STATE OF MICHIGAN

IN THE 30TH CIRCUIT COURT FOR THE COUNTY OF INGHAM

PEOPLE OF THE STATE OF MICHIGAN,

Plaintiff,

v

HERBERT MAURICE ALFORD,

Defendant.

OPINION AND ORDER

HON. CLINTON CANADY III

Docket No.: 15-696-FC

At a session of said Court held in the City of
Lansing, County of Ingham, State of Michigan,
this 28th day of November, 2016

PRESENT: The Honorable Clinton Canady III
30th Circuit Court Judge

This matter is before the Court on Defendant's *Motion in Limine to Exclude Expert Testimony* pertaining to the use of STRMix, a probabilistic genotyping software application, pursuant to MRE 702 and the factors set forth by the United States Supreme Court in *Daubert v Merrell Dow Pharmaceuticals, Inc.*[1] The Court held a hearing regarding Defendant's Motion on Wednesday, November 16, 2016. During the hearing, the Court heard testimony from two experts – Dr. John Buckleton and Jeffrey Nye. At the conclusion of the hearing, the Court indicated it would issue a written decision to rule on the issues presented.

This case arises out of the shooting death of Michael Adams on October 18, 2011. Charges against Defendant were authorized shortly thereafter on October 21, 2011. Defendant was arrested and subsequently arraigned in the 54-A District Court on May 23, 2015 on the charges of Open Murder[2], Felon in Possession of a Firearm[3], and Felony Firearm[4] as a Habitual

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[1] *Daubert v Merrell Dow Pharmaceuticals, Inc*, 509 US 579; 113 S Ct 2786; 125 L Ed 2d 469 (1993)

[2] MCL 750.318

Offender, Fourth Offense. A preliminary examination was held on July 13, 2015 and July 29, 2015; Defendant was subsequently bound over on all charges. Defendant filed a written waiver of arraignment with this Court on August 6, 2015. The trial in this matter was originally scheduled for February 16, 2016; however, due to the need for further DNA testing by the prosecution and further discovery by the defense, the trial was adjourned to July 25, 2016. A second adjournment of trial was granted for virtually the same reasons – additional discovery as well as additional time to review recently received discovery. The trial is presently scheduled to commence on December 5, 2016.

This Court having received the Motion, all supporting documents, exhibits and correspondence; having held a formal hearing on the merits; and being fully apprised of the issues, states the following:

FINDINGS OF FACT

As part of the investigation in this case, swabs were taken of several areas of a vehicle and tested for DNA using the traditional method. In addition, the Michigan State Police (MSP) Crime Lab performed a statistical evaluation of the DNA obtained from the front driver side door swab along with buccal swabs from Defendant, Herbert Alford. The DNA was processed using the polymerase chain reaction (PCR) and the PowerPlex® Fusion System. The profiles were evaluated using STRMix, a probabilistic genotyping software application used to statistically evaluate complex DNA evidence and generate a match probability from the results of the DNA analysis. Interpretations of item LS11-3679-26Ax (buccal swabs from Herbert Alford – DNA extract) were performed assuming that the DNA profile originated from three individuals. The prosecution's hypothesis (H^1) was that the three individuals included Defendant and two

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[3] MCL 750.224(f)
[4] MCL 750.227(b)

unrelated, unknown contributors. In contrast, the defense's hypothesis (H^2) was that the DNA profile originated from three unrelated, unknown contributors.

On July 24, 2016, the MSP Forensic Science Division issued Lab Report LS11 – 3679, Record Number 8, which indicated that, based on the DNA typing results obtained, it is at least 1.9 septillion times more likely if the observed DNA profile from the front driver side door swab originated from Defendant and two unrelated, unknown contributors than if the data originated from three unrelated, unknown individuals. As a result, the likelihood of ratio of the two competing hypotheses stated above favored the prosecution's hypothesis. The instant Motion filed by the defense seeks to exclude the results obtained using STRMix, as well as any testimony pertaining to the use of STRMix, as inadmissible pursuant to MRE 702 and *Daubert, supra.*

Dr. John Buckleton, a forensic scientist employed by the New Zealand government, testified during the *Daubert* hearing as an expert in the field of DNA interpretation. Dr. Buckleton also works for the ESR (Environmental Science and Research) in New Zealand as the principal scientist and was one of the three creators of STRMix.[5] STRMix is a fully continuous probabilistic genotyping software application that interprets and evaluates complex DNA mixtures. STRMix was created in 2011 and produced jointly by the government of New Zealand and South Australia. Although initially intended to be utilized exclusively as an Australian tool, used in Australia and New Zealand only, today STRMix is utilized in Canada, England, Scotland, and the Republic of Ireland as well as 12 laboratories across the United States. STRMix has also been utilized by the U.S. Army, FBI, California Department of Justice and a laboratory located in Eerie County, New York State.

