

COUNTY COURT  
COUNTY OF ST. LAWRENCE STATE OF NEW YORK

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THE PEOPLE OF THE STATE OF NEW YORK,

-against-

**DECISION & ORDER**

DNA Analysis Admissibility  
Ind. #: 2015-15

ORAL NICHOLAS HILLARY,

Defendant.

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*Mary E. Rain, District Attorney, Canton, for the People.*

*William Fitzpatrick, District Attorney, Syracuse, for the People.*

*The Legal Aid Society, New York (Jessica Goldthwaite of counsel), for the Defendant.*

*The Legal Aid Society, New York (Richard Torres of counsel), for the Defendant.*

*Dumas & Narrow, Canton (Peter Dumas of counsel), for the Defendant.*

*Emery, Celli, Brinckerhoff & Abady, New York (Earl Ward of counsel), for the Defendant.*

*Siegel, Teitelbaum & Evans, LLP, New York (Norman Siegel of counsel), for the Defendant.*

*The Legal Aid Society, New York (Clinton Hughes of counsel), for the Defendant.*

*The Bronx Defenders, New York (Adnan Omar Sultan of counsel), for the Defendant.*

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**CATENA, J.:**

A motion was filed by defendant to preclude the prosecution from offering expert testimony as to the use of, or any results produced by, the forensic software tool STRmix alleging that the use

of this software for probabilistic genotyping is not generally accepted in the relevant scientific and legal communities as required by *Frye v. United States*, 293 F. 1013 (see, *People v. Middleton*, 54 NY2d 42 [“the test is not whether a particular procedure is unanimously indorsed by the scientific community, but whether it is generally acceptable as reliable”]). The defendant also filed a motion to preclude the use of a modified random match probability statistic (“RMP”). The defendant also challenged the admissibility of the evidence. The people filed an affirmation in opposition to the motion dated June 24, 2016, and oral argument was held on Friday July 1, 2016. By decision and order dated July 11, 2016, this court granted a limited *Frye* hearing on the issue of whether STRmix can “generate results accepted as reliable within the scientific community generally” on extreme mixture ratios where the DNA from the minor contributor is low template. Trial foundation for the admissibility of the evidence was made part of the hearing (*People v. Wesley*, 83 NY2d 417, 429). The hearing was held on Monday July 25, 2016, at the courthouse in Canton, New York. Further oral argument was held on the record on August 17, 2016.

On October 24, 2011, the Potsdam Police Department received a call from a neighbor of the victim stating that she heard moans and the word “help” coming from the victim’s apartment. An officer of the Potsdam Police Department arrived at the apartment at approximately 5:16 p.m., knocked on the door, and heard what sounded like someone walking around the apartment. Shortly thereafter, the Officer entered the apartment with the landlord and found the victim unconscious in the bedroom. No one else was in the apartment and the victim was pronounced dead at 7:18 p.m. that evening. The cause of death was determined to be strangulation.

As part of the investigation, the police collected dozens of samples of DNA from multiple areas in the apartment including the body and clothing of the victim. The police also obtained a

sample of the defendant's DNA as he had lived briefly with the victim, having an intimate relationship with the victim's mother. Because this was a New York State Police investigation, the New York State Police crime lab processed the samples. The defendant was excluded from all samples taken at the apartment where comparisons could be made except for a DNA mixture profile from fingernail scrapings taken from the victim's left hand. Due to insufficient genetic information, the defendant could neither be included nor excluded as a possible contributor to the mixture.

Beginning in 2013, the New York State Police crime lab contacted Cybergentics, Inc., to run the data obtained from the fingernail scrapings through their probabilistic genotyping software program called TrueAllele. The results were inconclusive. Nonetheless, the defendant was indicted for the victim's murder in 2014 and the New York State Police crime lab sent its data at the behest of the prosecution to the Institute of Environmental Science and Research ("ESR") which ran it through their probabilistic genotyping software program called STRmix<sup>1</sup>. The People also requested their expert, Dr. John S. Buckleton, one of the developers of STRmix, to calculate a random match probability statistic which was presented in a report dated July 1, 2016.

Dr. Buckleton conceded at the hearing that no internal validation studies were performed by the New York State Police crime lab for the use of STRmix on casework samples developed at the

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<sup>1</sup>District Attorney Fitzpatrick first contacted Dr. Buckleton by email on November 2, 2015, stating in pertinent part "I am currently assisting a colleague in prosecuting a murder case in Saint Lawrence County . . . On 10/24/2011 a 12 year old boy [ ] was strangled to death in his apartment in Potsdam NY. No physical evidence was discovered at the scene except for [ ] fingernail scrapings . . . Those scrapings were analyzed at the New York State Police crime lab and the DNA profile generated appears to be consistent with a mixture of two individuals with the victim as the major contributor and the obligate alleles (7) being consistent with the defendant. I am hoping that you or someone you recommend might be able to provide a statistical weight to the results using a likelihood ratio or some other method. I can provide the analyst's report and the electropherograms if you decide to take a look."

lab. As a result Dr. Buckleton was forced to pick and choose data from different “reliable sources” and input parameters into the program in such a way that he believed the system would tolerate<sup>2</sup>.

