ORIGINAL

FILED

OCT 23 2019

Tammy M. Howard, Clerk
Superior & State Court
Douglas County, GA

IN THE SUPERIOR COURT OF DOUGLAS COUNTY
STATE OF GEORGIA

STATE OF GEORGIA

Plaintiff

Versus **CASE NO. 17CR00938**

ADEDOJA OLANIYI BAH

Defendant

ORDER - TrueAllele

This matter came before the Court on Defendant Adedoja O. Bah's Motion to Exclude the State's Expert Testimony from Georgia Bureau of Investigation (GBI) Forensic Biology Crime Laboratory Scientist Ashley Hinkle as to testing, analysis and interpretation of two swabs (vaginal and facial) using Developer Cybergenetics' TrueAllele® Casework System. TrueAllele uses probabilistic genotyping to separate and then examine and analyze multiple sources of DNA contained in a particular mixture where human visual testing and analysis has reached its limits due to a number of factors (besides the number of contributing individuals) are scientific and non-scientific and which exponentially increase the challenge to objectively and correctly analyze DNA samples.

Bah moved to exclude on the basis that the processes and procedures underlying the TrueAllele system do not qualify for admission under *Harper v. State*[1] as the State has not shown that TrueAllele "has reached a scientific stage of verifiable certainty, or in the words of Professor Irving Younger, whether the TrueAllele "rests upon the laws of nature."[2] Essentially, Bah's overall contention is like that in *Caldwell v. State* and "essentially [is] ... the manner in which [TrueAllele] ... declares a "match[]" and in its probability calculations."[3]

Bah's specific objections, stated during the hearing, and as understood by this Court, were that the source code of the TrueAllele has not been reviewed because such review has been frustrated by Cybergenetics' refusal to make available the source code for examination, that there have been articles and studies that have questioned in certain

[1] 249 Ga. 519, 524-526, 292 S.E.2d 389 (1982)
[2] *Harper v. State*, 249 Ga. 519, 525, 292 S.E.2d 389, 395 (1982).
[3] 260 Ga. 278, 279, 393 S.E.2d 436 (1990).

aspects of the TrueAllele system, and that there has been no independent review of TrueAllele. As to this last, Bah contends that the published peer review studies and studies where Cybergenetics or an entity with a financial interest in or some relationship with Cybergenetics studies do not qualify.

The State contemporaneously moved that this Court take judicial notice that TrueAllele is admissible under *Harper*.

A reported evidentiary hearing was held October 16, 2019 on whether TrueAllele in general and as applied to the specific testing performed in this case by Hinkle is admissible under *Harper*. Besides Hinkle, who testified to her work in this case, Emily M. Schmidt[4] with the GBI testified as to the TrueAllele system in general and the GBI's validation of the software and implementation of the system in January 2018.

After review of the record, for the reasons below, the Court DENIES Bah's Motion to Exclude finding that evidence derived using TrueAllele is admissible under *Harper*, specifically finding that the TrueAllele probabilistic genotyping system has reached the stage of veritable certainty so that the testing and results "rest upon the laws of nature." The Court further finds that Hinkle's testimony is admissible under *Harper* as she testified that she was knowledgeable of and abided by the protocols established and employed by the GBI for use in the TrueAllele system while carrying out the testing, analysis and interpretation of results from the two buccal swabs submitted to the GBI by the Douglas County Sheriff's Office in this case.[5]

With regards to Bah's contention about TrueAllele's source code not having been reviewed because of Cybergenetics' refusal to make available the source code for examination, Bah has not made such a request.[6] Moreover, Bah has not begun to make the materiality showing that an expert's "testimony regarding the source code bore a logical connection to facts supporting the existence of error in his [DNA] results" as required by *Cronkite v. State*, 293 Ga. 476, 745 S.E.2d 591 (2013) or that an expert could timely

[4] Schmidt, a forensic biology technical leader, was admitted by the Court without objection from the defense as an expert in the areas of DNA, DNA testing and TrueAllele. Schmidt's curriculum vitae was admitted without objection as State's Exhibit #1.
[5] The written results of Hinkle's testing were admitted for this hearing without objection as State's Exhibit #13.
[6] Cybergenetics in 2017 established a method for defense experts to request access to the source code for inspection purposes. See State's Exhibit #3 (4-VUier folder/"6-Source code" folder/Access to Source Code.pdf) and page 9 the *Nundra* 2019 decision (Decatur Superior Court which is Exhibit A of the State's Bench Brief filed August 26, 2019.

examine the source code which review Schmidt testified would take between 8-1/2 to 10 years to complete.[7]

There have been *Harper* hearings in two other jurisdictions which the State admitted without objection the 2019 written rulings.[8] The Court has reviewed those rulings and incorporates portions of each the rulings into this order.