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[5] Dr. Buckleton testified that the other two creators' names are Jo-Anne Bright and Duncan Taylor.

"Probabilistic genotyping" refers to the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios and/or infer genotypes for the DNA typing results of forensic samples. Probabilistic genotyping is not intended to replace the human evaluation of the forensic DNA typing results or the human review of the output prior to reporting; rather, probabilistic genotyping is simply a tool to assist the DNA analyst in the interpretation of forensic DNA typing results.

A probabilistic genotyping system is comprised of software, or software and hardware, with analytical and statistical functions that entail complex formulae and algorithms. Particularly useful for low-level DNA samples (i.e., those in which the quantity of DNA for individuals is such that stochastic effects may be observed) and complex mixtures (i.e., multi-contributor samples, particularly those exhibiting allele sharing and/or stochastic effects), probabilistic genotyping approaches can reduce subjectivity in the analysis of DNA typing results. Historical methods of mixture interpretation consider all interpreted genotype combinations to be equally probable, whereas probabilistic approaches provide a statistical weighting to the different genotype combinations. Probabilistic genotyping does not utilize a stochastic[6] threshold. Instead, it incorporates a probability of alleles dropping out or in. In making use of more genotyping information when performing statistical calculations and evaluating potential DNA contributors, probabilistic genotyping enhances the ability to distinguish true contributors and non-contributors.

There are two main approaches to probabilistic genotyping: the semi-continuous method and fully continuous method. The semi-continuous method focuses only on the alleles present in

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[6] "Stochastic" means characterized by conjecture or involving or containing a random variable or involving chance or probability. *The American Heritage Dictionary* (1982)

the profile and addresses all possible genotype combinations of the observed alleles in conjunction with a probability of drop-out and drop-in. Analysis parameters such as peak height variation, mixture ratios and stutter percentages are not typically utilized by semi-continuous software systems, although these elements may be considered during the initial manual evaluation of this data. The fully continuous method generally utilizes more of the biological information in the profile, such as peak heights, stutter percentages and mixture ratios. The weighting of genotype combinations as more or less probable may be inferred from the data through methods such as Markov Chain Monte Carlo (MCMC) samplings from probability distributions. [7] As noted above, STRMix employs the fully continuous model of DNA profile interpretation.

Following its creation and development, STRMix went through developmental validation. Developmental validation of a probabilistic genotyping system is the acquisition of test data to verify the functionality of the system, the accuracy of statistical calculations and other results, the appropriateness of analytical and statistical parameters, and the determination of limitations. Developmental validation may be conducted by the manufacturer/developer of the application or the testing laboratory. Developmental validation should also demonstrate any known or potential limitations of the system. According to Dr. Buckleton, every version of STRMix goes through a developmental validation, and each time a new version of STRMix is produced, the new version is developmentally validated. In 2016, a research paper called Developmental Validation of the STRMix Expert Software for Interpretation of Forensic DNA Profiles was published, and Dr. Buckleton was part of the group that authored this paper. This paper was one of approximately 17 other published articles in various magazines in the forensic

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[7] See People's Exhibit 4, SWGDAM "Guidelines for the Validation of Probabilistic Genotyping Systems"

science community regarding the validation of STRMix. Dr. Buckleton also added that, prior to publication, each article was reviewed by two anonymous referees from the forensic science community.

In addition to developmental validation, each individual laboratory that has purchased and implemented STRMix has done its own internal validation (often more than one if the lab has used more than one version). Internal validation of a probabilistic genotyping software system is the accumulation of test data within the laboratory to demonstrate that the established parameters, software settings, formulae, algorithms and functions perform as expected. In accordance with the FBI Quality Assurance Standards, internal validation data may be shared by all locations in a multi-laboratory system.

When asked about the functionality and operation of STRMix, Dr. Buckleton stated that the program applies standard mathematical methods with the interpretation of complex DNA profiles to assign a weight to the DNA evidence. He also noted that STRMix does not play any role in the detection or discovery of a DNA profile; it simply interprets the DNA profile that has been presented to the computer program. Dr. Buckleton then testified that STRMix differs from prior methods of DNA interpretation in that it applies mathematical methods to a DNA profile, which allows it to utilize information in the profile that was previously wasted. The most relevant information, according to Dr. Buckleton, is the "peak height".[8]

In regards to the mathematical formula used as the basis for STRMix, Dr. Buckleton indicated that there were two mathematical bases – standard mathematics and empirical calculation models. The mathematical principle supporting STRMix's probabilistic genotyping

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[8] "Peak height" refers to a trace on a piece of paper that makes a peak at the height and other positions. Dr. Buckleton referenced an electropherogram to further explain this concept.

is the Monte Carlo Markov Chain, which was developed by Adrey Markov. The Markov Chain was invented in the late 90s, 20th century, while the Monte Carlo Method was invented in the late 1940s but could not be implemented in any meaningful way until the 1950s – 1960s. According to Dr. Buckleton, this is a very powerful mathematic technique that could not be given proper utilization until the advent of computers. On the other hand, the empirical calculation models are models that are derived from experimentation and speak to the height expected for a certain amount of templates or the "stuttering" expected. Dr. Buckleton explained that "stuttering" is a missed copying of the DNA or a desired after-effect of the DNA.

The Court also heard testimony from Jeffery Nye, who is currently employed as the Assistant to the Director responsible for quality assurance at the Michigan State Police Forensic Science Division.[9] Prior to his current position, Nye worked as the DNA Technical Leader for the Forensic Science Manager, specifically for the DNA discipline, responsible for training and processing developmental validations and other things of that nature. Nye has been qualified as an expert in the field of Forensic DNA over 100 times in numerous jurisdictions throughout the state of Michigan, and he was qualified as an expert by this Court in the same field.

With regard to STRMix, Nye testified that he was responsible for collecting, purchasing and implementing STRMix as a tool for the MSP Forensic Lab. Nye also indicated that he trained MSP employees how to operate STRMix, completed the internal validation of STRMix for MSP, wrote the validation policy, and wrote policies and procedures related to the use of STRMix. The MSP Forensic Lab purchased STRMix in May of 2015. The first training session included 10-12 MSP scientists and was taught by two of the code developers, one of which was

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[9] MSP has eight laboratories, three of which have DNA laboratories.

Dr. Buckleton. STRMix went live in March of 2016, and so far, the MSP Forensic Lab has utilized STRMix to analyze DNA in over 350 cases.

Nye also testified that he is a member of SWGDAM and explained that, in selecting STRMix, he followed the SWGDAM guidelines. In terms of validating STRMix for use at the MSP Forensic Lab, Nye indicated that there were two basic types of validations that needed to occur, both of which were completed before STRMix was adopted for use at the MSP Forensic Lab: developmental validation and internal validation. Nye explained that developmental validation is primarily done by the developer of new technology and includes a certain set of criteria that must be followed in order to utilize the new technology in any laboratory. In contrast, internal validation is specific to each laboratory environment, and certain internal tests are completed to ensure the new technology operates as expected. Nye also noted that internal validation is particularly useful to assist with development of internal procedures and policies related to the use of STRMix.

One particular method utilized during the internal validation process was the use of "mock samples" for case work. Nye explained that mock samples consist of taking DNA already contained in the laboratory from individuals and putting them together in a mixture. This procedure creates the "ground truth" of the components of the mixture, or stated differently, the scientists will know who contributed to the mixture. Next, the mixture is put into the software to ascertain whether the scientist can parse out the contributors and come up with the correct answers as far as who are contributors, what portions, etc. Nye also indicated that the MSP scientists worked with adjudicated cases where the ground truth was not known so they would know what was previously reported. Those portions were also run through the software and subsequently compared to what was previously reported.

Nye testified that STRMix did very well in MSP's internal validation and that it helped clarify many of the interpretations. He further explained that, part of the reason MSP wanted to implement STRMix was not only to assist with the interpretation, but also to help streamline and standardize MSP Lab processes. In addition, because MSP has a large number of DNA scientists, the use of a program like STRMix helps bring everyone to a more consistent way of interpreting DNA as opposed to having several individuals with different interpretations of the same DNA. Nye noted that, as part of the internal validation process, MSP forensic scientists received 35-40 hours of formal training during which they went through the validation results, including evaluating any strengths or weakness of the program and testing their own mixtures.

In addition to this formal training, each MSP scientist who would be operating STRMix was required to take a competency test. According to Nye, the point of a competency test is to basically evaluate the way each scientist understood and properly applied the STRMix application, within MSP's developed policies and procedures, and whether they were able to reach proper conclusions. Nye stated that, while the scientists understood all the principles behind STRMix, the competency tests were basically to evaluate the scientists' learning process. Nye also indicated that Amber Smith, the scientist who evaluated the DNA collected in the present case, was also required to complete a competency exam, and she did "very well."[10] Nye also noted that, in addition to Amber Smith's evaluation, the results of her STRMix analysis were reviewed by a peer as well as an administrator.

CONCLUSIONS OF LAW

The specific issue in the present Motion is the admissibility of the forensic DNA testing results performed on the swabs taken from the front driver's side door of a vehicle deemed to be

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[10] Amber Smith's competency examination was submitted to the Court as People's Exhibit 7, which indicated that she earned a score of 98%

of evidentiary value during the investigation. The MSP Forensic Laboratory conducted DNA testing on the swabs, and the results were interpreted using the relatively new software program referred to as "STRMIX". Defendant argues that testimony and evidence related to the STRMix analysis performed by MSP should be excluded pursuant to MRE 702 and *Daubert* because the scientific evidence and testimony is not based on sufficient facts or data, and it is not the product of reliable principles and methods. In addition, Defendant asserts that STRMix evidence and testimony is inadmissible because the principles and methods of STRMix were not reliably applied to the facts of this case. Lastly, Defendant contends that prosecution witness Amber L. Smith is not qualified to testify regarding STRMIX evidence in this matter.

I. MRE 702

MRE 702 has imposed an obligation on the trial court to ensure that any expert testimony admitted at trial is reliable.[11] In other words, MRE 702 requires the trial court to ensure that each aspect of an expert witness's proffered testimony—including the data underlying the expert's theories and the methodology by which the expert draws conclusions from that data—is reliable.[12] While the exercise of this gatekeeper role is within a court's discretion, a trial judge may neither "abandon" this obligation nor "perform the function inadequately."[13] This gatekeeper role applies to *all stages* of expert analysis. MRE 702, which governs the admissibility of expert testimony, provides:

> If the court determines that scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education may testify thereto in the form of an opinion or otherwise if (1) the testimony is based on sufficient facts or data, (2) the testimony is the product of

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[11] *Gilbert v DaimlerChrysler Corp*, 470 Mich 749, 780; 685 NW2d 391, 408 (2004)

[12] *Id.* at 779

[13] *Id.* at 780

> reliable principles and methods, and (3) the witness has applied the principles and methods reliably to the facts of the case.

MRE 702 mandates a searching inquiry, not just of the data underlying expert testimony, but also of the manner in which the expert interprets and extrapolates from those data. Thus, it is insufficient for the proponent of expert opinion merely to show that the opinion rests on data viewed as legitimate in the context of a particular area of expertise (such as medicine). The proponent must also show that any opinion based on those data expresses conclusions reached through reliable principles and methodology.[14] When expert testimony is based only on speculation, the trial court should exclude the testimony.[15] However, if the basic methodology and principles employed to reach a conclusion create a sound foundation for the conclusion reached, the expert testimony is admissible.[16]

A. Sufficient Facts or Data

MSP Lab Report LS11-3679, Record Number 3 was completed on October 31, 2012. That report indicated that the testing to item number LS11-3679-2x (front driver side door swab) revealed the presence of "at least two unidentified donors, at least one of which is male ..." At the time of this report, no known comparison sample to a possible suspect existed. In 2015, a comparison sample was obtained by search warrant from Defendant, Herbert Alford. The sample was sent to the MSP Lab for testing and is designated as LS-3679-26Ax.

As noted above, STRMix does not play a role in the detection of a DNA profile; rather, it simply interprets the DNA profile presented to the computer program. STRMix is undoubtedly the newest form of probabilistic genotyping software currently on the market, and STRMix

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[14] *Gilbert, supra* at 782

[15] *Phillips v Deihm,* 213 Mich App 389, 402; 541 NW2d 566 (1995)

[16] *Nelson v American Sterilizer Co (On Remand),* 223 Mich App 485, 492; 566 NW2d 671 (1997)

applies mathematical methods to the profile, which allows profile information previously wasted to be utilized; however, probabilistic genotyping as a method of evaluating and interpreting DNA is not novel science. Instead, it is a more innovative method of DNA profile interpretation that allows complex and lower-level DNA profiles to be tested using a form of mathematics that is "decades old."

In this case, a trained MSP forensic scientist input the DNA profile information obtained from the front driver side door and the buccal swab from Defendant into the STRMix program. Based on the DNA typing results obtained, it was found to be at least 1.9 Septillion times more likely that the observed DNA profile from the front driver side door swab originated from Defendant and two unrelated, unknown contributors than if the data originated from three unrelated, unknown individuals. Although Defendant challenges the ultimate conclusion, he has failed to present a meritorious argument that would tend to show that the results obtained using the STRMix program were not based upon sufficient facts or data. The Court finds that probabilistic genotyping software such as STRMix is actually capable of determining a likelihood ratio based on statistical evaluation of DNA profiles, and in this particular case, the results obtained were based upon sufficient facts and data.

B. Reliable Principles and Methods

The Court also finds that any expert testimony relating to the use of STRMix and the results obtained would be based on reliable principles and methods. As noted above, the STRMix program relies on a form of statistical analysis known as probabilistic genotyping. In this process, DNA profiles are applied to mathematical algorithms. The algorithms then compare different statistical models to the actual data and weigh the probability that the model matches the data. The result is a likelihood ratio, which explains the probability of the data given two competing hypotheses. The likelihood ratio is based on the frequency of the DNA type in the population. The algorithms used by STRMix are based on the Markov Chain Monte Carlo Method, which was first developed in the 1950s and is a technique widely used in weather forecasting, computational biology and linguistics, genetics, engineering, physics, aeronautics, the stock market, and social sciences. Notably, at least two other courts in Michigan, as well as courts in New York, Pennsylvania, Virginia and Ohio have deemed the principles and methods utilized by STRMix and other probabilistic genotyping software (such as TrueAllele, a competitor program that preceded the creation of STRMix) reliable and therefore, admissible.

C. Principles and Methods Applied Reliably to Facts of Case

Defendant also argues that prosecution witness Amber L. Smith is not qualified to testify regarding STRMix evidence in this matter, and therefore, any potential testimony she might give should be excluded. Although Ms. Smith did not testify at the *Daubert* Hearing, her curriculum vitae (CV) was admitted into evidence as People's Exhibit 3. A review of her CV indicates that Ms. Smith is a Forensic Scientist employed at the MSP Lab who has been extensively trained in the application of STRMix and has been subject to both internal competency testing as well as external proficiency testing.

Specifically, Ms. Smith has undergone a 32-hour STRMix training workshop with two of the creators of STRMix, John Buckleton, and Jo-Anne Bright. In addition to her STRMix training, Ms. Smith has also participated in many hours of training in the area of DNA Analysis: Armed Xpert, DNA Mixture Analysis (24 hours), Mixture Interpretation: Principles, Protocols and Practice Workshop (8 hours), FBI DNA Auditor Training (16 hours), Maxwell 16, Powerplex 16, Y-STRs & Hamilton Robotics Training (12 hours), Forensic Y STR Training (3 hours), Plexor HY and AB 7500 Real-Time PCR System Training (8 hours), Population

Statistics and Forensic DNA Analysis (24 hours), FBI Combined DNA Index System (CODIS) Training (40 hours), Generating DNA Profiles from Difficult Samples (3 hours), Mid-America 2007 Forensic DNA Conference (16 hours), Forensic Statistics Workshop: The Calculations Behind Popstats (2 days), and the Mid-America 2006 Forensic DNA Conference (16 hours), which included an eight hour Statistics Workshop. Jeffery Nye also gave extensive testimony detailing the internal validation and training process of MSP Forensic Scientists, such as Amber Smith, who were certified to use STRMix.

Defendant asserts that Ms. Smith is not qualified to give testimony related to STRMix because she is not a medical doctor, does not have a PhD, is not a mathematician, and has not authored any academic or peer reviewed work regarding the use of STRMix; however, Defendant has not provided the Court with any authority that would suggest that any of the above-referenced qualifications are required in order for her testimony to be admissible. The prosecution has indicated to the Court that Ms. Smith's anticipated testimony will detail the standards and methods used by MSP in determining the number of contributors to a DNA sample, the factors for when a profile can be conditioned to one donor, and the parameters for determining whether a person of interest is a contributor sample or not. The purpose of her testimony in this regard is to demonstrate protocols and standards of analysis focused on obtaining the most complete assessment possible.

As previously noted, the factors that the courts of this state may consider in determining whether expert opinion evidence is admissible under MRE 702 have been amended explicitly to incorporate the standard set forth in *Daubert.*[17] As stated in the staff comments that follow MRE 702, the purpose of that amendment was to emphasize the trial court's role as gatekeeper to

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[17] *Gilbert, supra*

exclude expert testimony that is unreliable because it is based on unproven theories or methodologies in conformance with *Daubert.* Importantly, this standard of reliability focuses on the scientific validity of the expert's methods rather than the soundness of his or her specific conclusions.[18] Thus, under *Daubert,* an expert's opinion is reliable if it is based on the "methods and procedures of science" rather than "subjective belief or unsupported speculation."[19]

Based on this Court's reading of the documents submitted in this case and according to the testimony presented during the hearing in this matter, it appears that Defendant does not argue that the evidence at issue is the result of faulty methodology or theory, and this Court is not inclined to so find. Indeed, the Polymerase Chain Reaction (PCR) testing method and its statistical analyses that were utilized in this case have been widely accepted by Michigan courts as reliable.[20] Rather, relying on Smith's report, Defendant argues that the facts of this case suggest imperfect execution of laboratory techniques or procedures. However, despite Defendant's challenge to Ms. Smith's training and experience with regard to her operation of STRMix, her education and experience relates to her qualifications, and not to whether her testimony is based on reliable principles and methods that she applied reliably to the facts of this case. In other words, challenges of this nature go to the weight of Ms. Smith's testimony, not to its admissibility.[21]

Based on the foregoing, the Court finds that the prosecution has met its burden of showing that the anticipated testimony related to the use of STRMix will demonstrate that the witness has applied the principles and methods reliably to the facts of this case. Therefore, Ms.

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[18] *Daubert, supra* at 589

[19] *Id.* at 589-590

[20] See *People v Coy*, 258 Mich App 1, 9-12; 669 NW2d 831 (2003); see also *People v Lee*, 212 Mich App 228, 281-283; 537 NW2d 233 (1995) ("trial courts in Michigan may take judicial notice of the reliability of DNA testing using the PCR method").

[21] *Coy, supra* at 11

Smith's testimony related to her use of STRMix and the results obtained in this case is relevant and admissible pursuant to MRE 702.[22]

II. *Daubert* Factors

"When evaluating the reliability of a scientific theory or technique, courts consider certain factors, including but not limited to (1) whether the theory has been or can be tested, (2) whether it has been published and peer-reviewed, (3) its level of general acceptance, and (4) its error rate if known,"[23] and (5) "the existence and maintenance of standards controlling the technique's operation."[24] It is well-established that the proponent of evidence "bears the burden of establishing relevance and admissibility."[25]

A. Testing

The Court finds that both the testimony and documentary evidence demonstrate that the STRMix program has received adequate validity testing. One of the three developers of STRMix, Dr. Buckleton, a recognized expert in the field of DNA analysis and statistical interpretation, testified that these validation tests comported with FBI Quality Assurance Standards by a properly accredited laboratory. Additionally, various forensic science laboratories across the U.S. have independently tested and validated STRMix: the Federal Bureau of Investigation, the Erie County Forensic Laboratory (NY State), the United States Army Criminal Investigation Laboratory, the California Department of Justice, the Texas Department of Public Safety, the San Diego Police Department, DNA Labs International, the

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[22] Defendant also raises the issue of LS11-3679-2Ax, Report Number 6, where MSP tested the DNA profile that was later analyzed using STRMix, but the results of the former analysis indicated that "due to the complexity of the profile, no conclusions can be made." However, the Court cannot find that this has a negative bearing on the reliability of STRMix. Conversely, it appears that, under the circumstances presented herein, STRMix fulfilled its stated purpose of interpreting a complex DNA profile that had previously been incapable of interpretation.

[23] *People v Kowalski*, 492 Mich 106, 131; 821 NW2d 14 (2012)

[24] *Daubert, supra* at 594

[25] *Gilbert, supra* at 781

Idaho State Police, DFS (District of Columbia), Michigan State Police, Scottsdale Police Department Crime Laboratory, and the San Diego Sheriff's Crime Laboratory.

Notably, Defendant was given the opportunity to independently test the DNA profile evidence and to have his own expert review the information/results. However, presumably based on the results obtained, Defendant chose not to request a report, and he does not intend to call an expert to rebut the results obtained from the STRMix program. While the Court draws no inference from Defendant's decision one way or another, it is important to note that Defendant was given the opportunity to conduct independent testing in accordance with due process. Based on the foregoing, the Court finds that there is no question that STRMix is capable of being tested and in fact, has been tested in numerous jurisdictions throughout the country.

B. Peer-Review

Likewise, there is no dispute that the validation studies referenced above have been published for peer review in many of the leading journals of the DNA community, including *Forensic Science International: Genetics*, the *Australian Journal of Forensic Sciences*, *Electrophoresis*, and the *Journal of Theoretical Biology*. Dr. Buckleton testified that he was aware of approximately 17 published articles regarding different aspects of STRMix. He also noted that, prior to being published, each of the articles had to be reviewed by two anonymous scientists in the DNA community to ensure that the information contained in each paper comported with scientific standards as well as the standards of each journal. Additionally, various authorizing bodies have looked at STRMix, such as the New York State Forensic Science Commission. Having found that the STRMix program has been sufficiently published and peer reviewed, the Court concludes that the prosecution has met its burden with regard to this reliability factor.

C. Level of General Acceptance

The Court also finds that the prosecution has met its burden with regard to proving that STRMix is generally accepted in the relevant scientific community. As noted above, each of the 12 laboratories that utilize STRMix in the U.S. have developed and implemented internal validation procedures that adhere to SWGDAM guidelines. SWGDAM stands for the Scientific Working Group on DNA Analysis Methods, and it is a group of approximately 50 scientists representing Federal, State, and Local forensic DNA laboratories in the United States and Canada. SWGDAM is sponsored by the FBI, and the scientist-members meet twice a year to create guidelines for various things, including probabilistic genotyping. Dr. Buckleton also noted that, during the validation process, he and the developers hand-calculated some of the tested samples in order to verify that the output from the software was correct.

Further, in regards to the general acceptance of STRMix in the scientific community, Dr. Buckleton indicated that the forensic science field in North America and much of Europe is moving or has already moved towards the adoption of probabilistic genotyping for the interpretation of DNA as opposed to the conventional method of DNA typing known as the Combined Probability of Inclusion (PCI). Specifically, according to Dr. Buckleton, approximately 52% of North American Laboratories have now purchased STRMix and have either gone live or are in the process of validation. The evidence and testimony presented clearly support a finding that the prosecution has satisfied its burden with regard to this *Daubert* factor.

D. Error Rate

There is also no dispute that information regarding STRMix's error rate is known, and information pertaining to any potential error rate has been discussed and reviewed in the public domain. To date, no known error rate has been developed with STRMix. However, Dr.

Buckleton noted that STRMix has a very well-studied error rate that is primarily dominated by the type of sample involved. By "well-studied", Dr. Buckleton explained that he and others have studied the rate of false inclusion, which is the error of greatest significance for a range of different sample types. Specifically, there are two ways to create a false conclusion – a false inclusion or a false exclusion. Dr. Buckleton testified that DNA has always had a potential for false inclusion by the person coincidentally having the correct alleles to fit in the mixture (i.e., the false inclusion rate); the DNA false inclusion rate increases as the template gets low, and the number of contributors gets high. The question was whether STRMix increased that rate, and according to Dr. Buckleton, STRMix did not increase that rate. Also, as it pertains to the error rate, Dr. Buckleton testified that there were two "miscodes" that created a small error one way or another in the area of error statistics, but they did not have inclusion or exclusion either way. Dr. Buckleton indicated that the error rate or known false occlusions did not undermine his confidence in STRMix. Importantly, of the thousands of tests run to date, the only errors reported involved extremely low levels of DNA.

E. Standards Controlling Operation

Lastly, the Court finds that the prosecution has met its burden with regard to proving the existence and maintenance of standards controlling STRMix's operation. Prior to being adopted by individual laboratories, STRMix had to be developmentally validated. As Jeffery Nye testified, prior to making the decision to purchase STRMix for use at the MSP Lab, he reviewed the published peer review journal articles regarding STRMix's developmental validation. Once he was satisfied that STRMix comported with SWGDAM validation guidelines, he purchased STRMix for use at the MSP Lab and began developing and implementing procedures for internal validation. This internal validation included numerous tests to see how the software handled different DNA mixtures, with up to four contributors, under as many different scenarios as possible. Also, as noted above, mock samples of DNA already contained within the MSP Lab were combined with other DNA profiles in an effort to test if contributors could be parced out, and if so, in what portions. Adjudicated case samples were also utilized during the internal validation process as a method of testing the software's accuracy.

Aside from the SWGDAM guidelines already in place for use of this type of software, Nye also developed his own internal instruction manual specific to the MSP Lab, which he classified as a set of working instructions with certain parameters so that MSP scientists stay within the guidelines set forth and so that the MSP Lab can provide reports with conclusions that are acceptable. Specifically, this internal instruction manual sets forth working instructions on how to use the STRMix software, how MSP scientists are to evaluate how the software works, and different diagnostic tools to assist with their analyses. The instructions also operate as a guide for MSP scientists as to how to interpret and actually report their conclusions. Beyond the development of policies and testing for purposes of internal validation, Nye also indicated that MSP scientists underwent 34-40 hours of formal STRMix training with Dr. Buckleton. In addition to the formal training, each scientist that was to use STRMix was required to pass a competency test.

Although Defendant challenges MSP's internal validation methods as being insufficient, he does not articulate what, if anything, would be necessary in addition to the internal guidelines that are already in place. Moreover, the Court would again note that Defendant's dissatisfaction with the level of training imposed on MSP forensic scientists certified to operate STRMix would go to the weight of the testimony and evidence introduced – not admissibility. Likewise, Defendant's challenge to the likelihood ratio STRMix outputs and its corresponding qualitative equivalent conclusion does not affect the reliability and admissibility of STRMix evidence as a whole under *Daubert* or MRE 702. In *Daubert*, the United States Supreme Court held that general acceptance of a scientific theory was not a necessary precondition to the admissibility of scientific evidence under FRE 702, as long as "the reasoning or methodology underlying the testimony is scientifically valid" and applicable to the facts in issue.[26] Pertinent evidence based on scientifically valid principles will satisfy those demands.[27] The trial court need not "admit only evidence that is unassailable" or investigate "whether an expert's opinion is necessarily correct or universally accepted."[28] Based on the foregoing, the Court finds that the prosecution has met its burden of demonstrating the existence and maintenance of standards/guidelines controlling STRMix's operation.

CONCLUSION

For the reasons set forth herein, the Court finds that evidence and testimony related to the use of STRMix satisfies the reliability criteria set forth in *Daubert* and MRE 702; therefore, said evidence is hereby deemed relevant and admissible. Although no appellate court in Michigan has addressed the use of STRMix as a statistical method of evaluating DNA profile evidence under *Daubert* and MRE 702, the fact that two other Michigan trial courts have deemed the use of such evidence to be reliable and admissible is highly persuasive under the circumstances.[29]

THEREFORE, IT IS ORDERED that Defendant's *Motion in Limine to Exclude Expert Testimony* pertaining to the use of STRMix is hereby **DENIED.**

IT IS SO ORDERED.

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[26] *Daubert, supra* at 592-593

[27] *Id.* at 592-594; see, also, *Kumho Tire Co, Ltd v Carmichael,* 526 US 137, 149-150; 119 S Ct 1167; 143 L Ed 2d 238 (1999).

[28] *People v Unger*, 278 Mich App 210, 218; 749 NW2d 272 (2008)

[29] See *People v Elamin Muhammad,* unpublished opinion of the 14th Circuit Court, issued December 15, 2015 (Docket No. 14-65263-FC) and *People v Markesse Irby*, 37th District Court, Docket No. 16-254-FC, *Daubert* Hrg Tr 6/21/2016

Hon. Clinton Canady III (P23262)
Circuit Court Judge

PROOF OF SERVICE

I hereby certify I served a copy of the above Order upon Plaintiff and Defendant by placing it in sealed envelopes addressed to attorney for Defendant and attorney for Plaintiff and depositing it for mailing with the United States Mail at Lansing, Michigan, on November 28, 2016.

Melissa J. Hoover (P75921)
Law Clerk