STATE OF NEW YORK
COUNTY COURT : COUNTY OF NIAGARA

THE PEOPLE OF THE STATE OF NEW YORK

-vs-

VINCENT BULLARD-DANIEL, **Indictment No. 2015-088**
Defendant

Appearances by: Robert A. Zucco, Esq.
John P. Granchelli, Esq.
Assistant District Attorneys
Appearing for the People

Christopher A. Privateer, Esq.
Assistant Public Defender
Appearing for Defendant

FRYE HEARING DECISION

MURPHY, J.

Defendant is charged with Predatory Sexual Assault (Penal Law §130.95 [1][a]) and Burglary in the First Degree (Penal Law §140.30 [1]). During pretrial proceedings, the Court learned that the People intended to introduce DNA evidence as part of their case in chief. Defense counsel was provided with copies of the DNA report. Following his review of the report, defense counsel raised the question of the admissibility of the report as well as testimony relating to the report

and thereafter sought a *Frye* hearing (see *Frye v United States*, 293 F 1013 [D.C. Cir. 1923]). After consideration of written submissions, the Court concluded that it would conduct a *Frye* Hearing.

The specific issue here is the admissibility of the forensic DNA testing results performed on a number of items of evidence discovered at the crime scene (the victim's house) and on cuttings from a dried red-stained area of a sock found in Defendant's bedroom. DNA testing on those items was conducted by the Eric County Central Police Services Forensic Laboratory ("the Lab") and the results were interpreted using a relatively new software program referred to as "STRmix."[1]

The parties have provided the Court with voluminous submissions in support of their respective positions. Those submissions include references to relevant cases, articles from scientific journals, and expert affidavits. The Court recognizes that the science behind DNA analysis and statistical probabilities is complex. This Court, however, previously rendered a Decision involving the admissibility of a DNA "kit" (see *People v Borden*, Decision attached to People's Memorandum of

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[1]According to the STRmix website (http://strmix.esr.cri.nz), "STRmix is a breakthrough for forensic analysts as it can assist investigations using DNA evidence that was previously considered too complex to interpret. The software has been developed by New Zealand Crown research institute ESR, with Forensic Science South Australia."

Law, dated December 23, 2015) and therefore is familiar generally with the scientific principles at issue.

Before summarizing the testimony from the *Frye* Hearing, the Court believes that some background discussion of DNA analysis and interpretation is necessary. Rather than attempt to reinvent the wheel, the Court has taken the liberty of quoting at length from Judge Michael Coccoma's recent decision involving a similar probabilistic genotyping program:

> 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.
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> 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) productivity - 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 results whereas a mathematically programmed computer can infer a genotype 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) 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 aproaches:

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

(2) fully continuous - incorporation of biological parameters.

(*People v Wakefield*, 47 Misc3d 850, 852-854 [Sup Ct, Schenectady Co 2015] footnotes omitted).[2]

THE FRYE HEARING

The *Frye* hearing was held on January 11, 14, and 21, 2016. The People's only witness was **Dr. John Simich**, the Director of the the Lab (I-12).[3] Dr. Simich testified that he was also the "DNA technical leader" for the Lab, and taught forensic science at SUNY Buffalo at both the graduate and undergraduate levels. Dr. Simich has been conducting DNA analysis since 1993 and the Lab has always used commercial "kits." The "kits" contain "all of the components that are required for the polymerase chain reaction [PCR] process to proceed and to

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[2]*Wakefield* involved the issue of whether "Cybergenetics True Allele Casework," otherwise referred to as TrueAllele, met the *Frye* standard. That court concluded that it did.

[3]The *Frye* hearing consists of two volumes, but each hearing date is consecutively paginated. The January 11 Hearing references will be preceded by ("I"), the January 14 Hearing References by ("II"), and the January 21 Hearing references by ("III").

generate the DNA results" (I-21). The Lab has used different kits over the years (I-19). The kits are used to "generate the PCR reaction and to look at the STR [short tandem repeat] genetic markers that are provided in the kit" (I-21). According to Dr. Simich, PCR/STR testing is used in all forensic labs worldwide.

After the PCR/STR process is complete, an instrument called a Genetic Analyzer reads the "various amplified fragments of DNA, and then that translates it into something that a human can see which is the electropherogram" (I-24). Once the Lab generates a DNA profile from the sample, that profile is compared to an individual - victim, suspect, or elimination sample - "to determine if they are the source of that DNA" (I-27). An electropherogram is a print-out of the "graph of the various DNA types that were identified at each of the genetic markers" (I-27). Exclusion can be made by visual comparison of the electropherograms. If there is no exclusion, the Lab needs "to determine the weight of the evidence" (I-28).

The electrophoresis step produces a chart, which gives the value of the DNA marker at a certain point and the "strength" of the signal (a measure of how many of the DNA molecules were examined at a particular value) (I-32). In July 2015, the Lab began using STRmix to make this calculation. STRmix allows the Lab to

report the results as a likelihood ratio.[4]

STRmix uses "continuous probability genotyping" software (I-34). That software uses information that has been available for "years" (I-34). STRmix was recommended by different scientific organizations as "the best way to perform reporting of the weight of the DNA evidence" (I-34). A "continuous" software program like STRmix, according to Dr. Simich, is "more discriminating;" it looks at "all of the information" (I-35).

Dr. Simich testified about various scientific organizations that review the software programs: SWGDAM (Scientific Working Group for DNA Analysis Methods), NIST (National Institute of Standards and Technology), and ISFG (International Society of Forensic Genetics). According to his undisputed testimony, all three have recommended STRmix. STRmix addresses the problem of mixed samples, that is, DNA with more than two contributors. STRmix "is able to break [the DNA sample] down into its component mixtures" (I-38).

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[4]Different computer software has been used by the Lab over the years to calculate a *probability* ratio, expressed in a mathematical term, e.g., one in 500,000 individuals. In a *likelihood* ratio, the results are expressed as follows: a match between the suspect and the evidence is (x number) of times more probable than a coincidental match.

Dr. Simich discussed the concept of "probabilistic genotyping,"[5] as used in the calculation step of DNA analysis, and testified that the principle "has been around for many years." (I-40). He described the two steps involved in the process: deconvolution and statistical analysis. Deconvolution breaks a mixture "down into the individual contributors and generate[s] DNA profiles for each of them" (I-41). Statistical analysis determines "the likelihood ratio of a person of interest [the Lab] is asked to compare to" (I-41).

Dr. Simich was familiar with some of the mathematical analysis methods and principles used in the deconvolution process, for example, the MCMC (Markov Chain Monte Carlo) model, and the Metropolis-Hastings algorithm. MCMC is a standard statistical modeling process. STRmix also employs Bayes' theorem, which is a general scientific principle of the likelihood ratio. Bayes' theorem was developed in the early 1700s and has been used for centuries in various scientific disciplines without controversy (I-45).

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[5]According to the Draft Guidelines for the Validation of Probabilistic Genotyping Systems, published by SWGDAM and introduced into evidence as People's Exh. 3, "A probabilistic genotyping system is comprised of software, or software and hardware, with analytical and statistical function that entail complex formulae and algorithms. Particularly useful for low-level DNA samples and complex mixtures, probabilistic genotyping approaches can reduce subjectivity in the analysis of DNA typing results, as compared to historical methods of mixture interpretation (e.g., deconvolution of the mixture into individual components), and quantifies uncertainty in the analysis."

After reviewing the STRmix software, Dr. Simich concluded that the science behind it was generally accepted within the forensic lab community. He further concluded that the software was reliable, based upon his review of peer-reviewed journals (I-48). The creators of STRmix provided Dr. Simich with a report of their internal validation process (I-50). The Lab also conducted its own validation study of STRmix and published a report, which was submitted to the New York State Commission on Forensic Science DNA Subcommittee ("the DNA Subcommittee) (I-54; see People's Exh. 2). The Lab study concluded that STRmix "does reliably deconvolute DNA profiles and provide likelihood ratios that can be used for casework" (I-55). The Lab underwent an external audit by the National Forensic Science Training Center in August 2015, after it had begun using STRmix. The Lab undergoes a regular accreditation process as well as an internal audit (I-25-26).

Dr. Simich testified that he had considered other software programs, including Forensic Statistical Tool (FST) and TrueAllele. He concluded that "STRmix is accurate and reliable and can be utilized to generate likelihood ratios for mixture deconvolutions" (I-59).

Dr. Simich testified about the approval of STRmix by the New York State Commission on Forensic Science ("the Commission"). The Commission is the

"organization that actually will evaluate and grant... New York State accreditation" (I-60). The DNA Subcommittee, made up of experts in various scientific disciplines related to DNA analysis, evaluates the DNA aspect of forensic labs in New York. Dr. Simich appeared before the Subcommittee three times and presented his validation studies; Dr. Buckleton, one of the creators of STRmix, also appeared before the Subcommittee. In May 2015, the Subcommittee voted 4-0 (with one member abstaining) on a binding recommendation to the Commission to allow the Lab to use STRmix for casework analysis (see minutes of the meeting of the DNA Subcommittee approving STRmix, People's Exh. 5; letter from the Subcommittee to the Chair of the Commission with the binding recommendation, People's Exh. 6) (I-63). The DNA Subcommittee also issued a general recommendation on the use of probabilistic genotyping software (People's Exh. 7).

Dr. Simich testified without any contradiction that STRmix is used in other labs in Australia and New Zealand, and by USACIL (United States Army lab), the California Department of Justice, and the FBI. He was aware that some labs use FST (New York City's Office of the Chief Medical Examiner, or "OCME") or TrueAllele (Virginia, some labs in Pennsylvania). He believed that other labs in

New York State have purchased STRmix and will be using it soon, including the OCME, which will be replacing FST.

On cross-examination, Dr. Simich explained why he selected STRmix for the Lab over other software programs. He admitted that there were other acceptable methods to perform forensic statistics (I-79) and explained the differences among the various accepted methods (I-80). He opined that, in this case, the DNA profile was "15,000 times more probable if the sample originated from [Defendant] and three unknown unrelated individuals because it's a four-person mixture rather than if it originated from four unknown unrelated individuals in the U. S. population" (I-88).

Dr. Simich was asked about the "reproducibility" of the results reached by STRmix, in the context of his testimony that every time a sample was analyzed there would be a different likelihood ratio (I-115). He testified that variations among the different results were not "statistically significant" (I-115). The People rested, relying solely on the testimony of Dr. Simich and the accompanying exhibits.

Defendant presented the testimony of **Dr. Gary Skuse**, who teaches biological sciences at the Rochester Institute of Technology, with a specialization

in a field called bioinformatics, which involves the interaction between biology and computers (III-4). His experience with DNA forensics consists of working "with criminal defense attorneys primarily helping them understand the processes that go into using DNA in criminal cases and help them interpreting the results" (III-6-7). He testified in the *Wakefield* case about the "way the DNA was isolated, the way the laboratory interpreted the DNA results" (III-7). With respect to STRmix, he reviewed various articles as well as material from the company, and the protocols established by the Lab. He criticized the amount of "human intervention and human judgment" involved in setting up the software (III-9). He was "interested that a laboratory acknowledged that the software itself gives different answers every time it's run" (III-9). He discussed the notion of "objective science" and opined that STRmix was not acceptable in accordance with general scientific principles (III-10).

On cross-examination, Dr. Skuse conceded that he had no training in forensic DNA analysis and that he had never been to the Lab. He apparently has visited the Monroe County Forensic Laboratory on rare and sporadic occasions. He had never used the STRmix program (III-50).

On re-direct examination, Dr. Skuse was critical of what he called "directed science," that is, "you're doing something to achieve a result that you expect" (III-55). In his view, there was an intrinsic bias with directed science (III-56). He was also critical of the peer review process in biological publications that has evolved over the past few years (III-56-57).

Defendant rested, and the parties provided the Court with further written submissions; oral argument was held on February 25, 2016.

THE LAW

THE FRYE STANDARD

Frye established the general proposition that scientific expert witnesses are only permitted to give opinion evidence when their testimony is based upon scientific principle or discovery that has passed the mere experimental stage and become demonstrable scientific knowledge generally accepted as valid within the relevant scientific community. Even though the Federal system, and a number of states, have moved away from the *Frye* standard to one embracing a more hands-on gatekeeper function for the trial judge (see *Daubert v Merrell Dow Pharmaceuticals, Inc.*, 509 US 579 [1993]), New York continues to follow the

Frye approach. Initially, the proponent of the evidence provides case citations indicating that other courts have already addressed the issue and approved its admissibility. Such cases can come from any competent court and jurisdiction, whether in the United States or elsewhere. The proponent will also typically reference learned scientific treatises, published papers, books or other learned writings demonstrating acceptance of the scientific principle within the applicable scientific community (see *People v Hughes*, 59 NY2d 523 [1983]). When there are no such published materials, or when they are sparse or conflicting, the proponent must augment his proffer by expert testimony at a pretrial *Frye* hearing.

At such a hearing, the proponent bears the burden of proof. The standard that the proponent must meet does not seem to have been clearly delineated by New York courts. At oral argument, the People indicated they were unable to find any specific authority on this issue (Transcript of Feb. 25, 2016, at 21). The People rejected Defendant's suggestion that the appropriate standard is, "beyond a reasonable doubt," and argued that the more appropriate standard is, "preponderance of the evidence." In *Daubert*, the U.S. Supreme Court stated that, like any preliminary question regarding the admissibility of evidence, the standard is "a preponderance of proof" under the Federal Rules of Evidence (*Daubert,* 509 US at 590 n 10). Such a standard has been suggested in New York (see *People v*

Owens, 187 Misc2d 838 [Sup Ct, Monroe Co 2001]). To the extent that it is necessary for this Court to apply a legal standard, the "preponderance of the evidence" test seems more appropriate and it has been that standard that this Court has applied in the analysis of the issues in this hearing.

The proponent of the evidence must establish that the scientific principles and techniques he advocates, when properly performed, generate consistent results accepted generally as reliable within the relevent scientific community (see *People v Wesley*, 83 NY2d 417 [1994]). At such a hearing, it is not the court's duty to reach its own conclusion about the reliability of the proposed scientific procedure, but rather to determine whether most of the relevant scientific community believes the procedure or technique under consideration is reliable (see *id.*). As Justice Mark Dwyer reminded us: "a court assessing the admissibility of evidence under Frye is not charged with deciding the validity of novel scientific procedures. It would hardly be sensible to assign that task to the judiciary, most of which is patently unqualified to perform the task as is this court. Judges should be 'counting scientists' votes,' and not 'verifying the soundness of a scientific conclusion'" *(People v Collins*, 49 Misc3d 595 [Sup Ct, Kings Co 2015], quoting *Parker v Mobil Oil Corp.*, 7NY3d 434, 446-447 [2006], quoting *People v Wesley*, 83 NY2d 417, 439 [1994][Kaye, C.J., concurring]).

While the issue of the admissibility of DNA has long since been resolved, new issues have arisen regarding the interpretation of the results of DNA testing. There are numerous cases in New York regarding software programs that interpret DNA results, although none involve STRmix. Although the scientific principles underlying the STRmix program are similar to the principles if not identical to the programs that have been considered, and almost universally accepted by courts in New York, this case concerns the first judicial review, as far as this Court is aware, of STRmix in New York. For that reason, the Court decided to conduct a *Frye* hearing.

The People argue, and the Court agrees, that the only question before it is whether the scientific principles underlying the STRmix software are accepted generally in the relevant scientific community. The People contend that STRmix is a form of probabilistic genotyping, which is accepted generally in the scientific community of forensic DNA analysis. There is only one reported decision involving STRmix, from Michigan, where the court applied *Daubert*, and upheld the admissibility of the DNA test results (*People v Muhammad* [14th Cir. Ct, Muskegon Co, Dec. 15, 2015][attached to the People's submission of Dec. 23, 2015]). This Court is aware that all of the New York decisions involving software programs similar to STRmix have found the tests results to be admissible, with one

exception that this Court finds distinguishable.

Defendant's primary objection to the admissibility of the results of the DNA testing, advanced in the Memorandum of Law received on February 16, 2016, is that the relevant scientific community for purposes of deciding whether STRmix is accepted is "an insular community of professionals whose careers and livelihoods focus on the prosecution of criminal cases and upon the 'discovery' of inculpatory evidence." Defendant urges this Court to "take the warnings of Frye and Leone to heart."[6] Although the People's proof was limited to the testimony of Dr. Simich and the accompanying exhibits, the Court concludes that his testimony, in conjunction with a number of other factors, supports the admissibility of DNA testing undertaken in this case.

First, Dr. Simich was thoroughly familiar with the application of the STRmix software. While he could not expound on the underlying mathematics, his Lab conducted validation studies (People's Exh. 2) and he reviewed numerous articles regarding the software. As noted in *Muhammad*, the mathematical models are themselves non-controversial and have been widely used in fields such as weather forecasting, computational biology, linguistics, genetics, engineering,

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[6]Presumably, Defendant is referring to the admonition in *People v Leone* (25 NY2d 511, 518 [1969]) that scientific "tests" can have an undue influence on juries and therefore, courts must be "most careful in admitting into evidence the results of such tests unless their reasonable accuracy and general scientific acceptance is clearly recognized."

physics, aeronautics, finance, and social sciences. As the director of a forensics lab, Dr. Simich is well-qualified to critique software programs like STRmix. The Court was impressed by his background, education and wealth of practical experience generally on forensic DNA and on the STRmix program specifically. At least one other court has credited Dr. Simich's work on this particular topic (*People v Muhammad*, supra). Dr. Simich is, in the Court's opinion, part of the relevant scientific community for *Frye* purposes.

With all due respect to Dr. Skuse and not in any way to denigrate the intelligence and experience that he so obviously possesses, this Court does not believe that he can be can considered as an expert in the field of forensic DNA analysis in general or on the specific topic of the scientific acceptance of probabilistic genotyping as utilized.[7]

Although the Court would have preferred to hear from other experts in the relevant scientific community,[8] Dr. Simich's testimony cannot be considered in a vacuum. He appeared before the Commission on three occasions. He testified

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[7]Having said that, this Court is not making a finding on whether he is qualified as an expert to testify at a jury trial about questions related to DNA in general.

[8]For example, in the only case of which the Court is aware that STRmix was the subject of an admissibility hearing, there was testimony from Dr. Simich and Dr. Buckleton, the New Zealand scientist who helped develop STRmix. Some of the other cases reviewed by the Court discussed the testimony of several experts, on both sides of the issue, and thus those courts had the benefit of hearing from a greater portion of the relevant scientific community.

that, following his initial presentation of the Lab's validation studies, he performed additional experiments and reorganized data at the request of the Commission (I-62). At Dr. Simich's second appearance, the Commission required additional work, so he reorganized "all of the material and performed additional studies following the SWGDAM guidelines and then made the final presentation to the DNA Subcommittee in May of 2015" (I-62).

The role of the Commission and the DNA Subcommittee in this Court's decision, while not dispositive, certainly cannot be discounted. In 1994, the Legislature created the Commission (Executive Law Art. 49-B) to "develop minimum standards and a program of accreditation for all forensic laboratories in New York state . . . and approval of forensic laboratories for the performance of **specific forensic methodologies**" (Executive Law §995-b [1], emphasis added). To achieve its mission, the Commission is designed to "ensure that forensic analyses, including forensic DNA testing, are performed in accordance with the highest scientific standards practicable" (Executive Law §995-b [2][b]). Insofar as relevant here, the Commission, "[u]pon the recommendation of the DNA subcommittee . . . shall designate one or more approved methodologies for the performance of forensic DNA testing" (Executive Law §995-b [11]). Moreover, the Commission is charged with promulgating standards "for a determination of a

match between the DNA records contained in the state DNA identification index and a DNA record of a person submitted for comparison therewith" (Executive Law §995-b [12]).

The record establishes that the DNA Subcommittee met on May 29, 2015, and voted unanimously (4-0, with one abstention) "to issue a binding recommendation to the [Commission] that the use of STRmix by [the Lab] be approved for forensic casework" (People's Exhs. 5 and 6). The DNA Subcommittee met again on August 14, 2015, to discuss a June presentation by Dr. Michael Coble at the National College for Forensic Science Litigation on the topic of "Software Systems for Interpreting Low Level Samples and Complex Mixtures" (People's Exh. 7). The letter sent to the Commission following that meeting is informative. It states in relevant part:

> The Subcommittee indicated that the presentation addresses some of the challenges involved in handling complex mixtures and some of the advantages of using probabilistic models to aid in interpretation. Subcommittee members agreed that Dr. Coble's presentation substantiates the need to embrace new technologies, especially when challenging mixtures require additional analytical methods to assist in their interpretation. The presentation addressed the benefits of using these software tools and revealed that those laboratories not using deconvolution software tools are at a disadvantage. Members noted that interpretations without the software were "all over the road."
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> In sum the Subcommittee members expressed that they are pleased that New York State labs are moving forward to validate these software systems. All Subcommittee members were resolute that the development and use of these software tools is a significant advancement and will greatly assist laboratories in the analysis, interpretation and reporting of DNA mixtures.

The Commission voted on June 19, 2015, to approve the binding recommendation of the DNA Subcommittee.

The Court finds it significant that the DNA Subcommittee, which consists of scientists in various disciplines, voted unanimously to approve STRmix. The DNA Subcommittee consists of scientists in the fields of molecular biology, population genetics, laboratory standards and quality assurance, and forensic science (Executive Law §995-b [13][a]). As noted by the court in *People v Rodriguez* (_ Misc3d _ [Sup Ct, NY Co 2013]), "It would be bizarre indeed for a body of such highly accomplished forensic scientists, charged by law with this solemn duty, to recommend software program for use in DNA analysis unless confident that it was firmly based upon principles and methodology accepted as reliable by colleagues in the field."

In addition to the votes of the bodies appointed by State law to consider the use of various forensic DNA methodologies, the Court is also faced with the almost unanimous approval of the courts that have considered similar software programs. Of course, there is no reported case in New York regarding the admissibility of the STRmix software program, but the Court is persuaded by the analysis of those courts that have reviewed similar programs (see *People v Megnath*, 27 Misc3d 405 [Sup Ct, Queens Co 2010][Low Copy Number analysis];

People v Rodriguez, supra [FST] [attached to People's Memorandum dated Dec. 23, 2015]; *People v Garcia*, 39 Misc3d 482 [Sup Ct, Bronx Co 2013][FST]; *People v Styles*, 40 Misc3d 1205[A] [Sup Ct, Kings Co 2013][FST]; *People v Wakefield*, supra [TrueAllele]; *People v Belle*, 47 Misc3d 1218[A][Sup Ct, Bronx Co 2015][FST]; *People v Debraux*, 50 Misc3d 247 [Sup Ct, NY Co 2015][FST]; *People v Lopez*, 50 Misc3d 632 [Sup Ct, Bronx Co 2015][FST]).

Only two of the New York cases are worth discussing in detail. The first is *People v Wakefield* (supra), which involved TrueAllele. TrueAllele, like STRmix, involves probabilistic genotyping. The Court recognizes that STRmix and TrueAllele are not identical and in fact Defendant argues that the differences between the two are so significant that the *Wakefield* decision cannot be used to support a ruling in favor of STRmix. The Court also recognizes that TrueAllele is a competitor of STRmix.[9] Indeed, the Court was advised during its consideration of the scheduling of the *Frye* hearing that Dr. Perlin might testify on behalf of Defendant. That ultimately did not happen and this Court draws no inference, either favorable or unfavorable, because of the omission.

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[9]In one of Defendant's many submissions to the Court, dated November 3, 2015, there is a letter from Dr. Mark W. Perlin, the Chief Scientific and Executive Officer of TrueAllele, to Jerry D. Varnell, Contract Specialist, Procurement Section, Department of Justice, Federal Bureau of Investigation. Dr. Perlin was responding to the FBI's decision that STRmix was the only software that satisfied its requirements for DNA interpretation technology.

In any event, the court in *Wakefield* discussed at length the role of the Commission and the DNA Subcommittee, both of which voted to approve TrueAllele, and concluded that "approval" by the Commission and the DNA Subcommittee "clearly constitutes 'general acceptance'" (*Wakefield*, 47 Misc3d at 856). After discussing the expert testimony adduced at the *Frye* hearing and the legal acceptance of TrueAllele, Judge Coccoma in Wakefield concluded that "computerized probabilistic approaches and likelihood ratio principles" used by TrueAllele "are superior to current methods" (*id.* at 858). The court stated that there was a "plethora of evidence" in favor of TrueAllele and "there is no significant evidence to the contrary" (*id.*). The same is true here.

People v Collins (49 Misc3d 595 [Sup Ct, Kings Co 2015]) is the outlier among the forensic DNA software program cases in New York. *Collins* involved FST, used by OCME. At least two other trial courts, at the time that *Collins* was decided, had already ruled in favor of FST as being generally accepted in the forensic DNA community. In *Collins*, the People presented testimony from national experts on DNA forensics and the DNA subcommittee's vote approving FST. In response, the defendant presented testimony from an expert referred to by the court as "the father of American DNA analysis." The court in *Collins* rejected the view of the other courts that had considered whether FST was generally

accepted in the relevant scientific community, and minimized the weight given to the DNA Subcommittee's approval of FST. With all due deference to the *Collins* court, this Court does not believe that it is in a position to assess the reliability of STRmix; rather, its role is simply to determine whether the scientific principles behind the STRmix software are accepted generally in the relevant scientific community. That does not mean that there must be unanimity within the scientific community (see *People v Middleton*, 54 NY2d 42, 49 [1981]).

Additionally, Justice Dwyer's criticism in *Collins* that validation studies are not "conclusive" because they are only tautological begs the question. This Court has considered People's Exhibit 2, the Lab's 41-page STRmix Implementation and Internal Validation Study-2015, and finds that it tests the program's assumptions in a variety of ways and that the program properly handles problematic issues such as stutter, drop-in and peak height parameters. Moreover, page 41 of the Study references other validation experiments and tests of the STRmix program and thus supports this Court's conclusion that it has found general acceptance within the relevant scientific community.[10]

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[10]The court in *Collins* was presented with an impressive group of scientists on both sides of the issue, some of whom testified that the manner in which the drop-in and drop-out rates are assessed at each locus by the FST program is not generally accepted within the DNA community. The Court here was presented with no such evidence to the contrary.

The *Collins* decision was criticized in *People v Carter* (50 Misc3d 1210[A] [Sup Ct, Kings Co 2016]), the latest case involving FST. The *Carter* court found that there was "a possible lack of objectivity guiding the testimony of several of the defense experts in Collins" and that the recommendation of the DNA subcommittee is entitled to greater weight than the court in *Collins* gave it.

The last submission by Defendant, received by the Court on February 16, 2016, perhaps in an attempt to lighten the tone of these otherwise dreary briefs, contains the following quotation from Ernest Rutherford: "If your experiment needs a statistician, you need a better experiment."[11] The analysis of DNA is not an experiment; the science behind it is well-established. All that STRmix, TrueAllele, FST, and others of their kind are doing is improving the ability of forensic labs to confirm or deny the identity of DNA samples, particularly when multiple sources

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[11]In the Court's research to put this quotation in its proper context, it found the quotation to be, "If your experiment needs statistics, you ought to have done a better experiment." Without impugning the integrity and brilliance of Rutherford, a Nobel Prize winner in Chemistry (although his true field was Physics), the Court makes two points. First, Rutherford died in 1937 and it is unlikely that he could have envisioned the scope and breadth of scientific advances that have been made in the late 20th and early 21st centuries, particularly in the fields of genetics and computing. Second, Rutherford has also been widely quoted for the following: "The energy produced by the breaking down of the atom is a very poor kind of thing. Anyone who expects a source of power from the transformation of these atoms is talking moonshine." With the advent of supercomputers, the future is already a thing of the past.

are involved.

Dr. Skuse's chief criticism of STRmix in his testimony does not relate to probabilistic genotyping in general or even to STRmix in particular but to a line in the Lab protocol that "says that STRmix should only be run one time because - well, actually the way it says it is results tend to vary. So each time a sample is analyzed it should only be run once" (III-16). That issue is addressed by Dr. Simich in his cross-examination as follows: there is a different result "if you run the program twice with the same input . . . [b]ecause the MCMC process is a random process, and it generates a random number to begin the process every time you do the analysis. So you will get a different likelihood ratio every time you . . . put the same data in" (I-114-115).

In a broader and and more general sense, Dr. Skuse countered that "traditional scientists" will do an experiment three times and if the results are "close, you report them . . . or you figure out what's wrong and try it again" (III-12).

The Court finds that whether the procedure is performed once as recommended, or three times (or more) as Dr. Skuse seems to suggest, it does not affect the question this Court is called upon to decide, namely, general acceptance of the probabilistic genotyping procedure within the relevant scientific community.

Of course, this Court would expect that the statement referred to above would add another arrow in the quiver of defense counsel that would be used to undermine the STRmix results when the issue is presented to the trial jury, but it does not affect the issue of the general acceptance of STRmix within the relevant scientific community.

People v Muhammad (supra) is the only other reported case in the country regarding the admissibility of STRmix. There, the court concluded as a preliminary matter that "statistical evaluation of the DNA analysis's results is a matter of evidentiary weight, not admissibility." Thus, the court's determination of admissibility falls into the category of dicta. Nonetheless, the court reached several conclusions, which are persuasive insofar as this Court is faced with identical issues. First, the *Muhammad* court found that STRmix "received adequate validity testing." Indeed, Dr. Buckleton testified in *Muhammad* and it was anticipated, based on preliminary representations made to this Court by the People, that he would testify here. His testimony could have resolved several questions raised by the cross-examination testimony of Dr. Simich and the direct testimony of Dr. Skuse. Nothwithstanding Dr. Buckleton's failure to testify here, Dr. Simich's

testimony was sufficient to meet the People's burden of establishing, by a preponderance of the evidence, that STRmix was generally accepted in the relevant scientific community. Significantly, Dr. Simich testified in *Muhammad* and that court found his testimony relevant and significant. Dr. Simich reported the results of the Commission and the DNA subcommittee and the *Muhammad* court discussed those results in a positive light.

In conclusion, the Court would like to commend the parties for their passionate and thorough advocacy on behalf of their respect positions. Contrary to the statement in the last submission by defense counsel, received by the Court on February 16, 2016, the Court does not expect its decision to be "unassailable throughout the state for the remainder of eternity." The Court is aware that there is a case pending in Erie County, with a *Frye* hearing scheduled, on this very issue. As other laboratories throughout New York and the country adopt STRmix, courts will deal with the same questions presented here. At oral argument the parties agreed that there were other programs similar to STRmix being used in labs. Dr. Simich testified that he considered several programs before settling on STRmix. This Court's decision is based on the testimony adduced at the hearing, the accompanying exhibits, and the relevant case law. It may be among the first words

in New York courts on the admissibility of STRmix, but the Court certainly does not expect it to be the last.

This constitutes the Decision and Order of the Court.

Dated: March 10, 2016

Hon. Matthew J. Murphy
Niagara County Court Judge

GRANTED

MAR 10 2016

BY_____
JUDY A. VACANTI
COURT CLERK