DISTRICT OF COLUMBIA COURT OF APPEALS

No. 03-CF-853

ORLANDO ROBERTS, APPELLANT,

v.

UNITED STATES, APPELLEE.

Appeal from the Superior Court of the
District of Columbia
(F-771-01)

(Hon. Robert I. Richter, Trial Judge)

(Argued November 28, 2006 Decided February 15, 2007)

Alice Wang, Public Defender Service, with whom *James Klein* and *Andrea Roth*, Public Defender Service, were on the briefs, for appellant.

Valinda Jones, with whom *Kenneth L. Wainstein*, United States Attorney at the time the original briefs were filed,[*] and *Roy W. McLeese III*, Assistant United States Attorney, were on the brief, for appellee.

Before FARRELL, RUIZ, and BLACKBURNE-RIGSBY, *Associate Judges*.

FARRELL, *Associate Judge*: A jury found appellant guilty of first-degree sexual abuse, crediting the testimony of thirteen-year-old K.W. that in January 2001 he drove her to the Stadium Armory parking lot in Southeast Washington and forced her to have sexual intercourse with him. (Though unrelated to her, appellant lived in the same home as K.W.). Some weeks later, K.W. told her mother of the assault after the mother saw open sores on the child's genitals that were later determined to be herpes. Medical testimony allowed the

[*] Jeffrey A. Taylor, who succeeded Mr. Wainstein as United States Attorney, was on the supplemental brief filed by appellee.

jury to infer that the onset of the herpes coincided with when K.W. said she had been assaulted by appellant, who had the same form of herpes the child developed.

The issues in this appeal, however, arise from evidence of a DNA match which the FBI found after examining semen removed from panties K.W. had worn on the day of the assault and comparing it to the known DNA profile of appellant. Dr. Frank Samuel Baechtel, a DNA expert from the FBI forensic laboratory, testified that appellant's DNA profile and K.W.'s profile were both consistent with DNA found in the recovered semen. He further opined, using the FBI's highly conservative estimate for cases involving so-called mixed samples, that the statistical chance of finding a person at random who could have been a contributor to the DNA on the panties was no greater than 1 in 410,000 among four major population groups in the United States.

On appeal, appellant makes a variety of challenges to the admissibility of Dr. Baechtel's opinion, arguing particularly (a) that the expert could not properly offer a match-probability statistic without also providing the jury with an "error rate," that is, a "false positive probability to represent the chance of a false match caused by laboratory error" (Br. for Appellant at 21); and (b) that the FBI's method of interpreting mixed samples, which contain DNA of two or more persons, "relies on unwarranted assumptions about the number of contributors and their individual DNA profiles" (Reply Br. for Appellant at 7). We hold that, while appellant could properly explore these matters on cross-examination of Dr. Baechtel or through expert testimony of his own, in order to attack the weight of the DNA evidence, they did not render inadmissible Dr. Baechtel's opinion either that appellant could not be excluded as a contributor to the semen found on K.W.'s clothing or

as to the probability of a random match.

Appellant further argues that the judge erroneously barred him from arguing to the jury an exculpatory interpretation of the DNA evidence that could reasonably be inferred from Dr. Baechtel's own testimony. Although we agree that FBI protocols furnished a basis for appellant to argue that genetic material found at a locus of one of the tested samples was exculpatory, any prejudice he suffered from the preclusion of that argument is insufficient to justify reversal. Finally, appellant contends that the admission of out-of-court statements of FBI forensic scientists through Dr. Baechtel's testimony violated his constitutional right to confront witnesses. Under a recent decision of ours, we agree that appellant's Sixth Amendment right was violated; but because he did not object to this evidence on confrontation grounds, we apply plain error analysis and again find no basis for reversal.

I.

To put appellant's arguments concerning the DNA evidence in context, some background regarding how the FBI derived and interpreted the DNA samples and made its match estimate is necessary.

Methods of Analysis and Statistical Methods

The FBI laboratory used two complementary scientific techniques to identify the

DNA found in this case.[1] The first technique, called polymerase chain reaction (PCR), takes a targeted segment of a DNA sample and duplicates it over and over again to create enough DNA material for analysis. The second technique involves determining the specific genetic variations, or "alleles," in the DNA samples at specific sites ("loci") along the DNA thread. The particular variations examined in this case are called short tandem repeats, or "STRs." They were examined at thirteen loci which have been adopted as a national standard for use in the Combined DNA Identification System (CODIS) established by Congress in 1994. The PCR-based analysis using the thirteen STR loci has been explained by the Supreme Court of New Hampshire as follows:

> At each locus, an individual's genetic code contains a combination of chemical markers organized into a pattern. These chemical patterns repeat themselves and these repeats can be chemically cut apart from one another. At any particular chromosomal locus, an individual will have a characteristic inherited from each of his or her parents, known as an allele. Further, at any given locus, a person will have DNA with a specific number of repeats of these alleles from each parent. Thus, for example, a person's PCR-based STR DNA profile for a particular DNA locus could contain a ten-repeat allele from his or her mother and a twelve-repeat allele from his or her father. STR testing involves the examination of short repeats and distinguishes between individuals by comparing the number of repeats at certain loci.

State v. Whittey, 821 A.2d 1086, 1093 (N.H. 2003).

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[1] DNA, which stands for deoxyribonucleic acid, is genetic material in the form of microscopic chromosomes located in the nucleus of human body cells. A chromosome is a very thin thread of DNA surrounded by other materials; the DNA thread is double, consisting of two strands — which may be separated for purposes of analysis — twisted to form a helix or twisted ladder. *See* National Research Council, *The Evaluation of Forensic DNA Evidence* (1996) (NRC II), at 12-13.

The FBI conducted the PCR/STR analysis using two commercial kits called Profiler Plus (Profiler) and Cofiler that together can identify all thirteen CODIS loci. Profiler and Cofiler are processed by an automated system, and the results of the process appear in the form of an electropherogram, or graph that displays a series of different-colored peaks of different heights.[2] A DNA analyst, or examiner, interprets the data displayed on the electropherogram to determine the DNA profile, *i.e.*, the alleles seen at all the examined loci. Once the DNA profiles from the evidence and known samples are determined, the DNA profile from the evidence is compared to the DNA profiles from known individuals to see if any of those individuals can be excluded as possible contributors to the evidence (or "questioned") DNA. A person can be excluded as a possible source if he has a DNA allele at a locus that is not found among the alleles at the same locus in the evidence sample. But if the alleles in the known sample are consistent with the alleles in the evidence, there is a match, in the sense that "the donor of the known sample cannot be conclusively eliminated as the source of the questioned sample." *Id*. at 1094. The analyst then calculates how frequently the allelic profile found in the evidence would be expected to be seen in a defined population, as a benchmark for the significance of that match. "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." *United States v. Trala*, 162 F. Supp. 2d 336, 343 (D. Del. 2001), *aff'd*, 386 F.3d 536 (3d Cir. 2004), *vacated on other grounds*, 126 S. Ct. 1078 (2006).

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[2] If a peak represents an allele, the type of allele — the number of short-tandem-repeat (STR) patterns in that allele — is indicated by the peak's location on the horizontal axis of the electropherogram within each locus. The number of STRs in the allele determines its designation; that is, a "24" allele means that 24 repeats have been observed.

Using databases the FBI has generated to approximate the actual frequencies of the alleles in various population groups, the examiner ordinarily calculates the probability of a random match by multiplying the frequency of each of the alleles in the profile (while correcting for limitations in current genetic knowledge about those frequencies).[3] However, for a mixed DNA profile, in which the number of alleles at a locus indicates the presence of two or more contributors and there is no way to distinguish among the contributors, the FBI essentially adds the frequencies of all possible combinations of alleles observed at the locus to obtain a combined frequency for that locus. Then the combined frequencies of the alleles at all examined loci are multiplied together to obtain the match statistic for the entire DNA profile. This statistical formula does not require identification of individual contributors and thus produces a ratio much more conservative than if the frequency of alleles were determined for a single-source profile.[4]

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[3] "In other words, the statistical frequency of the DNA profile is calculated using . . . the product rule," *Trala*, 162 F. Supp. 2d at 343, which holds that "if two events are independent of each other, the probabilities of each event occurring can be multiplied, and the resulting product is the probability of both events occurring." *State v. Link*, 25 S.W.3d 136, 144 (Mo. 2000).

[4] So, for example, a 1999 study of the frequency of alleles found at the thirteen CODIS loci in several major population groups concluded, based on the probability formula for single-source samples, that "[t]he most common profile frequency derived from the 13 core STR loci is less than 1 in 10 billion in all [the studied] populations, and usually the estimates are substantially more rare." Bruce Bodowle, *et al.*, "*Population Data on the Thirteen CODIS Core Short Tandem Repeat Loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians,*" 44 (6) J. FORENSIC SCI. 1277, 1284 (1999) (R. 3671-3680). *See also* U.S. Dep't of Just., Off. of the Inspector General, *The FBI DNA Laboratory: A Review of Protocol and Practice Vulnerabilities* (May 2004), at 6 ("Scientists have determined that, in general, when DNA profiles consist of the alleles present at [the thirteen CODIS] locations the probability that two unrelated individuals will have the same DNA profile purely by chance is less than 1 in 200 billion."). In comparison, using the formula for mixed samples, the most common profile frequency derived in this case was 1 in 410,000 — a far more common frequency.

The DNA Samples in this Case

Samples were cut from several places in the crotch of the underwear worn by the child, K.W., at the time of the assault. Semen was extracted from some of those cuttings, and the semen samples were processed to separate sperm from other substances. Because too little DNA was extracted from the resultant three sperm samples, they were combined before being amplified and run through the PCR/STR automated typing instrument, and were labeled Q1-3/4/6M. The corresponding non-sperm samples (Q1-3F, Q1-4F, and Q1-6F) were processed individually. The four resulting DNA samples were first analyzed using the Profiler kit, which tests nine of the thirteen CODIS loci, plus the amelogenin site, which tests the sex of the DNA contributor(s).

The results of the Profiler test showed that all four samples were "unresolvable" mixed samples, meaning that while each contained alleles from more than one contributor, the alleles could not be reliably divided into individual pairs corresponding to each contributor's unique DNA profile.[5] Samples Q1-3F and Q1-3/4/6M contained male and female DNA; the other two contained only female DNA. Only the Q1-3F sample was tested at additional loci using Cofiler, because the Q1-3/4/6M sample did not have enough

[5] In other words, while it could be determined that there were four alleles at each examined locus, it could not reliably be said which two of the four alleles belonged to which contributor. *See*, *e.g.*, President's DNA Initiative, *available at* http://www.dna.gov/glossary/#I (last visited Jan. 18, 2007) ("irresolvable mixture" is "[a] DNA profile where multiple individuals have contributed biological material and no profile is more or less apparent than any other and the developed alleles cannot be isolated to a single source").

DNA left after the Profiler test to test using Cofiler. The Cofiler test identified an additional four loci in the Q1-3F sample.

According to Dr. Baechtel, all of appellant's and K.W.'s alleles could be seen in the alleles found at the thirteen loci in the Q1-3F sample. Thus, he concluded that both appellant and K.W. were possible contributors to the mixed DNA in that sample. The alleles found at the nine Profiler loci examined in the Q1-3/4/6M sample also were compared to the alleles found at the same nine loci in appellant's and K.W.'s known DNA samples. All of the alleles possessed by appellant and K.W. were consistent with the alleles present in the Q1-3/4/6M sample, so Dr. Baechtel also concluded that appellant and K.W. were possible contributors to that mixed sample.

After he concluded that neither appellant nor K.W. could be excluded as possible contributors to those samples, Dr. Baechtel calculated a match probability statistic that estimated (in his words) "how likely it is to go out into the general population and find someone who has a DNA profile such that they could have contributed to that [DNA evidence sample]." The statistic he reported was based on sample Q1-3F, which was the most informative because it contained thirteen loci as opposed to only nine loci in the Q1-3/4/6M sample. The resulting estimates of the probability of a random match were approximately 1 in 410,000 African-Americans; 1 in 5.5 million Caucasians; 1 in 3.5 million for Southeastern Hispanics; and 1 in 8.5 million for Southwestern Hispanics.

