In the Circuit Court for Prince George's County
Case Number: CT 02-0381X

IN THE COURT OF APPEALS
OF MARYLAND

No. 99

September Term, 2004

ANTHONY EUGENE YOUNG

v.

STATE OF MARYLAND

Bell, C.J.
Raker
Wilner
Harrell
Battaglia
Greene
Eldridge, John C. (Retired, Specially
Assigned),
JJ.

Opinion by Raker, J.

Filed: July 19, 2005

The primary issue we address in this appeal is whether the trial court erred in admitting evidence that there was a DNA "match" in the absence of accompanying statistical evidence. We conclude that the court did not err and hold that when a DNA method analyzes genetic markers at sufficient locations to arrive at an infinitesimal random match probability, expert opinion testimony of a match and of the source of the DNA evidence is admissible.

I.

The Grand Jury for Prince George's County charged Anthony Eugene Young with, *inter alia*, three counts of second degree sexual offense and three counts of third degree sexual offense. A jury in Prince George's County convicted petitioner of one count of second degree sex offense.

At trial, the State presented the following evidence: On September 27, 2001, a thirteen year-old boy participated in an internet chat room called "Gay Twenties." Young, who was thirty-seven at the time, participated in the chat room as well. Young contacted the boy via instant messenger[1] and telephone and arranged a rendevous at the boy's apartment. The next day, Young visited the boy's home, and the two engaged in oral and anal sex. On October 2, Young visited the boy's home unannounced and again engaged him in anal sex.

---

[1]An instant message is an internet-based cross between an e-mail and a telephone conversation. One person, operating under a "screen name," types a message to another person. The second person receives that message instantly and may reply. As such, two or more people can have a "conversation."

During the second encounter, the boy's mother returned home from work. After Young left, the boy eventually disclosed to his mother what had occurred. Later that night, the mother and child contacted the police. The boy was taken to the hospital where he was examined.

Identification was the primary issue at trial. The State offered three types of identification evidence. First, the State presented testimonial evidence, primarily that of the boy. Young challenged the testimonial evidence, emphasizing the boy and his mother's failure to identify Young in a police photo array and claiming that the boy was not credible. Second, the State tendered evidence that Young participated in the chat room. Young did not dispute that evidence.[2] Third, the State presented DNA evidence.

The DNA evidence consisted of an analysis of two DNA samples. The first was obtained from the boy by a forensic nurse who examined him at the hospital and took a swab of his rectal area. The second was procured by an officer of the Prince George's County Police Department who, with Young's consent, took two swabs of Young's mouth.

In this appeal, Young challenges the testimony of Rupert Page, a forensic DNA analyst for the Prince George's County Police Department, who examined the samples on behalf of the State. The court received Page as an expert in profiling and forensic serology. Page testified that other than identical twins, no two people have the same DNA profile. He then described his testing of the anal swabs from the boy and the oral swabs from Young.

---

[2]Young testified and acknowledged that he frequented the "Gay Twenties" chat room. He denied, however, any knowledge of or contact with the boy.

Page explained that he used a process called differential extraction to separate the sperm cells from the boy's skin cells on the anal swab. He testified that he made a microscope slide of the sperm cells, obtained a DNA profile from the slide, and compared the profile to Young's profile obtained from the oral swabs.

In response to the State's questions, Page repeatedly testified that the two DNA profiles "matched." Page did not provide any basis for this conclusion, other than to state that his conclusion was based on his comparison of the two samples. He did not identify which DNA sequences he reviewed, and only on cross-examination did he note that he employed the polymerase chain reaction ("PCR") method. Page did not testify to the probability that a random person's profile would have matched the profile taken from the boy. Defense counsel objected repeatedly, arguing that, based on *Armstead v. State*, 342 Md. 38, 673 A.2d 221 (1996), the witness was required to provide probability statistics to accompany and support his conclusion. For example, defense counsel stated as follows:

> "Your Honor, the Armstead case concluded . . . . My understanding is that the Court of Appeals concluded that the legislature intended to render the sexual statistics admissible, not just the raw evidence of DNA match, and what the State seems to be trying to do is to say there is a match as opposed to providing what the statistical information was that was provided to give the jury a chance to make that determination."

The court permitted the witness to testify that the DNA profiles "matched," but did not allow him to testify that Young was the source of the DNA obtained from the anal swab. Instead, the court admitted into evidence Page's DNA report, over defense counsel's

objection. In this report, Page noted that he employed the PCR method and the AmpFISTR Profiler Plus PCR Amplification Kit and AmpFISTR Cofiler PCR Amplification Kit to examine DNA markers along a combined thirteen loci and a gender identification locus.[3] Page concluded, "The sperm fraction of the Anal Swab (R1) contains DNA from a male. To a reasonable degree of scientific certainty (in the absence of an identical twin), Anthony Young (K1) is the source of the DNA obtained from the sperm fraction of the Anal Swab (R1)."[4] Page's report contained no statistical data to support his conclusion.

Young's cross-examination of Page focused on the whereabouts of a particular piece of evidence not presented at trial and on the significance of Page's references to "technical artifacts" in his comparison of the DNA samples. Young did not ask Page any questions about statistics.

The State relied heavily on the evidence that the DNA samples matched. In its opening statement, the State argued that the DNA evidence showed "a perfect match, all the way down the line" and that the "DNA evidence will prove conclusively that Anthony Young was the source of the semen recovered from [the victim's] anus, removing any doubt you may have whatsoever, leading to the only conclusion, and that is the conclusion that Anthony Young is guilty of the charges submitted to you." In its closing statement, the State argued that the DNA evidence revealed "an exact match" "straight down the line." In its

[3]AmpFISTR Profiler Plus PCR Amplification Kit and AmpFISTR Cofiler PCR Amplification Kit are commercial products marketed by Applied Biosystems.

