At a Term of the Supreme Court of
the State of New York held for the
County of Schenectady, New York at
the City of Schenectady, New York
on the 30th day of January, 2015

PRESENT: HON. MICHAEL V. COCCOMA
SUPREME COURT JUSTICE

STATE OF NEW YORK
SUPREME COURT: COUNTY OF SCHENECTADY

THE PEOPLE OF THE STATE OF NEW YORK

-against-

JOHN WAKEFIELD

                              Defendant

DECISION AND ORDER

Indictment No. A-812-29

The Defendant John Wakefield is charged with Murder in the First Degree (PL §
125.27(1)), Murder in the Second Degree (PL § 125.25(1)(a)(vii)), Murder in the Second Degree
(PL § 125.25(3)), Robbery in the First Degree (PL § 160.15(1)), and Robbery in the First Degree
(PL §160.15(3)).

The People seek to introduce at trial scientific evidence of deoxyribonucleic acid
(DNA) using a probabilistic genotype analysis. The Defendant does not argue that the principles
and procedures applied to the evidence in this case to derive the DNA data prior to entry into the
Cybergenetics TrueAllele Casework software are novel nor does the Defendant argue that the use
of statistical models and likelihood ratios in reporting the probative value of DNA evidence is
novel. Instead, the Defendant asks the Court to suppress that evidence as being novel in that it

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abandons the human element in analysis and it analyzes data that falls below the thresholds incorporated in standard practice by DNA laboratories.

Peter H. Willis, Esq., appeared on behalf of the People; the Defendant appeared in person and by Frederick Rench, Esq. and Catherine Bonventre, Esq. A hearing was held over numerous days at which the Court had a full opportunity to consider the evidence presented in this proceeding, including the testimony offered and the Exhibits received (see attached Table A). The Court further had the opportunity to observe the demeanor of the witnesses - Dr. Mark W. Perlin, Dr. Barry W. Duceman and Jay Caponera - and has made determinations on issues of credibility with respect to these witnesses and the weight to give to their respective testimony. The Court has also considered the arguments of counsel and the points of law referenced in their respective Memorandums.

Since Cybergenetics TrueAllele Casework has never been accepted in a New York Court, it is by nature novel scientific evidence. To be admissible in New York Courts, it must pass the Frye test as first formulated in Frye v United States, 293 F. 1013 (1923) and subsequently adopted by the New York Court of Appeals in People v Middleton, 54 NY2d 42 (1981). That protocol requires that expert testimony be based on a scientific principle or proceeding which has been "sufficiently established to have gained general acceptance in the particular field in which it belongs" (Frye, at 1014). A Frye inquiry is concerned with the basis of an expert's opinion and not whether the particular opinion is sound (Lugo v New York City Health & Hosps. Corp., 89 AD3d 42 [2nd Dept 2011]). In other words, Frye is not concerned with the reliability of an expert's conclusions, but instead with whether the expert's deductions are based on principles that have gained general acceptance as reliable (see Nonnon v City of

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New York, 32 AD3d 91 [1st Dept 2006]).   And in deciding the admissibility of novel scientific evidence, a court may consider "opinions, texts, laboratory standards or scholarly articles" as well as expert testimony (see People v Wesley, 83 NY2d 417 [1994]).

DNA identification is a powerful forensic tool for solving and preventing crime. Two common sources of data ambiguity in biological evidence are DNA mixtures from multiple contributors and low-template (evidence samples below the threshold) DNA. Although some American laboratories are moving to quantitative modeling of DNA mixture data, most still use Combined Probability of Inclusion (CPI) or Combined Likelihood Ratio (CLR), using the qualitative Boolean logic of all-or-none allele (the number of repeated words) events. Both approaches apply thresholds to the DNA data that cut off quantitative information. Their analysts subjectively apply these analytical or stochastic thresholds manually to data peaks to decide whether or not they believe the evidence peak represents an allele in the genetic material. But the more complex data that has mixtures or low-template DNA limits the applicability of such qualitative procedures.

Computer interpretation methods use more of the quantitative short tandem repeat (STR) peak height data rather than thresholds and have been used for over 20 years. Computers offer three principal advantages in the interpretation process: (1) productively - eliminates the often time-consuming human review of cases that are impossible to solve, (2) information - human review typically makes simplifying assumptions that can discard considerable identification information containing DNA evidence whereas a computer can use a statistical model to fully examine the quantitative peak height data, and (3) objectivity - human mixture interpretation methods sometimes use the suspect genotype (pair of allele) to help infer or report

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results whereas a mathematically programmed computer can infer a genotype directly from the evidence data without using any suspect information and then afterward compute a match likelihood ratio (LR) statistic from this genotype.