In reviewing a trial court's order on a particular DNA testing system, the Georgia Supreme Court in *Caldwell v. State*[9] set forth a "brief genetic biological primer" which is provided below in relevant part:[10]

> A cell is the basic unit of all living organisms.... The human body has more than 10 trillion cells. A cell has two main parts—the nucleus and the cytoplasm. The nucleus contains two important types of structures: chromosomes and nucleoli. The cytoplasm is all the material inside the cell membrane outside the nucleus. The nucleus contains the cell's genetic program, a master plan that controls almost everything the cell does. It sends instructions to cytoplasm, which is the cell's chemical "factory," to take amino acids and build proteins—to construct an arm, a leg, a head, and ultimately a total, functioning human body.
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> A chromosome is composed mainly of DNA and associated proteins and stores and transmits genetic information. In each human cell there are 46 chromosomes, arranged in pairs of 22 plus two sex chromosomes (represented by X for female and Y for male).
>
> DNA is an abbreviation for deoxyribonucleic acid, its chemical structure. It is a molecule that carries the body's genetic information. It is contained in every cell with a nucleus in every living organism.
> In 1953, James Watson, an American scientist, and Francis Crick, a British

[7] Schmidt testified that a source code is the language that the software system reads to conduct the business of the software system.

[8] See State's Exhibit #3 (1-Reliability folder which contains the "Admissibility Rulings" folder) for the two rulings. The file names are Howell2019GA.pdf and Nundra2019GA.pdf and reflect trial court rulings from Coweta and Decatur counties. The State tendered a listing of 22 Georgia cases spanning a time period of March 2018 through October 9, 2019 in which TrueAllele evidence and testimony has allegedly been admitted. (The 22nd case is a Coweta March 2018 case listed at the bottom of State's Exhibit 8.) The list was admitted without objection. See State's Exhibit #7. One case is a federal case which ruling was premised on *Daubert v. Merrell Dow Pharm., Inc.*, 509 U.S. 579, 582, 113 S. Ct. 2786, 2791, 125 L. Ed. 2d 469 (1993). Another case is Douglas Superior Court case (18CR00747 JAMES DEWAYNE SHELTON). Cited by the State, It is a June 2019 jury trial on murder and aggravated assault charges. The State has alleged that TrueAllele testimony was admitted without objection. The Court cannot verify this as the record does not contain the trial transcripts. A non-particularized motion for a new trial has been filed. The motion does not appear to have been heard. State's Exhibit #9 shows 7 Georgia cases. The exhibit is dated April 2019.

[9] 260 Ga. 278, 393 S.E.2d 436 (1990).

[10] See also TrueAllele Computer Interpretation of DNA Mixtures - EMS 101119 FINAL (Powerpoint created by Schmidt and testified to during hearing; on State's Exhibit #2(b)); and Howell2019GA.pdf, page 2 (*Caldwell* cite).

scientist, working together at Cambridge University in England, discovered the chemical and spatial structure of the DNA molecule. It was a "double helix" in which two chains of nucleotides, running in opposite directions, are held together between pairs of bases reminiscent of the rungs of a ladder, and coiled like a spring. It looks like a twisted rope ladder or a spiral staircase. Wherever their derivation—human, animal or vegetable—all DNA molecules have this shape.

The long threads that make up the sides of the DNA ladder are made up of alternating units of phosphate and sugar called deoxyribose. The "rungs" of the "ladder" are made up of four compounds called *bases.* ... The order of the bases in one strand of the DNA ladder determines the order of the bases in the other strand. Each rung on the DNA ladder is known as a "base sequence," or a "base pair," and constitutes a bit of information. There are approximately 3 billion bits of information, or base sequences, in a molecule of DNA—that is, the genetic code in the nucleus of each cell of the human body consists of approximately 3 billion bits of information. The DNA molecule is tightly coiled within the nucleus of a cell like a ball of yarn. Unraveled, a molecule of DNA is approximately six feet in length.

