

United States District Court, D. Delaware

UNITED STATES OF AMERICA, Plaintiff,

v.

John Walter Trala, and Melissa Bailey, Defendants

No. CR. A. 00-23-GMS

Sept. 17, 2001

Keith M. Rosen, Assistant United States Attorney, Wilmington, Delaware, Colm F. Connelly, United States Attorney, for Plaintiff United States of America.

Penny Marshall, Assistant Federal Public Defender, Wilmington, Delaware, for Defendant John Walter Trala.

MEMORANDUM OPINION

SLEET, J.

ORDER

For the reasons stated in the court's memorandum opinion of this date, IT IS HEREBY ORDERED that the Motion to Exclude Expert Testimony on DNA Analysis (D.I.74) filed by the defendant, John Walter Trala is DENIED.

I. INTRODUCTION

On January 14, 2000, John Walter Trala ("Trala") was charged by indictment with robbery while armed, conspiracy, and using a firearm during a crime of violence in connection with the robbery of a bank in Bear, Delaware. At a location outside of the bank, a black ski mask and red jacket were collected by the FBI and sent to the FBI laboratories. A report dated August 15, 2000, indicated that a DNA sample taken from the ski mask matched a known DNA sample of Trala. The Government intends to use this evidence at trial.

On December 5, 2000, the defendant filed a motion in limine challenging the admissibility of the government's expected expert trial testimony on the results of the analysis of the DNA sample recovered from the scene of the alleged crime. This challenge is mounted pursuant to Rule 702 of the Federal Rules of Evidence. According to the defendant, the DNA evidence should be excluded because it fails to meet the standards for admissibility described in *Daubert v. Merrell Dow Pharmaceuticals*, 509 U.S. 579, 113 S.Ct. 2786, 125 L.Ed.2d 469 (1993). The court conducted an evidentiary hearing on the issue from May 7, to May 10, 2001. Upon consideration of the evidence introduced at the Daubert hearing and the parties' arguments, the court finds that the expert testimony at issue is relevant, reliable, and would assist the jury in making related determinations. Thus, the court will deny the defendant's motion. The reasons for the court's decision are set forth in detail below.

II. BACKGROUND

A. Testifying Experts

At the evidentiary hearing, the court heard testimony from three expert witnesses for the government and one expert witness for the defendant. Dr. Bruce Budowle, Brendan Shea, and Dr. Ranajit Chakraborty were called by the government. Dr. William Shields was called by the defendant.

Dr. Budowle, the government's primary witness, is a Senior Scientist at the FBI Laboratory Division in Washington, D.C. Dr. Budowle testified about the basic concepts of DNA, different types of DNA typing, with specific emphasis on the typing and kits used in this case, and other issues concerning the reliability of the typing used in this case.

Brendan Shea is a Forensic Examiner employed by the FBI DNA Analysis Unit I. As a forensic examiner, Shea is responsible for supervising a team of biologists that performs the various stages of DNA amplification and analysis. Shea testified about the PCR-STR typing as it was conducted specifically in this case.

Dr. Chakraborty is the Allan King Professor of Biological Sciences, Population Genetics, and Biometry at the Human Genetics Center, University of Texas at Houston. Dr. Chakraborty testified about statistics, population genetics, and DNA analysis.

The defendant's witness, Dr. Shields, is a professor at the State University of New York, College of Environmental Science and Forestry. Dr. Shields testified about the reliability of PCR/STR typing as well the reliability of the statistical methods used.

B. Description of DNA Testing

1. Basic Concepts of DNA ¹

Each human body contains a large number of cells, each of which descends from successive divisions of the fertilized egg that was its origin. Virtually all non-reproductive cells in the body contain identical copies of a complex structure called deoxyribonucleic acid or, DNA. This structure represents the genetic code for that individual. The DNA is in the form of microscopic chromosomes, which are located in the nucleus of a cell. A chromosome is a thread of DNA surrounded by other materials, mainly protein. A fertilized egg contains 23 chromosomes, with one member of each pair being contributed by the mother and father, respectively. Each cell contains identical, duplicates of the 46 cells from the fertilized parent cell. Therefore, each cell in the human body has the same DNA.

The structure of DNA consists of two strands, coiled in the form of a double helix (i.e., a twisted ladder). Each strand is composed of a string or a sequence of nucleotide bases held together by a sugar-phosphate backbone. To use the ladder metaphor, running between the sugar-phosphate strands (the side rails of the ladder) are billions of rungs, each of which is composed of two bases. There are only four possible types of bases--A,

T, G, C. "A, T, G, C" represent adenine, thymine, guanine, and cytosine, respectively. The order in which the base pairs appear on the DNA ladder constitutes an individual's genetic code.

