IN THE DISTRICT COURT OF DOUGLAS COUNTY, NEBRASKA

THE STATE OF NEBRASKA, Plaintiff, vs. CHARLES SIMMER, Defendant.	)	CASE I.D. CR16-1634 ORDER ON DEFENDANT'S MOTION IN LIMINE TO PRECLUDE DNA EVIDENCE

INTRODUCTION

This matter came on for hearing on three non-consecutive days, May 12, June 26, 2017 and January 12, 2018 on Defendant's Motion in Limine to preclude the State from introducing any and all testimony concerning DNA testing and the results of said testing pursuant to *Daubert v. Merrell Dow Pharmaceuticals*, 113 S.Ct. 2786 (1993) and *Schafersman v. Agland Co-op*, 262 Neb. 215 (1998).. The State was represented by Deputy Douglas County Attorney, Amy G. Jacobsen. The Defendant was represented by Douglas County Public Defender, Thomas C. Riley.

On May 12, 2017, evidence was presented by the State from Dr. Mark Perlin of Cybergenetics through testimony and several exhibits addressing TrueAllele DNA analysis.

On June 26, 2017 further evidence was presented through Mellissa Helligso regarding the DNA testing conducted by UNMC Human DNA Identification Laboratory. Ms. Helligso holds a B.S. in Medical Technology from UNMC and a Masters of Forensic Science from Nebraska Wesleyan University. Ms. Helligso's testing yielded results for Y-STR DNA. Ms. Helligso's work was analyzed and served as the basis for Dr. Perlin's analysis. The Defendant did not challenge the acceptance of the work done by Ms. Helligso and the UNMC laboratory.

On January 12, 2018, the Defense presented testimony via phone from Nathanial Adams, a Systems Engineer from Forensic Bioinformatic Services, Inc. in Fairborn, Ohio. Mr. Adams holds a B.S. degree in Computer Science from Wright State University in Dayton Ohio.

The State's proposed findings were received January 18th, 2018 and the Defendant's on the 22nd. This Court finds the evidence adduced by the State from both Dr. Mark Perlin and Mellissa Helligso is admissible under the Daubert/Schafersman standards. The Court will further address the issues starting with the initial analysis conducted at the UNMC laboratory followed by the work conducted by Cybergenetics.

The testimony and evidence of all three witnesses provide insight into the differences between the more traditional PCR-STR process (human analysis) and that utilized by Cybergenetics and TrueAllele (probabilistic genotyping). It is helpful to outline these procedures.

BACKGROUND

Once a laboratory obtains a DNA profile (either full or partial) from the evidentiary sample, the lab will be provided known DNA profiles from the suspect, victim, and other individuals who may be likely contributors to the evidentiary DNA sample. The known DNA profiles are then compared to the evidentiary profiles which results in one of three conclusions, i.e. (1) excluded, (2) not excluded, and (3) inconclusive. If an individual is not excluded, the technician then determines the frequency probabilities of the evidentiary sample alleles and the alleles from the known sample would be found in the population.

Analysts measure the peak heights and the thresholds in relative fluorescent units (RFU). To determine if an allele is present in the evidentiary sample, laboratories, like

UNMC, that conduct human analysis of DNA mixture samples review the RFU peak heights generated by the instrument (genetic analyzer or DNA sequencer) used to measure the presence of an allele at a given location. If an allelic peak falls above a certain threshold, it will be counted as present; if it falls below that threshold, it will be counted as absent. If the peak reaches the line, then the peak counts as part of the analysis, and the analysis of that allele ends.

Due to the low relative fluorescent units of "shadow peaks," human analysis generally excludes these artifacts. In order to cast a wider net, laboratories employ different standards to determine the threshold. Sometimes, analysts declare an allelic peak a match if the peak rises above 120 relative fluorescent units, and sometimes the cut off is 80 relative fluorescent units. Employing different thresholds may yield different results. Ultimately, forensic science labs commissioned studies to establish and validate stochastic and analytical thresholds in order to eliminate this subjectivity. At the same time, the field also sought ways to improve statistical calculations in mixture cases by utilizing computer analysis and incorporating the Likelihood Ratio approach.

