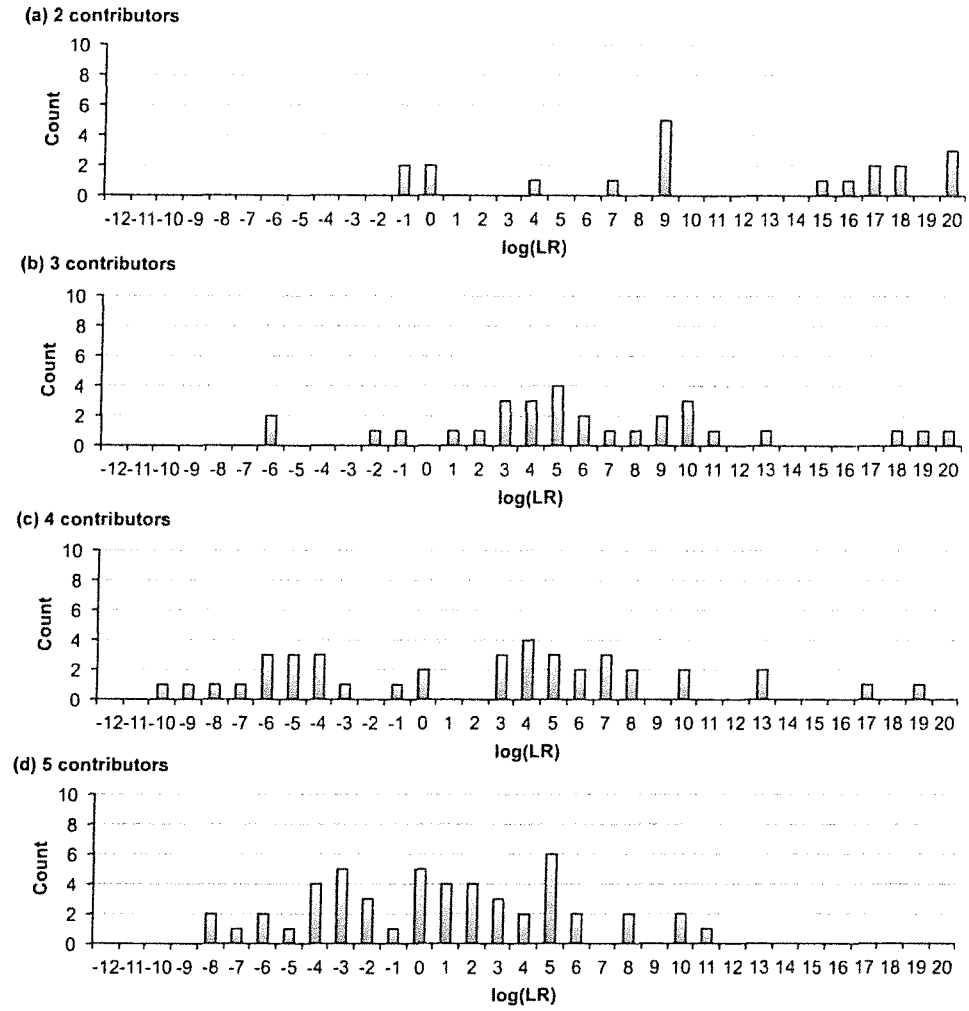

FIG. 5—*Sensitivity (200 pg). Histograms of the log(LR) distribution for mixtures having (a) 2, (b) 3, (c) 4, and (d) 5 contributors. Average replicated log (LR) scores were used.*

using their weight, quantity, and log(LR) values (Fig. 1). The scatterplots of positive match results were roughly linear ($r^2 = 0.505$), and for two contributors showed the expected log(LR) reductions for equal contributor weights and high DNA amounts. The average regression slope across all groups was 13.33 log(LR)/log(DNA), with a standard error of 0.74. This slope value means that a 10-fold change in contributor DNA amount yields about a trillion-fold change in LR (Table 3).