A gene is a particular DNA sequence located along a chromosome, ranging from a few thousand to tens of thousands of base pairs, that produces a specific product in the body. In other words, a gene is a site (a sequence of letters) on the DNA that encodes for a protein. A marker is a site on the DNA that does not code for proteins; the marker is also known as the locus (or location). Tr. at A34. In essence, the specific base sequence on the gene acts as an encoded message to the body to produce certain amino acids, which ultimately combine to form a protein. The function of a given gene is determined by the order of bases in the gene. The position that gene occupies along the DNA thread is known as its locus.

Human beings share more biological similarities than differences. Thus, over 99% of human DNA does not vary from person to person. Each person's DNA, however, has certain regions where the rungs of the ladder will be different. This area where a locus is different is polymorphic. The possible arrangements of base pairs that could occur in one of these polymorphic areas (i.e., the alternative forms of a gene that an individual could possess) are known as alleles. These alleles can result from differences in single base pairs, differences in multiple base pairs, or differences in the number of base pairs found in a given region. The individual genetic makeup described by the alleles is known as the genotype. In forensic analysis, the genotype for a group of analyzed loci is called the DNA profile. When a sample of DNA is typed, the lab examiner looks at predetermined polymorphic loci, identifies the alleles that make up the DNA sequence at those polymorphic loci, and then determines how likely it is for this sequence to appear in a given population.

2. Description of DNA testing

In this case, the laboratory used a method of DNA typing known as PCR/STR typing. In PCR/STR typing, a process known as polymerase chain reaction, or PCR, is used to amplify targeted loci of the sample of DNA by replicating the process by which DNA duplicates itself naturally. Thus, the lab is able to produce a substantial number of specific, targeted segments of DNA which can then be typed and compared. Short Tandem Repeats, or STRs, are a group of loci which are used to type and compare the DNA. Finally, statistics are used to evaluate how likely it is that a similar match would occur if the DNA sample were drawn randomly from the population. The court will briefly further describe the typing methods used below.

a. PCR Amplification Process²

PCR, a sample preparation technique, is a laboratory process for copying a short segment of DNA millions of times. The PCR process is analogous to the process by which cells replicate their DNA naturally. See *United States v. Gaines*, 979 F.Supp. at 1435. By using this process, a lab can produce a substantial number of specific, targeted segments of

DNA which can then be typed and compared. PCR allows the laboratory to amplify only those specific DNA regions which exhibit genetic variations within the population, allowing for DNA typing. Moreover, the PCR process enables the analysis of very tiny amounts of DNA. PCR also permits the analysis of old and/or degraded DNA samples.

The PCR process is comprised of three steps. First, the double-stranded segment of DNA is separated, or denatured, into two strands by heating. This denatured DNA strand forms a template that can allow the manufacture of a new strand that is identical to its former complimentary strand.

Next, each of the single-strand segments are hybridized with primers. Primers are short DNA segments that are designed to bind with the template at particular loci. The primers are designed to compliment a sequence just outside of a target sequence of bases.

Finally, each primer serves as a starting point for the replication of the target sequence. In this third step, a type of enzyme called a polymerase becomes active. In essence, the polymerase facilitates repeated additions of bases to the primer until a new, complimentary strand of the targeted DNA locus is created.

This process is repeated a number of times, creating an exponentially increasing number of copies of the targeted area of the original DNA. Eventually, the PCR amplification process yields a sufficient quantity of the DNA sample to be typed. If the laboratory wants to type the DNA sample at multiple sites, it can add additional primers which will bind simultaneously to their respective target sites. This process is known as multiplexing. According to Dr. Budowle, multiplexing allows the laboratory to minimize the chance of human error and contamination in the PCR process. Using current technology, the FBI laboratory can multiplex up to fifteen or sixteen markers with reliable results.

b. Short Tandem Repeats³

The PCR process is performed to amplify a targeted locus (or loci) for analysis. These loci are selected because they are polymorphic, thus, making them amenable to typing. One group of such loci involve a class of repeated units, distributed widely throughout the DNA structure, known as short tandem repeats ("STRs"). A tandem repeat involves multiple copies of an identical DNA sequence arranged in direct succession in a particular region of a chromosome. A STR is a tandem repeat in which the core repeat units are just a few base pairs. Loci containing STRs are scattered throughout the chromosomes in enormous numbers. Such loci have a fairly large number of alleles and are usually capable of unique identification. See *Commonwealth v. Rosier*, 425 Mass. 807, 685 N.E.2d 739, 742 (Mass.1997).