II.

Appellant questions the admissibility of the DNA evidence on essentially two grounds. His first challenge is to the failure of the FBI's statistical formula for determining match probability to take into account "false positive rates." He then questions the scientific reliability of the FBI's method of interpreting samples of mixed DNA. We treat these issues *seriatim* after summarizing the relevant legal principles.

Although the decision whether to admit expert testimony is ordinarily reviewed for abuse of discretion, "[w]here the question of the general acceptance of a new scientific technique is raised," this court reviews *de novo* the trial court's determination whether the techniques from which the evidence is derived have gained general acceptance. *United States v. Porter,* 618 A.2d 629, 635 (D.C. 1992) (citing *Jones v. United States*, 548 A.2d 35, 40 (D.C. 1988)). In conducting that review, the court may consider "not only expert evidence of record, but also judicial opinions in other jurisdictions, as well as pertinent legal and scientific commentaries." *Id*. The court evaluates the admissibility of novel scientific evidence by the standard first announced in *Frye v. United States*, 54 App. D.C. 46, 293 F. 1013 (1923): where expert testimony is not based on a "well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs." *Id*. at 47, 293 F.2d at 1014; *see also Bahura v. S.E.W. Investors*, 754 A.2d 928, 943 n.15 (D.C. 2000) (affirming that *Frye* test remains in effect in the District of Columbia). "[U]nder *Frye*, the proponent of a new technology must demonstrate by a preponderance of the evidence that this technology has been generally accepted in the

relevant scientific community." *Porter*, 618 A.2d at 633. "The issue is consensus versus controversy over a particular technique, not its validity," *Jones*, 548 A.2d at 42; unanimity among scientists is not required. *Porter*, 618 A.2d at 634; *see State v. Copeland*, 922 P.2d 1304, 1319 (Wash. 1996).

A.

Appellant argues that because the FBI "omit[s] from its statistical analysis any estimate of the chance of a false match caused by laboratory error," scientists significant in number and expertise regard that method of analysis as unreliable and misleading (Reply Br. for Appellant at 2). In his view, to be admissible Dr. Baechtel's estimate of the chance of a coincidental match had to factor in, or at least be accompanied by, an acknowledgment that the FBI's estimate of random match probability "typically overstates the significance of a DNA match by several orders of magnitude, as the chance of a false match by laboratory error typically ranges from 1 in 100 to 1 in 1,000" (*id*. at 6). This argument is not based on any assertion of laboratory error committed in this case ("Mr. Roberts does not contend that the . . . DNA evidence is inadmissible . . . because the FBI's methods and procedures were not 'performed correctly' in this case," *id*. at 3); rather, it relies on "industry-wide error rate data," including published results of double-blind proficiency testing, to argue that "some estimate of the false positive probability is . . . necessary for an accurate and reliable statistical evaluation of a DNA match" (Br. for Appellant at 26-27; emphasis omitted).

Viewing this as a claim of inadmissibility rather than of a defendant's right to bring the frequency (or not) of laboratory error leading to false matches to the attention of a jury,

we reject it. The assertion that a "general error rate for . . . laboratories over time" should be "estimated and combined with the random match probability" was repudiated by the National Research Council (NRC) of the National Academy of Sciences in its authoritative 1996 report concerning forensic use of DNA Evidence.[6] Relying substantially on the scientific consensus reflected in that report, courts have since refused to exclude DNA evidence because the testing laboratory did not calculate and report an error rate, or combine an error rate with its match statistics. Illustrative is *People v. Reeves*, 109 Cal. Rptr. 2d 728 (Cal. App. 2001), where the court relied on "the considered conclusions reached by the NRC, a body composed of . . . a distinguished cross-section of the scientific community," to conclude that "a probability statistic derived when a 'laboratory error rate' is combined with a DNA profile's random match probability . . . is not sanctioned by the weight of scientific opinion," at least as a condition of admitting DNA profile evidence. *Id.* at 752-53 (internal quotation marks omitted); *see also id*. at 753 ("[O]ur decision does not preclude cross-examination on the subject of laboratory error, or the possibility that such errors were committed in a particular case."). The court in *United States v. Trala, supra*, likewise relied on NRC II's "belie[f] that a calculation that combines error rates with match probabilities is inappropriate," to conclude that disputes based on rates of alleged laboratory error present "an issue of weight and not an issue of admissibility." 162 F. Supp. 2d at 351.[7] Appellant cites no case in which DNA evidence has been excluded because an

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[6] The NRC twice convened special committees of molecular biologists, population geneticists, and other experts to make recommendations concerning the use of DNA technology for forensic purposes. The first report was issued in 1992. *See* National Research Council, *DNA Technology in Forensic Science* (1992) (NRC I). The second report, issued in 1996, updated the first in light of rapid advances in the field of DNA analysis. *See* NRC II, *supra* note 1.

[7] *See also United States v. Ewell*, 252 F. Supp. 2d 104, 113-14 (D.N.J. 2003); *United* (continued...)

error rate — either particular to a laboratory or extrapolated from industry-wide performance — was not acknowledged by the government along with its random probability match.

The NRC II report gave several reasons for rejecting such a requirement. "The question to be decided," it said,

> is not the general error rate for a laboratory or laboratories over time, but rather whether the laboratory doing DNA testing in this particular case made a critical error. The risk of error in any particular case depends on many variables (such as number of samples, redundancy in testing and analyst proficiency), and there is no simple equation to translate these variables into the probability that a reported match is spurious.

NRC II at 86; reprinted at Record (R.) 3154-3155. Moreover, beyond the fact that "[t]o establish [an error] rate accurately, it would be necessary for each laboratory to undergo many thousands of [proficiency test] trials," the "pooling of [such] test results across laboratories . . . could penalize the better laboratories," for "multiple errors on a single test by one laboratory could substantially affect the overall estimated false-match error rate" (*id*. at 86; R. 3155). Then, too, estimating error rates "is almost certain to yield wrong values, because "[w]hen errors are discovered, they are investigated . . . and [a] laboratory is not likely to make the same error again, so the error probability is correspondingly reduced" (*id*.). Ultimately, NRC II concluded, while "[n]o amount of attention to detail, auditing, and proficiency testing can completely eliminate the risk of error[, t]here is a better

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[7](...continued)
States v. Shea, 957 F. Supp. 331, 340 (D.N.H. 1997), *aff'd*, 159 F.3d 37 (1st Cir. 1998); *Commonwealth v. Fowler*, 685 N.E.2d 746, 748, 752-53 (Mass. 1997).

approach" than to resort to an illusory general error rate: "the best protection an innocent suspect has from a false match is an independent test, and that opportunity should be made available if at all possible" (*id*. at 24; R. 3125).

Appellant argues that even if the NRC rejected combining random match probability and laboratory error rate "into a single figure," to estimate the statistical significance of a DNA match "without any consideration of the chance of a false match caused by laboratory error" is inaccurate and misleading (Reply Br. for Appellant at 5). But, whether combined in a single ratio or reported separately, NRC II was deeply skeptical that a "general error rate" based on the performance of different laboratories operating at different times (*i.e.*, after past errors have been detected and corrected for) would be reliable or meaningful. Moreover, appellant's jury was not denied "any consideration" of the risk of false positive matches occurring: Dr. Baechtel was cross-examined fully about the possibility and historical evidence of such errors, and nothing prevented appellant from presenting expert testimony — he did not — about the incidence of laboratory error industry-wide and how that could affect the random match estimates by the FBI or other laboratories. Finally, appellant could also have obtained independent testing of the DNA samples at issue to establish the fact or probability of a false match, but did not do so. In sum, the *Frye* standards of admissibility did not require, as a condition of admitting Dr. Baechtel's estimate of the probability that someone else had provided the DNA matching appellant's profile, testimony by the government about laboratory error rates not shown to have any relation to the FBI's testing practices in particular, or to the testing done in this case.

B.

Appellant argues that scientists significant in number and expertise reject the FBI's method, as employed by Dr. Baechtel here, of interpreting mixed samples of DNA (*i.e.*, samples containing DNA from more than one contributor), "because it relies on unwarranted assumptions about the number of contributors and their individual DNA profiles" (Reply Br. for Appellant at 7). The argument has narrowed as this appeal has progressed. It began as a claim that there are no generally accepted methods for interpreting mixed-DNA samples, because there are no reliable methods for identifying the number of contributors, determining the individual genotypes (or profiles) of each contributor, or distinguishing between indications of a true DNA allele and indications of other by-products or "artifacts" of the PCR/STR testing process, such as "stutter."[8] Appellant cites no cases in which DNA evidence was found inadmissible under *Frye* (or a similar admissibility standard) for these reasons, and the government cites numerous decisions holding that application of the PCR/STR process to mixed samples either raises no issue of admissibility or has been shown to be generally accepted and reliable.[9] We

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[8] "An artifact is a result that does not come from the things one actually intends to test." *Whittey*, 821 A.2d at 1096. "Stutter" is "[a] minor band or peak [on the electropherogram generally] appearing one [STR] repeat unit smaller than a primary STR allele." President's DNA Initiative, *supra* note 5, http://www.dna.gov/glossary/#S ("Stutter").

[9] *See, e.g., Whittey*, 821 A.2d at 1096 ("mixed samples . . . are one of the most common things that scientists encounter in forensic science . . . [and] mixture interpretation has been examined extensively and is not a new concept"; holding that any difficulties in interpreting mixed samples do not undermine general acceptance of the PCR/STR method as applied to mixed samples, and thus are matters of weight not admissibility); *People v. Smith*, 132 Cal. Rptr. 2d 230, 249-50 (Ct. App. 2003) (application of generally accepted PCR/STR method to mixed samples is not a "novel" scientific technique under *Frye*; even if *Frye* applied, use of PCR/STR method to analyze and interpret mixed samples is generally accepted, and trial court's findings, "which were based on extensive expert testimony, and [an] exhaustive (continued...)

agree with that conclusion; the various articles from science journals cited by appellant do not persuade us that any existing disagreement about the general reliability of interpreting mixed samples presents an issue of admissibility,[10] rather than one on which he was free to cross-examine Dr. Baechtel or present contrary expert testimony to the jury.

Appellant has since focused his argument more sharply on Dr. Baechtel's finding, with respect to one of the evidence samples, that a peak at the 27 position, see note 2 & accompanying text, *supra*, in one locus (the "FGA" locus) on the electropherogram represented stutter and not an allele. Appellant contends that Dr. Baechtel drew scientifically unacceptable inferences from things such as relative peak heights at the FGA locus and the number of peaks at other loci to conclude that there were only two contributors to the DNA at that locus, hence that the 27 peak — which did not match appellant's profile — was stutter and not an allele of a potentially third contributor. As a claim of inadmissibility, we reject this argument as well. To understand why, it is

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[9](...continued)
review of the [scientific] literature and case law," supported conclusion that laboratory's methods for analyzing and interpreting mixed DNA samples are generally accepted, so that any remaining dispute about results goes to weight not admissibility); *People v. Henderson*, 132 Cal. Rptr. 2d 255, 267-70 (Ct. App. 2003) (same); *Trala*, 162 F. Supp. 2d at 349 (rejecting claim that PCR/STR testing process contained complications that make interpretation of mixed-DNA samples unreliable; because FBI laboratory protocols control for effects of artifacts such as stutter, challenges to application of generally accepted PCR/STR method to mixed samples go to weight, not admissibility, under federal admissibility standards).

[10] As the government points out, four of the articles appellant cites reported the results of an ongoing series of "challenge" studies conducted by the National Institute of Standards and Technology (NIST), which tested the outer limits of a laboratory's ability to analyze and interpret test results from extremely difficult mixed samples. Despite the deliberately challenging nature of those studies, the NIST scientists concluded that the PCR/STR method produced reliable results when used on mixed samples, and that the mistakes detected involved the most complex mixed samples and were not likely to occur in real case work.

necessary to review Dr. Baechtel's testimony on the point more closely. We observe initially, however, that appellant does not explain why, even if Dr. Baechtel's analysis of one locus of one DNA sample was scientifically defective, that made his interpretation of the many other loci in the combined Q1-3/4/6M and Q1-3F samples, at all of which alleles consistent with appellant's profile were found, similarly flawed so as to be inadmissible.

As explained earlier, the Q1-3/4/6M sample from K.W.'s panties was tested at nine of the CODIS loci, and individual alleles corresponding to appellant's and K.W.'s alleles at the same loci were found at each of them.[11] At one of the nine loci — the FGA locus — the sample showed five peaks in the 20, 23, 24, 27 and 28 positions on the horizontal axis of the electropherogram. Appellant and K.W. both have a 24 allele at the FGA locus; appellant also has a 28 allele and K.W. has a 20 allele at that locus; and it is not disputed that the 23 peak was stutter. The dispute arose over the 27 peak at the FGA locus, which Dr. Baechtel interpreted to be stutter.

Before looking at the known profiles from appellant and K.W., and before interpreting the 27 peak, Dr. Baechtel inferred the number of contributors from the number and relative height of the peaks at the 20, 24, and 28 positions. In particular, the fact that the height of the 24 peak was approximately the sum of the heights of the 20 and 28 peaks convinced him that there were alleles from two contributors at the 24 position,[12] which

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[11] The Q1-3F sample, tested at all thirteen CODIS loci, was likewise seen to have matching alleles from appellant and K.W. at each location.

[12] As he explained, even if contributors share alleles, the number of contributors can be determined by examining relative peak heights: "speaking generally, if individuals share a DNA type [an allele] and they were equally contributing to the DNA mixture, then the (continued...)

meant that there were four alleles (20, 24, 24, 28) at the FGA locus before the 27 peak was interpreted. Because people have two alleles (one from each parent) at each locus, and there were already four alleles at the FGA locus, there were at least two contributors at that locus. Thus, any additional allele, such as a 27 allele, would have to come from a third contributor. To test the hypothesis that the 27 peak was an allele, Dr. Baechtel looked for evidence of a third contributor at all other loci in that sample, and at all the loci in the Q1-3F sample. Seeing no such evidence, he concluded that the 27 peak was not an allele, hence no indication of the presence of a third contributor.

Appellant challenges Dr. Baechtel's consideration of peak intensity, as measured by peak height (here at the 24 peak), as well as his seeking confirmation outside the disputed FGA locus, contending that scientists regard these as unreliable indicators of the number of contributors (Reply Br. for Appellant at 8). But the support furnished by the scientific studies appellant proffers falls short of establishing a sufficient expert controversy over Dr. Baechtel's procedure. *See State v. Marcus*, 683 A.2d 221, 231 (N.J. App. 1996) ("For scientific evidence to be admissible, we only require that the scientific technique or procedure be accepted as scientifically reliable, not that it produce results which are beyond all legitimate debate."). Taking the second objection first, it has been recognized that "interpret[ing] the electropherogram data from one locus by referring to test results from other loci . . . is . . . standard procedure in the field."[13] FBI protocols call for this

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[12](...continued)
height of that [allele] would be twice what it is for one of the [alleles] because there's two doses of it."

[13] *State v. Whittey*, New Hampshire Super. Ct., Order of May 22, 2001, at 19 (reprinted at R. 3095), *aff'd Whittey*, 821 A.2d at 1096.

examination of "all loci" in determining whether an aberrant peak is stutter or an allele,[14] and appellant cites no court decision disallowing or disapproving the FBI's practice in this regard. Dr. Baechtel explained that "a third contributor [at the FGA locus] would have contributed DNA types [or alleles] at other locations also . . . . [T]hey could share some types with the two individuals present, but they would also have types not the same as those individuals. There was no indication [elsewhere] of yet a third person contributing." Appellant has not shown that this step in distinguishing alleles from artifacts involves scientifically unaccepted reasoning.

Nor was Dr. Baechtel out of the scientific mainstream in considering peak heights as a measure of the number of contributors, in keeping with FBI practice.[15] Indeed, an authority relied on by appellant acknowledges that "severe . . . imbalance" at a peak may reflect shared alleles at that peak in the manner Dr. Baechtel described. *See* John Buckleton, *et al*., *Forensic DNA Evidence Interpretation*, at 232-33 (2005) ("From . . . validation experiments, it has become clear that where alleles were shared between two contributors, post-PCR, the area of the shared allele was approximately the sum of the two contributors."). Appellant maintains that the presence of two contributors sharing alleles at

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[14] *See* FBI Short Tandem Repeat Analysis Protocols §§ 10.4.2, 10.4.2.1 (2001) (reprinted at R. 3546); *see also* Dep't of Just., Forensic Science Commc'ns, 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)*, at 5 (February, 2000) (DAB Article) (reprinted at R. 3690) ("It may be difficult to be confident regarding the number of contributors in some complex mixtures of more than two individuals; however, the number of contributors often can be inferred by reviewing the data at all loci in a profile.").

[15] See DAB Article, *supra* note 14 ("Interpretation of DNA mixtures requires careful consideration of factors including . . . detectable alleles; variation of . . . peak . . . intensity; and the number of alleles").

the 24 peak could not reliably be inferred from adding the heights of adjoining peaks; at most scientists would agree, he states, that "*if two contributors shared the 24 allele*, then the heights of the unshared 20 and 28 peaks should add up to approximately the height of the 24 peak" (Supp. Br. for Appellant at 15; emphasis by appellant). But this elusive distinction is not made by nor apparent from the authorities appellant discusses.[16] Although appellant was free to present experts to the jury challenging Dr. Baechtel's inference from peak heights to the number of contributors, he has not shown that that methodology is rejected by the scientific community.

Finally, appellant argues that Dr. Baechtel was caught in an internal contradiction when, on the one hand, he determined the number of contributors at the FGA locus (*i.e.*, two) but then used a statistical calculus for "unresolvable" mixed samples which assumes that the number of contributors cannot be ascertained. We agree with the government that the contradiction is more apparent than real. Dr. Baechtel testified that, in the case of an unresolvable or "indistinguishable" mixed sample, the analyst cannot reliably decide which pair of alleles at a locus belongs to which of several contributors; the alleles, that is, cannot reliably be divided into individual pairs corresponding to each contributor's unique DNA profile. In such cases, the FBI uses the highly conservative method described earlier to estimate the probability of a random match, one that, among other things, requires "no

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[16] *See also*, *e.g.*, T.M. Clayton, *et al*., *Analysis and Interpretation of Mixed Forensic Stains Using DNA STR Profiling*, 91 FORENSIC SCI. INT'L 61 (1998) (within a single locus "allele peak areas are additive for any shared alleles . . . [h]ence, at any locus where there is a single shared allele, if the two DNA templates were admixed in a 1:1 ratio, then the peak area of the shared allele should be about twice those of the unshared alleles"). Only a strained reading of this and similar texts enables appellant to argue that the "additive" height of a peak in relation to its adjoining ones says nothing about *whether* alleles are shared at that peak and by how many contributors.

assumptions . . . about the identity or number of contributors to the mixture." *State v. Roman Nose*, 667 N.W.2d 386, 394 n.5 (Minn. 2003). But that is not to say that an analyst cannot determine the number of contributors to a mixed sample, as Dr. Baechtel did; he concluded that there were four alleles at the FGA locus, hence two contributors, even though he could not tell conclusively which pair of the alleles belonged to which contributor.[17] Appellant has not shown that Dr. Baechtel's use of a particular random match formula — one far more favorable to the defense than in the case of a single-source sample — so contradicted his opinion that there were only two contributors at the FGA locus as to render it inadmissible.

III.

The issue of what the 27 peak represented arises again, however, with respect to appellant's claim that the trial court erroneously prohibited him from arguing to the jury that the peak was, indeed, an allele and thus either showed the presence of an unexplained third contributor to the Q1-3/4/6M sample or "excluded Mr. Roberts as a potential contributor" (Reply Br. for Appellant at 11). In the latter regard, appellant asserts that, despite Dr. Baechtel's opinion that the alleles could not reliably be divided into pairs and attributed to individual contributors, the jury should have been allowed to hear argument

[17] Appellant's assertion that merely by examining the 24 peak in relation to the heights of adjoining ones (20 and 28) and concluding therefrom that there were two contributors to peak 24, Dr. Baechtel was "rel[ying] on [an unacceptable] determination of individual DNA profiles" from mixed samples (Supp. Br. for Appellant at 12), does not persuade us. As the government points out, "saying that two contributors' alleles can be seen in a mixed sample is not the same as saying that the alleles . . . can conclusively be divided into allele pairs or profiles corresponding to each . . . contributor's unique DNA profiles" (Supp. Br. for Appellee at 12). In any case, on this point as well appellant has raised an issue going to the weight of Dr. Baechtel's testimony, not its admissibility.

that at the FGA locus the alleles were in two pairs, 20 & 24 and 27 & 28, which served to exclude him from the sample because his alleles at that locus are 24 & 28.

The trial judge barred appellant from arguing these inferences because they had no "basis in the evidence, ultimately, from an expert opinion," appellant having called no expert to rebut Dr. Baechtel's opinion that peak 27 was not an allele. Appellant asserts that the judge ignored reasonable inferences the jury could draw from Dr. Baechtel's own testimony. Specifically, FBI protocols that Dr. Baechtel referenced help DNA examiners to distinguish false peaks (including stutter) from true alleles. Because research has shown that a stutter peak usually appears one position to the left of a peak representing a true allele, the FBI's STR protocols contain tables of average stutter-peak to allele-peak ratios at each of the CODIS loci. Dr. Baechtel acknowledged that under these ratios a peak at the FGA locus would typically represent stutter if its height were less than twelve percent of the height of the peak it precedes, but that the height of the 27 peak was twenty-five percent of the height of the 28 peak, or more than double the average twelve-percent guideline for stutter. He nonetheless concluded that the 27 peak was not an allele because of other factors, including the absence of signs of a third contributor at any other locus. Appellant contends that the jury might reasonably have rejected Dr. Baechtel's reasons for not adhering to the FBI's own peak height ratio and found the 27 peak to be a true allele.

"[A]n attorney plainly is entitled to make reasonable comments on the evidence and urge such inferences from the testimony as will support the [party's] theory of the case." *Finch v. United States*, 867 A.2d 222, 229 (D.C. 2005) (citation and internal quotation marks omitted). Although "[d]eciding whether a comment made by counsel is a reasonable

inference [from the evidence] . . . is usually a task best suited to the trial judge," *Gardner v. United States*, 698 A.2d 990, 1001 (D.C. 1997) (citations and internal quotation marks omitted), defense counsel should have "wide latitude" in drawing such inferences, particularly since "the prosecutor[, arguing both first and last,] has ample opportunity to rebut the inferences suggested by defense counsel." *United States v. DeLoach*, 164 U.S. App. D.C. 116, 121-22, 504 F.2d 185, 190-91 (1974). Here, there was a sufficient basis in the FBI's peak height ratios for an argument that the 27 peak was an allele, and for the further argument that this cast reasonable doubt on Dr. Baechtel's conclusions that there were only two contributors at the FGA locus and that appellant could not be excluded as one. Indeed, appellant did argue for two transcript pages, without objection, that the expert's deviation from the FBI ratio ("that's the only time he calls something stutter where the relationship between the two exceeds the stutter percentage") undermined his "opinion," and the jury could hardly have been in the dark as to what Dr. Baechtel's opinions were. An explicit argument that the 27 peak represented an allele and as such cast doubt on the DNA identification of appellant would have found support in the evidence, particularly given the fact (acknowledged by the government) that "[a]s with any scientific process, interpretation of electropherogram or other test results always involves an element of subjectivity" (Br. for Appellee at 52 n.67 (quoting affidavit of Dr. Arthur Eisenberg)). The argument should have been permitted.

But to say that the judge erred in not allowing the defense to argue these points is not to say that the refusal to do so was reversible error. Dr. Baechtel explained fully to the jury why he had not adhered to the average peak height ratio and found instead that the 27

peak was not an allele;[18] and appellant presented no expert witness of his own to offer a different interpretation. The jury thus would have heard only defense counsel opposing Dr. Baechtel's explanation of why the FBI's protocol ratios, though presumptive in application, are not the whole equation. Further, Dr. Baechtel testified — again without contradiction by a defense expert — that even if there was a 27 peak allele at the FGA locus, that would not exclude appellant as a contributor because it would not erase the evidence of the alleles at that locus matching his and the victim's;[19] and a 27 allele did not appear at any of the other eight loci examined in the Q1-3/4/6M sample. Equally important, appellant's DNA was consistent with DNA found at all thirteen loci analyzed in the Q1-3F sample, which (because it contained thirteen rather than nine loci) was used as the basis for the random match statistic reported by the FBI. In sum, it is difficult to see how a dispute over conclusions about the DNA profile shown at a single locus of one sample could have affected evidence that overall placed appellant's DNA convincingly on the tested fragments from the victim's garment.

Finally, K.W. testified in detail, and in basic conformity with statements she had made to a girlfriend and a police detective, that appellant had forced her to have sexual

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[18] He explained, in sum, that if a peak exceeds the average stutter ratio the examiner may, but is not required to, call it a true allele; that an examination of other loci in the examined DNA sample is usually required before a final determination can be made about a possible stutter peak; and that especially when interpreting mixed samples, the examiner is required to base his conclusions on all loci observed in the tested sample, where he found no evidence of the presence of a third contributor.

[19] *See* President's DNA Initiative, *supra* note 5, http://www.dna.gov/glossary/#E ("Exclusion — The elimination of an individual as the source of a biological sample. This occurs when one or more types from a specific location in the DNA of a known individual are not present in the type(s) for that specific location in the DNA obtained from an evidence sample.").

intercourse with him in the Stadium Armory parking lot, and her testimony was corroborated by the evidence that she had contracted a form of genital herpes at a time coinciding approximately with when she said she had been raped by appellant, who had the same type of herpes. All told, any harm appellant suffered from being unable to argue exculpatory inferences related to the 27 peak is too insignificant to have affected the verdict. *See Kotteakos v. United States*, 328 U.S. 750, 765 (1946).

IV.

Appellant contends, lastly, that his right to confront his accusers was violated because, although Dr. Baechtel testified and was cross-examined at length about his opinion that appellant could not be excluded as a contributor to the evidentiary DNA and about the probability of a random match, he had not done the original analysis of the DNA in this case, and the FBI scientists who did so were not called by the government as witnesses. Appellant argues that Dr. Baechtel's opinion was "based on" the testimonial conclusions of those scientists (Reply Br. for Appellant at 18), which he was entitled to confront by cross-examination under *Crawford v. Washington*, 541 U.S. 36 (2004). He concedes that, because he did not object on constitutional grounds — or, indeed, on any ground — to the government's failure to call these witnesses, our review is for plain error. *See United States v. Olano*, 507 U.S. 725 (1993).

The government disputes the premise of appellant's argument, *i.e.*, that Dr. Baechtel's opinion derived from the work and conclusions of other FBI employees. It points to his description of the way in which the FBI laboratory performs DNA testing, and

the role he played in that process here. As Dr. Baechtel explained, the FBI conducts DNA analysis through teams consisting of a serologist, who inventories materials submitted for examination and conducts tests to determine if the materials contain blood, semen, or other biological fluids suitable for DNA analysis; a PCR/STR technician who prepares test samples for DNA-typing and operates the instrument that actually determines the DNA types found in the samples; and an examiner (also called an analyst) who manages the team, interprets the data produced by the DNA-typing instrument, and memorializes those conclusions in a formal report. In this case, Dr. Baechtel was not the original examiner; that job had been performed by Dr. Maribeth Donovan, who no longer worked for the FBI and was not called as a witness by either side. As Dr. Baechtel acknowledged, he had not done the original "hands-on work" in the case and in a sense was "testifying in the place of Dr. Donovan." At the same time, Dr. Baechtel testified that the opinions he was testifying to were his own. He explained that all FBI DNA reports are subjected to two levels of review before being issued. In the first or more intensive review, the original examiner's report is given to a second examiner who "sit[s] down with that information and go[es] through it as if it was his or her own case." That was Dr. Baechtel's role here. He took "the case . . . as having been given to [him]" without regard to "what the actual examiner [had] decided." He went "through it as if it's my case . . . and [came] to [his own] conclusions and . . . interpretation," only then comparing them to the first examiner's interpretation. After this "technical" or "peer review" was complete, he transmitted the report, which he signed only because he agreed with its conclusions, to the unit chief for a final "administrative review."

Appellant nevertheless argues that Dr. Baechtel "relied on Dr. Donovan's analysis to bolster his own conclusions" (Reply Br. for Appellant at 19 n.13), citing as an example his admission on redirect that Dr. Donovan had "incidentally reach[ed] the same conclusion" as he about the 27 peak. Appellant points out further that, although the written report of the analysis was not introduced in evidence, Dr. Baechtel referred to it from time to time in explaining, for example, that the serology tests had been "presumptively positive" for the presence of blood and semen on the victim's panties. The government concedes in its brief that Dr. Baechtel "based his conclusions on foundational tests conducted by other [FBI] scientists . . . including serological studies that indicated the presence of semen . . . on the panties" (Br. for Appellee at 63).

Our review of the record confirms that, at least in part, Dr. Baechtel's opinion that appellant could not be excluded as a contributor to the DNA evidence rested on the conclusions reached by the team that did the actual laboratory analysis and set forth those conclusions in the report he reviewed. Further, our recent decision in *Thomas v. United States*, No. 03-CF-1125, 2006 D.C. App. LEXIS 655 (D.C. Dec. 28, 2006), leaves no room for dispute that the conclusions of FBI laboratory scientists — the serologist, the PCR/STR technician, and the examiner — admitted as substantive evidence at trial are "testimonial" under *Crawford, supra*, thus subject to the requirements of cross-examination and declarant-unavailability confirmed by that decision. Just as *Thomas* held that reports setting forth the results of analysis of drugs by DEA chemists are testimonial because they "are created expressly for use in criminal prosecutions," 2006 D.C. App. LEXIS 655, at *28-29, so the FBI laboratory scientists here were "forensic expert[s] employed by a law enforcement agency, . . . tasked by the government" to perform tests providing the basis for

"critical expert witness testimony . . . against appellant at his criminal trial." *Id*. at *24. To the extent that their conclusions were used as substantive evidence against appellant at trial, he was therefore entitled to be "confronted with" the conclusions in the manner the Sixth Amendment requires, that is, through the opportunity for cross-examination of the declarant.

In urging a different view, the government points out that (1) *Crawford* did not deal with expert testimony, (2) the Court there recognized that the Confrontation Clause "does not bar the use of testimonial statements for purposes other than establishing the truth of the matter asserted," *Crawford*, 541 U.S. at 59 n.9, and (3) courts have since held that *Crawford*

> does not undermine the established rule that experts can testify to their opinions on relevant matters, and relate the information and sources upon which they rely in forming those opinions. This is so because an expert is subject to cross-examination about his . . . opinions and, additionally, the materials on which the expert bases his . . . opinions are not elicited for the truth of their contents; they are examined to assess the weight of the expert's opinion.

Br. for Appellee at 70 (quoting *People v. Thomas*, 30 Cal. Rptr. 3d 582, 587 (App. 2005)); *see also United States v. Henry*, No. 04-3076, 2007 U.S. App. LEXIS 627 (D.C. Cir. January 12, 2007) (while "the Supreme Court in *Crawford* altered Confrontation Clause precedent, it said nothing about the Clause's relation to Federal Rule of Evidence 703" and

"did not alter an expert witness's ability to rely on (without repeating to the jury) otherwise inadmissible evidence in formulating his opinion under [that rule]").[20]

But reliance on the expert witness paradigm does not help the government here. It concedes that "some of the test results on which Dr. Baechtel's opinion was based . . . were offered as substantive evidence" (Br. for Appellee at 72); moreover, no instruction was given to the jury limiting consideration of any of those results to an evaluation of his opinion, rather than for their "truth" in linking appellant to the DNA evidence. *See In re Melton, supra* note 20, 597 A.2d at 906-07. And appellant cites contrary decisional law that, in the *Crawford* setting at least, "[t]he distinction between a statement offered for its truth and [one] offered to shed light on an expert's opinion is not meaningful." *People v. Goldstein*, 843 N.E.2d 727, 732-33 (N.Y. 2005). We leave resolution of that issue to another case where, as in *Henry, supra*, the underlying hearsay was not "repeat[ed] to the jury" or, at the least, was admitted with instructions precluding its use as substantive evidence. In light of the government's admission that this is not such a case, appellant was erroneously denied the right to cross-examine witnesses whose conclusions formed part of the DNA evidence against him.[21]

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[20] This court follows FED. R. EVID. 703. *See In re Melton*, 597 A.2d 892, 901 (D.C. 1991) (en banc) (holding that testimony of psychiatrists concerning out-of-court events derived from prior hospital records and hearsay from family members was admissible in civil commitment case because such information is commonly and reasonably relied on by psychiatrists to reach opinions about patient's future dangerousness).

[21] This case, of course, was tried without benefit of the decision in *Crawford*, but appellant is entitled to application of its holding. *See Griffith v. Kentucky*, 479 U.S. 314, 318 (1987).

As stated earlier, however, appellant made no confrontation objection to the government's failure to call the scientists other than Dr. Baechtel as witnesses, so to win reversal he must demonstrate plain error. *See Olano, supra*. He has not done so, for the reason alone that the government's failure to call Dr. Donovan, the PCR/STR technician, or the serologist — any or all of them — did not "seriously affect[] the fairness, integrity, or public reputation of [the] judicial proceedings." *Thomas*, 2006 D.C. App. LEXIS 655, at *12 (quoting *Johnson v. United States*, 520 U.S. 461, 467 (1997)) (in turn quoting *Olano*, 507 U.S. at 732); *see also Harris v. United States*, 602 A.2d 154, 160 (D.C. 1992) (en banc) ("ultimate focus" of plain error analysis "is on whether the asserted errors jeopardized the very fairness and integrity of the trial and contributed to a miscarriage of justice").

First, Dr. Baechtel's independent analysis of the DNA test results and own application of statistical standards were, at a minimum, key constituents of the opinions he stated tying appellant's DNA to the victim. And Dr. Baechtel was cross-examined for nearly two-hundred transcript pages about the kinds of tests performed at the FBI's forensic laboratory, the scientific foundation for those tests and the statistics introduced with evidence of a DNA match, the operating and quality-assurance protocols followed by the laboratory, and the bases for his conclusions about the DNA evidence. It is nearly inconceivable to us that questioning of Dr. Donovan, the PCR/STR technician, or the serologist would have varied materially from this cross-examination or proved any more fruitful in undermining the FBI's conclusion of a DNA match.[22] Further, as in *Thomas*, appellant "could have subpoenaed and cross-examined [those team members] if he doubted

[22] Appellant, for example, has never suggested how the results of the serology tests indicating the presence of semen and possible presence of blood on K.W.'s panties were inaccurate.

[their] findings, qualifications, or methodology," 2006 D.C. App. LEXIS 655, at *57, but he did not. Nor, as mentioned earlier, did he call his own experts to dispute Dr. Baechtel's conclusions or seek to have the DNA samples analyzed independently — "[t]he best protection an innocent suspect has from a false match." NRC II at 25 (reprinted at R. 3125). Finally, as explained in part III, *supra*, the DNA evidence was strongly confirmed by — even if it did not "simply corroborate[]," in the government's words — the other evidence of appellant's guilt, including scientific evidence that he had the same strain of herpes the child contracted at a time consistent with when she asserted he had raped her.

All told, the procedures leading to appellant's conviction were fair and the evidence supporting it was reliable. *See Thomas*, 2006 D.C. App. LEXIS 655, at *59 ("*Crawford* did not hold that confrontation is always necessary for reliable fact finding."). Any limitation on his ability to cross-examine those who analyzed the DNA evidence connecting him with the crime does not justify reversal to prevent "'a miscarriage of justice [that] would otherwise result.'" *Olano*, 507 U.S. at 736 (quoting *United States v. Young*, 470 U.S. 1, 15 (1985)).

The judgment of the Superior Court is

Affirmed.