A sequence of three bases on the DNA molecule is known as a codon. Groups of codons form genes. A gene is a unit of inheritance composed of a segment of DNA and carrying coded information associated with a specific function. It contains a certain number of base pairs in a certain order. The instructions for making specific proteins from the 20 amino acids contained in a cell are carried by specific genes. The genetic code lies in the order of the bases in the DNA molecule, organized in genes. ... Every human being inherits half of its genes from each of its parents. It is the order of the base sequences, organized in genes, that determines all of the characteristics of a living organism—the color of our eyes, the shape of our ears, and thousands of other traits. Within the DNA in the nucleus of every cell in the human body is all the genetic information needed to form another human body.

Each gene is a continuous segment of DNA along the molecule and is located at a specific site, known as a locus, upon a specific chromosome. Genes may be of different lengths and follow one another along the DNA molecule. Each gene differs from the next because the sequence of order of base pairs in one gene is not identical to the following one. [Further, Schmidt testified that as the *Caldwell* at 282 court likewise found "DNA from no two people, outside of identical twins, contains the same sequential pattern."]

The discovery of the structure of DNA by Watson and Crick, recognized as one of the major scientific events of the Twentieth Century, caused an explosion in biochemistry, molecular biology and related sciences, and the technology thereof. Among its vast biological implications are ... applications to medical diagnostics and forensic identification. Now knowing the structure

> of DNA, and its immutable rules, and knowing that genetic information and instructions are transmitted by varying sequences of matched base pairs, molecular scientists were able to decipher much of the genetic codes.

Identification and fragmentation (i.e., separation) of DNA from 1970 forward has led to new technologies being developed over the years "involving the use of polymerase chain reaction ("PCR") as part of the process of extracting, amplifying, and profiling a DNA sample in preparation of making DNA comparisons."[11] Analysis and interpretation is based on statistical modeling "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."[12]

However, Schmidt testified that for multiple contributors, human analysis is often flawed and incomplete due to a number of factors that are both scientific and non-scientific and which exponentially increase the challenge to objectively and correctly interpret DNA samples.[13] This is where computer analysis using probabilistic statistical modeling comes into play through probabilistic genotyping systems such as TrueAllele and STRmix® used by the Federal Bureau of Investigation ("FBI").

> Probabilistic genotyping software (PGS) is the most recent purported advancement in forensic DNA analysis. Probabilistic genotyping refers to "the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios (LRs) and/or infer genotypes for the DNA typing results of forensic samples ('forensic DNA typing results')."[14]
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> ....
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> The software weighs potential genotypic solutions for a mixture by utilizing

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[11] See Howell2019GA.pdf, page 2 for quote and case citations.
[12] Id. at page 3.
[13] See also id. at page 3.
[14] SWGDAM's Guidelines for the Validation of Probabilistic Genotyping Systems. See also footnote 26 and associated text *infra*. A particular defendant's DNA is not part of the 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 [defendant's] ... genotype to the corresponding genotype which was previously inferred. Where the [defendant's] ... genotype corresponds with the inferred genotype, the previous determined probability is obtained. This probability that is associated with the [defendant's] ... genotype is then divided by the probability of a random person in the population having the same genotype ... in order to provide context for assessing whether it is ... a coincidence the [defendant's] genotype is present or whether it is more likely present because the [defendant] ... actually contributed it. The result ... is a match statistic referred to as the ... LR." Howell2019GA.pdf, pages 4-5.

> more DNA typing information ... and accounting for uncertainty in random variables within the model .... Probabilistic genotyping software has been demonstrated to reduce subjectivity in the interpretation of DNA typing results and, compared to binary interpretation methods, is a more powerful tool supporting the inclusion of contributors to a DNA sample and the exclusion of non-contributors. ...The DNA typing data and probabilistic genotyping results require human interpretation and review in accordance with the [FBI's] Quality Assurance Standards for Forensic DNA Testing Laboratories.[15]

In *Caldwell*, the State proposed to use the Lifecodes DNA system. However the assumptions undergirding Lifecodes had not been subject to rigorous studies, and more importantly, validated independently by the State.

Instead in *Caldwell*, the State relied solely on peer-review publications or what is better known as the *Frye v. United States*[16] "counting heads" approach to establish general acceptance in the scientific and therefore legal community. However, as Bah has argued, and the State acknowledges, *Frye's* counting scientific head approach was found in *Harper* inappropriate because of what the approach engenders, that is competing experts, "limits on what any 'expert' may understand" and "wide variations in intradisciplinary opinions."[17]

As such, (and presumably because legal experts lack the education and training to understand the extremely complex interlocking scientific and mathematical knowledge on the level required to independently test a scientist's work),[18] the existence of peer review publications in a *Harper* analysis is but one factor and not necessarily a dispositive factor here as the 7 peer review articles were all partially written by personnel associated with or who have controlling influence of Cybergenetics. These 7 articles have spawned 515

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[15] *United States v. Gissantaner*, 1:17-CR-130, 2019 WL 5205464, at *5-6 (W.D. Mich. Oct. 16, 2019)(evaluating STRmix under *Daubert*). See also Howell2019GA.pdf, pages 3-6.

[16] 293 F.1013, 1014, (DC Cir. 1923).

[17] *Harper*, supra at 525. Schmidt testified that these issues are also seen in some legal cases and legal publications reviewing the TrueAllele system as well as studies conducted by the United States President's Council of Advisors and Science and Technology (PCAST) which published a report in 2016. Schmidt noted however the 2016 report by PCAST was outdated by the time it was published due to ongoing modifications to the TrueAllele system and that PCAST's findings were superseded by 37 other reports. Bah cited to but did not tender for admission into evidence an article in the *Harvard Journal of Law and Technology* as illustrative of problems with elevating TrueAllele to veritable scientific and legal certainty. The basis was the PCAST report and issues with TrueAllele's reliability, which Schmidt noted was a critical and heavily tested in validation studies.

[18] In much the same way, Schmidt during examination noted that she was not educated or trained on understanding legal concepts and terms often present in law articles and commentary about TrueAllele.

articles, studies, and theses which cite at least one the seven.[19]

Instead, the standard under *Harper* is a

> determination from evidence presented to it ... by the parties; in this regard expert testimony may be of value. Or the trial court may base its determination on exhibits, treatises or the rationale of cases in other jurisdictions. See *United States v. Lopez*, 328 F.Supp. 1077 (E.D.N.Y.1971); McCormick on Evidence, "Judicial Notice," p. 746. The significant point is that the trial court makes this determination based on the evidence available to him rather than by simply calculating the consensus in the scientific community. Once a procedure has been recognized in a substantial number of courts, a trial judge may judicially notice, without receiving evidence, that the procedure has been established with verifiable certainty, or that it rests upon the laws of nature.[20]

As shown below, TrueAllele has reached that stage in both the scientific arena and in state, federal, and military courtrooms across the country (and worldwide). In addition to the 22 Georgia cases cited in footnote 8, TrueAllele was used to identify remains in the World Trade Center disaster and was part of the basis to grant Johnny Lee Gates a new trial in Muscogee Superior Court in January 2019 by way of an extraordinary motion for new trial.[21] Forty-two states besides Georgia along with Washington, D.C., Puerto Rico, the military (Marines and Air Force) as well as 5 countries in 705 cases have as of April 2019 have admitted (sometimes stipulated) TrueAllele evidence. Of the 705 cases, 89 went to trial and scientists testified for the prosecution using TrueAllele.[22] Greater still, in one hundred and ten times, TrueAllele has assisted the defense, at trial and during post-conviction proceedings, resulting in acquittals and exonerations.[23] Between 2009 and 2019, including *Howell* and *Nundra*, there have been 23 admissibility challenges.[24] Schmidt testified that TrueAllele has never been rejected by a court because of a failure to meet *Harper* (or *Daubert* or *Frye*).[25] Admissibility of TrueAllele has cleared the appellate hurdle

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[19] See State's Exhibit #10.
[20] *Harper*, supra at 525-526.
[21] See State's Exhibit #5. The case has been docketed and is pending in the Georgia Supreme court. See S19A1130.
[22] See State's Exhibit #9 and State's Exhibit #8 (section – Criminal cases where Cybergenetics scientists have testified for prosecution on TrueAllele evidence).
[23] See #8 (section – Criminal cases where Cybergenetics has assisted the defense using TrueAllele).
[24] See State's Exhibit #8. The case has been docketed and is pending in the Georgia Supreme court. See S19A1130.
[25] Bullet, another probabilistic genotyping system developed by the Serological Research Institute, was denied admission under *Daubert* in *U.S. v. Williams*, 382 F.Supp.3d 928 (N.D. Ca. April 29, 2019)(pre-trial motion).

in Pennsylvania in *Commonwealth v. Foley*, 38 A.3d 882 (Pa.Super. 2012), 3 years after trial and conviction in 2009.

Moreover, TrueAllele does not suffer from *Caldwell's* lack of testing and independent validation. Schmidt testified that True Allele has been independently validated 4 times by the GBI in 2016-2019[26] on three basis, sensitivity (which is the measure of the correct person being wrongfully excluded as exemplified by the rate of false exclusions), specificity (which is measure of the wrong person being included as exemplified by the rate of false inclusions), and reproducibility (which is the extent that the same answer is given to the same question repeatedly). Schmidt also testified to validation studies that have been conducted by 36 other independent labs, both private and governmental.[27]

Additionally, Schmidt testified that True Allele (as well as the operating of the software by the GBI) complies with the FBI's quality assurance standards and the guidelines established by the Scientific Working Group on DNA Analysis Methods ("SWGDAM), which is a group of approximately 50 scientists representing federal, state, and local forensic DNA laboratories in the United States and Canada."[28]

With regards to Bah's contention that there have been articles and studies that have questioned in certain aspects of the TrueAllele system, the Court in *Caldwell* held that a "trial court [does not have to] ... exclude ... scientific evidence unless [it is] convinced there is no possibility of error. No procedures are infallible."[29] Likewise, no system is error free. Schmidt testified to protocols implemented by the GBI to address error rates observed in the validation studies for sensitivity and specificity through establishing upper and lower limits so that no one is falsely included or excluded, respectively, and to address reproducibility through the analyzing of each sample twice and excluding as inconclusive results that are more than 2 band units.[30]

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[26] See also State's Exhibit #2(a)(Powerpoint created by and testified to by Schmidt); GBI2016v1, GBI2016v2 and GBI2017 in 2-Validation/1-Studies folder on State's Exhibit #3; and ReadMe.pdf in 2-Validation/1-Studies folder on State's Exhibit #3.

[27] Id. This folder also contains other validation studies.

[28] See State's Exhibit #6. Schmidt testified to her and other scientists' training and education on TrueAllele as well as the required semi-annual proficiency testing of the lab by an outside vendor and the lab's maintaining audited compliance with the FBI's quality assurance standards. Schmidt conducted two of the GBI validations and reviewed and approved the other two validations. She is responsible for creating policies and procedures for TrueAllele analysis, and has completed a validation for the Palm Beach, Florida Police Department.

[29] 260 Ga. at 287.

[30] See also State's Exhibit #2(a)(Powerpoint created by and testified to by Schmidt).

Hinkle, the scientist who conducted the testing in this case, testified that she was familiar with, understood, and abided by the protocols established for TrueAllele.

Finally, the mathematics in TrueAllele are a combination of two concepts, Bayesian Statistics[31] and the Markov Chain Monte Carlo[32] algorithm that have been used since the 1700's and the 1950's, respectively.

Conclusion

The Court DENIES Bah's Motion to Exclude finding that the TrueAllele system is admissible under *Harper.* After considering the evidence, the Court finds that TrueAllele's probabilistic genotyping system has reached the stage of veritable certainty so that the testing, analysis and interpretative results "rest upon the laws of nature."

The Court further finds that Hinkle's testimony is admissible under *Harper* as she testified that she was knowledgeable of and abided by the protocols established and employed by the GBI to use the TrueAllele system in carrying out the testing, analysis and interpretation of results from the two buccal swabs submitted to the GBI by the Douglas County Sheriff's Office in this case. Evidence based on TrueAllele is admissible at trial with the weight of the evidence to be assigned by the trier of fact.

SO ORDERED this October 22, 2019.

CYNTHIA C. ADAMS
Judge, Superior Court
Douglas Judicial Circuit

JUDGE'S DISTRIBUTION LIST:

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[31] See *Oteng-Amoako v. HSBC Bank USA*, 13 CV 5760 PAC FM, 2015 WL 2399847, at *2 (S.D.N.Y. May 19, 2015)("The Bayesian Theorem is named after Rev. Thomas Bayes (1701–1761) and postulates a theory of relating current probability to prior probability. It has proven useful in drawing statistical inferences").

[32] See *Gissantaner*, at *7 (The Monte Carlo and Markov Chain processes were synergized in the '50s to '70s to become Monte Carlo Markov Chain (also called the Markov Chain Monte Carlo).... It has become a dominant and mainstream methodology for solving this type of complex problem from the '70s onwards, and is applied throughout many fields such as physics, engineering, geoscience, medicine, and a great many others").