Once the amount of DNA is amplified by the PCR process; the analyst proceeds to identify fragments of different sizes by their migration in an electric field. In order to detect variations, analyst use a process known as electrophoresis. During the PCR amplification of the STR fragments, the primers that are used contain fluorescent tags,

which become incorporated into the STR fragments during amplification. During electrophoresis, the amplified fragments will pass through a gel and eventually pass through a detection window at the end of the gel. The fragments can be passed through either a flat slab gel or through a small-diameter capillary that contains a gel or liquid polymer. The difference between these two methods is that the flat gel permits multiple samples to be run at the same time, while capillary electrophoresis only permits one sample to be run at a time. The scientific principles underlying both techniques are the same.

After the fragments pass through the detection window at the end of the gel, a laser fires, striking the fluorescent tags, and causing the tags to emit light. A camera will detect the light and convert it into data. By measuring the amount of time that it takes a particular fragment to reach the laser, the laboratory will be able to determine the size of the fragment and, therefore, it will be able to determine the number of sequence repeats. The faster a fragment moves through the window, the smaller it is in size and vice versa.

The data generated is analyzed by an accompanying computer software program which determines the size of the alleles based on the rate at which they reach the window. The software used in this case is known as Genescan and Genotyper. The software detects the light being emitted and converts it into peaks of different sizes. The analyst then compares the configuration of these peaks against known reference standards in order to determine the number of alleles present at the target loci in a given sample. The signal must be of a certain strength, that is, the peak must be high enough to be interpreted before the FBI laboratory will have enough confidence in the data to make an interpretation.

c. Cofiler and Profiler Kits⁴

In this case, the PCR process was used to amplify thirteen STR loci. The thirteen STRs typed in this case are the core DNA markers used in the development of the Combined DNA Index System, or CODIS. CODIS is a national database containing DNA profiles of convicted felons.⁵ In order to amplify the DNA samples at these particular loci, the laboratory used two kits that contain the materials necessary to accomplish this result. These kits are known as the Profiler Plus and Cofiler DNA typing Systems and are manufactured by Perkin Elmer Applied Biosystems.

These kits contain three basic materials, primers, a reaction mix and polymerase. The kits also contain the fluorescent tags that allow the amplified DNA fragments to be detected during the electrophoresis phase. The reaction mix is a mix of chemicals used in any form of PCR testing that, in essence, creates the proper chemical environment for the PCR process to occur. The reaction mix is not locus specific. The polymerase is a class of enzymes that enable bases to be added to the primer. It too, is not locus specific.

The elements of the kits that are locus-specific are the primers. The primers are small fragments of DNA designed to bind with particular loci when the two strands of the DNA sample are separated. These primers do not represent new methods of performing PCR,

or even modifications of the PCR process. The primers are simply known sequences of DNA bases which have been identified as occurring in every human on the boundary of the locus to be tested.

3. Statistical Methodology⁶

Once two DNA samples (i.e., what was found on the evidence and the defendant's DNA) are typed at a number of STR loci and are found to be sufficiently similar such that they could have originated from the same source, the analyst must determine the significance of the comparison. In other words, the analyst must determine how common or rare the particular DNA profile is based on population frequency data. The analyst does this by calculating the profile frequency. The profile frequency is simply the probability that an unrelated person chosen at random from the population would have the same DNA profile as the unknown sample.

The analyst will determine the statistical frequency of a particular DNA profile by multiplying the frequency of each of the alleles in the profile, and then correcting the result to account for inbreeding⁷ or substructuring⁸ effects in the population. In other words, the statistical frequency of the DNA profile is calculated using a statistical concept known as the product rule. In correcting for inbreeding, the FBI uses a value noted as "theta." This concept of using the theta inbreeding coefficient correction has been known since the 1950s. The FBI uses a theta value of .01 as is recommended by the NRC II. See NRC II at 122.⁹ In order to calculate the allelic frequencies, the FBI has generated a series of databases which are used to approximate the actual frequencies of the alleles in various population groups. In addition, the FBI applies a tenfold tolerance limit to statistical calculations, as recommended by the National Academy of Sciences. This means that the FBI will increase a calculated profile frequency by a factor of ten in each case to correct for genetic or sampling variation that might occur.