Different DNA profiles require different statistical treatment. For example, DNA mixture profiles (DNA samples that include more than one contributor) create unique analytical and statistical challenges. In 2006, the International Society of Forensic Genetics issued a consensus document "to define a generally acceptable mathematical approach for typical mixture scenarios and to address open questions where practical and generally accepted solutions do not yet exist."

Helligso testified that the Omaha Police submitted items from the crime scene to the DNA lab for purposes of subjecting them to testing and analysis of any DNA detected

on the items of evidence. Typically the UNMC DNA lab subjects evidentiary items to PCR-STR analysis. In this case the levels of DNA available for testing are low and instead of the typical analysis, Helligso subjected the evidence to Y-STR testing.

Y-STR testing only compares genetic markers from the Y (male) chromosome and is not as definitive as the autosomal DNA testing done by UNMC which includes pairs of alleles generated from both parents.

Subsequent to the UNMC testing, the State hired Cybergenetics to analyze the DNA extracted from the evidentiary items. Cybergenetics utilizes a computer program called TrueAllele to analyze the DNA evidence. It should be noted that Cybergenetics utilizes the same data collected by UNMC.

The testimony of Perlin and Helligso provides the court with information concerning the differences between "probabilistic genotyping" used by TrueAllele and the traditional methodology used by UNMC.

The data collected by UNMC and used by both entities consists of graphs showing peak heights attributed to genetic markers (alleles) at predetermined locations (loci) on genes. The intensity of the DNA is represented by the height of the peak and allows the technician to determine if certain alleles are present.

Because forensic samples are not pristine, may contain low levels of DNA, and often reveal the presence of multiple contributors to an evidentiary sample, each lab has protocols to be used to determine the presence of alleles and to determine major and minor contributors in a mixed sample. The protocols list a peak threshold that must be exceeded before the technician calls the presence of an allele. If a peak is visible, but

does not meet or exceed the peak height threshold, that peak is not considered as being present.

By utilizing this method, technicians develop a partial profile generated by the alleles determined to be present in the evidentiary sample. This partial profile is then compared to the known profile of suspected contributors to the DNA in the evidentiary samples. The known profile is generated by taking a buccal swab from a suspect or witness as well as obtaining samples from the bodily fluids of crime victim. Thus full profiles are generated from the known samples.

These known samples are compared to the evidentiary samples which results in one of three conclusions, i.e. (1) excluded, (2) not excluded, and (3) inconclusive. If an individual is not excluded, the technician then determines the frequency of the evidentiary sample alleles and the alleles from the known sample would be found in the general population. Y-STR is a variation of this procedure.

Dr. Perlin's program eliminates the human element of examining the evidence and instead utilizes "all peak heights" regardless of their strength and evaluates them using an algorithm of pre-programmed probabilities.

The testimony and exhibits from Dr. Perlin include an exhaustive explanation of how TrueAllele works and how, in his opinion, probabilistic genotyping is superior to the human method in common use across the country. Perlin testified that in 1994, his private company, called Cybergenetics, began commercializing a computerized DNA interpretation technology called TrueAllele. Cybergenetics markets TrueAllele as an automated system for interpreting DNA evidence. Computer analysis by TrueAllele is not a substitute for the DNA collection or amplification process. Instead, the process remains

the same until the point of the DNA statistical analysis. In other words, law enforcement still collects the sample, submits it to the laboratory, and the lab uses traditional amplification processes to produce data suitable for statistical interpretation.

TrueAllele assesses the same data that is produced and analyzed by the lab, in this case UNMC. However, instead of traditional human analysis where a person manually examines the allelic peaks, the TrueAllele operator inputs the data into the computer program. The program, in turn, subjects that data to a computer analysis.

The TrueAllele computer program relies on a form of statistical analysis called probabilistic genotyping. Probabilistic genotyping involves applying the information derived from DNA profiles to complex mathematical formulas known as algorithms. The algorithms compare different statistical models to the actual data and weigh the probability that the model matches the data. Using that probability, technicians can generate a likelihood ratio using traditional statistical methods.

Specifically, TrueAllele relies on a class of algorithms derived from a Bayesian statistical analysis called Monte Carlo-Markov Chain (MCMC) modeling. The MCMC statistical approach has been used in a variety of situations to successfully model many complex data sets; however, the Defense contends MCMC's application to forensic DNA is arguably new and unique to TrueAllele.

ANALYSIS

The *Daubert* standard was adopted to replace the Frye standard by the Nebraska Supreme Court in *Schafersman v. Agland Coop*, 262 Neb. 215, 631 N.W.2d 862 (2001). The Court followed the trend of other states as well as the Federal Circuits in reasoning that the Frye standard calling for only general acceptance of the technique or theory within

the relevant scientific community did not establish adequate reliability of the method in question. As a result, the U. S. Supreme Court established a test that lists a number of factors to be considered by a judge when determining whether a scientific method or technique is sufficiently reliable to be used as evidence at trial. These considerations include:

> **(1)** whether the theory or technique can be, and has been, tested; (2) whether the theory or technique has been subjected to peer review and publication; (3) the known or potential rate of error, and the existence and maintenance of standards controlling the technique's operation; and (4) the 'general acceptance' of the theory or technique.

Schafersman, 262 Neb. at 225 citing *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U. S. 579, 113 S. Ct. 2786 (1993).

The *Daubert* test allows judges to serve as the "gatekeeper" in determining what evidence will be allowed at trial. Using DNA for identification is widely accepted as evidenced by the Nebraska legislature's findings regarding its reliability. Neb. Rev. Stat. §29-4118(1) (Supp. 2001) specifically states in part that "DNA testing has emerged as the most reliable forensic technique for identifying purposes when biological material is found at a crime scene." Neb. Rev. Stat. §29-4118 (2) allows DNA to either "establish the guilt or innocence of a criminal defendant" or to "have significant probative value to a finder of fact." Clearly from the language of this statute, the legislature has manifested its intention that DNA evidence be admitted in criminal proceedings. Y-STR has been used in criminal cases in Nebraska in the past. The instant case is the first time TrueAllele DNA analysis has been used in a criminal case in Nebraska. While TrueAllele analysis uses more advanced techniques applying probabilities through the use of computers than

traditional analysis, this Court did not hear evidence that any scientific developments call into question the reliability of TrueAllele evidence.

Turning to the testimony and evidence offered via Dr. Mark Perlin, the Court at the outset finds that the TrueAllele DNA evidence is relevant and will help the finder of fact in determining the issues in this case. Dr. Perlin is the Chief Scientific and Executive Officer of Cybergenetics, a company he founded. He holds a B.A. in Chemistry, a Ph.D. in Mathematics, an M.D. in Medicine and a Ph.D. in Computer Science. The Court finds Dr. Perlin is an expert in probabilistic genotyping. Exhibit No. 8 was received and included numerous admissibility rulings from over 10 different judges in the United States. Dr. Perlin has testified at least 11 times in admissibility hearings on TrueAllele in the United States, and in each case the evidence has been admitted.

It is important to note that the TrueAllele analysis system does not do any additional biological analysis than a standard PCR-STR analysis. It does not alter in any fashion the methods in which DNA is collected. It does not alter the manner in which DNA is extracted from the biological samples collected at the scene or the known samples collected from suspects and witnesses. It does not alter the typing of the amplified DNA. The TrueAllele system uses data produced by UNMC using the same procedures and techniques that have been repeatedly validated and accepted as evidence in courts in Nebraska. The important distinction between the analysis conducted by UNMC and Cybergenetics is that the TrueAllele analysis uses all the data without being hindered by thresholds or low-level DNA results.

(1) whether the theory or technique can be, and has been, tested;

True Allele has been tested in 34 validation studies. Dr. Perlin offered the Defense two ways the TrueAllele casework can be tested. The Defendant can hire groups with software to run the testing themselves. Or, the Defendant can run the TrueAllele software himself. Cybergenetics makes the software available to opposing counsel for free on the internet. Nathaniel Adams, the defense expert, who holds a B.A. in computer science, has chosen to never use TrueAllele. He did not run the TrueAllele on the evidence in the instant case. The Court finds that the theory of technique used by Cybergenetics can be tested.

Nathanial Adams testified that because no one other than people from Cybergenetics have reviewed the source code for the TrueAllele software, that the system cannot be validated. Cybergenetics has agreed to allow the source code to be reviewed as demonstrated in Exhibit 12. However, Nathanial Adams testified that despite the offer to review source code, he is not able to do so because that is not something he does and there is not enough time to do the review. The Court finds from the testimony and from the "method" section of Exhibit 8 that Cybergenetics conforms to the 2015 SWGDAM guidelines for how probabilistic genotyping systems like TrueAllele should be validated. SWGDAM stands for the Scientific Working Group of DNA Analysis Methods.