Interpretation Invariance

There were eight test groups, two for DNA quantity (high, low) and four different contributor numbers (2, 3, 4, and 5 individuals). The slope parameter describes an important aspect of interpretation behavior, namely how contributor DNA amount affects match information. Finding similarity in the slope parameter between the groups' regression results would suggest that TrueAllele's interpretation behavior is relatively invariant across these conditions. Such interpretation invariance would show that TrueAllele behaves consistently, regardless of the number of contributors or amount of DNA.

Consider, for example, the interpretation of a two-person high-template mixture, relative to that of a five-person low-template mixture. The peak height data for these two situations would look entirely different. On average, there is more identification information in a 1 ng two-person mixture than in a 200 pg five-person mixture, as seen in the 4 ban difference in respective y-intercept values of −14.9 and −18.6 (Table 3). But their respective slopes of 11.4 and 13.3 are similar, indicating a consistent information response to changes in contributor DNA amount.

Analysis of covariance (ANCOVA) was used to test this similarity hypothesis. The covariate was the slope of a regression line (Fig. 2). The null hypothesis was that the slopes (across the eight groups) were the same. To reject the null hypothesis, there would need to be a significant difference between the slopes. (The intercept values were expected to differ, as each DNA mixture group had its own average identification information.)

The eight groups showed different intercept values (Table 3), expressing group differences in DNA detectability (x-intercept) and identification information (y-intercept). There was no significant difference in regression line slope ($p = 0.3478 > 0.05$), and so the null hypothesis could not be rejected (Table 4). Table 3 indicates the slope invariance across four different contributor numbers (2, 3, 4, and 5) and DNA template amounts (1 ng and 200 pg). This invariance shows that TrueAllele's overall information response to DNA data does not significantly depend on a particular mixture's number of contributors or template amount.

TABLE 6—*Sensitivity. Sensitivity statistics were calculated for the eight groups (quantity and contributor number) as the average of two replicate log(LR) values. (a) The minimum, mean, maximum, and standard deviation (ban) use the smallest values across three ethnic populations. (b) The number of false exclusions are binned by log(LR) value (rows), with a total of 59 events.*

	1 ng				200 pg			
ncon	2	3	4	5	2	3	4	5
(a) Summary statistics								
N=	20	30	40	50	20	30	40	50
Min	0.219	−11.422	−8.994	−11.315	−0.722	−5.970	−9.719	−7.883
Mean	14.084	10.476	6.789	4.723	11.388	6.656	2.691	1.276
SD	6.209	6.542	8.375	5.716	7.572	6.323	7.258	4.725
Max	20.799	20.789	20.304	19.923	20.799	20.723	19.665	11.483
	1 ng				200 pg			
log(LR)	2	3	4	5	2	3	4	5
(b) False exclusions								
−1			1	2	2	1	1	1
−2			1	2		1		3
−3			2	2			1	5
−4				1			3	4
−5			1	1			3	1
−6						2	3	2
−7			2				1	1
−8			1				1	2
−9			1				1	
−10							1	
−11								
−12		1		1				
Total	0	1	9	9	2	4	15	19

TABLE 7—*Sensitivity varies with mixture weight. The true inclusion rate (one minus the false exclusion rate) based on positive log(LR) counts is shown for mixture weight ranges. There were a total of 280 observations, divided equally between the 1 ng and 200 pg DNA levels.*

N=	Mixture Range, %	1 ng, %	200 pg, %
4	0–1	0	0
20	1–5	40	0
17	5–10	82	24
33	10–25	100	91
39	25–50	100	100
25	50–100	100	100
140			

Contributor Sufficiency

Each assumed unknown genotype provides another dimension that can explain the data. When too few contributors are assumed, genotype inference can be restricted. This restriction artificially sharpens genotype (and match) results for major contributors, and dissipates minor contributor genotypes (and matches). With a surplus of assumed (relative to actual) contributors, there is sufficient genotype dimensionality to resolve a mixture.

Every mixture item in this study was synthesized with a known number of contributing individuals. TrueAllele processed each 1 ng mixture over a full range (1, 2, 3, 4, 5, and 6) of assumed unknown contributors, that is, the one correct value and five alternative values. Duplicate log(LR) results for an inferred genotype were averaged together. Figure 3 shows match information regression lines for two-person mixtures (one line for each mixture contributor) as the number of contributors assumed by the computer's interpretation is varied.

Once TrueAllele had assumed a sufficient number of contributors (i.e., at least as many as the actual number), the match results remained consistent (Fig. 3). With an excess of assumed contributors, the log(LR) scatterplot values generally decreased. Most of the information slopes were negative, suggesting that match statistic decreases as excess assumed contributors are added.

For all actual contributor numbers (2, 3, 4, and 5), linear regression showed negative average slopes for interpretations that had an excess of contributors (Table 5). Note that the negative slope values were sufficiently greater than their standard errors to be statistically different from zero ($p < 0.01$). The slope magnitudes were small, with values ranging from −1.30 to −0.26, indicating little average reduction in log(LR). Thus, assuming extra contributors in TrueAllele preserves the average match result, without overstating the match statistic.

Inclusion Distribution

Sensitivity measures the extent to which a mixture interpretation method includes a contributor. The log(LR) measures the degree of match between a genotype inferred from an evidence item and the genotype of an individual who has contributed to that item, relative to a population genotype. Previous studies have shown that this match information (in ban units) correlates with how much of that contributing individual's DNA (on a logarithmic scale) is present in the item (17).

Sensitivity was determined for each of the eight test groups. Figure 4 shows the log(LR) frequency distribution for each match of the high DNA quantity group (1 ng) for separate contributor numbers (2, 3, 4, or 5), while Fig. 5 shows the distribution for the low DNA quantity (200 pg) groups. The bar charts show a leftward shift as contributor number increases, indicating a decrease in average identification information. Using less DNA (200 pg vs. 1 ng) further reduced the log(LR) score.

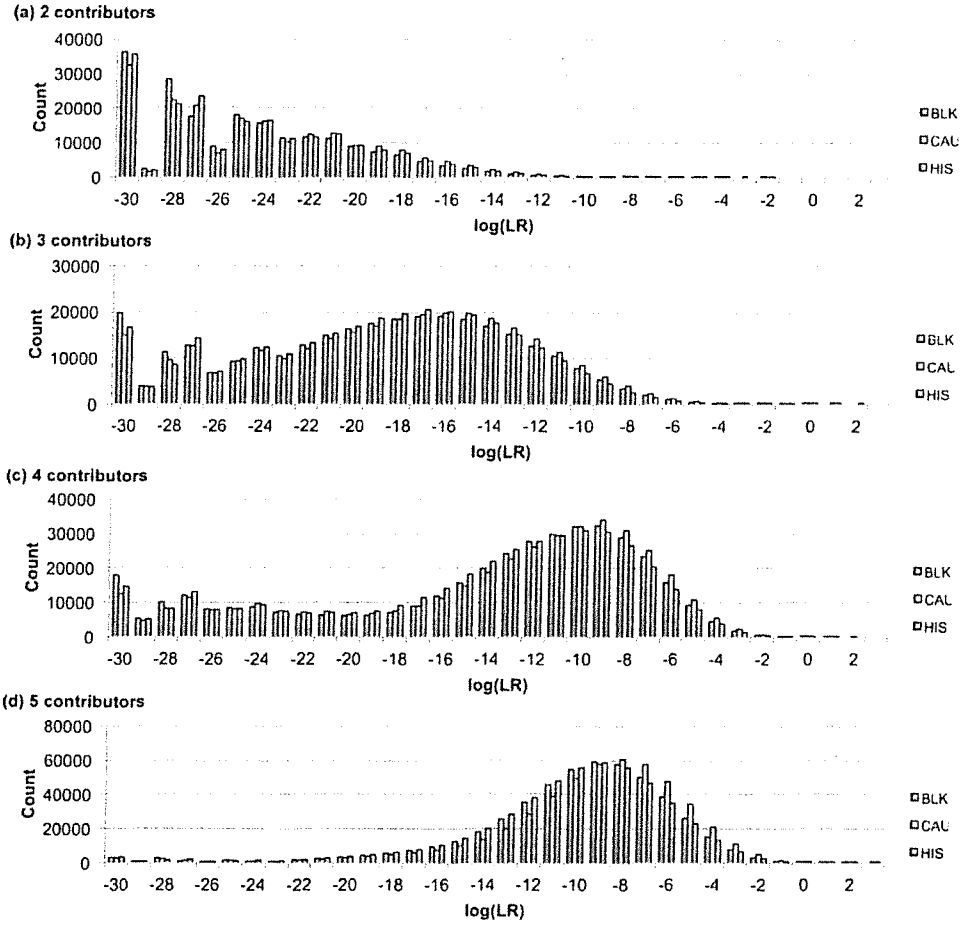

FIG. 6—*Specificity (1 ng). The log(LR) specificity distribution for mixtures having (a) 2, (b) 3, (c) 4, and (d) 5 contributors. The LRs were computed relative to 10,000 randomly generated profiles across the FBI African American (BLK, red), Caucasian (CAU, green), and Hispanic (HIS, blue) populations.*

These trends are quantified in Table 6a. The mean identification information for 1 ng mixtures decreased steadily from 14.084 ban with two contributors to 4.732 ban with five contributors. This decrease reflects the reduced amount of DNA in each contributor, as well as the uncertainty in separating their genotypes. The maximum values show that major contributors can produce definite genotypes that preserve all match strength, even with four other contributors present. The minimum values show more exclusion of known contributors with increasing contributor number. With a lower 200 pg template, the trends are similar, but start at a lower log(LR) level.

False exclusions increased with contributor number (Table 6b, Figs 4 and 5). The table rows stratify the false exclusion events by ban value. With 1 ng DNA, false exclusions with 2 or 3 contributors were rare (2%), but became more common (20%) with 4 or 5 contributors. There were more false exclusions when there was less DNA (200 pg), consistently increasing from 10% for two contributors to 38% with five contributors. There were a total of 59 false exclusions, of 280 observations (21%).

The true inclusion rate (i.e., 1 – false exclusion rate) was estimated as a function of mixture weight for common ranges used in forensic practice (Table 7). For full DNA amounts of 1 ng, mixture weights above 10% always gave a positive match result (no false exclusions), regardless of the number of contributors. This success rate fell to 82% in the 5–10% range, and down to 40% in the 1–5% range. With low-template amounts (200 pg), a positive identification was always made with a mixture weight over 25%. While the inclusion rate was 91% in the 10–25% mixtures, it dropped to 24% with 5–10% mixtures, and no matches were found below 5%. There were no inclusions when the mixture weight was under 1% ($N = 4 + 4$, for 1 ng and 200 pg).

Exclusion Distribution

Specificity measures the extent to which a mixture interpretation method excludes a noncontributor. The log(LR) measures the degree of exclusion (relative to a population) through the magnitude of a negative match value. A mismatch can occur between two genotypes, one inferred from an evidence item, and another from an individual who may have not contributed their DNA to that item. Previous studies have shown that such mismatches generally produce negative log(LR) numbers, with occasional positive values near zero (16).

To assess specificity, each inferred evidence genotype (using the first replicate) was compared with 10,000 genotypes that were randomly generated from an ethnic allele frequency distribution. This comparison was performed three times, once for each ethnic population.

Specificity was determined for each of the eight mixture subgroups. Figure 6 shows the empirical log(LR) distribution for mismatch with high DNA levels (1 ng) for each contributor number (2, 3, 4, or 5). Similarly, Fig. 7 shows the mismatch distribution for low DNA levels (200 pg). The figures show

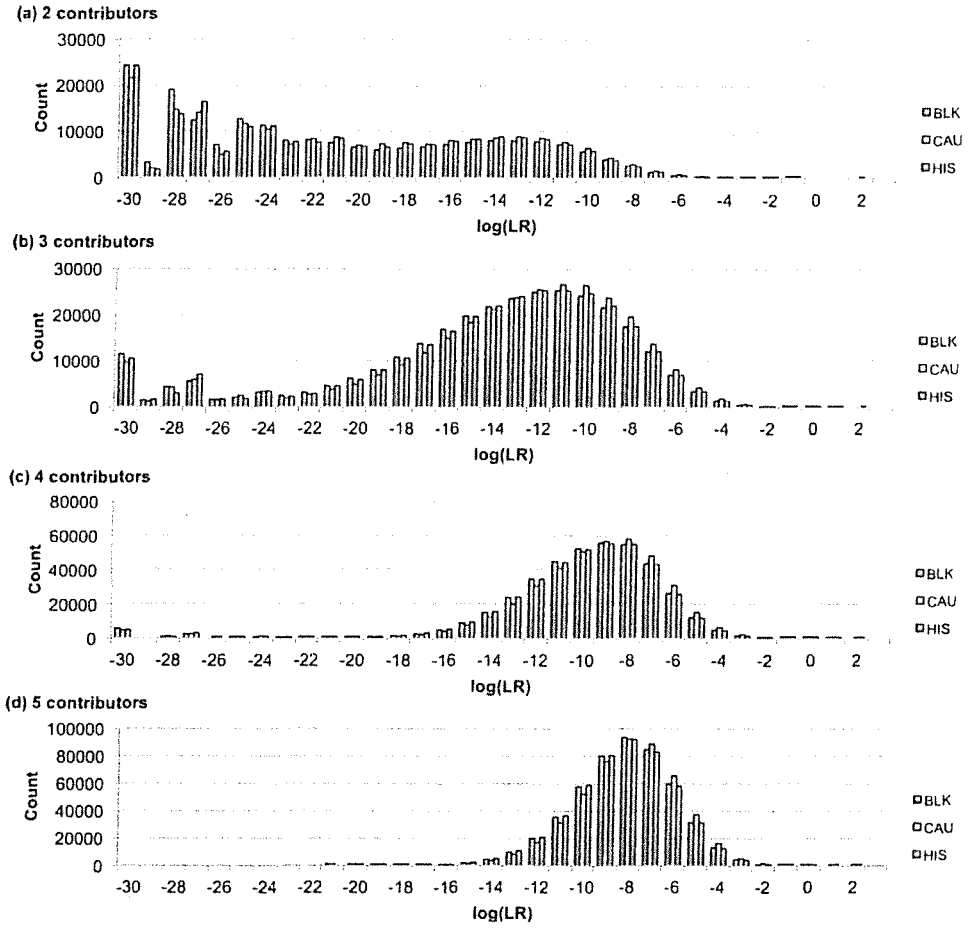

FIG. 7—*Specificity (200 pg). The log(LR) specificity distribution for mixtures having (a) 2, (b) 3, (c) 4, and (d) 5 contributors. The LRs were computed relative to 10,000 randomly generated profiles across the FBI African American (BLK, red), Caucasian (CAU, green), and Hispanic (HIS, blue) populations.*

TABLE 8—*Specificity. Specificity statistics were calculated for the eight groups (quantity and contributor number). (a) The minimum, mean, maximum, and standard deviation log(LR) values were averaged across three ethnic populations. (b) The total number of false inclusions is shown for each group, binned by log(LR) value (rows).*

	1 ng				200 pg			
ncon	2	3	4	5	2	3	4	5
(a) Summary statistics								
N=	600,000	900,000	1,200,000	1,500,000	600,000	900,000	1,200,000	1,500,000
Min	−30.000	−30.000	−30.000	−30.000	−30.000	−30.000	−30.000	−20.143
Mean	−23.904	−18.339	−13.878	−9.429	−20.247	−13.507	−9.517	−7.636
SD	4.608	5.990	7.183	4.536	6.821	5.986	4.048	2.218
Max	−1.514	1.511	2.140	3.202	0.410	1.878	2.006	1.671
	1 ng				200 pg			
log(LR)	2	3	4	5	2	3	4	5
(b) False inclusions								
0	0	18	142	1071	0	36	152	123
1	0	6	37	200	0	16	22	18
2	0	1	7	24	2	1	3	4
3	0	0	0	6	0	0	0	0
Total	0	25	186	1301	2	53	177	145

shrinkage toward zero information, as contributor number increases, for both high and low DNA amounts (1 ng and 200 pg).

These trends are quantified in Table 8. The mean values showed roughly equal specificity across the three different ethnic groups (Tables S1 and S2). At 1 ng (Table 8a), there was

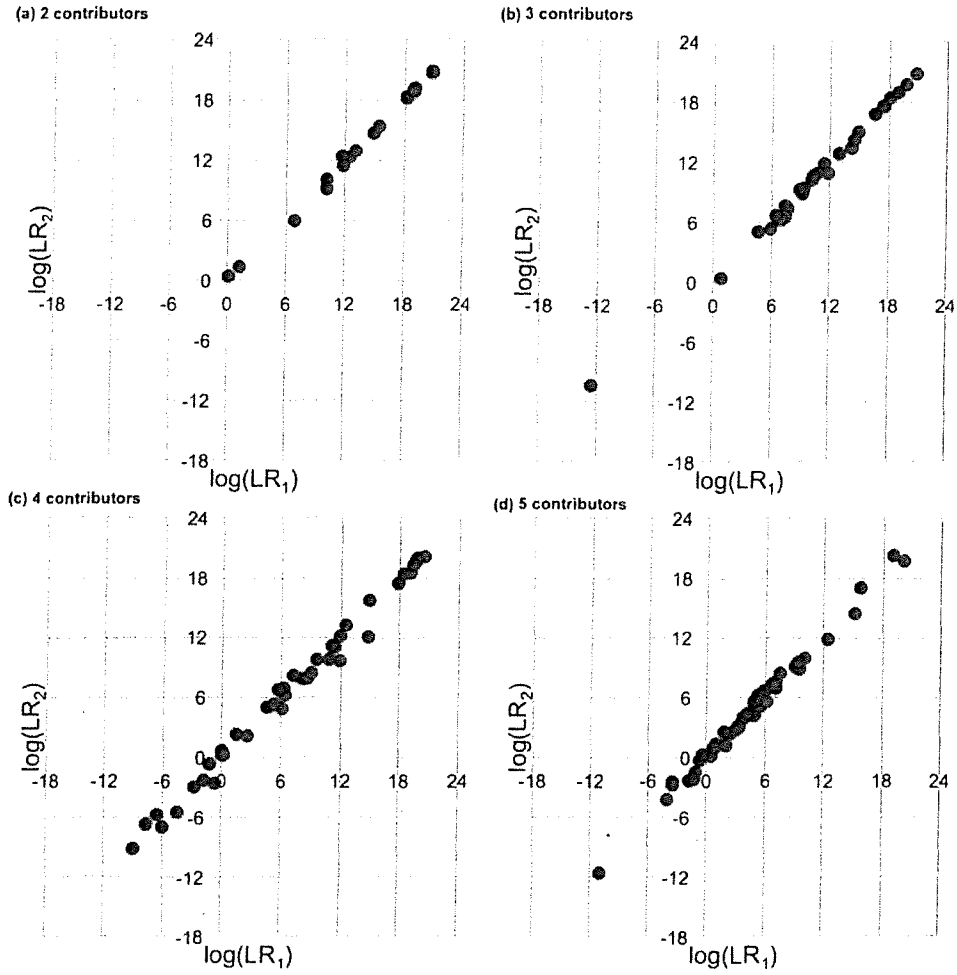

FIG. 8—*Reproducibility (1 ng). Scatterplots of paired log(LR) values for duplicate computer runs on the same mixture sample. The mixtures had (a) 2, (b) 3, (c) 4, and (d) 5 contributors. Each point shows the first (LR_1) and second (LR_2) replicates.*

shrinkage toward zero information when proceeding from two contributors (−24 ban) to five (−9 ban). The lower DNA amount (200 pg) showed the same progression, but the reduced genotype information was already closer to zero: −20 ban for two contributors, increasing to −7 with five contributors.