III. DISCUSSION

A. Standard for Determining the Admissibility of Scientific Evidence

Federal Rule of Evidence 702 governs the use of expert testimony in federal courts.¹⁰ The U.S. Supreme Court's decision in *Daubert v. Merrell Dow Pharmaceuticals*, 509 U.S. 579, 113 S.Ct. 2786, 125 L.Ed.2d 469 (1993), established a gatekeeping role for trial court judges in determining the admissibility of expert testimony on scientific evidence.

[T]he trial judge must determine at the outset, pursuant to Rule 104(a), 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 issue. This entails a preliminary assessment of whether the reasoning or methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology properly can be applied to the facts in issue.

Id. at 592-3. In other words, *Daubert* directed district court judges to insure that evidence presented by expert witnesses is relevant, reliable, and

When an expert bases opinion testimony on scientific knowledge, the testimony will not be admitted unless it is derived by the scientific method and is supported by "appropriate validation." *Daubert*, at 590. This standard of evidentiary reliability focuses on the scientific validity of the expert's methods rather than the soundness of his specific conclusions. *Id.* at 589 ("[the] inquiry into the reliability of scientific evidence requires a determination as to its scientific validity."); see also *Oddi v. Ford Motor Co.*, 234 F.3d 136, 145 (3d Cir.2000); *United States v. Shea*, 957 F.Supp. at 337. An expert's opinion is reliable if it is based on the "methods and procedures of science" rather than on "subjective belief or unsupported speculation"; the expert must have "good grounds" for his or her belief See *Daubert*, 509 U.S. at 589.

Although the Court in *Daubert* acknowledged that many factors could bear on the inquiry, the Court did set out some general observations to guide trial courts in determining if proffered expert testimony is sufficiently relevant and reliable to be admissible. In determining "whether a theory or technique is scientific knowledge that will assist the trier of fact," a court should consider "whether it can be (and has been) tested," "whether the theory or technique has been subjected to peer review and publication," "the known or potential rate of error, and the existence and maintenance of standards controlling the technique's operation, and whether the theory has been generally accepted. See *Daubert* at 593. The Court also emphasized that the inquiry envisioned by Rule 702 is "a flexible one," and noted that the "focus ... must be solely on principles and methodology, not on the conclusions they generate." *Id.* at 595.

In 1994, the Third Circuit first applied *Daubert* in *In re Paoli Railroad Yard PCB Litigation*, 35 F.3d 717 (3d Cir.1994)("Paoli II"). In discussing reliability, *Paoli II* adopted the factors outlined in *Daubert* and also noted the continuing vitality of *United States v. Downing*, 753 F.2d 1224 (3d Cir.1985), which also articulated factors to be considered in determining reliability. *Paoli II* held that in conducting an inquiry into the reliability of proposed expert testimony, "district court[s] should take into account all of the factors listed by either *Daubert* or *Downing* as well as any others that are relevant." *Paoli II*, at 742. These factors include:

- (1) whether a method consists of a testable hypothesis;
- (2) whether the method has been subjected 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
- (8) the nonjudicial uses to which the method has been put."

Paoli II, at 742 n. 8; see also *Elcock v. Kmart Corp.*, 233 F.3d 734, 745-46 (3d Cir.2000); *Oddi v. Ford Motor Co.*, 234 F.3d at 145. The *Paoli II* court also stated that the expert's testimony must also "fit", that is, it must assist the trier of fact. *Id.* at 743. "Admissibility thus depends in part upon "the proffered connection between the scientific

research or test result to be presented and particular disputed factual issues in the case." Id.

The test of admissibility is not whether a particular scientific opinion has the best foundation or whether it is demonstrably correct. *Oddi*, 234 F.3d at 145-46. Instead, the test is whether the "particular opinion is based on valid reasoning and reliable methodology." Id. (quoting *Kannankeril v. Terminix Int'l Inc.*, 128 F.3d 802, 806 (3d Cir.1997)). "The analysis of the conclusions themselves is for the trier of fact when the expert is subjected to cross-examination." Id. Lastly, although "conclusions and methodology are not entirely distinct from one another," the court "must examine the expert's conclusions in order to determine whether they could reliably flow from the facts known to the expert and the methodology used." Id.

B. Application of the Daubert/Paoli II factors¹¹

Applying the factors articulated by the Supreme Court in *Daubert* and by the Third Circuit in *Paoli II* to the evidence adduced during the evidentiary hearing, the court finds that the expert testimony concerning DNA analysis should be admitted, rather than excluded.

In addition, turning to a threshold issue, the court finds that the *Cofiler* and *Profiler* materials kits do not represent a separate part of the typing process, but rather, simply contain materials for beginning the PCR process. See *People v. Schreck*, 22 P.3d 68, 81 (Colo.2001). Therefore, the court concludes that "questions as to the reliability of the particular type of multiplex kit go to the weight of the evidence, rather than its admissibility." Id. (reversing lower court's decision to treat *Cofiler* and *Profiler Plus* materials kits as separate stages of the typing process that also had to meet *Daubert*'s standards of admissibility). Thus, the court will first briefly discuss the *Daubert/Paoli II* factors as they relate to PCR/STR typing.¹² The court will then turn to the defendant's specific challenges.

1. Whether the Theory or Technique Has Been Subject to Review?

The PCR/STR typing used in this case has been the subject of numerous published articles. At the outset, the court notes that the PCR process of amplifying relatively small samples of DNA into an analyzable quantity has received widespread acceptance in courts. See e.g., *United States v. Wright*, 215 F.3d 1020, 1027 (9th Cir.2000); *United States v. Beasley*, 102 F.3d at 1447; *United States v. Gaines*, 979 F.Supp. at 1433 at n. 4 and 1435; *United States v. Shea*, 957 F.Supp. at 345.

Although the PCR amplification process has been widely accepted in courts, the defendant accuses the government of trying to "lump STRs and PCRs together as having been accepted by the Courts." In effect, the defendant charges the government with trying to "bootstrap old precedent into a legal endorsement of the validity of the new test." Despite the defendant's contentions, the court finds other courts' acceptance of the PCR amplification process to be relevant in deciding if the method used in this case is reliable.

Moreover, the government has not lumped together PCRs and STRs, but rather, has demonstrated that both have been substantially peer reviewed. Finally, the court notes that the defendant's own expert agreed at the evidentiary hearing that as a general matter, PCR methodology has been sufficiently validated in the scientific literature. See Tr. at D14.

Regarding the thirteen STR loci used in this case, the government has offered sufficient evidence establishing that the use of the PCR process to amplify STR regions has also been subjected to peer review. "The abundance of literature available on the use of STRs for forensic DNA typing shows that it has become an established technology worthy of being used as court evidence." See Tr. at A112 to 113 (referring to a peer reviewed article in scientific journal, *Nucleic Acids Research*). In addition, the government submitted evidence that there are more than 1000 articles on the subject. Tr. at A111. Finally, the government also demonstrated that the thirteen STR loci used in this case have undergone extensive scrutiny because they were chosen after a series of tests done by a consortium of twenty-one laboratories. See Tr. at A91-93.

Given the testimony presented at the hearing, the court finds that the use of the PCR process to amplify the thirteen STR loci used in this case has been subjected to sufficiently vigorous peer review that it was likely that "substantive flaws in [the] methodology" have been detected. See *Daubert*, 509 U.S. at 594.

2. Known or Potential Error Rate

The testimony at the hearing indicated that the FBI's method of performing PCR/STR analysis is designed to produce consistently responsible results within established measurement error conditions. Tr. at A158. The FBI protocol for performing PCR/STR analysis has been designed to eliminate any potential technological errors and establish an acceptable range of measurement error. Tr. at B78. The FBI methodology has been developed to result in a zero error rate within acceptable measurement error conditions (error being understood as yielding an incorrect result), if the methodology is followed and properly calibrated instruments are used. Tr. at B131.

3. Standards Controlling Technique's Operation

The FBI maintains an extensive protocol for the performance of the PCR/STR process, which provides guidance to the forensic examiners and biologists on each step of the process. Specifically, the protocol provides a procedure for performing each stage of the amplification and typing process, from extracting the samples through the typing stage. The protocol was developed after research and validation studies by the FBI laboratory research unit as well as after internal validation studies.

The FBI also maintains a Quality Assurance manual, which provides a further layer of controls on the operation of the PCR/STR technique. These controls include, but are not limited to: maintaining separate rooms with dedicated equipment for pre and post

amplification samples, using of gloves, masks and pipettes and separating the extraction of the sample to be analyzed and the reference samples.

In light of these quality control and quality assurance procedures, the court finds that there are sufficient standards controlling the operation of the PCR/STR typing technique.

4. General Acceptance

The court finds that PCR/STR profiling is generally accepted by the relevant scientific community. The government presented testimony that the technique is not only widely accepted in the United States, but is also accepted internationally. See Tr. at A126-27. In its 1996 Report, the NRC II Committee remarked that "it is not surprising that PCR-based typing is widely and increasingly used in forensic DNA laboratories in this country and abroad." NRC II, at 70.

Thus, the court finds, based on the expert testimony, that PCR/STR typing is generally accepted within the scientific community of forensic geneticists.

5. Relationship of Technique to Established Reliable Methods

The government presented testimony that other forms of DNA typing such as RFLP/VNTR, DQ-alpha, and Polymarker, have all been previously validated as reliable and have previously achieved general acceptance in the scientific community. See Tr. at A64. The government has demonstrated that the PCR amplification of the thirteen STR loci is similar to these predecessor technologies. See Tr. at A63 (explaining that PCR principles are the same regardless of the number of markers tested) and 82 (explaining that the concept of using STR analysis is no different from the concept of typing mixtures under predecessor methodologies). Because the PCR/STR method of typing is related to established reliable methods, the court finds that this is yet another factor that weighs in favor of a finding of reliability within the meaning of Daubert.

6. Nonjudicial Uses to Which the Method Has Been Put

Finally, the government has demonstrated that the typing at issue has been used outside of the judicial context. For example, the PCR amplification process is used in such fields as medical research and agriculture. See Tr. at A56. STRs have been used in paternity testing, tumor identification, and in the identification of human remains from mass disasters. See Tr. at A127. Again, the court finds that this factor weighs in favor of admitting the expert's testimony.

C. Defendant's Challenges to Admissibility

The defendant challenges the admissibility of the DNA evidence at issue in several ways. First, the defendant challenges the reliability of the PCR amplification process claiming that contamination may occur and the amplified product is only as good as the

original sample. The defendant also contests whether the PCR/STR typing used in this case is as reliable with mixed samples. Second, the defendant suggests that the FBI improperly influenced the development of the Cofiler and Profiler Plus kits. Finally, the defendant challenges whether both the PCR/STR typing process and the statistical methods used in this case properly account for error rates. The court will address these issues in turn.

1. General Reliability Challenges

a. Contamination

The defendant maintains that the "primary concerns with the PCR segment of the process is that contamination may often occur and that the amplified product is only as good as the original sample." The defendant supports this claim by citing to twenty-five published articles. In citing to these articles, the defendant states that "[o]utside the forensic realm notice has been made of problems that have occurred with PCR as a starting process."¹³ While these problems may be true outside the forensics realm, the government presented ample evidence at the hearing that the FBI protocol for PCR/STR analysis contains substantial controls and procedures for preventing contamination. Because there is evidence that the government has taken steps to prevent contamination of the DNA sample, the court concludes that the defendant's vague, broad assertion that samples amplified by the PCR can become contaminated does not warrant the exclusion of the DNA evidence in this case.

b. Procedures Used in this Case

The defendant also characterizes the FBI's protocols as "watered down." The defendant further alleges that the FBI examiner in this case, Brendan Shea, was "not required to note whether he followed the [FBI's] protocol nor the amount actually used for future examination." As the court has already described, the FBI has established that it has protocols and quality assurance controls in place to assure that its methods are sufficiently reliable. The defendant is not challenging the soundness of the methods of the FBI's protocols, but rather the conclusions that are drawn. See *Daubert*, at 589. Thus, the court finds that the challenges that the defendant makes to the procedures used in this case are more relevant to the weight of the evidence and not its admissibility.

c. Alleged Inherent Flaws in the System

The defendant contends that inherent flaws in the system may render unreliable the PCR/STR typing done with the Cofiler and Profiler Plus materials kits in combination with Genoscan and Genotyper software. Specifically, the defendant points to the "concepts of allelic drop out, stutter, and differential amplification and problems that may have to "be explained away through numbers set by laboratories to obtain a profile."¹⁴ The defendant also argues that the government has not established that the PCR/STR typing used in this case is as reliable with a mixed sample of DNA as it is with a single source of DNA. The government presented evidence that its laboratories have protocols

in place in order to control for these types of inherent flaws. Specifically, Dr. Budowle testified that laboratories set interpretation thresholds below which the laboratory will not interpret a peak as an allele. See Tr. at B143. Dr. Budowle further explained that as a result of an empirical study, the interpretation thresholds set by the FBI are designed to prevent these types of known inherent flaws from causing errors in interpreting a profile. See *id.* at B143-45. In light of the controls to reduce the effects of inherent flaws such as stutter or allelic drop out, the court finds that the defendant's challenges are directed to the weight of the evidence and not its admissibility.