(2) whether the theory or technique has been subjected to peer review and publication;

While TrueAllele was first used in a criminal trial in 2009 it is a technique of first impression in Nebraska courts. TrueAllele has been around for more than twenty years. It is not a new or novel approach in the science world. TrueAllele uses probability and

computers, neither of which are new or novel, to pick up where the human brain has left off. TrueAllele has been repeatedly peer reviewed and has been subject to publication. The Court received as part of Exhibits 6 and 7, numerous articles and reports published about TrueAllele. Likewise, the Court received copies of various validation studies as part of Exhibit 6 and 7. Seven peer reviewed validation studies have been done on TrueAllele and have been published in scientific papers. Along with that, there are 27 unpublished validation studies largely done in collaboration with crime laboratories. The Court further notes that according to Dr. Perlin, this is an unusually large number of validation studies. Most science disciplines only do one validation study. As important as the number of times TrueAllele has been validated is, it is equally noteworthy that there is no significant evidence to the contrary. The Court heard no testimony suggesting there has ever been a validation study that refuted the reliability of TrueAllele.

(3) the known or potential rate of error, and the existence and maintenance of standards controlling the technique's operation;

Error rate can be measured in two ways. One way is through validation studies. Validation studies are tests that are done where known data is put into a method, like a computer program for calculating match statistics, and the results are assessed and measured for errors. TrueAllele has been subject to numerous validation studies.

Another way to calculate error rate is mathematically derived using information theory from one evidence genotype. This is based on probability theory looking at what the expected distribution of match statistics are and to what extent you would get a false positive. The various validation studies received and reviewed by this Court demonstrate that TrueAllele has been subject to both of these methods for measuring error rate.

TrueAllele follows written procedures within the laboratory of how to carry out the TrueAllele process in a way that each group has internally validated.

(4) the 'general acceptance' of the theory or technique."

TrueAllele reports have been used in criminal cases in over two-thirds of the states in the United States. TrueAllele has been accepted in the scientific community beyond the courtroom as evidence by its use in identifying mass casualty victims in the 9/11 attack on the World Trade Center in 2000. Cybergenetics was tasked with using TrueAllele to analyze all the victim remains from 2700 missing people and make a match comparison between the two data sets and provide the Office of the Chief Medical Examiner in New York City with the results. TrueAllele has also been involved with over 10 cases with the Innocence Project leading to DNA exoneration. Dr. Perlin noted that there are 443 scientific articles that refer back to TrueAllele articles. These are people writing articles that are a part of the scientific community. Further, there are seven crime labs currently using TrueAllele every day for their DNA mixture interpretation.

CONCLUSION

The Supreme Court of the United States has explained that not every factor of *Daubert* needs to be considered in determining the reliability of testimony. *Kumho Tire Co. v. Carmichael*, 526 U. S. 137, 119 S. Ct. 1167, 143 L. Ed.238, (1999). The Court concluded that:

> A trial court may consider one or more of the more specific factors that *Daubert* mentioned when doing so will help determine that testimony's reliability. But, as the Court stated in *Daubert*, the test of reliability is "flexible," and Daubert's list of specific factors neither necessarily nor exclusively applies to all experts or in every case. Rather, the law grants a district court the same broad latitude when it decides how to determine reliability as it enjoys in respect to its ultimate reliability determination. See

General Electric Co. v. Joiner, 522 U. S. 136, 143, 139 L.Ed.2 508, 118 S.Ct. 512(1997). *Kumho Tire* at 141-42

The Court finds that the evidence produced by the State after careful cross-examination by the Defense sufficiently meets the criteria for admissibility outlined in Daubert to the extent necessary.

DATED this 22 day of February, 2018.

BY THE COURT:

Thomas A. Otepka
District Court Judge

cc: Amy G. Jacobsen
Thomas C. Riley

CERTIFICATE OF SERVICE

I, the undersigned, certify that on February 5, 2018 , I served a copy of the foregoing document upon the following persons at the addresses given, by mailing by United States Mail, postage prepaid, or via E-mail:

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FOURTH DISTRICT COURT
DOUGLAS COUNTY, NEBRASKA