For two contributors, false inclusions were rarely seen (Table 8b, Figs 6 and 7), with none occurring at 1 ng and just 2 events at 200 pg (N = 600,000). The table rows stratify the false inclusion events by ban value. The false inclusion level increased with contributor number, reaching a maximum rate of 0.0867% with five contributors in 1 ng of DNA (1301 events of 1,500,000 comparisons). The other seven subgroups had appreciably lower error rates (Table 8b). There were few false matches beyond an LR of 10, and essentially none (six events in 8,400,000) with an LR > 1000.

Reproducibility Comparison

The reproducibility of a DNA interpretation method describes how well a match statistic is independently replicated on the same data. Once two (or more) interpretations have been made on the same data group, an interpretation method's reproducibility can be quantified using a within-group standard deviation. This statistic measures the log(LR) variation (about the average interpretation result) for each mixture contributor within the group.

There is expected interpretation variation arising from the MCMC statistical sampling. Scatterplots show that when genotypes are concordant, so too are the DNA match statistics (Figs 8 and 9). Each point gives the pair of log(LR) values from two concordant computer runs, independently run using the same parameter settings. As these points line up along the 45 degree equi-information line, TrueAllele's reproducibility is visually evident.

Table 9 gives the within-group standard deviation (σ_w) values for each group. Small σ_w values were found in all eight subgroups, never exceeding half a ban. These small σ_w values quantitatively confirm TrueAllele's reproducibility. In forensic practice, two independent computer runs on an evidence item can provide reporting confidence.

Conclusions

The computer interpretation of DNA evidence is a 21st century necessity. With ever-increasing numbers of STR loci, DNA mixtures having three or more contributors, low-level or degraded samples, and the potential for subjective examination bias (22,30), human analysts cannot be expected to fully process