Probabilistic genotypes have been recognized by regulatory bodies such as the Scientific Working Group on DNA Analysis Methods (SWGDAM)[1] in its 2010 "Interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories" and the American National Standards Institute (ANSI) in the 2011 article "Data format for the interchange of fingerprint, facial & other biometric information" as a valid approach to DNA Interpretation and reporting. There are two probabilistic approaches:

(1)   semi-continuous[2] - information is determined from the allele present - peak heights are not considered, and

(2)   fully continuous[3] - incorporation of biological parameters.

Cybergenetics TrueAllele Casework is a fully continuous probabilistic approach that analyzes the electropherograms (EPG) (computerized DNA data that a local laboratory extracted and amplified) and considers the genotypes (pair of alleles) at every locus (pair of DNA sentences) of each contributor, taking into consideration the mixture weights of the contributors, the DNA template mass, polymerase chain reaction (PCR) stutter, relative amplification, DNA degradation, and the uncertainties of all these variables. Its genetic calculator uses Markov chain

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[1]A forensic DNA advisory group to the FBI director that is comprised of forensic scientists who serve as DNA technical leaders or CODIS administrators in their laboratories.

[2]e.g. LRmix, Like LTD, FST, Lab Retriever, Armed Expert, Geno Proof Mixture.

[3]e.g. TrueAllele Casework, STRmix, DNA-View Mixture Solution, DNAmixtures

Monte Carlo (MCMC)[4] to give the probabilities of all the different possibilities, not just a maximum possibility, and by using Bayes theorem[5], it decomposes that calculation into a prior probability and a likelihood function that compares genotypes relative to a population and computes a match LR.

The Defendant's expert, and others, question this approach. They argue that there is a lack of validation software, it is costly and time consuming, and it uses "black box" technology. The acknowledged success of Cybergenetics TrueAllele Casework has begun to erode these barriers and there is a move in the direction of probabilistic modeling, but the use thereof would still represent a minority of casework. However, the test is not whether a particular procedure is unanimously endorsed by the scientific community (Cornell v 360 W. 51st St. Realty, LLC, 22 NY3d 762 [2014]), but whether it is generally accepted as reliable (People v Wernick, 89 NY2d 111 [1996]).

PEER REVIEW

There have been numerous articles published relative to Cybergenetics TrueAllele Casework (see People's Exhibit 15) in all the leading journals of the DNA community, including the American Journal of Human Genetics, the Journal of Forensics Sciences (the Official Scientific Journal of the American Academy of Forensic Sciences), Forensic Science International: Genetics, Plos One, Genometrics, The Croatian Medical Journal, and Science and

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[4]This was first published in the 1950's, and according to Dr. Perlin, "he would be hard pressed to know any field where MCMC has not been used" (October 6, 2014 Transcript, p. 45).

[5]An algebraic (p (A/B) = p (B/A) p (A)/p(B)) way to work out the likelihood of something in the face of some particular piece, or pieces, of evidence in use since 1812.

Justice. Prior to being published, each of these articles had to be reviewed by two anonymous scientists in the DNA community to ensure a quality assurance that the manuscript and scientific results are up to the standards of the level of that journal, that the results are reported properly, that the results make sense, and that the conclusions that are drawn from the data are supported by the data. In addition thereto, there have been numerous forensic collaborations (see People's Exhibit 16) with other scientists in the DNA community.

VALIDATION STUDIES

Dr. Perlin testified that Cybergenetics TrueAllele Casework's source code is a trade secret, which he will not reveal. The Defendant argues that without that code, no outside scientist can replicate or validate Dr. Perlin's methodology and, therefore, Cybergenetics TrueAllele Casework evidence should not be admissible in this case. However, scientists can, and have, validated the reliability of Cybergenetics TrueAllele Casework even though the source code underlying the process is not available to the public. Cybergenetics TrueAllele Casework has undergone 20 unpublished validating studies and 6 published validation studies (People's Exhibits 3, 4, 5, 6, 7, 27) to confirm that the laboratory is producing the same type of reliable results or determining the extent of reliability for the method or technology that's already been developmentally validated. Four of these were independent validation studies - Massachusetts, Virginia, and 2 by the New York State Police as addendums to People's Exhibit 5 (People's Exhibits 30 and 31). Without exception, each of these validation studies found Cybergenetics TrueAllele Casework to be sensitive (the extent to which interpretation identifies the correct person) and specific (the extent to which the interpretation does not misidentify the wrong

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person). And Cybergenetics TrueAllele Casework was shown to have provided objectivity, achieved greater genotype accuracy, and proved reproducible (the extent to which the interpretation gives the same answer to the same question).

