IN THE SUPERIOR COURT OF DECATUR COUNTY
STATE OF GEORGIA

STATE OF GEORGIA	)	
V.	)	CASE NO. 18-CR-134
THADDUS NUNDRA, RONNIE MCFADDEN, LOUIS OUSLEY,	)	
Defendants.	)	

ORDER

COMES NOW This Court, having read and considered all motions, responses, all arguments by Defendants and the State of Georgia, the record of this Court, and the applicable law, hereby admits the following under case precedent and legal authority and ORDERS the following:

TrueAllele in DNA Analysis

TrueAllele® is a probabilistic genotyping computer system that interprets DNA evidence using a statistical model. TrueAllele is used to analyze DNA evidence, particularly in cases where human review might be less reliable or not possible. A definite genotype can be readily determined when abundant DNA from one person produces unambiguous genetic data.

However, when data signals are less definitive, or when two or more people contribute to the evidence, uncertainty arises. This uncertainty is expressed in the derived contributor genotype, which may describe different genetic identity possibilities. Such genotype uncertainty may translate into reduced identification information when a comparison is made with a suspect. The DNA identification task can thus be understood as a two-step process:

1.) Objectively inferring genotypes from evidence data, accounting for allele pair uncertainty using probability, and

2.) Subsequently matching genotypes, comparing evidence with a suspect relative to a

population, to express the strength of association using probability.

The match strength is reported as a single number, the likelihood ratio (LR), which quantifies the change in identification information produced by having examined the DNA evidence. The TrueAllele Casework system is Cybergenetics computer implementation of this two-step DNA identification inference approach. Cybergenetics began developing TrueAllele 22 years ago, adding a mixture module 17 years ago. The casework system underwent many rounds of testing and model refinement over 10 years before it was used in criminal casework, with the current version 25 released in 2009. The TrueAllele computer objectively infers genotypes from DNA data through statistical modeling, without reference to a known comparison genotype. To preserve the identification information present in the data, the system represents genotype uncertainty using probability. These probabilistic genotypes are stored on a relational database. Subsequent comparison with suspects or other individuals provides identification information that can be used as evidence.

TrueAllele's Widespread Acceptance

TrueAllele has been used in over 500 criminal cases, with expert witness testimony given in over 50 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.

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.[1] The TrueAllele calculation is entirely objective: when it determines the genotypes for the contributors to the mixture evidence, the computer has no knowledge of the comparison genotypes. Genotype comparison and match statistic determination are only done after genotypes have been computed. In this way, TrueAllele computing avoids human examination bias, and provides a fair match statistic.

TrueAllele is Reliable

There is no genuine controversy as to the validity and reliability of the TrueAllele method. To the contrary, computer analysis of uncertain data using probability modeling is the scientific norm. Forensic science researchers see this as the best approach. 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

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

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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.[2]

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.[3]

Conducting such validations is consistent with the FBI's 2010 Scientific Working Group on DNA Analysis Methods (SWGDAM) interpretation guidelines. TrueAllele

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[2] (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.

[3] (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.

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. TrueAllele has been admitted into evidence after opposition challenges in eighteen courts. Jurisdictions that have admitted TrueAllele include California, Florida, Indiana, Louisiana, Massachusetts, Nebraska, New York, Ohio, Pennsylvania, South Carolina, Tennessee, Virginia, Washington, Northern Ireland and Australia.

Eighteen 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 (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.

DR. MARK PERLIN

Dr. Mark Perlin (hereinafter referred to as "Dr. Perlin") testified he has been called to court as a 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 Exhibit 1, and the Court declared him an expert in DNA evidence interpretation and likelihood ratio (LR). 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 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 Exhibit 3.

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

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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. See Exhibit 2.

Dr. Perlin testified thirty-six validation studies have been conducted on TrueAllele either by Cybergenetics, independent crime labs, or collaboration of both; studies, twenty-three are internal validation studies. See also Exs. 6A & 76 (containing 34 validations studies); Ex. 2, folder labeled "validation" contains 39 files.

Seven of thirty-six 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

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the method.[4] Here, although the majority of the publications have been by Cybergenetics, other entities have also reviewed TrueAllele's method.[5]

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.[6] 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.[7] Dr. Perlin testified the MCMC algorithm is considered one of the ten most widely used in computer science. TrueAllele's Visual User Interface (VUIer™) tool uses MATLAB programming language, which Dr. Perlin described as "a standard, high-level programming language for visualization, finding numerical solutions and problems." Bayesian Statistics are a technique that assigns "degrees of belief," or Bayesian probabilities, to traditional statistical modeling. In this interpretation of statistics, probability is calculated as the reasonable expectation of an event occurring based upon currently known triggers. Or in other words, that probability is a subjective process that can change as new information is gathered, rather than a fixed value based upon frequency or propensity.[8]

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[4] 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.

[5] .[5] See S. Greenspoon, L. Schiermeir-Wood & B. Jenkins, Establishing the Limits of TrueAllele Casework: A Validation Study, 60 Journal of Forensic Science, 1263 (2015).

[6] See also Ex. 9 binder titled "Method Reports"; Ex. 2.

[7] See also Ex. 15 binder titled "Other Papers"; Ex. 2.

[8] 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 Exhibit 15 and on the disc

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Dr. Perlin replied although TrueAllele was the first of its type, he believes probabilistic genotyping programs are "quite mainstream" given the current state of forensic science. He noted at least ten programs are available on the market.[9]

Dr. Perlin explained initially he had concerns about disclosing the TrueAllele source code, particularly in 2014; however, since the source code has been a continually litigated issue, Cybergenetics made a decision around 2017, to disclose its source code under specific conditions. Dr. Perlin testified the defense did not accept the offer nor has anyone else.

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.[10] Dr. Perlin further testified TrueAllele has a known error rate under a 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

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marked Exhibit 2 (located in "Foundation" folder filed within the "Other papers" file under "1-reliability"); Matthew Richey, The Evolution of Markov Chain Monte Carlo Methods, Math. Assoc. of America. (May 2010), which is included in the binder admitted into evidence as Exhibit 15 and on the disc marked Exhibit 2 (located in "Foundation" folder filed within the "Other papers" file under "1-reliability"); 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 Exhibit 15 "Other Papers" and on the disc marked Exhibit 2).

[9] See also Ex. 11 binder titled "Related Systems"; also see Ex. 2.
[10] See binder Ex. 15 "Other Papers"; also see ex. 2.

genotyping methods used before, such as the Modified Combined Probability of Inclusion (CPI), TrueAllele has a far lower error rate.

When asked about the California Department of Justice (CDOJ) study that revealed an 18% error rate with True Allele, Dr. Perlin referred to it as a "secret study" that he had learned about last year through a FOIA request; the study was not published nor were the results reported to the forensic community. Dr. Perlin testified once he reviewed the study, it was clear CDOJ had changed, or modified, some key features of TrueAllele and did not use the original program to calculate statistics; thus, the study demonstrated error rate when the program is not run correctly, rather than the accuracy of the program.

Conclusion

The Court finds the probabilistic genotyping program TrueAllele satisfies the Harper standard. Substantial evidence has been presented to the Court, which supports the admission of TrueAllele analysis, and no significant evidence has been presented to the contrary.

The procedure or technique in question, probabilistic genotyping, 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 in favor of probabilistic genotyping over other genotyping. The error rate for probabilistic genotyping is much less than that of other genotyping methods the Courts have already deemed scientifically reliable.

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 exhibits and treatises submitted on behalf of the State as shown in the record.[11] Finally, the Trial Court relies on the rationale of cases in other jurisdictions that the Court has reviewed.[12]

Based on all the evidence presented, this Court finds the TrueAllele analysis reliable as applied in this case, and the testimony of either Dr. Perlin or Emily Mathis 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 probabilistic genotyping is admissible at trial. The Trial Court finds that the State has met its burden under Harper. This matter remains scheduled for trial on February 11th, 2019.

IT IS SO ORDERED this 21st day of January, 2019.

Judge T. Craig Earnest
Superior Court Judge
South Georgia Circuit/ Pro Tempore

Prepared By:
Joe Mulholland
District Attorney
South Georgia Circuit

[11] See State's Ex. 2-15.
[12] See Ex. Binder 12, 13 "Admissibility Rulings" and "Legal Commentary"; see also Ex. 2.