

**IN THE SUPERIOR COURT OF THE VIRGIN ISLANDS
DIVISION OF ST. THOMAS-ST. JOHN**

PEOPLE OF THE VIRGIN ISLANDS,	)	CASE NO: ST-2015-CR-0000156
	)	
Plaintiff,	)	14 V.I.C. §§ 921 & 922(a)(1)
	)	14 V.I.C. §921 & 922(b)
-vs-	)	14 V.I.C. §§ 295(1) & 295(3) & 1081
	)	14 V.I.C. § 297(a)(2)
MEKEL BLASH,	)	14 V.I.C. §§ 475(a)(1) & 475(a)(2)
(D.O.B. 04/26/87)	)	14 V.I.C. § 442(1)
	)	14 V.I.C. §§ 1081 & 1083(1)
Defendant.	)	14 V.I.C. §2251(a)(2)(B)

MEMORANDUM OPINION AND ORDER

Before the Court is Defendant's Motion for Daubert Hearing on DNA Evidence, which was filed on February 12, 2018. The People of the Virgin Islands filed an opposition on March 19, 2018. The Court held a *Daubert* hearing on June 1, 2018, and the parties subsequently filed supplemental briefs.

I. BACKGROUND

On or about January 18, 2014, police officers with the Virgin Islands Police Department discovered James Malfetti dead in his apartment on St. John, Virgin Islands. A preliminary assessment of Malfetti's wounds suggested that an assailant stabbed him in the neck, which was later confirmed by an autopsy report. The officers on scene collected a white towel containing saturated blood from Malfetti's apartment for evidentiary purposes. Officers also collected swabs taken from Malfetti's vehicle. Both the towel and swabs were sent to the Federal Bureau of Investigation (FBI) Laboratory for further examination.

On September 30, 2014, Tarah R. Brown, a Forensic Examiner in the FBI DNA Casework Unit, issued her Report of Examination.¹ Brown conducted serological testing and nuclear deoxyribonucleic acid (DNA) typing for several pieces of evidence: three separate cuttings² of the white towel and swabs from the driver's door handle,³ steering wheel,⁴ and gear shift⁵ of Malfetti's vehicle.⁶ Regarding the three cuttings, male DNA existed in each piece. Brown concluded that, to

¹ Def.'s Mot. for Daubert Hr'g on DNA Evidence, Ex. C.

² The three cuttings were labeled as 1(1) (Cutting from bloodstain on towel), 1(2) (Cutting from stain on towel), and 1(3) (Cutting from stain on towel).

³ This swab was labeled as Item 19.

⁴ This swab was labeled as Item 20.

⁵ This swab was labeled as Item 21.

⁶ Def.'s Mot. for Daubert Hr'g on DNA Evidence, Ex. C. Along with the above-mentioned evidence, Brown conducted similar testing for a liquid blood sample (Item 4) and fingernail clippings (Items 5-14), all obtained from Malfetti's person. However, the remainder of this Memorandum Opinion will focus on the results from towel cuttings and swabs.

a reasonable degree of scientific certainty, Malfetti was the source of the DNA in Cutting 1(1).⁷ Cutting 1(2) presented a more complicated DNA mixture:

Male DNA is present in item 1(2). DNA from two or more individuals was obtained from item 1(2). To a reasonable degree of scientific certainty[,] item 4 (MALFETTI) is the major contributor of the DNA obtained from item 1(2). The result for the minor contributor to item 1(2) is not suitable for matching purposes; however, it may be utilized for exclusionary purposes.⁸

Brown reached a similar conclusion for Cutting 1(3):

Male DNA is present in item 1(3). DNA from three or more individuals was obtained from item 1(3). To a reasonable degree of scientific certainty[,] item 4 (MALFETTI) is the major contributor of the DNA obtained from item 1(3). The result for the minor contributors to item 1(3) is not suitable for matching purposes; however, it may be utilized for exclusionary purposes.⁹

Item 19 contained male DNA, but “[n]o comparison information for item 19 [could] be provided for item 4 (MALFETTI),” though the results could be used for exclusionary purposes.¹⁰ Item 20 contained DNA from two or more individuals, and Brown concluded that Malfetti was “potentially the major contributor of the DNA,” with the results for the minor contributors being unsuitable for matching purposes.¹¹ Lastly, item 21 also included DNA from two or more individuals, and the results were unsuitable for matching purposes.¹² Both items 20 and 21 could be used for exclusionary purposes.¹³

The following year, on April 17, 2015, detectives with the V.I.P.D. arrested Defendant Mekel Blash for the homicide of Malfetti.¹⁴ On August 26, 2015, DNA samples obtained from Blash were sent to the FBI Laboratory for examination and comparison, and Brown issued an amended Report of Examination on October 6, 2016, reflecting the implementation of new interpretation guidelines that use the probabilistic genotyping software STRMix.¹⁵ The conclusion for Cutting 1(1) remained the same: Malfetti was the source of the DNA. Cuttings 1(2) and 1(3), however, presented a different result.

Cutting 1(2) was interpreted under the assumption that two contributors were present.¹⁶ Brown concluded that Malfetti was the source of one of the contributors.¹⁷ Brown further

⁷ Def.’s Mot. for Daubert Hr’g on DNA Evidence, Ex. C.

⁸ *Id.*

⁹ *Id.*

¹⁰ *Id.*

¹¹ *Id.*

¹² *Id.*

¹³ *Id.*

¹⁴ The People’s Mot. in Opp’n to Def.’s Mot. for Daubert Hr’g on DNA Evidence 3.

¹⁵ *Id.*; Def.’s Mot. for Daubert Hr’g on DNA Evidence, Ex. D.

¹⁶ Def.’s Mot. for Daubert Hr’g on DNA Evidence, Ex. D.

¹⁷ *Id.*

concluded that the “results for item 1(2) are at least 11 times more likely if they originated from BLASH and an unrelated unknown individual than if they originated from two unrelated unknown individuals,” and this “analysis provides moderate support that BLASH is a contributor to the DNA.”¹⁸ Cutting 1(3) was interpreted under the assumption that three contributors were present, and Brown determined that Malfetti was one of the contributors.¹⁹ Regarding Blash, “[t]he DNA typing results . . . are at least 140,000 times more likely if they originated from BLASH and two unrelated unknown individuals than if they originated from three unrelated unknown individuals.”²⁰ Brown found that “[t]his analysis provides very strong support that BLASH is a contributor to the DNA.”²¹ Finally, regarding items 19, 20, and 21, Blash was excluded as a potential contributor of the DNA in those swabs.²²

In response to the change between the two reports, on February 12, 2018, Blash moved the Court for a *Daubert* hearing to seek the exclusion of the results in Brown’s 2016 report, with his main point of contention being Brown’s reliance on STRMix; the People opposed. Upon considering the arguments, the Court held a *Daubert* hearing on June 1, 2018. Because Brown was unavailable due to medical reasons, the People called Jerrilyn Conway, a forensic biologist with the FBI’s DNA Casework Unit, to testify to the scientific reliability of STRMix and her opinion on Brown’s analysis.

II. LEGAL STANDARD

Rule 702 of the Virgin Islands Rules of Evidence governs the admissibility of expert testimony:

A witness who is qualified as an expert by knowledge, skill, experience, training, or education may testify in the form of an opinion or otherwise if:

- (a) the expert’s scientific, technical, or other specialized knowledge will help the trier of fact to understand the evidence or to determine a fact in issue;
- (b) the testimony is based on sufficient facts or data;
- (c) the testimony is the product of reliable principles and methods; and
- (d) the expert has reliably applied the principles and methods to the facts of the case.

Similar to its federal counterpart, the standard adopted in *Daubert v. Merrell Dow Pharmaceuticals, Inc.*²³ guides the Rule 702 analysis:

Faced with a proffer of expert scientific testimony, . . . the trial judge must determine at the outset . . . whether the expert is proposing to testify to (1) scientific knowledge that (2) will assist the trier of fact to understand or determine a fact in

¹⁸ *Id.*

¹⁹ *Id.*

²⁰ *Id.*

²¹ *Id.*

²² *Id.*

²³ 509 U.S. 579 (1993).

issue[, which includes assessing] whether the reasoning or methodology underlying the testimony is scientifically valid and . . . can be applied to the facts in issue.²⁴

The standard enunciated in *Daubert* requires that courts consider the qualifications of the proffered expert, the reliability of that expert's proffered testimony, and the fit of the testimony to the particular facts of the case.²⁵

III. DISCUSSION

The primary point of contention is Brown's reliance on the probabilistic genotyping software STRMix in the interpretation of her DNA testing results. Before turning to the merits, a short discussion of DNA testing generally, and STRMix specifically, is necessary.

DNA, or deoxyribonucleic acid, is a molecule that encodes the genetic information in all living organisms and has been used in the criminal justice system as a means of identifying individuals since the late 1980s.²⁶ On a basic level, "DNA analysis involves comparing DNA profiles from different samples to see if a known sample may have been the source of an evidentiary sample."²⁷ To produce DNA profiles, the FBI uses the AmpFLSTR Identifiler Plus PCR Amplification Kit, which includes the amelogenin locus – used for sex determination – and 15 autosomal STR loci. Polymerase chain reaction (PCR) describes the biotechnical process by which the DNA profiles are determined.²⁸

To generate a DNA profile, DNA is first chemically extracted from a sample containing biological material, such as blood, semen, hair, or skin cells. Next, a predetermined set of DNA segments ("loci") containing small repeated sequences are amplified using the Polymerase Chain Reaction (PCR), an enzymatic process that replicates a targeted DNA segment over and over to yield millions of copies.

[T]he amplification process is designed so that the DNA fragments corresponding to different loci occupy different size ranges – making it simple to recognize which fragments come from each locus. At each locus, every human carries two variants (called "alleles") – one inherited from his or her mother, one from his or her father – that may be of different lengths or the same length.²⁹

²⁴ *Id.* at 592.

²⁵ See *United States v. Schiff*, 602 F.3d 152, 172 (3d Cir. 2010); see also *Edward v. GEC, LLC*, 67 V.I. 745, 762 (V.I. 2017) ("Rule 702 . . . is concerned with the qualifications, knowledge, methodology, and so forth[.]").

²⁶ MODERN SCIENTIFIC EVIDENCE: THE LAW AND SCIENCE OF EXPERT TESTIMONY § 30:1 (2017 ed.).

²⁷ *Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods*, PRESIDENT'S COUNCIL OF ADVISORS ON SCIENCE AND TECHNOLOGY, EXECUTIVE OFFICE OF THE PRESIDENT 1, 69 (Sept 2016).

²⁸ *United States v. Pettway*, 2016 WL 6134493, at *1 (W.D.N.Y. Oct. 21, 2016).

²⁹ *Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods*, PRESIDENT'S COUNCIL OF ADVISORS ON SCIENCE AND TECHNOLOGY, EXECUTIVE OFFICE OF THE PRESIDENT 1, 69 (Sept 2016).

After the PCR process is complete, DNA profile analysis and match determination is conducted through the use of several genetic markers – in this instance, short tandem repeats (STR).³⁰ STR “refers to segments of the genomic strand where known (short) sequences [of base pairs] repeat themselves a number of times.”³¹ Once complete, the PCR results and STRs are analyzed by capillary electrophoresis:

After amplification, the lengths of the resulting DNA fragments are measured using a technique called capillary electrophoresis, which is based on the fact that longer fragments move more slowly than shorter fragments through a polymer solution. The raw data collected from this process are analyzed by a software program to produce a graphical image (an electropherogram) and a list of numbers (the DNA profile) corresponding to the sizes of the each of fragments (by comparing them to known “molecular size standards”).³²

The electropherograms display different peaks at each of the predetermined STR markers and corroborating numbers that appear underneath each peak, normally two numbers per locus, to represent the amount of recorded repeats.³³ With their experience, DNA analysts can use the electropherograms to determine if the profile contains DNA from a single-source or if multiple contributors are present.³⁴ A locus with more than two numbers would evince that DNA from more than one person was present in the analyzed sample, i.e., a mixed profile with multiple contributors.³⁵

Once a profile is created for the DNA collected from evidentiary samples, analysts can compare that profile with a reference sample, e.g., a sample from a known contributor such as a victim or suspect. From this comparison, and pre-STRMix, an analyst could reach one of three determinations: a match exists between the evidentiary sample and the reference sample;³⁶ the reference sample is excluded as a potential contributor given the differences between the two DNA samples; or the comparison is inconclusive, which means that the evidentiary sample is of limited quality or quantity, and cannot be used to match to a reference sample.³⁷ If the analyst finds a match, she can then assign a weight to that conclusion by using a statistical analysis, usually by way of a computer software.³⁸

³⁰ See *Young v. State*, 879 A.2d 44, 50 (Md. 2005).

³¹ MODERN SCIENTIFIC EVIDENCE: THE LAW AND SCIENCE OF EXPERT TESTIMONY § 30:2 (2017 ed.).

³² *Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods*, PRESIDENT’S COUNCIL OF ADVISORS ON SCIENCE AND TECHNOLOGY, EXECUTIVE OFFICE OF THE PRESIDENT 1, 69 (Sept 2016).

³³ See *United States v. Wrensford*, 2014 WL 1224657, at *3 (D.V.I. Mar. 25, 2014).

³⁴ *Id.*

³⁵ *Id.*

³⁶ *Id.* It is important to note that a “match” is not the equivalent of making “a conclusive identification of a crime suspect as the source of the unknown DNA sample.” *Young*, 879 A.2d at 51. “Rather, the suspect simply has been ‘included’ as a possible source of the DNA material, because the suspect’s DNA sample has matched the crime scene DNA sample at a certain number of critical alleles.” *Id.*

³⁷ *Wrensford*, 2014 WL 1224657, at *3.

³⁸ See *Pettway*, 2016 WL 6134493, at *1; *People v. Pike*, 53 N.E.3d 147, 164 (Ill. App. Ct. 2016) (“The final step [in DNA testing] is to provide a statistical context for the match[.]”).

The last step – assigning a weight to the evidence through a statistical analysis – is where STRMix becomes relevant to the discussion. STRMix is a probabilistic genotyping software that calculates a likelihood ratio for DNA typing results:

Probabilistic genotyping refers to the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios (LRs) and/or infer genotypes for the DNA typing results of forensic samples . . . Probabilistic genotyping is a tool to assist the DNA analyst in the interpretation of forensic DNA typing results. 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.

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 . . . and complex mixtures . . . , probabilistic genotyping approaches can reduce subjectivity in the analysis of DNA typing results.³⁹

The FBI began using STRMix in its forensic laboratories in 2015 to assign statistical weights to its DNA typing results. It is STRMix's scientific reliability that Blash challenges here.

A. Ms. Jerrilyn Conway is qualified to testify as an expert in forensic serology and DNA analysis.

Rule 702 requires that the witness in question be “qualified as an expert by knowledge, skill, experience, training, or education.”⁴⁰ Courts have interpreted this requirement liberally. No particular degree or formal qualifications are required; in fact, years of practical experience and training will suffice. When considering qualifications, a court can consider education, practical experience, study, research, and general background.⁴¹ Further, experts should not be excluded simply because the trial judge does not believe them to be the best qualified. Determining “[w]ho is ‘best’ qualified is a matter of weight upon which reasonable jurors may disagree.”⁴² Experts must, at a minimum, possess skill or knowledge greater than the average layman.⁴³

At the *Daubert* hearing, Conway, a forensic examiner with the FBI DNA Casework Unit, testified to her training and experience as a forensic examiner. Having been with the FBI for about

³⁹ *Guidelines for the Validation of Probabilistic Genotyping Systems*, SCIENTIFIC WORKING GROUP ON DNA ANALYSIS METHODS, 1, 2 (June 2015).

⁴⁰ V.I.R.E. 702.

⁴¹ See *In re Catalyst Litigation*, 2010 WL 4721333, at *3-4 (Super. Ct. July 2, 2010). It is important to note that “[q]ualifications are relative, being more or less useful depending on the expert’s familiarity with the subject that fits, or is relevant to, the matter to be decided by the trier of fact.” MODERN SCIENTIFIC EVIDENCE: THE LAW AND SCIENCE OF EXPERT TESTIMONY § 1:14 (2017 ed.). “Qualifications, therefore, cannot be evaluated in the abstract[; in other words,] the issues of qualifications, reliability and fit are inextricably entwined and, in practice, cannot easily be disentangled.” *Id.*

⁴² *Holbrook v. Lykes Bros. S.S. Co., Inc.*, 80 F.3d 777, 782 (3d Cir. 1996).

⁴³ See *Elcock v. Kmart Corp.*, 233 F.3d 734, 741 (3d Cir. 2000).

18 years, Conway began her tenure as a Forensic Biologist after completing three months of training to become a qualified serologist, six to seven months of training in DNA analysis, and a competency exam. She was later qualified as a forensic examiner after completing a two-year training program that required an interpretation exam and competency exam at the end of the training period. According to her Curriculum Vitae, she has performed serological analysis of about 1,300 evidentiary items in about 200 cases, STR analysis of about 400 samples in about 150 cases, and reported serological and DNA analyses from about 650 cases. Conway has also been previously qualified as an expert in forensic serology and DNA analysis in both federal and state courts. Regarding the use of STRMix specifically, Conway has undergone specialized training with the developers of STRMix and has helped develop the training process within the FBI for STRMix.

The People moved the Court to recognize Conway as an expert in forensic serology and DNA analysis for the purpose of testifying to her opinions with respect to the analyses performed in 2014 and 2016. At the *Daubert* hearing, the Court found that Conway was qualified as an expert witness in the field of forensic serology and DNA analysis, and the Court reiterates that finding here.

Therefore, Conway meets the qualification prong of Rule 702.

B. STRMix is scientifically reliable.

Blash's main contention concerns the scientific reliability of STRMix, as well as Conway's inability to explain certain aspects of the evaluation performed by Brown, the analyst who authored the 2014 and 2016 reports.

Rule 702, as qualified by *Daubert* and its progeny, requires that the technique or process used by the expert be scientifically valid and reliable, as well as relevant.⁴⁴ When testifying to scientific knowledge, "the expert's opinion must be based on the 'methods and procedures of science' rather than on 'subjective belief or unsupported speculation[.]'"⁴⁵ The Third Circuit has delineated several factors to consider when determining whether a technique or methodology is scientifically sound:

- (1) whether a method consists of a testable hypothesis;
- (2) whether the method has been subject to peer review;
- (3) the known or potential rate of error;
- (4) the existence and maintenance of standards controlling the technique's operation;
- (5) whether the method is generally accepted;
- (6) the relationship of the technique to methods which have been established to be reliable;
- (7) the qualifications of the expert witness testifying based on the methodology; and

⁴⁴ See *In re Catalyst Litigation*, 2010 WL 4721333, at *4.

⁴⁵ *In re Paoli R.R. Yard PCB Litigation*, 35 F.3d 717, 742 (3d Cir. 1994) (quoting *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 590 (1993)).

(8) the non-judicial uses to which the method has been put.⁴⁶

These factors are neither exhaustive nor dispositive.⁴⁷ In relying on these factors, courts have considerable flexibility in determining the reliability of an expert's proffered testimony, and "[t]he focus, of course, must be solely on principles and methodology [rather than] the conclusions that they generate."⁴⁸

Based on the totality of the information provided, the Court finds that STRMix is scientifically valid, reliable, and relevant. Not only has STRMix been subjected to several peer-reviewed studies that have produced favorable results, but the FBI has carefully created legitimate standards within its DNA testing laboratories to control STRMix's operation. Though fairly new, STRMix has also been accepted as scientifically reliable in numerous courts, both at the federal and state level. Further, Conway's exceptional qualifications and experience provides weight in favor of STRMix's reliability and general acceptance within the scientific community.

Indeed, research regarding the reliability, validation, and underlying principles of STRMix has been published in a multitude of peer-reviewed journals such as *Forensic Science International*, *Australian Journal of Forensic Sciences*, and *Journal of Forensic Sciences*. As the court in *State v. Wakefield* noted, the articles are "reviewed by . . . scientists in the DNA community to ensure a quality assurance that the manuscript and scientific results are up to the standards of the level of that journal, that the results are reported properly, that the results make sense, and that the conclusions that are drawn from the data are supported by the DNA."⁴⁹ Further, the FBI has instituted several standard operating procedures and policies that govern the DNA Casework Unit's work, as well as the use of STRMix, and those policies and procedures align with the standards established by the International Organization for Standardization (ISO)⁵⁰ and Quality Assurance Standards for Forensic DNA Testing Laboratories. Conway testified to the fact that the FBI laboratories undergo accreditation by an outside accreditation body to ensure that the laboratories are satisfying ISO standards for testing laboratories, and the DNA Casework Unit specifically is audited against national DNA casework standards by other DNA experts in the field.

As mentioned above, STRMix has also been subjected to validation studies by both its developers and the FBI itself. Developmental validation involves "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."⁵¹ Conway testified to the fact that a developmental validation study was performed by the developers of STRMix prior to the FBI implementing STRMix in its laboratories. The FBI also conducted its

⁴⁶ See *Wrensford*, 2014 WL 3715036, at *5.

⁴⁷ *Id.*

⁴⁸ *Daubert*, 509 U.S. at 594-95.

⁴⁹ *State v. Wakefield*, 9 N.Y.S.3d 540, 543 (Supr. Ct. Feb. 9, 2015).

⁵⁰ According to its website, "ISO is an independent, non-governmental international organization with a membership of 161 national standards bodies." *About ISO*, INTERNATIONAL ORGANIZATION FOR STANDARDIZATION, <https://www.iso.org/about-us.html> (last visited on August 22, 2018).

⁵¹ *Guidelines for the Validation of Probabilistic Genotyping Systems*, SCIENTIFIC WORKING GROUP ON DNA ANALYSIS METHODS, 1, 5 (June 2015).

own internal validation study prior to implementing STRMix. This study allowed the FBI to test STRMix in its laboratories to ensure that the software worked with the instruments and profiles developed in those laboratories. According to Conway, the validation study involved the use of over 300 mixtures of DNA from known contributors and around 200 non-contributor DNA samples that were analyzed against those mixtures. In total, the study included about 60,000 tests. The findings were published in the *Forensic Science International: Genetics*, which, as stated above, is a peer-reviewed journal. These studies no doubt lend credence to the existence of legitimate and controlled standards governing STRMix's operation within the FBI's laboratories.

In arguing that STRMix is unreliable, Blash expresses concerns about the source code of STRMix, its error rate, and how that potentially affects the LR's being produced in criminal cases. Specifically, Blash notes that the STRMix version used by the FBI to produce the 2016 amended report, Version 2.3.06, contained "software errors that could result in Likelihood Ratios that do not reflect reality."⁵² For support, Blash cites a 2017 law review article that highlights the problems within the software and its updates, as well as a publication from STRMix itself that discusses coding errors discovered in several software versions, including 2.3.06. Blash also points to a 2015 case out of New York, *People v. Hillary*, where the court disallowed the use of STRMix results.

Though Blash's concerns surrounding the unknown of STRMix's source code is anything but trivial, the Court does not find that these concerns warrant preclusion in this instance. Despite not having the specifics of STRMix's source code, the reliability of STRMix's output has been studied, validated, and declared suitable for DNA forensic testing by the FBI. One purpose of the internal validation study was to allow the FBI laboratories to initiate STRMix runs in a controlled setting where the tested DNA mixtures were known mixtures, i.e., the number of contributors and percentage of bodily fluids from each contributor was known prior to running STRMix.⁵³ At the *Daubert* hearing, Conway testified that the statistical weights provided by STRMix are reviewed to ensure that they look appropriate based on the profile and her interpretation of the profiles. The Court agrees that some errors likely exist within STRMix's code, as Conway herself conceded that no software can boast of being error free. However, the mathematics used in STRMix's calculations are not new to the field of DNA testing.⁵⁴ Whatever the effect that errors within the source code of STRMix might have on LR's, LR's represent the statistical weight of a determination made by a DNA analyst, based on her years of experience and training, rather than a computer code: that a particular suspect is a potential contributor to the DNA in an evidentiary sample. Hence, in the Court's view, the issue of whether errors in STRMix's code exist and whether those errors affect the LR's is a consideration for the jury when determining how much weight to assign

⁵² Def.'s Suppl. *Daubert* Br. 6.

⁵³ This fact distinguishes the case presented before the Court from that presented in *People v. Hillary*; there, the court precluded results from STRMix because the New York State Police crime laboratory failed to perform any internal validation study. *Hillary*, Case No. 2015-15, at 8 (N.Y. Sup. Ct. Aug. 26, 2016). Here, the FBI conducted internal validation studies, the results of which were published in peer-reviewed journals.

⁵⁴ See *People v. Bullard-Daniel*, 42 N.Y.S.3d 714, 721 (N.Y. Sup. Ct. 2016) ("[T]he mathematical models are themselves non-controversial and have been widely used in fields such as weather forecasting, computational biology, linguistics, genetics, engineering, physics, aeronautics, finance, and social sciences."). In fact, Conway testified that part of STRMix's code uses a method called Markov chain Monte Carlo in its statistical calculations, which is a method that is used in multiple fields of research beyond DNA testing.

to Conway's testimony about the 2014 and 2016 reports; that issue does not cause the methodology in question here to be precluded as unreliable.

The Court is not alone in refusing to preclude the admittance of STRMix results or testimony based on those results. In *United States v. Pettway*, the district court denied a defendant's motion in limine seeking to preclude DNA evidence derived from STRMix.⁵⁵ The court reasoned that the defendants "may press their contentions concerning the longevity and reliability of STRmix on cross-examination and through their own expert witnesses[, b]ut nothing in their motion demonstrates that a . . . preclusion of evidence is necessary or warranted[.]"⁵⁶ In *People v. Bullard-Daniel*, the New York trial court found STRMix to be admissible under the *Frye* standard as being generally accepted within the scientific community, despite only hearing testimony from one witness.⁵⁷ These cases, among others, provide persuasive support in favor of admitting STRMix as scientifically reliable.

The Court's gatekeeping responsibility requires, in part, that it determine whether the People have met their burden of showing, by a preponderance of the evidence, that STRMix is scientifically reliable. Based on Conway's testimony and the People's exhibits, the Court finds that the burden has been met here.

C. Conway's testimony fits the issues presented in this matter.

Because Rule 702 requires that the expert's testimony "help the trier of fact to understand the evidence or to determine a fact in issue," that testimony must "fit" the particular issue presented. Fit goes primarily to relevance and "requires a valid scientific connection to the pertinent inquiry as a precondition to permissibility."⁵⁸ Put simply, "[e]xpert testimony which does not relate to any issue in the case is not relevant and, ergo, non-helpful."⁵⁹ Though "[f]it is not always obvious, and scientific validity for one purpose is not necessarily validity for other unrelated purposes,"⁶⁰ the standard for analyzing fit is "not that high[] but is higher than bare relevance."⁶¹

At issue here is the DNA present on the evidentiary samples collected from Malfetti's apartment and vehicle, and whether Blash's DNA is found on any of those samples. Because the evidentiary samples contain a mixture of DNA from multiple possible contributors, STRMix was used to assign a statistical weight in the form of a LR to Brown's determination of whether Blash's DNA was included in the DNA mixture on the collected evidence. Therefore, the Court believes

⁵⁵ *Pettway*, 2016 WL 6134493, at *3.

⁵⁶ *Id.* at *2.

⁵⁷ *Bullard-Daniel*, 42 N.Y.S.3d at 721, 725-26.

⁵⁸ *In re Paoli R.R. Yard PCB Litigation*, 35 F.3d at 743 (quoting *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 591-92 (1993)).

⁵⁹ *Daubert*, 509 U.S. at 591.

⁶⁰ *United States v. Ford*, 481 F.3d 215, 219 n.6 (3d Cir. 2007) (quoting *In re TMI Litigation*, 193 F.3d 613, 670 (3d Cir. 1999)).

⁶¹ *Id.* (quoting *In re Paoli R.R. Yard PCB Litigation*, 35 F.3d 717, 745 (3d Cir. 1994)) (internal quotation marks omitted).

that Conway's testimony about Brown's reports and STRMix's results as reflected in the 2016 report is absolutely relevant and will "help the trier of fact" in the determination of whether Blash's DNA was present on the collected evidence.

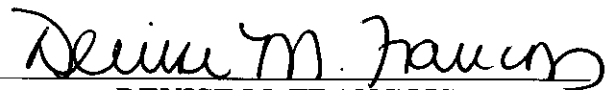
IV. CONCLUSION

When expert testimony is challenged under *Daubert*, the proponent bears the burden of showing that the testimony satisfies the standards required by Rule 702 and *Daubert*. The People have met that burden. Therefore, the Court will deny Blash's motion. Accordingly, it is hereby

ORDERED that Defendant's Motion for a Daubert Hearing on DNA Evidence is **DENIED**; and it is further

ORDERED that a copy of this Memorandum Opinion and Order shall be directed to Attorney W. Mark Wilczynski (Law Office of W. Mark Wilczynski, P.C.), Assistant Attorney General H. Timothy Perry (Virgin Islands Department of Justice), and the Bureau of Corrections on behalf of the Defendant and its record.

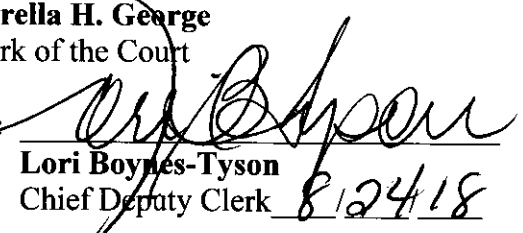
Dated: August 24, 2018



DENISE M. FRANCOIS
Judge of the Superior Court
of the Virgin Islands

ATTEST:

Estrella H. George
Clerk of the Court

By: 

Lori Boynes-Tyson
Chief Deputy Clerk

8/24/18