[4]Young later testified that he did not have an identical twin.

rebuttal argument, the State responded to Young's challenges to the testimony of identification and the victim's credibility by pointing to the DNA evidence. In response to Young's emphasis of the failure to identify him in the photo array, the State said, "That's a red herring. You know why? Because it doesn't make any difference, because the DNA says it was Anthony Young who had anal intercourse with [the victim]. So don't be fooled by that."

The jury found Young guilty of one count of second degree sexual offense. The court sentenced Young to a term of twenty years incarceration.

Young noted a timely appeal to the Court of Special Appeals. In an unreported opinion, that court affirmed. The Court of Special Appeals appears to have relied on two bases. First, the court distinguished *Armstead v. State*, 342 Md. 38, 673 A.2d 221 (1996). The court explained that while a DNA match based on a comparison of one locus is virtually meaningless without accompanying statistical testimony, a match at thirteen different loci has such a low random match probability that there is no requirement of accompanying statistical data. Second, the court held that even if statistical evidence were required, the error was harmless beyond a reasonable doubt.

We granted Young's petition for a Writ of Certiorari. 384 Md. 157, 862 A.2d 993 (2004). Young raises the following issue:

> "Whether it was error to admit 'expert testimony' that there was a DNA 'match' in the absence of any foundation for such an assertion."

We agree with the Court of Special Appeals and hold that the Circuit Court did not err in admitting the expert's testimony of a match in conjunction with testimony that to a reasonable degree of scientific certainty, the defendant was the source of the DNA evidence. Accordingly, we affirm.

II.

In this Court, Young argues that the trial court erred in overruling his objections to Page's testimony. He contends that *Armstead* requires the admission of contextual statistics when the State asserts that there is a DNA match. According to Young, stating that DNA profiles match without providing the statistical probability is meaningless, because DNA statistics vary based on the defendant's ethnic group or the number of loci examined. In Young's view, Page's testimony thus had no probative value and was irrelevant.

The State responds that the DNA evidence was relevant and admissible, without any testimony about statistical probability. According to the State, *Armstead* did not require testimony about statistical probability. Rather, this Court's strong statements about the admissibility of statistical probability testimony should be viewed in the context of Armstead's questioning of the testimony's admissibility and the controversy within the scientific community about the validity of such evidence. In addition, the State argues that scientific advances in DNA testing since *Armstead* have eliminated any uncertainty about the meaning of the term "match." The State contends that in all cases, the probability that

another person besides an identical twin has the same DNA profile has become so remote that an expert witness can testify to a DNA match without explaining the statistical probability. In the alternative, the State argues that even if the court erred, the error was harmless beyond a reasonable doubt. Given the scientific advancements resulting in a remote probability that another individual has an identical profile to Young, the jury could not have been swayed by testimony of the probability.

We conclude that scientific advances in DNA profiling enable an examiner employing particular methods and analyzing genetic markers at a sufficient number of loci to testify, to a reasonable degree of scientific certainty, to the source of the DNA evidence. We hold that in such circumstances, as in the instant case, the expert is not required to accompany his "match" testimony with contextual statistics. Accordingly, the Circuit Court did not err in admitting the expert's testimony of a match.

III.

We have described the science of DNA evidence as follows:

> "Deoxyribonucleic acid ('DNA') is the organic material that provides the genetic instructions for all individual hereditary characteristics. *See Armstead v. State,* 342 Md. 38, 51, 673 A.2d 221, 227 (1996); *United States v. Hicks,* 103 F.3d 837, 844 (9th Cir. 1996); *Commonwealth v. Curnin,* 409 Mass. 218, 565 N.E.2d 440, 441 n.1 (1991); *State v. Carter,* 246 Neb. 953, 524 N.W.2d 763, 775 (1994), *overruled on other grounds*, *State v. Freeman*, 253 Neb. 385, 571 N.W.2d 276 (1997); *State v. Vandebogart,* 136 N.H. 365, 616 A.2d 483, 485 (1992); *State v. Cauthron,* 120 Wash.2d 879, 846 P.2d 502, 508 (1993). The

importance of DNA for forensic purposes is that DNA does not vary within an individual and, with the exception of identical twins, no two individuals have the same DNA configuration. *See Nelson v. State,* 628 A.2d 69, 75 (Del. 1993); *State v. Williams,* 574 N.W.2d 293, 297 (Iowa 1998); *Curnin,* 565 N.E.2d at 441 n.1, 445; *Carter,* 524 N.W.2d at 775; *Vandebogart,* 616 A.2d at 485-86; *State v. Copeland,* 130 Wash.2d 244, 922 P.2d 1304, 1315 (1996); George Bundy Smith & Janet A. Gordon, *The Admission of DNA Evidence in State and Federal Courts,* 65 FORDHAM L. REV. 2465, 2465 (1997).