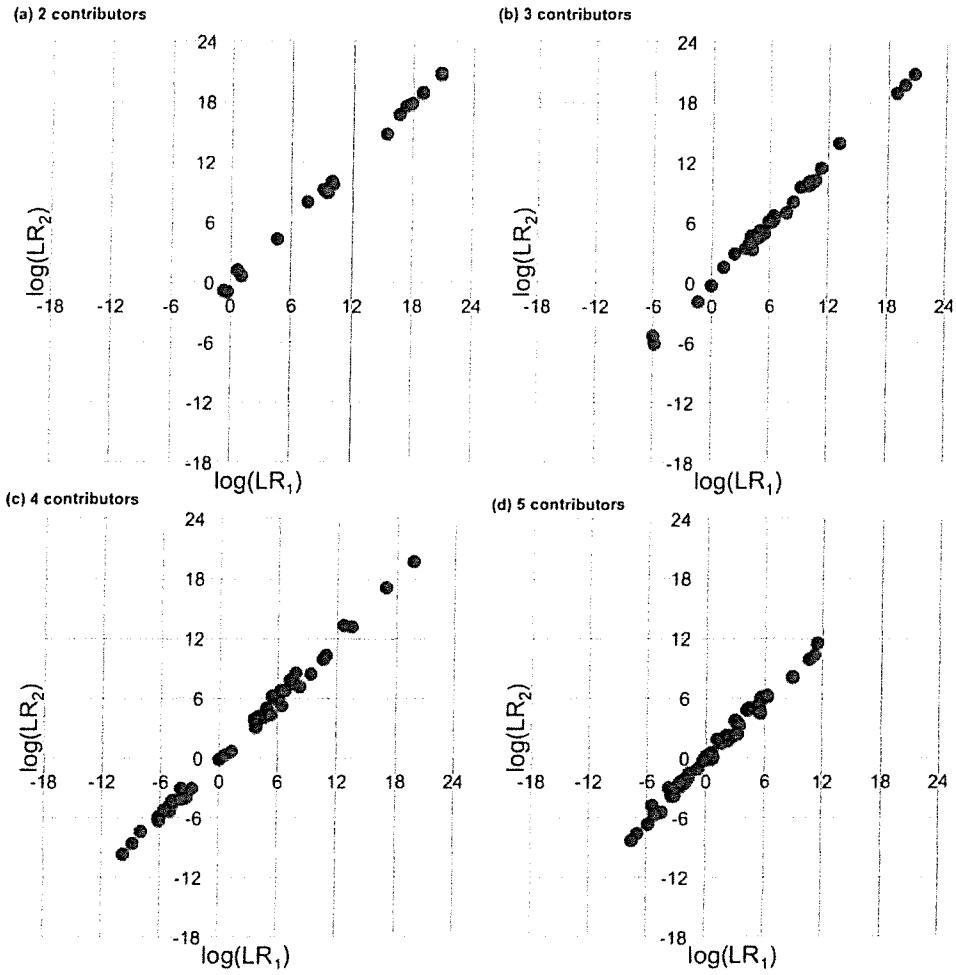

FIG. 9—*Reproducibility (200 pg). Scatterplots of paired log(LR) values for duplicate computer runs on the same mixture sample. The mixtures had (a) 2, (b) 3, (c) 4, and (d) 5 contributors. Each point shows the first (LR_1) and second (LR_2) replicates.*

TABLE 9—*Reproducibility. The table shows the within-group standard deviation σ_w (ban) for each of the eight test groups, at both 1 ng and 200 pg DNA template amounts.*

ncon	1 ng	200 pg
2	0.189	0.171
3	0.281	0.205
4	0.430	0.255
5	0.287	0.254

all the data. Such thorough and objective mathematical DNA mixture interpretation is the province of machines (31).

To be forensically useful, interpretation methods must be fully tested on realistic data. When software programs cannot robustly resolve challenging mixtures, their casework applicability becomes limited (e.g., DNAMIX, I-3, LoComatioN, LSD, PENDULUM). For over 10 years, TrueAllele has been extensively assessed in validation studies performed by crime laboratories and Cybergenetics, with publication in peer-reviewed journals (15–19).

This TrueAllele validation study used randomly generated DNA mixtures of known composition that were representative of actual casework. The samples contained up to five contributors, for both high- and low-template amounts. The study assessed the efficacy of the computer's genotype modeling, as quantified by LR.

The computer's mixture weight values were found to be reliable. The computed match information varied with DNA quantity in a predictable way that did not significantly depend on contributor number or template amount. Excess assumed contributors did not materially affect the conclusions.

The match statistic determination of inclusion and exclusion gave reproducible match values. The system was highly sensitive, preserving considerable identification information. It was also extremely specific, providing large exclusionary match statistics. Error rates were determined for false inclusions and exclusions. Inclusion accuracy was tabulated as a function of mixture weight.

This in-depth experimental study and statistical analysis establish the reliability of TrueAllele for the interpretation of DNA mixture evidence over a broad range of forensic casework conditions.

Conflict of Interest

Dr. Mark Perlin is a shareholder, officer, and employee of Cybergenetics, Pittsburgh, PA. Jennifer Hornyak is an employee of Cybergenetics. Garett Sugimoto and Dr. Kevin Miller are employees of the Kern Regional Crime Laboratory, a government

agency that provides expert DNA testimony in criminal cases and uses the TrueAllele Casework system.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1 Specificity (1 ng). The statistics for specificity were calculated for each contributor group across all three FBI ethnic populations.

Table S2 Specificity (200 pg). The statistics for specificity were calculated for each contributor group across all three FBI ethnic populations.