IN THE SUPERIOR COURT OF BEN HILL COUNTY
STATE OF GEORGIA

STATE OF GEORGIA

vs.

BATTLE, ALEXANDER DARELLE

INDICTMENT NO(S):
16CR-082

ORDER

This case is before the Court on the State's intent to present evidence at trial of DNA analysis performed by the Georgia Bureau of Investigation using TrueAllele software. On April 7, 2019, the Court held an evidentiary hearing on the admissibility of the TrueAllele DNA results under Georgia's legal standard as established in Harper v. State, 249 Ga. 519 (1982).

After conducting the hearing and considering the evidence presented, the record of the case and the arguments of counsel, the Court hereby finds that the TrueAllele DNA results in this case do meet the Harper standard, will be admissible at trial and further makes the following findings of fact and conclusions:

For decades, DNA evidence has routinely been admitted in the courts of the State of Georgia, including advancements in the science and technology, after the courts assessed these advancements for reliability and validity. See Caldwell V. State, 260 Ga. 278 (1990) (holding restriction fragment length polymorphism (RFLP) analysis of DNA admissible); Redding v. State, 219 Ga. App. 182 (1995) (holding advancement of scientific techniques in DNA under polymerase chain reaction (PCR) admissible); Thrasher v. State, 261 Ga. App. 650 (2003) (holding STR/PCR DNA testing is a method that has been accepted as valid by Georgia courts); Shabazz v. State, 265 Ga. App. 64 (2004) (affirming admission of Y-STR DNA analysis from PCR derived profiles); Vaughn v. State, 282 Ga. 99 (2007) (affirming admission of mitochondrial DNA at trial).

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At the hearing on this matter, the trial court heard from Emily Schmidt, a forensic biologist and technical leader, at the Georgia Bureau of Investigation (GBI) Crime Laboratory. After hearing her qualifications and upon a motion by the State, the Court recognized her as an expert in forensic DNA analysis and TrueAllele software. Mrs. Schmidt provided expert testimony to include an explanation regarding long-established procedures involving DNA extraction and PCR techniques that are utilized in the preparation of DNA profiles for comparison purposes. She explained that TrueAllele software does not change in any manner the established validity of that method nor the reliable method of generating DNA profiles. But rather, TrueAllele provides the ability to analyze complex mixtures of DNA (2 or more) using a computer software program. Traditionally, once a PCR DNA profile is generated, a human analyst compares them to a known sample of DNA. If a match is obtained, then provides statistical weight to a given match by utilizing the long-standing statistical association technique known as the Random Match Probability (RMP). This analysis of the peak height thresholds is most commonly used for a single DNA profile of a single contributor. Humans analysts are limited in their ability to interpret complex mixtures because of the applied thresholds, and generally these mixtures provide an inconclusive result due to human limitations of time and mathematical ability to analyze the possibilities to separate the mixture of DNA.

Thus, TrueAllele provides this component as a probabilistic genotyping software to analyze DNA evidence based upon long accepted statistical and mathematical models from Bayesian statistical analysis and the Markov chain Monte Carlo (MCMC) algorithm. This probabilistic analysis includes consideration of DNA's known biological and PCR properties, and the prevalence of certain DNA variants in the population.

TrueAllele begins by analyzing a DNA mixture obtained from an item of evidence. When analyzing allele locations of DNA in this mixture, TrueAllele considers the overlapping DNA components, or alleles, present from each contributor's DNA. The alleles are observed by peaks of varying heights and locations on an electropherogram. TrueAllele considers that each individual contributor to the mixture of DNA contributes one or two alleles at a given location. Those alleles at any locations are that individual's genotype.

TrueAllele provides a deconvolution of a mixture of DNA wherein the entire group of alleles are assessed at a particular location of the DNA mixture and considers the likelihood of different possibilities of sorting and pairing the alleles into separate genotypes. Utilizing known biological principles, TrueAllele determines which proposed configurations of genotypes are more likely and assigns a probability that reflects the likelihood the proposed genotype correctly explains the DNA mixture.

Once each 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 known genotype to the corresponding genotype that has been inferred from the item of evidence and a probability is obtained. That probability compared to the known sample of DNA is then divided by the probability of a random person in the population having the same genotype. This result is then expressed as 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 person of the known sample actually contributed their DNA to the mixture versus a match existing by coincidence.

The aforementioned procedure is repeated on a number of different locations of the DNA mixture. The LR's determined for each location is then multiplied together to obtain a final LR

reflecting 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 swabbings from the tee-shirt from item 1 (item 6) and Alexander Battle is approximately 100 trillion times more probable than a coincidental match to an unrelated person in the population."

Reliability

The TrueAllele method of analysis meets the standards for both validity and reliability; computer analysis for uncertain data using probability modeling is the scientific norm. The reliability of the mathematical concepts of True Allele, Bayesian Statistics and the Markov Chain Monte Carlo (MCMC) algorithm, have been utilized since the 1700's and 1950's respectively. The PCR generated DNA profiles TrueAllele analyzes are the same profiles analyzed by other methods of admissible DNA analysis that have existed for decades and previously determined to be admissible in courts of this state.

Cybergenetics, the company that developed TrueAllele software, in addition to other independent crime labs or a combination of both groups, have performed validation studies upon the software. Thirty-six (36) validation studies have been conducted to establish the reliability of the TrueAllele method and software in the areas of reproducibility, specificity, and sensitivity. Seven of these studies have been published in peer-reviewed scientific journals, for both laboratory-generated and casework DNA samples. Other validation studies provided to the court were "laboratory-generated." Two of those "laboratory-generated" studies were performed at the GBI Crime Laboratory by Emily Schmidt.[1] Other crime laboratories like the Kern County

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1. Hornyak, Schmidt, Perlin, *Georgia Bureau of Investigation Forensic Biology Unit TrueAllele Validation* (Cybergenetics , GBI Forensics Biology Unit: September, 2016); Schmidt, *TrueAllele GlobalFiler Performance Check* (GBI Forensics Biology Unit: August, 2017).

Regional Crime Laboratory (Bakersfield, CA) and Virginia Department of Forensic Science conducted their own validation studies by independent scientists prior to their crime laboratories were permitted to use TrueAllele for casework.

Reproducibility

Reproducibility concerns the consistency of the results of the analysis as expressed in the LR. Sensitivity speaks to 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.

These validation studies work in accordance with the FBI's 2010 Scientific Working Group on DNA Analysis Methods (SWGDAM) interpretation guidelines as well as the 2015 SWGDAM validation guidelines for probabilistic genotyping systems.

TrueAllele's Widespread Acceptance

TrueAllele results have been reported in 43 of 50 states. TrueAllele results have been admitted in the following states and countries: 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. Although ten (13) crime laboratories have purchased the True Allele system, eight (8) labs to include the GBI Crime Lab are operational after having independently validated the TrueAllele system.

TrueAllele was utilized to identify human remains from the World Trade Center disaster. Both prosecutors and defense attorneys, to include the Innocence Project, have utilized TrueAllele

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match statistics. TrueAllele has been admitted into evidence in the state of Georgia after a <u>Harper</u> hearing in Decatur County, Georgia, and Coweta County, Georgia.[2]

Emily Schmidt

Emily Schmidt has testified as an expert witness in the field of forensic biology and DNA analysis between 30 to 40 times. She testified to her credentials, also provided her *curriculum vitae*, and the Court recognized her as an expert in forensic biology, DNA and TrueAllele. Mrs. Schmidt spent two years performing two different validation studies on the TrueAllele software. She has also been through two separate trainings on TrueAllele by Dr. Mark Perlin and thereafter provided training to the analysts at the GBI crime lab. Schmidt provided the court with the science of DNA analysis and the later process using TrueAllele to calculate LRs, using a powerpoint slide show, which is State's Exhibit 10. Within this slide show, she further explained the validation process to include sensitivity, specificity and reproducibility.

The TrueAllele method and source code is made available to opposing experts for review, examination and questions at their office in Pittsburgh, Pennsylvania for Cybergenetics or through a Skype-style video conference. TrueAllele remains objective since the computer determines the evidence genotypes without any knowledge of the comparison reference genotypes which precludes bias in the DNA data. The LR is only calculated later by comparing evidence genotypes with reference genotypes.

Schmidt testified that the GBI with its policies and procedures for TrueAllele abides by the FBI's Quality Assurance Standards. Schmidt testified that TrueAllele uses MCMC computing,

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[2] State v. Nundra, McFadden, and Ousley, 18CR134 (Decatur Co. Sup. Ct. 01.29.19); State v. Baugh and Howell, 2017-CR-618 (Coweta Co. Sup. Ct. 03.22.19).

one of the oldest and well-adopted methods, dating back to the 1950's, as well as the long-accepted Bayesian methods.

TrueAllele's reliability was established by the evidence presented in this case. Ashley Hinkle, another forensic biologist, trained by Emily Schmidt and Dr. Mark Perlin, in the use of TrueAllele, testified that she performed the TrueAllele analysis in the instant case in accordance with her training, procedures and requirements from the GBI and TrueAllele.
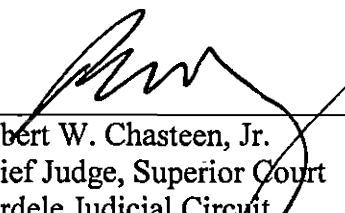
Conclusion

The Court finds TrueAllele software satisfies the Harper standard. The procedure or technique in question, TrueAllele's method of probabilistic genotyping, has reached a scientific stage of verifiable certainty. There has been substantial peer review of the subject matter. Numerous validation studies have been conducted that recognize TrueAllele's reliability.

The Court makes this determination from evidence presented to it at hearing in the form of expert testimony from Emily Schmidt and Ashley Hinkle. The Court also bases its determination upon all the exhibits and treatises submitted on behalf of the State as shown in the record, to include other courts contained in the DVD admitted as State's Exhibit 2.

Based upon the foregoing, the Court further 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 both Emily Schmidt and Ashley Hinkle would substantially assist the trier of fact in understanding the evidence. The TrueAllele analysis are scientifically reliable and testimony concerning the results are admissible at trial. The trial court finds that the State has met its burden under Harper.

SO ORDERED, this __11__ day of May, 2019, *nunc pro tunc*, the 7th day of April, 2019.

Robert W. Chasteen, Jr.
Chief Judge, Superior Court
Cordele Judicial Circuit

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