"The molecular structure of DNA is commonly referred to as a 'double helix,' which resembles a spiraling ladder, and which is composed of twisted double strands of repeated sequences of 'nucleotides.' *See Armstead,* 342 Md. at 51, 673 A.2d at 227; *State v. Tankersley,* 191 Ariz. 359, 956 P.2d 486, 490 (1998); *Williams,* 574 N.W.2d at 297; *Curnin,* 565 N.E.2d at 445; *Carter,* 524 N.W.2d at 775; *Vandebogart,* 616 A.2d at 486; *Copeland,* 922 P.2d at 1315; Smith & Gordon, *supra,* at 2465-66. The sides of the ladder are composed of the 'nucleotides,' which are organic bases that pair with one another to form the 'rungs' of the double helix. *See Curnin,* 565 N.E.2d at 445-46; *Carter,* 524 N.W.2d at 775; *Cauthron,* 846 P.2d at 508; Smith & Gordon, *supra,* at 2466. It is the repeating sequence of base pairs along the DNA double helix that comprise 'genes,' which determine the unique physiological traits of human beings. *See Armstead,* 342 Md. at 51-52, 673 A.2d at 227; *Hicks,* 103 F.3d at 845; *Tankersley,* 956 P.2d at 490 n.2; *Carter,* 524 N.W.2d at 775; *Vandebogart,* 616 A.2d at 486; *Cauthron,* 846 P.2d at 508; Smith & Gordon, *supra,* at 2466. The specific position that a gene occupies is called its 'locus.' *See* Smith & Gordon, *supra,* at 2466. An individual's entire complement of DNA is known as the 'genome.' *See Vandebogart,* 616 A.2d at 486; Smith & Gordon, *supra,* at 2467.

"The vast majority of the base pair sequences of human DNA are identical for all people. *See Armstead,* 342 Md. at 52, 673 A.2d at 227; *Hicks,* 103 F.3d at 845; *Nelson,* 628 A.2d at 75; *Williams,* 574 N.W.2d at 297; *Carter,* 524 N.W.2d at 775;

> *Copeland,* 922 P.2d at 1315; Smith & Gordon, *supra,* at 2466. There are, however, a few DNA segments or genes, called 'polymorphic loci,' which are highly variable among individuals. *See Nelson,* 628 A.2d at 75; *Williams,* 574 N.W.2d at 297; *Curnin,* 565 N.E.2d at 446; *Carter,* 524 N.W.2d at 775; *Vandebogart,* 616 A.2d at 486; *Cauthron,* 846 P.2d at 509. The alternative forms of these individual polymorphic gene fragments are called 'alleles.' *See Tankersley,* 956 P.2d at 490 n.2; *Curnin,* 565 N.E.2d at 446; *Cauthron,* 846 P.2d at 509; Smith & Gordon, *supra,* at 2466. It is these polymorphisms that have great significance for forensic DNA analysis because they provide the basis for DNA identification. *See Armstead,* 342 Md. at 52, 673 A.2d at 227; *Hicks,* 103 F.3d at 845; *Nelson,* 628 A.2d at 75; *Curnin,* 565 N.E.2d at 441 n.1, 446; *Cauthron,* 846 P.2d at 509; Smith & Gordon, *supra,* at 2467."

Gross v. State, 371 Md. 334, 339 n.1, 809 A.2d 627, 630 n.1 (2002).[5]

The polymerase chain reaction ("PCR") method of DNA analysis is an amplification procedure that reproduces repeatedly a short segment of DNA, making it possible to analyze

---

[5]At the time of our decision in *Armstead v. State,* 342 Md. 38, 673 A.2d 221 (1996), restriction fragment length polymorphism ("RFLP") analysis was the most common method used in forensic DNA analysis. RFLP involves the use of the DNA loci that contain "variable number tandem repeat" ("VNTR") sequences, which are stretches of DNA in which a short nucleotide core sequence of base pairs is repeated in tandem along the chromosome. *See id.* at 52, 673 A.2d at 227-28; George Bundy Smith & Janet A. Gordon, *The Admission of DNA Evidence in State and Federal Courts,* 65 Fordham L. Rev. 2465, 2467 (1997). As a result of VNTR sequencing, the length of a given allele, which is measured by the number of repeated base pairs, varies from person to person. *See State v. Vandebogart,* 616 A.2d 483, 486 (N.H. 1992). VNTR loci particularly are useful in forensic DNA analysis because they have a very large number of different alleles. *See Armstead,* 342 Md. at 52, 673 A.2d at 227. RFLP analysis yields distinct DNA profiles because the exact number of repeats, and therefore the length of the VNTR region, varies from one allele to another, and different VNTR alleles can be identified by their length. *See* Smith & Gordon, *supra,* at 2467. DNA fragments containing VNTRs are detected by specially constructed molecular "probes," which are short segments of single-stranded DNA with radioactive components that bind to specific DNA sequences. *See id.*

minute or degraded samples.[6] *See United States v. Hicks,* 103 F.3d 837, 845 (9th Cir. 1996); *State v. Tankersley,* 956 P.2d 486, 489-90 (Ariz. 1998); Committee on DNA Forensic Science, National Research Council, *The Evaluation of Forensic DNA Evidence* 70 (1996) [hereinafter "NRC II"].

PCR analysis begins with a three-step process to amplify the DNA sample: (1) denaturization (the DNA is heated to separate the two strands); (2) annealing (primers containing nucleotide sequences that are complementary to the DNA region being amplified are added to the DNA sample, which bond to the gene when cooled); (3) extension (the gene is "copied" repeatedly in order to produce a larger sample of DNA for analysis). *See Hicks,* 103 F.3d at 845. The PCR method can be carried out in a laboratory, with results obtained in a significantly shorter time than with the previously common restriction fragment length polymorphism ("RFLP") analysis. NRC II at 70. Additionally, the PCR method usually permits an exact identification of each allele, sidestepping RFLP's measurement uncertainties. *Id*. These advantages, along with the method's utility for analyzing minute DNA samples, have resulted in a vast expansion in the use of the PCR method. *Id.*; *see State*

---

[6]DNA RFLP evidence is admissible pursuant to statute. In *Armstead*, this Court held that Md. Code (1973, 1995 Repl. Vol., 1995 Cum. Supp.) (current version at Md. Code (1973, 2002 Repl. Vol., 2004 Cum. Supp.)), § 10-915 of the Courts and Judicial Proceedings Article eliminated the discretion of trial judges generally to weigh the probative value of DNA evidence against its prejudicial effect, but that the trial courts retained the discretion to determine whether DNA evidence was logically relevant and reliable in individual cases. *See Armstead,* 342 Md. at 62-63, 673 A.2d at 232-33. Young did not challenge at trial and does not challenge on appeal the admissibility of DNA PCR evidence. Accordingly, we do not address the issue. *See* Md. Rule 8-131.

v. Belken, 633 N.W.2d 786, 798 (Iowa 2001) (noting that "the PCR method has emerged as the predominant method of DNA typing").

