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. 201 1 ;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.q. 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.

Judge Emory L. Palmer
Superior Court Judge
Coweta Judicial Circuit