2. Claim that the FBI Improperly Influenced the Development of the Materials Kits

The defendant suggests that the court cannot assess whether the Cofiler and Profiler Plus materials kits used in this case have been widely accepted because the FBI somehow improperly controlled the DNA typing industry by forcing Perkin Elmer Biosystems (the maker of the kits) to manufacture the Profiler Plus and Cofiler materials kits "consistent with the FBI's wishes." Furthermore, the defendant accuses the government's expert, Dr. Budowle, of trying to "force the industry into his methods," and says that his influence caused a "lack of real checks on the FBI product." The court is not persuaded by this argument. As the government correctly asserts, the record does not support this contention. Moreover, this charge is not evidence which would show that the materials kits used in this case are unreliable. Instead, if the defendant seeks to question the FBI's relationship to the kits used in this case, this argument would be better made in challenging the weight of the evidence before the jury.

3. Error Rate Challenges

a. Error Rate in the Laboratory

The defendant accuses the government of claiming that their methodology creates a zero error rate within acceptable measurement conditions. According to the defendant, such a claim is illogical. The defendant also charges the government with attempting to avoid the issue of error rate by not responding to the problems generated by PCR based testing by claiming that "one should assume that the machinery works correctly all the time and that human error does not exist because everyone follows the protocols."

As the government points out in its reply, its experts did not deny the potential for measurement errors. However, the FBI has determined an acceptable range of measurement error for its PCR/STR typing methodology. Thus, if the methodology is followed and properly calibrated instruments are used, the error rate for the methodology is zero. Error is understood in this context as an incorrect result. This does not mean that errors do not occur, but rather that the FBI has conducted studies and has attempted to control for typical errors.

The court also finds persuasive the conclusions drawn by the NRC II concerning laboratory error rates:

It is difficult to arrive at a meaningful and accurate estimate of the risk of such laboratory errors. For one thing, in this rapidly evolving technology, it is the current practice and not the past record of a laboratory that is relevant, and that necessarily means smaller numbers and consequent statistical uncertainty. For another, the number of proficiency tests required to give an accurate estimate of a low error rate (and it must be low to be acceptable) is enormous and would be outlandishly expensive and disruptive. We believe that such efforts would be badly misplaced and would use resources that could much better be used in other ways, such as improving laboratory standards. No amount of attention to detail, auditing, and proficiency testing can completely eliminate the risk of error.

NRC II, at 24-25.

In light of the evidence that the FBI attempts to control for laboratory error, the court finds the defendant's challenge to be unpersuasive.

b. Error Rate in Statistical Methodology

"The defense maintains the position that the DNA evidence is inadmissible because there are no scientifically valid statistical methods that address both the probability of a coincidental match between two people who share common genetic characteristics and the probability that a match would mistakenly be reported due to laboratory error." The defendant also asserts that the "state of science is not such that this issue is a matter of weight."¹⁵

The court does not agree. In making its determination, the court finds the conclusions announced in the 1996 NRC II to be persuasive: "[W]e believe that a calculation that combines error rates with match probabilities is inappropriate." NRC II, at 87. Moreover, the defendant's own expert, Dr. Shields, does not believe that both the probability of a match and the probability of error should be included as a part of a likelihood ratio analysis. Rather, Dr. Shields stated that "there is more information if you provide the two estimates separately, and then somebody who is listening can make a decision on their own about what it means." Tr. at C167. As the court has already explained, Rule 702 does not require consensus, only valid methodology. Thus, contrary to the defendant's assertion, the court finds that this challenge is more an issue of weight and not an issue of admissibility.

IV. CONCLUSION

For the foregoing reasons, the court finds that the expert testimony concerning DNA evidence meets the requirements of Rule 702 of the Federal Rules of Civil Procedure. Therefore, the court will deny the defendant's motion. The court will issue an order to this effect in conjunction with its opinion.

¹ This description of the basic concepts of DNA is derived from the National Research Council, *The Evaluation of Forensic DNA Evidence* (1996), at pp. 12-14, 60-65 [hereinafter NRC II]. Both the government and the defendant agree that the NRC II is widely regarded as one of the definitive publications on the use of DNA evidence in the field of forensics. See also e.g., *United States v. Gaines*, 979 F.Supp.

1429, 1431-32 (S.D.Fla.1997) (citing *United States v. Shea*, 957 F.Supp. 331, 333 (D.N.H.1997)); *Virgin Islands v. Penn*, 838 F.Supp. 1054, 1058 (D.Vi.1993).

² See Tr. at 45-59. See generally, NRC II, at 69-71. See also *United States v. Hicks*, 103 F.3d 837, 844-45 (9th Cir.1996); *United States v. Beasley*, 102 F.3d 1440, 1445 (8th Cir.1996); *United States v. Shea*, 957 F.Supp. at 334.

³ See generally Tr. at 64-87; *Commonwealth v. Rosier*, 425 Mass. 807, 685 N.E.2d 739, 742 (Mass.1997)

⁴ See generally Tr. at A87-90

⁵ All of the samples in the CODIS data bank are typed at the same thirteen STR loci, thus enabling law enforcement to compare unknown samples with samples in the data bank. CODIS was developed by a consortium of twenty-one laboratories to test various STR markers to determine which would be the best to use in the CODIS data bank. The thirteen used in this case were selected for CODIS and are, therefore, known as the CODIS core loci.

⁶ See Tr. at 164-196; *United States v. Shea*, 957 F.Supp. at 335-337.

⁷ Inbreeding refers to the mating of two persons who are more closely related than if they were chosen at random. See NRC II, at 98.

⁸ Substructuring refers to the tendency toward decreasing genetic heterogeneity and allelic independence exhibited by ethnically homogeneous, non-randomly mating populations. In other words "a substructured population may be defined as one in which the probability of a random match between two of its members is greater than the likelihood of such a match between two members of the population at large." See *United States v. Chischilly*, 30 F.3d 1144, 1153 (9th Cir.1994).

⁹ The parties dispute whether the use of .01 for theta is a conservative estimate or not. The government claims that empirical studies demonstrate that .01 is "highly conservative." In contrast, the defendant's expert recommended a theta value of .05. In the court's assessment, this dispute goes to the weight of the evidence and not the reliability.

¹⁰ On December 1, 2000, Rule 702 was amended in response to Daubert and Kumho Tire Rule 702 now reads:

If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise, if (1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles and methods, and (3) the witness has applied the principles and methods reliably to the facts of the case. (Additions emphasized in bold). In the advisory committee notes, the committee stated that this amendment "affirms the trial court's role as gatekeeper and provides some general standards that the trial court must use to assess the reliability and helpfulness of proffered expert testimony ." Fed.R.Evid. 702 advisory committee's note.

¹¹ The court will not address the first factor, whether the methodology at issue has a testable hypothesis, or the seventh factor, concerning the qualifications of the expert witnesses. The parties do not dispute that the hypotheses behind the methodologies at issue in this case can be tested. The hypothesis of PCR/STR DNA typing is that with proper procedures an expert can determine the allelic types of given DNA samples at the thirteen core STR loci. The statistical methodology in this case is premised on the hypothesis that, given a DNA profile at thirteen core loci, an analyst can determine the random match frequency of that profile in various major population groups.

As to the qualification of the experts, the court has already accepted Dr. Budowle, Dr. Chakraborty, and Dr. Shields as experts. The court deferred a determination of Mr. Shea's qualifications to testify as an expert until the time of trial. See Tr. at A59.

¹² The court also finds that statistical methodology used in this case meets the requirements of Daubert/Paoli II. See e.g., *United States v. Gaines*, 979 F.Supp. at 1441.

¹³ None of these articles were presented, explained or offered into evidence by the defendant at the evidentiary hearing. Moreover, the defendant's brief offers no explanation as to how these materials relate to the issue presently before the court.

¹⁴ As the court has explained, the rate at which the different DNA fragments move through the gel is converted into a pattern of peaks to be read by an analyst for interpretation. The concepts of stutter, allelic dropout and differential amplification all relate to whether a peak is able to be interpreted.

¹⁵ The defendant also challenges the use of the product rule (which involves multiplication of allelic frequencies) and the "relevance of small unrepresentative databases."

The court acknowledges that there has been debate about the use of the product rule, see *United States v. Shea*, 957 F.Supp. at 341, however, Rule 702 does not require consensus, see *id.* at 343. As the government correctly points out, the 1996 NRC II effectively ended much of this debate. NRC II at 122 (recommending that the calculation of profile frequencies be made with the product rule and discussing ways to account in a conservative way for likely negative systematic effects). Moreover, the government has directed the court's attention to cases which find that the use of the product rule is sufficiently reliable to be admissible under Daubert. See e.g., *United States v. Gaines*, 979 F.Supp. at 1441; *United States v. Shea*, 957 F.Supp. at 342-43.

Concerning the size of the population databases used by the FBI to calculate random match frequencies, the government presented evidence that these databases are based on convenience samples drawn from various sources, including paternity test laboratories. These databases contain more than a statistically sufficient number of samples to permit the calculations of valid allelic frequencies. Moreover, the FBI has published up to forty-one of these databases with the underlying raw data also being available to the public.

In light of this evidence, the court finds that these types of arguments relate to the weight of the evidence and not whether the statistical methodology is valid.