SCIENTIFIC COMMUNITY

On May 20, 2011 the New York State Commission on Forensic Science DNA Subcommittee unanimously approved Cybergenetics TrueAllele Casework for use by the New York State Police for their forensic casework. Pursuant to Executive Law § 995-b(13), this Subcommittee was comprised of a chair appointed by the chair of the Commission who then appointed six other members to the subcommittee, one of whom shall represent the discipline of molecular biology and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall represent the discipline of population genetics and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall be representative of the discipline of laboratory standards and quality assurance regulation and monitoring and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall be a forensic scientist and be appointed upon the recommendation of the commissioner of the department of health, one of whom shall be representative of the discipline of population genetics and be appointed upon the recommendation of the commissioner of criminal justice services and one of whom shall be representative of the discipline of forensic science and be appointed upon the recommendation of the commissioner of criminal justice services - all respected scientists who do research on different areas of DNA analysis. The subcommittee in this case consisted of Jack Ballantyne,

Ph.D., Chairman, George Carmody, M.D., Eric Buell, Ph.D., Charles Hirsch, Ph.D., Mark

Batzen, Ph.D., Anne Welsh, Ph.D., and Ranajit Chakraborty, Ph.D. (Defendant's expert). It was

their duty to assess and evaluate all DNA methodologies proposed to be used for forensic

analysis. In that regard, it reviewed and evaluated Cybergenetics TrucAllele Casework over 1 ½

years and heard presentations by Dr. Perlin, Joe Galdi (runs the DNA laboratory in Suffolk

County), J. D. Bellvose, Russ Gedick (the DNA technical lead at the Albany laboratory), and Dr.

Barry W. Duceman (Director of the Biological Science Section of the New York State Police

Forensic Investigation Center) before recommending its use by the New York State Police.

Thereafter, on July 15, 2011 the full Commission on Forensic Science

unanimously approved Cybergenetics TrueAllele Casework technology for forensic casework

<u>without any mention of the type of forensic casework and without limitation</u> (People's Exhibit

12). This full Commission was composed of the chair of the New York State Crime Laboratory

Advisory Committee, the director of a forensic laboratory located in New York State, the director

of the Office of Forensic Services within the Division of Criminal Justice Services, two scientists

having experience in the areas of laboratory standards or quality assurance regulation and

monitoring, a representative of a law enforcement agency, a representative of prosecution

services, a representative of the public criminal defense bar, a representative of the private

criminal defense bar, two members-at-large, and an attorney or judge with a background in

privacy issues and biomedical ethics. The committee in this case consisted of Sean M. Byrne,

Esq., Chairman, Gina L. Bianchi, Esq., Kathleen Corrado, Ph.D., Joseph D'Amico, Hon. William

T. Fitzpatrick, Richard W. Jenny, Ph.D., Hon. Peter J. McQuillan, Hon. James A. Murphy, III,

Peter Neufeld, Esq., Marvin E. Schechter, Esq., Barry Scheck, Esq., Nirav R. Shah, M.D.,

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M.P.H., Marina Stajic, Ph.D., and Ann Willey, J.D., Ph.D. It was their duty, *inter alia*, to evaluate and approve or reject any forensic methodology. In that regard, it sets minimum standards designed to increase and maintain the effectiveness, efficiency, reliability, and accuracy of forensic laboratories in accordance with the highest scientific standards practicable.

This approval by the New York State Commission on Forensic Science DNA subcommittee and the full Commission on Forensic Science clearly constitutes "general acceptance." Nevertheless, the New York State Police still undertook three separate validation studies specifically designed around the Quality Assurance Standards of the FBI to ensure that Cybergenetics TrueAllele Casework was a reliable way to interpret mixed and single-source DNA evidence and provide its DNA laboratory with a standardized interpretation approach that thoroughly examined data, eliminated examiner bias, accurately preserved identification information, quantified match strength (whether positive and negative) and yielded reproducible results prior to its use thereof. These studies proved that Cybergenetics TrueAllele Casework is reliable, and that is the standard for admissibility (see People v Wernick, 89 NY2d 111 [1996]).

LEGAL ACCEPTANCE

Cybergenetics TrueAllele Casework has also been used in the World Trade Center 9/11 victim identification,[6] the Allegheny County Crime Lab in Pittsburgh, the country of Oman, the United Kingdom Forensic Science Service and 23 states[7] (People's Exhibit 29, page 4). In

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[6] The Office of the Chief Medical Examiner of the City of New York asked Cybergenetics TrueAllele Casework to deconvolute mixtures from victim remains from the site relative to the 2,700 missing persons.

[7] Kern County, California and the State of Virginia are presently using Cybergenetics TrueAllele Casework for all forensic casework.

that regard, there have been admissibility hearings in Pennsylvania, Virginia, California, Ohio, and, now, New York, as well as in Northern Ireland, Australia, and England, with Cybergenetics TrueAllele Casework being admitted in all but the England case (there was no decision in that case).

This case is similar to the situation the Court of Appeals was presented with, and sanctioned, in People v Wesley, *supra*. At the time of the hearing in that case only three laboratories in the world were performing RLFP based DNA typing. The only articles written on the subject were authored by scientists affiliated with those laboratories and many law enforcement entities, including the FBI, had not employed the technique. At the time that Court considered the issue the scientific community had not widely adopted the procedure, but it still found that RLFP based profiling had been accepted as reliable within the scientific community.

EXPERT TESTIMONY

While the superiority of continuous systems like Cybergenetics TrueAllele Casework has been acknowledged for over a decade, implementation has lagged (People's Exhibit No. 25). The problem, according to Dr. Perlin, is one of education, not lack of general acceptance. In that regard, Dr. Perlin has given over 50 talks, testified in numerous court proceedings (domestically and internationally), and has been the keynote speaker for the American Academy of Forensic Sciences, the International Conference on Forensics Inference and Statistics, and the International Symposium on Human Identification (Promega). He has even been a lecturer for the American Bar Association at several continuing legal education programs.

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The National Institute of Standards and Technology (NIST), the scientific wing of

the United States Department of Commerce, whose mission is to advocate science in the United

States and guide the forensic DNA community, uses Cybergenetics TrueAllele Casework to

insure that its scientific reference material used in testing laboratories is what they describe it as

(to assess a mixture weight and thereby determine the variability of different amplifications).

This means that Cybergenetics TrueAllele Casework is used, albeit indirectly, by almost every

laboratory in the United States since they all obtain control samples from NIST. Michael D.

Coble and John M. Butler, both from the NIST Applied Genetics Group, gave a presentation

entitled "Exploring the Capabilities of Mixture Interpretation Using True Allele Software" on

September 3, 2011 at the 24th Congress of the International Society for Forensic Genetics. They

concluded by summarizing their results and finding that Cybergenetics TrueAllele Casework

makes better use of the data than the RMNE (random man not excluded) approach, the statistical

equivalent of CPI. And this was not the only time that NIST acknowledged the effectiveness and

reliability of Cybergenetics TrueAllele Casework - at the Green Mountain DNA conference on

July 28 - 30, 2014 in Burlington, Vermont, Michael D. Coble presented the results of a study

entitled "Mix 13: Overview and Lessons Learned" and reported that Cybergenetics TrueAllele

Casework was the only expert system to correctly exclude the suspect in a controlled study

involving 100 laboratories, it made poster presentations at conferences for the International

Symposium on Human Identification and the International Society for Forensic Genetics, and it

even put on a webinar two-part series pertaining to probabilistic gene typing and advocated the

use of this method (October 8, 2014 Transcript, page 561).

FINDINGS

The evidence shows that computerized probabilistic approaches and likelihood ratio principles used by Cybergenetics TrueAllele Casework are superior to current methods. Moreover, Cybergenetics TrueAllele Casework has been demonstrated to be one of, if not, the most advanced method of interpreting DNA profiles from mixed and low-template DNA. It has been proved to be more accurate than CPI and CLR, preserves more of the identification information, eliminates examiner bias, produces a match value which human review may not, and permits standardization of mixture reporting whereas human review approaches can lead to very different match statistics on the same DNA data.

Here, there is a plethora of evidence in favor of Cybergenetics TrueAllele Casework, and there is no significant evidence to the contrary. The Court recognizes that the lack of critical work does not guarantee the absence of controversy; however, the reality is that Cybergenetics TrueAllele Casework has been around since 1999, a time frame that would certainly allow for a thorough critical review to be put forth if it was warranted.

Based upon the evidence produced at this hearing, the Court finds:

(1)   that Cybergenetics TrueAllele Casework has been empirically tested and found to be relevant, reliable, and accurate,

(2)   that Cybergenetics TrueAllele Casework has been subjected to favorable peer review and extensive publication,

(3)   that Cybergenetics TrueAllele Casework's average efficacy has been proved to be at least 4 ½ orders of magnitude more efficacious than human review on the same data,

(4)   that Cybergenetics TrueAllele Casework has been validated and found to be reproducible,

(5)   that the various scientific principles used by Cybergenetics TrueAllele

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Casework have been long ago accepted and endorsed by the scientific community, and

(6)   that the on-going administrative investigation at the New York State Police Forensic Investigation Center has no bearing on the validation studies performed in July 2013 and/or March 2014 (see Affidavit of Timothy J. Munro, sworn to January 23, 2015).

CONCLUSION

Accordingly, the Court finds that Cybergenetics TrueAllele Casework is not novel but instead is "generally accepted" under the Frye standard. The Court therefore DENIES the Defendant's Motion to Preclude, subject to sufficient foundational showings by the People as to their experts' qualifications and adherence to accepted procedures for collection, storage, or analysis of such evidence (cf People v Kelly, 288 AD2d 695 [3rd Dept 2001]).

THIS SHALL CONSTITUTE THE DECISION AND ORDER OF THE COURT.

Dated: February 9, 2015
       at Cooperstown, New York

       ENTER

Hon. Michael V. Coccoma
Supreme Court Justice

To: John Wakefield
       Frederick Rench, Esq.
       Catherine Bonventre, Esq.
       Peter H. Willis, ADA, Schenectady County District Attorney's Office
       Clerk of the Court

TABLE A

People's Exhibits:

1.   Curriculum Vitae - Dr. Mark W. Perlin

2.   Computer Interpretation of Quantitative DNA Evidence

3.   PLOS One - "An Information Gap in DNA Evidence Interpretation"

4.   Journal of Forensic Sciences - "Validating TrueAllele DNA Mixture Interpretation"

5.   Journal of Forensic Sciences - "New York State TrueAllele Casework Validation Study"

6.   Science and Justice - "DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information"

7.   Journal of Forensic Sciences - "TrueAllele Genotype Identification on DNA Mixtures Containing Up to Five Unknown Contributors"

9.   Virginia TrueAllele Validation Study: Casework Comparison

10. PLOS One - "TrueAllele Casework on Virginia DNA Mixture Evidence: Computer and Manual Interpretation in 72 Reported Criminal Cases"

11. DNA Subcommittee approval letter

12. Commission on Forensic Science approval letter

15. Citation Index

16. Forensic Collaborations

17. Workshop announcement

18. 9th International Conference on Forensic Inference and Statistics Abstracts

19. Exploring the Capabilities of Mixture Interpretation Using TrueAllele Software

20. The New Standard Reference Material 2391e:PCR-based DNA Profiling Standard

21. Examination of DNA Mixture Proportion Variability Using Multiple STR Typing Kits and NIST Standard Reference Material 2391c, Component D

22. Certificate of Analysis

23. Mix13: Overview and Lessons Learned

24. Annual Review of Statistics and Its Application 2014 - "Statistical Evaluation of Forensic DNA Profile Evidence"

25. Forensic Science International: Genetics - "The interpretation of single source and mixed DNA profiles"

26. Science and Justice - "A comparison of statistical models for the analysis of complex forensic DNA profiles"

27. Establishing the Limits of TrueAllele Casework: A Validation Study

28. Science and Justice - "A MCMC method for resolving two person mixtures"

29. TrueAllele Casework Supporting Data/Validation

30. New York State Police Crime Laboratory System TrueAllele Casework Validation Addendum - two and three person mixtures

31. New York State Police Crime Laboratory System True Allele Casework Validation Addendum - four person mixture and familial study

Defendant's Exhibit:

A. Forensic Science International: Genetics - "DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods"