SUPERIOR COURT OF WASHINGTON FOR KING COUNTY

STATE OF WASHINGTON,	)	
	)	
Plaintiff,	)	No. 10-1-09274-5 SEA
	)	
vs.	)	
	)	DECLARATION OF DR. KEVIN
EMANUEL FAIR,	)	MILLER
	)	
Defendant.	)	
	.)	
	)	
	)	

I, Kevin W.P. Miller, Ph.D., hereby declare as follows:

1. I am over 18 years of age and I am competent to make this declaration.

2. I hold academic degrees from Cornell University (Bachelor of Science in Animal Physiology), the Virginia-Maryland Regional College of Veterinary Medicine (Master's of Science in Pathophysiology), and the University of Cambridge, U.K. (Doctor of Philosophy in Molecular Anthropology). I completed internship training in forensic biology at the Forensic Science Service, U.K., and Post-Doctoral training at the University of California, Santa Barbara.

3. I have 20 years of experience in forensic science at all levels of government (local, state, regional, federal, and international) and in all positions within the laboratory (bench-level

scientist, DNA Technical Leader, and Laboratory Director). My forensic laboratory experience was gained in the following government laboratories: North Louisiana Criminalistics Laboratory, Federal Bureau of Investigation Laboratory, District of Columbia Metropolitan Police Department Laboratory (now called the D.C. Consolidated Laboratory), Kern Regional Crime Laboratory, and Los Angeles County Office of the Medical Examiner-Coroner. In addition to these positions, I have served as a forensic consultant to various District Attorney's Offices, Public Defender's Offices, Medical Examiner's Offices, and the United States Department of the Interior. I have also served as a national auditor of forensic laboratories, assessing casework programs in both public and private forensic laboratories under ISO/IEC17025:2005 and FBI Quality Assurance Standards across 11 states. I developed an award-winning Professional Science Master's Degree Program in Forensic Science at the California State University, Fresno, and have held academic appointments in Departments of Biology, Chemistry, Anthropology, and Criminology. I am currently employed as the Forensic Scientific Leader (Forensic Market Segment Manager) at Hamilton Robotics, a leading manufacturer of automated liquid handling systems for use in forensic laboratories.

4. During the course of my career, I have completed many independent research projects and implemented forensic casework enhancement programs related to human identification and degraded DNA. To this end, I have:

   a. Co-authored work that lead to a forensic patent with General Electric,

   b. Published 23 manuscripts in refereed scientific journals,

   c. Published five book chapters,

   d. Published one article within a trade publication,

e. Published five technical reports to state and federal government agencies,

f. Presented research findings at 41 national and international scientific conferences and symposia (with an additional seven abstracts),

g. Given 10 invited talks,

h. Constructed three forensic databases, one of which was the forerunner to the Missing Persons Index of the COmbined DNA Index System (CODIS),

i. Served as a forensic science subject matter expert for television, and

j. Participated in professional panels relating to the genetic identity of George Washington and his putative descendants, the identification of victims of the World Trade Center disaster, and implementation of the TrueAllele Caseworks System within forensic laboratories.

As part of my research, I have been instrumental in either the development or implementation of several forensic software programs into forensic practice, including the missing persons index of CODIS (development and implementation), RE/FACE facial recognition software (development), and TrueAllele probabilistic genotyping software (implementation).

5. Over the course of my career, I have participated in the following professional societies:

a. Scientific Working Group on DNA Analysis Methods (chair of the mtDNA subcommittee),

b. California Association of Crime Laboratory Directors,

c. American Academy of Forensic Sciences,

d. California Association of Criminalists,

e. American Association of Physical Anthropologists,

f.   American Chemical Society,

g.   Association of Forensic Quality Assurance Managers, and

h.   International Society of Forensic Genetics.

6.   As stated, I am familiar with Cybergenetics, and its TrueAllele software because the Kern Regional Crime Laboratory, under my direction, purchased the software and fully implemented it into forensic casework in 2014. In fact, we were the first ISO/IEC17025 Accredited Forensic Laboratory in the world to present TrueAllele data in a court of law. TrueAllele is a probabilistic genotyping computer system that interprets DNA mixture evidence using a bayesian statistical model. Each laboratory that brings a technology online for use in casework (whether it is new and novel or just new to the lab itself) is first required to perform and document validation studies. Our laboratory did this with the TrueAllele Caseworks system. Our work was fully vetted through and accepted by the scientific community, and was published in the Journal of Forensic Sciences (to date, no author has received negative feedback regarding the data contained therein):

Perlin, M.W., Hornyak, J.M., Sugimoto, G., and Miller, K.W.P. TrueAllele genotype identification on DNA mixtures containing up to five unknown contributors. Journal of Forensic Sciences, 60(4):857-868, 2015.

Accredited laboratories in other states have also gone through the process of independently validating the TrueAllele Caseworks system for forensic casework for the past five years. These laboratories have also had their work fully vetted through and accepted by the scientific community, and include such published works as (not an exhaustive list):

a.   Greenspoon, S.A., Schiermeier-Wood, L., and Jenkins, B.C. Establishing the

limits of TrueAllele® Casework: a validation study. Journal of Forensic Sciences, 60(5):1263-1276, 2015;

b. Perlin, M.W., Dormer, K., Hornyak, J., Schiermeier-Wood, L., and Greenspoon, S. TrueAllele Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. PLoS ONE, 9(3):e92837, 2014;

c. Perlin, M.W., Belrose, J.L., and Duceman, B.W. New York State TrueAllele® Casework validation study. Journal of Forensic Sciences, 58(6):1458-1466, 2013; and

d. Perlin, M.W., Legler, M.M., Spencer, C.E., Smith, J.L., Allan, W.P., Belrose, J.L., and Duceman, B.W. Validating TrueAllele® DNA mixture interpretation. Journal of Forensic Sciences, 56(6):1430-47, 2011.

7. My laboratory in Kern County, California, began to use TrueAllele automated methods of DNA mixture interpretation, because our analysts were unable to interpret complex data manually and mixture studies performed by the National Institute of Standards and Technology (NIST) began to show that there was a wide variation in DNA mixture interpretation results between forensic laboratories nationally (a scenario that is now playing out in national news reports of several laboratories across the country). It was our desire to minimize subjectivity and variation between analysts in our forensic case reporting. To this end, we constructed a series of DNA mixtures of two, three, four, and five individuals of known DNA type and quantity. We presented the experimental mixture data to our analysts and asked them to manually deduce how many individuals were in the mix and the DNA profile of each. We then asked them to use the TrueAllele

Caseworks software to determine the number and DNA types of individuals within the mixed samples. When analysts used manual methods of statistical calculation, a variety of mathematical models were employed. Analysts did not always agree on the statistical approach, and their results varied with the level of comfort they had with the data at hand (subjective inference about the case and level of analyst experience were primary factors in analyst comfort level). No analyst was comfortable rendering an opinion that they would report for mixtures of greater than two individuals. When the data were run through the TrueAllele software, however, analysts were able to discern all contributors and assign proper DNA types all of the time. Answers did not vary from analyst to analyst. Based upon these data, my laboratory chose to use TrueAllele and report its results for all DNA casework requests. The laboratory has used the TrueAllele Caseworks system to interpret DNA mixtures in casework since 2014.

8. Training analysts to use TrueAllele Caseworks involves discussion of both the theory of probabilistic genotyping and the mathematical formulae used. This training is in enough depth so that analysts may understand how the mathematical models work and how the variables that are able to be set through the program ultimately affect the final results. Analysts do not, however, learn the complexities of the mathematical proofs that are used to derive these formulae or the source code that underlies the software that causes it to provide the data that is ultimately reported.

9. It is not typical for labs to require that DNA analysts learn the mathematical proofs of the statistical formulae that are used in manual calculations or the source code underlying software that is used in calculations today. In fact, DNA analysts are required by national mandate to have taken only one statistics class and they have no computer science

educational requirements. Therefore, this level of mathematics and engineering is above

most individuals who work in the field. In actual fact, forensic laboratory analysts rely on

instrumentation that performs a wide array of mathematical calculations each and every

day on every analysis that is performed, without the analyst checking any of the

calculations (the analyst relies upon initial validation work and subsequent performance

checks) or knowing any of the source code for any of these procedures. To my

knowledge, lack of source code information has never been brought up as an issue in

court for any of these forensic workflow steps. Moreover, it strikes me has highly

irregular that any one particular step in any one particular workflow would suddenly

become singled out as an issue for source code revelation. If one is to discuss error in

DNA testing, then would one not want to capture an error rate for the entire workflow?

10. When speaking about the DNA interpretation portion of the workflow only, it is currently

common practice for DNA analysts to use Microsoft Excel spreadsheets to do genetic

calculations and to report the results of these spreadsheet calculations in court. The

spreadsheets that are used are generally made by a single individual in one lab and then

shared through social networks from individual to individual and, indeed, from lab to lab.

Only relatively recently has the idea of file integrity (i.e. corruption, data entry error, etc.)

been brought out as an issue. Now that ISO/IEC17025 standards are in effect for all

forensic laboratories, analysts will typically "validate" their Excel spreadsheets by

confirming that a formula is correct within a cell, that a hand-calculated and an

automatically calculated answers are the same, etc. However, I have never heard of a

forensic analyst requesting Excel source code from Microsoft for inspection as part of

this process. Rather, the assumption is that if the desired calculation works as expected in

Excel, then the underlying engineering of the Excel software product must be correct. In my current position, I work with forensic labs who desire to automate their liquid handling workflows. It is expected that software will be used to direct a given robot to dispense a required volume of liquid within a tolerated precision and, again, the gold standard is whether or not a DNA profile was generated at the end of the workflow and not necessarily that an exact level of fluid was dispensed. I am not aware of any laboratory or court that has ever requested the source code that was used to direct a liquid handling system to produce a DNA profile that was ultimately used in a criminal case.

11. I am confident that the TrueAllele Caseworks system provides reliable results, because my laboratory performed a reasonable validation study that was accepted within the scientific community (if the study were unreasonable, then it would not have been generally accepted by the scientific community). After our validation work was completed, I also asked Cybergenetics to perform blind DNA analysis on a criminal case using the same data that my analysts were using (Cybergenetics did not know anything about our analysis, and my analysts did not know anything about the Cybergenetics work). This was a difficult case of serial rape, with low level DNA on several evidentiary items. When it came time for discovery, I submitted two reports to the prosecution – one prepared by my analyst and the other by Cybergenetics staff. This was the first time that anyone who worked on the case saw work product other than their own. While the actual numbers were different between reports, the log values generated for each evidentiary item were the same. This, together with our laboratory validation, clearly demonstrated to me that the program worked as it was intended to work. I never requested the source code for the TrueAllele Caseworks software and, for the reasons that I highlighted above, I do

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1   not believe the source code is necessary for determining the reliability of the TrueAllele

2   Caseworks system for forensic use or court reporting.

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4   Under penalty of perjury under the laws of the State of Washington, I certify that the foregoing is

5   true and correct to the best of my knowledge and belief.

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7   Signed and dated by me this second day of April, 2016, in Reno, Nevada.

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9   _____
     KEVIN W.P. MILLER, Ph.D.

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