Once PCR amplification has been completed, analysis of the DNA profile and match determination can be conducted through the utilization of several different genetic markers. *See Tankersley,* 956 P.2d at 490. The markers employed by the laboratory in the instant case are short tandem repeats ("STR"). STRs are DNA sequences consisting of two to six base pairs. *See Commonwealth v. Rosier*, 685 N.E.2d 739, 742 (Mass. 1997); John M. Butler & Christopher H. Becker, U.S. Dep't of Justice, *Improved Analysis of DNA Short Tandem Repeats With Time-of-Flight Mass Spectrometry* 2 (2001). STRs particularly are useful in analyzing small DNA samples, because loci containing STRs are present with great frequency throughout the chromosomes. *See Rosier*, 685 N.E.2d at 742. The loci have a large number of alleles and usually are susceptible to unique identification. *Id.* The FBI has designated thirteen core STR loci and a sex-typing marker (amelogenin) for identification in its national database of convicted felons, the Combined DNA Index System ("CODIS"). *See* Butler & Becker, *supra*, at 2.[7]

DNA profiling typically is used to compare a suspect's DNA with a sample of DNA taken from a crime scene. *See Armstead,* 342 Md. at 52, 673 A.2d at 228. "DNA profiling"

---

[7]Due to the small number of alleles on many of the loci used in PCR-based tests, more loci are required for the same statistical power provided by a few loci using RFLP/VNTRs. National Research Council, Committee on DNA Forensic Science, *The Evaluation of Forensic DNA Evidence* 34 (1996) [hereinafter "NRC II"]. Twelve STR loci have a comparable discriminatory power to four or five VNTR loci. *Id.*

is a catch-all term for a wide range of methods employed to study genetic variations, including RFLP and PCR/STR typing. *See Tankersley,* 956 P.2d at 491. All types of DNA analysis involve three basic steps: (1) processing or typing of the DNA samples (to produce x-ray films that indicate the lengths of the polymorphic fragments); (2) match determination (comparison of the films to determine whether any sets of fragments match); and (3) statistical analysis (to determine the statistical significance of any match between the two DNA samples). *See id.*; *Nelson v. State,* 628 A.2d 69, 75 (Del. 1993). This three-step process produces two distinct, but interrelated, types of information: (1) molecular biological information (whether a match exists between an unknown DNA sample and a sample taken from a suspect); and (2) population genetics information (if a match exists, the statistical probability that the unknown sample came from a third party with the same DNA pattern as the suspect). *See Nelson*, 628 A.2d at 75.

DNA evidence cannot be attributed conclusively to one person unless examiners analyze the entire DNA molecules of the DNA evidence and the DNA sample from that person respectively. Two unrelated individuals can have identical DNA fragments that are examined in a particular type of DNA analysis — *i.e.*, identical DNA patterns at the targeted loci. *See Nelson,* 628 A.2d at 75; *State v. Williams,* 574 N.W.2d 293, 297 (Iowa 1998); *State v. Vandebogart,* 616 A.2d 483, 486 (N.H. 1992); *State v. Cauthron,* 846 P.2d 502, 513 (Wash. 1993) (en banc). The underlying theory of the forensic use of DNA testing is that as the number and variability of the polymorphisms analyzed increases, the odds of two

people coincidentally sharing the same DNA profile becomes vanishingly small. *Williams,* 574 N.W.2d at 297; *see also Commonwealth v. Crews,* 640 A.2d 395, 401 (Pa. 1994).

Therefore, when a DNA "match" has been declared, a conclusive identification of a crime suspect as the source of the unknown DNA sample is not being made. 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. *See Tankersley,* 956 P.2d at 490*; Williams,* 574 N.W.2d at 297; *Vandebogart,* 616 A.2d at 486; *Crews,* 640 A.2d at 401; George Bundy Smith & Janet A. Gordon, *The Admission of DNA Evidence in State and Federal Courts,* 65 Fordham L. Rev. 2465, 2472 (1997). The issue still remains of just how many other people in the population could share the same DNA profile with the suspect. *See Tankersley,* 956 P.2d at 490; Smith & Gordon, *supra,* at 2486.

Once a DNA match determination has been made, forensic scientists perform statistical analysis of population frequencies to estimate the statistical significance of the match, by calculating the likelihood that a random person (*i.e.*, not the person whose DNA actually was left at the crime scene) would match the crime scene sample, commonly referred to as the "random match probability." *See Tankersley,* 956 P.2d at 490; *Nelson,* 628 A.2d at 75; *Williams,* 574 N.W.2d at 297; *Watts v. State,* 733 So.2d 214, 224 (Miss. 1999) (en banc); *Vandebogart,* 616 A.2d at 486, 488; Smith & Gordon, *supra,* at 2473. In order to make a statistical evaluation of a declared match, it is necessary to know how frequently

a genotype occurs in the relevant reference population. *See State v. Carter*, 524 N.W.2d 763, 776, 780 (Neb. 1994). Genotype frequency calculations are performed to determine the relative frequency of a random match within a sample population database. *See Commonwealth v. Curnin,* 565 N.E.2d 440, 448 (Mass. 1991); *Carter,* 524 N.W.2d at 780; *Vandebogart,* 616 A.2d at 488; Smith & Gordon, *supra,* at 2473.

The statistical significance of a match is determined by a two-step process: first, an initial determination is made regarding the random match probability of each polymorphic locus (the "individual allele frequency"); second, the individual allele frequencies are combined to determine the overall probability of possessing the entire matched DNA segment (the "aggregate DNA profile frequency"). *See Curnin,* 565 N.E.2d at 448; *Watts,* 733 So.2d at 225; *Vandebogart,* 616 A.2d at 488; Smith & Gordon, *supra,* at 2473. These probability estimates are achieved using theoretical population genetics models in order to determine the frequency with which a given genetic pattern will occur in a defined population. *See Watts,* 733 So.2d at 225; *Vandebogart,* 616 A.2d at 488; Smith & Gordon, *supra,* at 2473-74.

Probability calculations generally are made using the "product rule." The product rule, also known as the "multiplication method," states that the likelihood of a match occurring for an entire DNA segment can be determined by calculating the match probability for each polymorphic allele and then multiplying those probabilities together. *See Armstead*, 342 Md. at 69-70, 673 A.2d at 236; *Williams*, 574 N.W.2d at 297; *Curnin,* 565 N.E.2d at

448; *Watts,* 733 So.2d at 224-25; *Vandebogart,* 616 A.2d at 488; *Cauthron,* 846 P.2d at 513. To give a basic example, if a matching DNA sample contains two independent alleles, and there is a 10% chance of a random match of the first allele and a 20% chance of a random match of the second, the product rule would suggest that there was a two percent chance that a random person in the population shared the same DNA profile (.10 x .20 = .02).

IV.

The State argues that recent scientific advances in DNA analysis have resulted in infinitesimal random match probabilities, thus eliminating the necessity for the State to accompany match evidence with statistical evidence. The State is correct, to a large degree. The State is incorrect, however, in claiming that *all* techniques for analyzing DNA evidence produce infinitesimal random match probabilities.

Nine years have passed since *Armstead* was decided.[8] As DNA analysis technology

---

[8]Admission of DNA evidence in Maryland, without the necessity of a *Frye-Reed* hearing, is governed by Md. Code (1973, 2002 Repl. Vol., 2004 Cum. Supp.), § 10-915 of the Courts and Judicial Proceedings Article. *See Armstead,* 342 Md. at 54-55, 673 A.2d at 228-29. In *Armstead*, we held that § 10-915 rendered the population genetics statistics supporting DNA RFLP match evidence admissible, as well as the raw DNA evidence, without the need for an individualized *Frye-Reed* hearing. *See id.* at 77, 673 A.2d at 240. This portion of *Armstead* dealt with Armstead's argument that population genetics statistics could not be admitted without an individualized *Frye-Reed* hearing. *Id.* at 48, 673 A.2d at 225. The State argues that *Armstead* did not decide whether the statistical evidence *had to be* admitted or whether the raw DNA evidence of a match could be admitted *without* such explanatory statistics. The State misreads *Armstead.*

Armstead is pellucid in its holding that § 10-915 rendered contextual statistics (continued...)

advances, examiners can utilize more precise techniques and view more loci. The fact remains that a match cannot identify the source of the relevant DNA sample conclusively unless the entire DNA molecule is viewed. Under certain circumstances, however, new technologies result in infinitesimal random match probabilities that would be deemed conclusive by all but mathematicians and philosophers. The instant case thus confronts us with the question of whether and to what extent these scientific advances have altered the holding of *Armstead* that contextual statistics *must* accompany match testimony.

Central to this question is whether, in such cases, a trial court may permit testimony of "source attribution." A witness testifying to "source attribution" or "uniqueness"[9] would

---

[8](...continued)
admissible *and* that testimony of a match is not admissible without accompanying statistics. We reasoned that testimony of a match without accompanying statistics would not be justifiable scientifically. We recognized that the inability of DNA testing to identify the defendant conclusively as the source of the DNA evidence made statistics a "necessary component of DNA evidence." *Id.* at 78, 673 A.2d at 241. We noted the General Assembly's deletion of the words "unique" and "uniquely" from what became § 10-915 as indicating that "the Legislature clearly recognized that the odds of random matching would be at issue whenever DNA evidence was presented." *Id*. at 78, 673 A.2d at 240. We then quoted the first National Research Council report as stating that "[t]o say that two patterns match, without providing any scientifically valid estimate (or, at least, an upper bound) of the frequency with which such matches might occur by chance, is meaningless." *Id.* at 78, 673 A.2d at 241 (quoting Committee on DNA Forensic Science, National Research Council, *DNA Technology in Forensic Science* 301 (1992) [hereinafter "NRC I"]); *see also* NRC II at 192 (stating that "it would not be scientifically justifiable to speak of a match as proof of identity in the absence of underlying data that permit some reasonable estimate of how rare the matching characteristics actually are").

[9]The terms "source attribution" and "uniqueness" appear to be used interchangeably. To the extent that the terms have been distinguished, authors have preferred "source attribution," in order to emphasize that the relevant reference population depends on the
(continued...)

state that in the absence of identical twins, it can be concluded to a reasonable scientific certainty that the evidence sample and the defendant sample came from the same person (*i.e.* from the same source). *See* L. M. Goos et al., *The Influence of Probabilistic Statements on the Evaluation of the Significance of a DNA Match*, 35 Can. Soc'y Forensic Sci. 77, 81 (2002). Source attribution would fulfill the need to give meaning to the term "match." Source attribution would inform the jury that the matching patterns are as unique as the Mona Lisa, and not as common as a picture with two eyes or even a four-leaf clover.[10]

The first report of the National Research Council unambiguously presented accompanying statistical testimony as necessary and emphasized the inappropriateness of testifying to the uniqueness of the genotype. The National Research Council recognized the potential for unique identification, but noted that the typing systems employed at that time

---

[9](...continued)
context of the case. Thus, the expert should calculate the probability that another person within the relevant population of potential sources of the DNA sample would share the DNA profile. The relevant population typically will not be the entire world population. For that reason, the expert attributes the source of the sample, rather than claiming that the defendant's DNA profile is "unique." *See* Bruce Budowle et al., *Source Attribution of a Forensic DNA Profile*, 2 Forensic Sci. Comm. No. 3 (July 2000), *at* http://www.fbi.gov/hq/lab/fsc/backissu/july2000/source.htm; DNA Advisory Board, *Statistical and Population Genetics Issues Affecting the Evaluation of the Frequency of Occurrence of DNA Profiles Calculated From Pertinent Population Database(s)*, 2 Forensic Sci. Comm. No. 3 (July 2000), *at* http://www.fbi.gov/hq/lab/fsc/backissu/july2000/dnastat.htm.

[10]*See Armstead*, 342 Md. at 78, 673 A.2d at 241 (quoting *United States v. Yee*, 134 F.R.D. 161, 181 (N.D. Ohio 1991) as stating that "[w]ithout the probability assessment, the jury does not know [whether the matching] patterns are as common as pictures with two eyes, or as unique as the Mona Lisa").

did not examine enough loci. The report stated as follows:

> "Can DNA typing uniquely identify the source of a sample? Because any two human genomes differ at about 3 million sites, no two persons (barring identical twins) have the same DNA sequence. Unique identification with DNA typing is therefore possible provided that enough sites of variation are examined.
>
> "However, the DNA typing systems used today examine only a few sites of variation and have only limited resolution for measuring the variability at each site."

Committee on DNA Forensic Science, National Research Council, *DNA Technology in Forensic Science* 74 (1992) [hereinafter "NRC I"]. The report then concluded that "[t]o say that two patterns match, without providing any scientifically valid estimate (or, at least, an upper bound) of the frequency with which such matches might occur by chance, is meaningless." *Id*. As a consequence of its comments about uniqueness, the report stated that the current DNA methods did not permit experts to testify to uniqueness. The report stated as follows: "Regardless of the calculated frequency, an expert should — given . . . the relatively small number of loci used and the available population data — avoid assertions in court that a particular genotype is unique in the population." NRC I at 92.

With the rapid scientific advances in DNA typing, the National Research Council presented an updated view of uniqueness in its 1996 report. Defining "uniqueness," the Committee stated that an evidentiary profile "might be said to be unique if it is so rare that it becomes unreasonable to suppose that a second person in the population might have the same profile." NRC II at 136. Addressing the comment of the 1992 report that, given the

small number of loci used, an expert should not testify to uniqueness, the 1996 report stated as follows:

> "Because more population data and loci already are available, and still more will be available soon, we are approaching the time when many scientists will wish to offer opinions about the source of incriminating DNA. . . .
>
> "We can say only that after one reaches some threshold, the point at which DNA testing is extensive enough to warrant an opinion as to the identity of the source becomes a matter of judgment. Does a profile frequency of the reciprocal of twice the Earth's population suffice? Ten times? One hundred times? There is no 'bright-line' standard in law or science that can pick out exactly how small the probability of the existence of a given profile in more than one member of a population must be before assertions of uniqueness are justified . . . . There might already be cases in which it is defensible for an expert to assert that, assuming that there has been no sample mishandling or laboratory error, the profile's probable uniqueness means that the two DNA samples come from the same person.
>
> "Opinion testimony about uniqueness would simplify the presentation of evidence by dispensing with specific estimates of population frequencies or probabilities. If the basis of an opinion were attacked on statistical grounds, however, or if frequency or probability estimates were admitted, this advantage would be lost. Nevertheless, because the difference between a vanishingly small probability and an opinion of uniqueness is so slight, courts that decide on a criterion for uniqueness and determine that the criterion has been met may choose to allow the latter along with, or instead of, the former, when the scientific findings support such testimony."

Id. at 194-95.

The National Research Council's conclusions make clear that once profile frequency reaches a certain level of infinitesimalness, there is no scientific basis for requiring statistical

testimony to accompany match testimony. The 1996 report accepted the concern about scientific justifiability articulated in the 1992 report and adopted as a rationale in *Armstead*; the 1996 report stated that "it would not be scientifically justifiable to speak of a match as proof of identity in the absence of underlying data that permit some reasonable estimate of how rare the matching characteristics actually are." NRC II at 192. It concluded, however, that once a profile may be considered unique, it is scientifically justifiable to testify to a match without accompanying statistics. *Id*. (stating that "[o]nce science has established that a methodology has some individualizing power, the legal system must determine whether and how best to import that technology into the trial process"). Additionally, the National Research Council concluded that at the point in which the profile is considered unique, source attribution would be an appropriate means to explain a match to the jury. *Id.* at 195; *see also* Bruce Budowle et al., *Source Attribution of a Forensic DNA Profile*, 2 Forensic Sci. Comm. No. 3 (July 2000), *at* http://www.fbi.gov/hq/lab/fsc/backissu/july2000/source.htm (concluding that in many forensic cases the random match probabilities are so small that source attribution may be appropriate); DJ Balding, *When Can a DNA Profile be Regarded as Unique?*, 39 Sci. & Justice 257, 260 (1999) (discussing the appropriateness of source attribution, but raising concerns of preempting the jurors' assessment of non-scientific evidence). As the excerpt from the NRC II report indicates, there appears to be wide agreement that defining "uniqueness" is not a statistical task; rather courts or legislatures can determine under what circumstances and with less than what statistical probability a profile

can be considered "unique." *See* NRC II at 137, 194; James F. Crow, DNA Forensics: Past, Present, and Future, Address at the Tenth International Symposium on Human Identification (1999) (*available at* http://www.promega.com/geneticidproc/ussymp10proc/content/01crow.pdf); B.S. Weir, Are DNA Profiles Unique?, Presentation to the Ninth International Symposium on Human Identification (1998) (*available at* http://www.promega.com/geneticidproc/ussymp9proc/content/25.pdf).

The 1996 National Research Council report convinced the Washington Supreme Court to repudiate in dramatic fashion its holding that an expert could not testify to uniqueness. In *State v. Cauthron*, 846 P.2d 502 (Wash. 1993) (en banc), experts testified that the DNA sample from the victims matched the defendant's DNA profile and that they had no doubt that the defendant was the source of the samples. Relying in large part on the 1992 National Research Council report, the Washington Supreme Court held that the trial court erred in permitting the experts to testify to uniqueness and to testify of a match without accompanying statistics. *Id*. at 515-16.

In *State v. Buckner*, 890 P.2d 460 (Wash. 1995) (en banc) (per curiam), an expert testified that the DNA evidence taken from the victim and the defendant matched, that the random match probability among people of European descent was one in 19.25 billion, and that the profile was unique. The court reversed, holding that the expert's testimony of uniqueness violated *Cauthron*'s holding. *Id*. at 462.

Following the release of the 1996 National Resource Council report, the court

reconsidered its decision. In *State v. Buckner*, 941 P.2d 667 (Wash. 1997) (en banc), a unanimous court repudiated its previous opinion. The court stated as follows:

> "The original opinion in this case also disapproved testimony in terms of statistical probabilities which implies or states that defendant is uniquely identified as the person in the human population who left the forensic sample. In 1993, this court accepted the proposition that an absolute identification of an individual could be made based upon DNA analysis provided that the technology exists to do so, because, except for identical twins, each individual's DNA is unique. *State v. Cauthron,* 120 Wash.2d 879, 900, 846 P.2d 502 (1993). At the time *Cauthron* was decided, we understood that this stage of technology would exist only when the entire DNA molecule could be compared to another entire DNA molecule. *Id.* It is now apparent that is not the case, as explained in the newest report of the National Research Council's Committee on DNA Forensic Science. *That report . . . states: 'The match probability computed in forensic analysis refers to a particular evidentiary profile. That profile might be said to be unique if it is so rare that it becomes unreasonable to suppose that a second person in the population might have the same profile*.' National Research Council, Commission on DNA Forensic Science: *The Evaluation of Forensic DNA Evidence* 136 (1996).
>
> "Thus, we now conclude there should be no bar to an expert giving his or her expert opinion that, based upon an exceedingly small probability of a defendant's DNA profile matching that of another in a random human population, the profile is unique. As in the case of all expert testimony, the opposing side will be able to challenge the expert's opinion and present its own experts."

Id. at 667-68 (emphasis added); *see also Burmingham v. State*, 27 S.W.3d 351, 356-57 (Ark. 2000) (holding that the trial court did not err in permitting an expert to testify that the defendant was the source of the DNA evidence taken from the victim, because the expert

had testified that the DNA evidence was analyzed at fifteen loci and that the random match probability was one in one trillion).

Similarly, following the NRC II report, the FBI adopted a policy that its expert witnesses may testify to a match without citing statistics, when the probability of a match is less than one in 260 billion. Julian Adams, *Nuclear and Mitochondrial DNA in the Courtroom*, 13 J.L. & Pol'y 69, 84-85 (2005); Paul Recer, *New DNA Technique Can't Miss, FBI Says*, Austin American-Statesman, Nov. 13, 1997, at A17.

We conclude that there exist methods of DNA analysis employing certain markers that, when tested along a minimum number of loci, yield DNA profiles with an astonishingly small random match probability. When the random match probability is sufficiently minuscule, the DNA profile may be deemed unique. In such circumstances, testimony of a match is admissible without accompanying contextual statistics.[11] In place of the statistics,

---

[11]Under Md. Rule 5-702, the trial court must determine that the expert's testimony "will assist the trier of fact to understand the evidence or to determine a fact in issue." The trial court should determine whether the witness is qualified, the appropriateness of the expert's testimony, and "whether a sufficient factual basis exists to support the expert testimony." Md. Rule 5-702. Testimony describing the methods employed in examining the DNA samples and calculating the match probabilities can lay the foundation for the trial court to determine that a sufficient factual basis exists for the DNA expert to testify to the source of the DNA evidence. Testimony of the probability calculations is not a necessary foundation to the expert's source attribution testimony. *See* Md. Rule 5-703(a). Md. Rule 5-703(a) states as follows:

> "**In general.** The facts or data in the particular case upon which an expert bases an opinion or inference may be those perceived by or made known to the expert at or before the hearing. If of a type reasonably relied upon by experts in the particular field

(continued...)

the expert may inform the jury of the meaning of the match by identifying the person whose profile matched the profile of the DNA evidence as the source of that evidence; *i.e.* the expert may testify that in the absence of identical twins, it can be concluded to a reasonable scientific certainty that the evidence sample and the defendant sample came from the same person. *See* L. M. Goos et al., *supra*, at 81.[12]

---

[11](...continued)

> in forming opinions or inferences upon the subject, the facts or data need not be admissible in evidence."

[12]Under certain circumstances, the expert's caveat should take into account the higher random match probability for close relatives, not only identical twins. *See* L. M. Goos et al., *The Influence of Probabilistic Statements on the Evaluation of the Significance of a DNA Match*, 35 Can. Soc'y Forensic Sci. 77, 81 (2002). The FBI's DNA Advisory Board recommends the following approach for considering the impact of close relatives on source attribution:

> "[T]he possibility of a close relative (typically a brother) of the accused being in the pool of potential contributors of crime scene evidence should be considered in case-specific context. It is not appropriate to proffer that a close relative is a potential contributor of the evidence when there are no facts in evidence to suggest this instance is relevant. However, if a relative had access to a crime scene and there is reason to believe he/she could have been a contributor of the evidence, then the best action to take is to obtain a reference sample from the relative. . . . Typing . . . will resolve the question of whether or not the relative carries the same DNA profile as the accused.
>
> "When a legitimate suspected relative cannot be typed, a probability statement can be provided. Given the accused DNA profile, the conditional probability that the relative has the same DNA profile can be calculated."

DNA Advisory Board, *supra*.

(continued...)

A defendant is not without recourse when the State's expert identifies the defendant as the source of the DNA evidence. The defendant has the opportunity, and the right, to challenge the expert's conclusion in cross-examination. *See* Md. Rule 5-703(c) (stating that "[t]his Rule does not limit the right of an opposing party to cross-examine an expert witness or to test the basis of the expert's opinion or inference"). Md. Code (1973, 2002 Repl. Vol., 2004 Cum. Supp.), § 10-915 of the Courts and Judicial Proceedings Article provides additional means for the defendant to challenge the expert's testimony that the defendant was the source of the DNA evidence. Under § 10-915(c), the party seeking to introduce the DNA evidence must, upon written request at least thirty days prior to the proceeding, provide the other party with a "statement setting forth the genotype data and the profile frequencies for the databases utilized." § 10-915(c)(2)(v). The defendant may cross-examine the expert on the statistics and the expert's conclusions based on those statistics. Additionally, the defendant can challenge the weight of the DNA evidence, by, for example, questioning the expert about laboratory errors and contamination. *See* § 10-915(c)(2)(i) and (ii) (requiring the party introducing DNA profile evidence, upon timely written request, to produce laboratory results and notes). Thus, in *Armstead*, we noted as follows:

---

[12](...continued)

When sufficient loci are analyzed, an expert can identify the defendant as the source of the DNA evidence, even taking into account related individuals. *See* Goos et al., *supra*, at 81 (stating that the "magnitude of random match probabilities commonly reported is approaching the point where the likelihood that two individuals would have the same type is remote, even if they are related").

> "By providing the opponent with detailed, case-specific information on the DNA analysis and giving the opponent more time to evaluate the information before trial, the amendments also indicate the Legislature's intent to establish the general reliability and admissibility of the evidence, permitting the opponent to attack the weight of the evidence through cross-examination."

342 Md. at 60, 673 A.2d at 231.

The method and marker employed in the instant case, PCR/STR along the thirteen loci recommended by the FBI and the sex-typing marker, produce "exceedingly small" random match probabilities. Budowle et al., *supra*. The thirteen STR loci selected by the FBI yield an average match probability of one in 180 trillion. James Crow, Remarks at the Meeting of the National Commission on the Future of DNA Evidence (May 7, 1999) (transcript *available at* http://www.ojp.usdoj.gov/nij/dnamtgtrans5/trans-h.html); David H. Kaye, *Bioethics, Bench, and Bar: Selected Arguments in Landry v. Attorney General*, 40 Jurimetrics J. 193, 199 n.38 (2000) (quoting Crow); *Belken*, 633 N.W.2d at 799 n.3 (citing Kaye); *see also Harvey v. Horan*, 285 F.3d 298, 305 (4th Cir. 2002) (denying rehearing and rehearing en banc) (discussing the low statistical probabilities for STR analysis along thirteen loci and the consequent ability "to confirm guilt or innocence beyond any question whatsoever"); Budowle et al., *supra* (stating that "[t]he average random match probability for unrelated individuals for the 13 STR loci is less than one in a trillion, even in populations with reduced genetic variability"). When thirteen STR loci are analyzed, the random match probability for related individuals, even including siblings, is sufficiently low as to be

characterized as unique.[13] *See* Budowle, *supra* (citing probabilities for thirteen STR loci as one in 40,000 among full siblings and one in a billion for other relatives and concluding that "source attribution should be possible routinely for scenarios where relatives of the suspect cannot be typed with typing results of the suspect from 11-13 of the CODIS STR loci"); Balding, *supra* at 259-60 (discussing the influence of brothers on uniqueness). We hold that a PCR/STR test along thirteen loci produces a sufficiently minuscule random match probability to make expert testimony of uniqueness admissible.

In the instant case, the State's witness testified, without citing any statistics, that the DNA sample taken from the victim's rectum matched the DNA sample provided by Young to the police. The State sought repeatedly to elicit testimony from Rupert Page that Young was the source of the DNA sample taken from the victim. While the Circuit Court sustained Young's objections to this questioning, the Circuit Court admitted Page's report. Page's report stated that he conducted a PCR/STR test to examine the anal swab from the victim and the oral swab from Young. The report contained a list of the thirteen STR loci and gender marker typed. Finally, in the report, Page concluded to a "reasonable degree of scientific certainty (in the absence of an identical twin)" that Young was the source of the DNA obtained from the boy. In other words, Page's testimony and his report (1) informed the Circuit Court that he had employed a DNA analysis technique that results in infinitesimal probabilities; (2) announced to the jury his conclusion that the DNA samples "matched"; and

[13]There is no indication that Young had a relative who could have been the source of the DNA evidence.

(2) explained to the jury that by "match" he meant that Young was the source of the DNA evidence. We hold that the Circuit Court did not err in admitting the testimony and the report, and, accordingly, we affirm the decision of the Court of Special Appeals.

JUDGMENT OF THE COURT OF SPECIAL APPEALS AFFIRMED. COSTS IN THIS COURT AND IN THE COURT OF SPECIAL APPEALS TO BE PAID BY PETITIONER.