The reason for this was because the New York State Police crime lab was not authorized by the New York State Commission on Forensic Science to generate data from DNA samples for STRmix

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<sup>2</sup>Dr. Buckleton testified that “[a]ll labs in the United States of America are following the SWGDAM guidelines”. The Scientific Working Group on DNA Analysis Methods (SWGDAM) provides guidelines for validation of probabilistic genotyping systems such as STRmix. As stated in the guidelines, “[v]alidation is a process by which a procedure is evaluated to determine its efficacy and reliability for forensic casework and/or database analysis.” Further, “[i]nternal validation studies 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 particular, complex mixtures and low-level contributors should be evaluated thoroughly during internal validation, as the data from such samples generally help to define the software's limitations, as well as sample and/or data types which may potentially not be suitable for computer analysis.”

STRmix has six laboratory specific parameters to determine prior to its use. Concerning one of these parameters called stutter ratios, Dr. Buckleton testified that he received data from the New York State Police crime lab to look at “forward stutter” which “did not serve the purpose” but nonetheless was used in the April 2016 analysis. Concerning “drop-in” rates, Dr. Buckleton stated that he inputted a zero drop-in rate as the crime lab did not “have a drop-in rate because they do not do low copy number on high sensitivity methods.” A “drop-in” rate greater than zero would have benefitted the defendant. And in his affidavit dated August 18, 2016, Dr. Buckleton further stated that he used a “drop-in rate” that was based partly on “our own experience.”

Dr. Buckleton further testified that “[b]est practice is clearly validation in the lab specifically, and that is -- the optimal way is the way we recommend. It's not available to me in this case because the New York State lab has not done the relevant validation. I have two options first with that. I have the option of doing the next best practice or not doing anything. I've done next best practice. I've done this a couple times before and I'm not pertaining it's best practice, and I have candidly acknowledged in my statement that exact fact. *What I've done is attempt to take data from different reliable sources that I think applies to the circumstance.* I'm also aware of the forgiveness of the system for slight inaccuracies in certain of the parameters, so I have input parameters in such a way that I believe the forgiveness of the system will tolerate any inaccuracies I've made” (emphasis supplied).

analysis<sup>3</sup>. And although ESR had performed the necessary internal validations to be accredited by the relevant agencies for the use of STRmix, those validations were specific to data generated by ESR. Here, the only data generated was from the New York State Police crime lab<sup>4</sup>.

“The New York State Commission on Forensic Science (the “Commission”) is the governmental body tasked with developing minimum standards and accreditation programs for all forensic laboratories in New York State. In addition, the Commission approves forensic laboratories to perform specific forensic methodologies. The Commission’s objectives are to increase and maintain the effectiveness, efficiency, reliability, and accuracy of forensic laboratories, ensure that forensic analyses are performed in accordance with the highest scientific standards practicable, and set forth minimum requirements for the quality and maintenance of equipment. The DNA Subcommittee of the New York Commission on Forensic Science (“DNA Subcommittee”) is the

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<sup>3</sup>The lab was authorized to generate data for TrueAllele analysis. The People stated at the August 17, 2016, oral argument that “each individual laboratory has to go through essentially an accreditation process to determine whether or not . . . they have the trained [personnel] and expertise to accurately employ [STRmix]”. The People further discussed the Onondaga County crime lab stating “Onondaga is going through . . . their own internal validation process to make sure that their people are properly trained to use STRmix, get accurate results with blind proficiency testing and then ultimately will present their process to ASCLD/LAB . . . for the accreditation process. Then that laboratory . . . has to go through a two year accreditation process in front of the Forensic Science Commission for that discipline.” It is clear that the New York State Police crime lab had not gone through the accreditation process and, thus, did not have the “trained [personnel] and expertise to accurately employ” STRmix. The People conceded this stating “there [were] no internal validation studies by the State Police regarding STRmix.”

<sup>4</sup>The Federal Bureau of Investigation’s quality assurance standards for Forensic DNA Testing Laboratories define “Forensic DNA analysis” as “the process of identification and evaluation of biological evidence in criminal matters using DNA technologies.” The quality assurance standards further define “internal validation” as “the accumulation of test data within the laboratory to demonstrate that established methods and procedures perform as expected in the laboratory.” Quality Assurance Standard 8.1.3 requires that internal validation be performed for forensic casework analysis.

body appointed by the Commission to perform accreditation of all DNA laboratories in New York. Further, the DNA Subcommittee is charged with assessing all DNA methodologies proposed to be used for forensic analysis. It has the sole authority to grant, deny, review, or modify a DNA forensic laboratory accreditation, which the DNA Subcommittee exercises by issuing a binding recommendation to the Commission. While the Commission can request that the DNA Subcommittee reconsider its findings, the DNA Subcommittee is the final decision maker regarding laboratory accreditation” (*U.S. v. Morgan*, 53 F.Supp.3d 732; Executive Law 995-b[1])<sup>5</sup>.

The Commission requires laboratories to comply with the standards promulgated by the American Society of Crime Laboratory Directors/ Laboratory Accreditation Board (“ASCLD/LAB”) (9 NYCRR §6190.3[b]). These standards require that DNA mixture interpretation be based on validation data (*id.*). Here, by sending its raw data to ESR, an accredited lab for STRmix analysis, the People argue that the New York State Police crime lab could bypass Commission approval for its participation in the STRmix process inasmuch as it did not run the computer program. This minimizes the importance of raw data generation in the STRmix process and emphasizes the People’s heavy reliance on the expertise of Dr. Buckleton to account for any deficiencies in the data<sup>6</sup>. Such reliance appears contrary to Commission and ASCLD/LAB requirements (*see, State v.*

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<sup>5</sup> “‘DNA testing methodology’ means methods and procedures used to extract and analyze DNA material, as well as the methods, procedures, assumptions, and studies used to draw statistical inferences from the test results” (Executive Law §995[3]).

<sup>6</sup>As the People stated at the August 17, 2016, oral argument “[Dr. Buckleton]’s just saying that, look, I’ve got this raw data from the State Police. There are some things I don’t know, so what I’m doing, what I, John Buckleton, am doing is I am taking the most stringent, conservative approach to my input of the STRmix data.”

*Wakefield*, 57 Misc.3d 850; see, *People v. Vincent Bullard-Daniel*, Co Ct. Niagara County, March 10, 2016, Murphy, J., Ind. No. 2015-88)<sup>7</sup>.

As stated by this court in its earlier order granting the pre-trial hearing herein, “the test pursuant to *Frye v. United States* (293 F 1013) poses the . . . question of whether the accepted techniques, when properly performed, generate results accepted as reliable within the scientific community generally . . . The issues of proper foundation and of the adequacy of laboratory procedures [] are not before [the Court at a *Frye* hearing]” (*People v. Wesley, supra*). To that end, this court notes that the New York State Commission on Forensic Science issued a binding recommendation for use of STRmix in the analysis of DNA profiles upon recommendation from its DNA Subcommittee (Executive Law §995-a; *People v. Wakefield, supra* at 856 [approval by the Commission constitutes general acceptance]). And STRmix was found by a New York State court after a *Frye* hearing to be generally accepted in the relevant scientific community (*People v. Vincent Bullard-Daniel, supra*). Based upon a review of the record, this court finds that STRmix has been developmentally validated and is generally accepted as reliable within the scientific community (*id.*; *People v. Muhammad*, 14<sup>th</sup> Cir. Ct., Muskegon Co, Dec. 15, 2015). Issues concerning the manner

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<sup>7</sup>ASCLD/LAB accreditation requirement 5.4.5.2 from ISO/IEC 17025:2005:

“Procedures for DNA profile interpretation must be based on validation data. The interpretation of a DNA profile containing a mixture of two or more individuals must be guided by a procedure that includes specific defined steps that will enable different analysts in the same laboratory to reach the same conclusion; and a competent person from outside the laboratory using the same procedure to understand how the conclusion was reached. DNA mixture interpretation procedures must be tested on mixture profiles from known contributors representing the range of mixture types (e.g., different numbers of contributors, mixture proportions, and template quantities) to which the procedure will be applied in casework. The results of this validation must be used to define the capabilities and limitations of the procedure and to verify that it produces the expected results (e.g., inclusions and exclusions).”

in which STRmix accounts for stochastic effects in its probability computations where mixture ratios are extreme and the minor contributor's DNA is low template goes to weight (*People v. Debraux*, 50 Misc.3d 247; *People v. Megnath*, 27 Misc.3d 405).

“The issue [now] shifts to a second phase, admissibility of the specific evidence--i.e., the trial foundation--and elements such as how the sample was acquired, whether the chain of custody was preserved and how the tests were made . . . Once *Frye* has been satisfied, the question is ‘whether the accepted techniques were employed by the experts in this case’. The focus moves from the general reliability concerns of *Frye* to the specific reliability of the procedures followed to generate the evidence proffered and whether they establish a foundation for the reception of the evidence at trial. The trial court determines, as a preliminary matter of law, whether an adequate foundation for the admissibility of this particular evidence has been established” (*People v. Wesley*, *supra* at 428-429). Here, the lack of internal validation by the New York State Police crime lab, as candidly admitted by Dr. Buckleton, precludes use of the STRmix results (*id.*; *see, State v. Wakefield*, *supra*; *see, People v. Vincent Bullard-Daniel*, *supra*).

Concerning RMP, while this court finds that it has been generally accepted as reliable within the scientific community under certain circumstances, the results produced in this case are unreliable based upon Dr. Buckleton's testimony that it cannot adequately account for the absence of defendant's alleles in the composite profile. As Dr. Buckleton stated, “the exact difficulty that we've come upon in this case and certain circumstances that the *Random Match Probability is not conservative and doesn't do a fair job for the defendant*, and this is one of those circumstances. The specific diagnostic is called a -- it's called a non-major allele between the profile and the accused. And we have a number of those where the accused has an allele that is not seen in the profile and

Random Match Probability is incapable of [punishing] the statistic for non-matches . . . So, in fact, it is the exact weakness of the 2p rule that has motivated me to make a probabilistic genotyping system” (emphasis supplied). Further, the defendant’s expert, Dr. Dan E. Krane, testified that “[t]he Random Match Probability is and has been considered generally accepted in many circumstances. The particulars of the evidence sample in this case do not fit within the category of those that would cause to be generally accepted. If I can put it just a different way. I’ve testified for many years that there is no generally accepted means of attaching a reliable statistical weight to a mixed sample, such as the evidence sample in this case where drop-out may have occurred, which, again, seems very likely to have occurred with the evidence sample in this case. So, on those two counts it would be quite inappropriate to rely upon a Random Match Probability approach to generate a statistical weight.”

Given Dr. Krane’s testimony, the use of RMP in this case where the People’s own expert witness testified that it “*is not conservative and doesn't do a fair job for the defendant*” must be precluded as unreliable (*People v. Wesley, supra*). In any event, even if this court were to agree with the prosecution that “[d]efendant’s concern with the methodology used by Dr. Buckleton in calculating the statistic goes to ‘the weight of the evidence, not its admissibility’”, to allow such evidence would be unduly prejudicial to the defendant (*People v. Morris*, 21 NY3d 588 [“Weighing the evidence’s probative value against its potential prejudice to the defendant is a matter of discretion for the trial court”]; *People v. Caban*, 14 NY3d 369 [“Evidence, though relevant, may be excluded where ‘it’s probative value is substantially outweighed by the danger that it will unfairly prejudice the other side or mislead the jury’”], quoting *People v. Scarola*, 71 NY2d 769, 777). In determining the motions herein, this court is reminded that “[f]orensic DNA analysis should be governed by the

highest standards of scientific rigor in analysis and interpretation” (*People v. Wesley, supra*)(Kaye, J., concurring). Neither the STRmix nor the RMP results may be used in this case (*id.*).

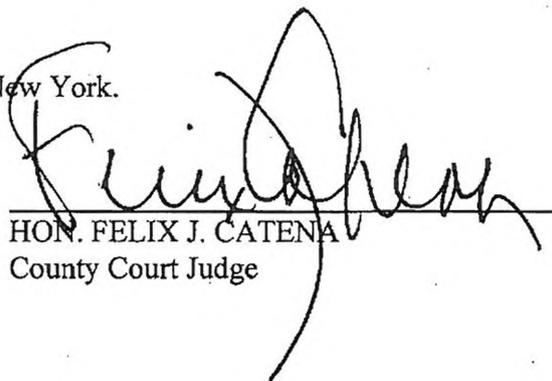
It is, therefore,

**ORDERED** that the defendant’s motion to preclude the prosecution from calling an expert witness to testify on their direct case regarding any conclusion reached by the use of STRmix is granted as the prosecution cannot lay a foundation for the introduction of evidence that had not been internally validated; and it is further

**ORDERED** that the defendant’s motion to preclude the prosecution from offering expert testimony as to any statistical results obtained by using the random match probability on the composite minor component of mixture is granted.

The above constitutes the decision and order of this Court.

Signed this 26<sup>th</sup> day of August, 2016, at Fonda, New York.

  
HON. FELIX J. CATENA  
County Court Judge

ENTER: