
No. 05-CO-333

DISTRICT OF COLUMBIA COURT OF APPEALS

Argued October 25, 2005

UNITED STATES OF AMERICA,

Appellant,

v.

RAYMOND A. JENKINS,

Appellee.

Appeal from the Superior Court of the District of
Columbia—Criminal Division

APPELLEE'S PETITION FOR REHEARING OR
REHEARING *EN BANC*

JAMES KLEIN

ALICE WANG

ANDREA ROTH

PUBLIC DEFENDER SERVICE
633 Indiana Avenue, NW
Washington, DC 20004
(202) 628-1200

ARGUMENT

This Court should grant rehearing or rehearing *en banc* for two reasons. First, the division's analysis of the admissibility of "cold hit" DNA match evidence effectively eviscerates key holdings of *Porter v. United States (Porter II)*, 618 A.2d 629 (D.C. 1992), because the division fails to require the government to present to the jury a match statistic that accurately estimates the chance that the cold hit is coincidental and, in reaching that conclusion, erroneously treats the scientific question of whether the government's proposed formula accurately estimates this probability as a matter of mere "relevance" to be determined by courts without reference to the views of the scientific community. Second, the opinion endorses bad science by stating that the statistical significance of a cold hit match is "best expressed" solely by the "random match probability" (RMP) or "rarity statistic," a formula that the government, the scientific community, and the division itself all recognize as an inaccurate estimate of the chance that a cold hit is coincidental. The opinion is the first appellate decision in the country to address the admissibility of a cold hit match and will govern all future cold hit cases in the District of Columbia. Because the opinion is inconsistent with *Porter* and incorrectly answers "question[s] of exceptional importance," App. R. 35(a)(2), it should be vacated and corrected on rehearing by the division or the *en banc* Court.

The division's mistaken endorsement of a scientifically rejected statistic as an accurate expression of the significance of a "cold hit" match stems from its failure to apply two key holdings of *Porter*: (1) that the probative value of a DNA match is determined by the chance that the match is coincidental; and (2) that the question of which statistical formula or method most accurately estimates the chance of a coincidental match is a scientific question, subject to the strictures of *Frye v. United States*, 293 F. 1013 (1923), and not a legal question for courts to decide as a mere matter of "relevance." A brief summary of these holdings follows:

First, *Porter* holds that DNA match evidence is not probative without an estimate of the chance that the match is merely coincidental. There are “two reasons why two DNA profiles would be consistent. One is that they do in fact come from the same individual; the other is that the match is a mere coincidence.” *Porter v. United States (Porter I)*, 1991 WL 319015, at *6 (D.C. Super. Sept. 20, 1991).¹ “[T]he most probative evidence” in a DNA case “is that which indicates whether or not the DNA . . . matches the DNA obtained from the suspect,” Slip op. at 19-20, or, logically, that which indicates the chance of the only other alternative, a coincidental match. Because jurors lack the scientific knowledge to independently assess this likelihood of coincidence, DNA match “evidence is probative” only if accompanied by an accurate statistical estimate of the “probability of a coincidental match.” *Porter II*, 618 A.2d at 631.² Other courts agree,³ as does the National Research Council in both of its seminal reports on DNA evidence.⁴

¹ A false match may also be caused by laboratory error, an issue not implicated by this appeal.

² See also *id.* at 631 (“So long as there is a consensus” that the “probability of a coincidental match” is “no greater than some very small fraction, then the evidence is probative and should be admitted on an appropriately conservative basis.”); *id.* at 640 (“[T]he probability of a coincidental match is an essential part of the DNA evidence”); *id.* at 640 (“We would not permit the admission of test results showing a DNA match . . . without telling the jury anything about the likelihood of that match occurring.” (citation omitted)).

³ See, e.g., *People v. Barney*, 10 Cal. Rptr. 2d 731, 742 (Cal. Ct. App. 1992) (“The statistical calculation step is the pivotal element of DNA analysis, for the evidence means nothing without a determination of the statistical significance of a match of DNA patterns.”); *State v. Williams*, 574 N.W.2d 293, 298 (Iowa 1998) (“We agree with the NRC Report which stated “[t]o say that two [DNA] patterns match, without providing any scientific valid estimate . . . of the frequency with which such matches might occur by chance, is meaningless.”); *Commonwealth v. Curnin*, 565 N.E.2d 440, 442 n.7 (Mass. 1991) (must tell jury the “likelihood of th[e] match occurring”); *Hull v. State*, 687 So.2d 708 (Miss. 1996) (“‘the ultimate results of DNA testing would become a matter of speculation’ without statistical evidence”); *State v. Vandebogart*, 616 A.2d 483, 494 (N.H. 1992) (“A match is virtually meaningless without a statistical probability expressing the frequency with which a match could occur. Thus, evidence of a match will not be admissible if it is not accompanied by a population frequency estimate that has been produced from a generally accepted method.”).

⁴ National Research Council, *DNA Technology in Forensic Science* 9 (1992) (“Interpreting a DNA typing analysis requires a valid scientific method for estimating the probability that a

Second, *Porter* holds that it is the province of scientists, not courts, to determine whether the government has chosen and correctly applied a statistical formula that accurately estimates the chance of a coincidental match. *Porter* rejected the argument that objections to the government's statistical formula merely "go to its weight" and held that "the calculation of statistical probability is an integral part of the process and the underlying method of arriving at that calculation must pass muster under . . . *Frye*." 618 A.2d at 640 (citation omitted).⁵ See also *Porter I*, 1991 WL 319015, at *26 ("Were the court to adopt the government's position [that statistical questions go only to weight], it would be for the jury to consider the competing views of scientists regarding the various matters which are relevant to a consideration of the validity of the FBI's probability estimate. . . . To state the proposition is to refute it."). Instead of declaring itself competent to delve into the realm of statistics and determine whether a given formula accurately estimates the chance of a coincidental match, the *Porter II* Court noted that scientists use the "random match probability" (RMP) to calculate this number⁶ and then looked to the

random person by chance matches the forensic sample at the sites of DNA variation examined. To say that two patterns match, without providing any scientifically valid estimate . . . of the frequency with which such matches might occur by chance, is meaningless."); National Research Council, *The Evaluation of Forensic DNA Evidence* 127 (1996) ("Suppose that a DNA sample from a crime scene and one from a suspect are compared, and the two profiles match at every locus tested. Either the suspect left the DNA or someone else did. We want to evaluate the probability of finding this profile in the 'someone else' case.").

⁵ See, e.g., JOHN M. BUTLER, *FORENSIC DNA TYPING* 270 (2d ed. 2005) ("When 'failure to exclude' is the interpretation for reference and evidence samples, then a statistical estimate of the significance of a [DNA] match is needed."); David H. Kaye & George F. Sensabaugh Jr., *Reference Guide on DNA Evidence*, in *REFERENCE MANUAL ON SCIENTIFIC EVIDENCE*, FEDERAL JUDICIAL CENTER 545 (2d ed. 2000) (noting that numerous courts have concluded that reliable statistical methodology must accompany science to be admissible).

⁶ In a non-cold-hit case like *Porter* where the suspect was first singled out and *then* found to match the DNA profile, the RMP – the probability that a randomly selected person would happen to share the profile – is the correct expression of the chance that the match is coincidental. 618 A.2d at 632 (noting that, because two profiles can match by chance, "scientists calculate the possibility that the match is merely a coincidence and that the two samples did not actually come from the same person"); *Porter I*, 1991 WL 319015, at *6 (observing that the FBI determines the

scientific community to determine whether the government correctly applied the RMP, focusing on the effect of population substructure on the reliability of the government's calculation. *Id.* at 636-42. Upon recognizing a lack of scientific consensus on this latter issue, *Porter* required the government to present a more conservative number upon which scientists could agree. *Id.* at 641-42.

The division's opinion upsets these key holdings of *Porter* in several ways that will set dangerous precedent for future DNA cases and, more generally, future *Frye* litigation. The division never attempts to, or acknowledges the need to, determine whether the government's proposed statistical formula is generally accepted by the scientific community as an accurate expression of the chance of a coincidental cold hit match. *Cf.* Slip op. at 2 (stating that "statistical evidence that expresses the significance of a match" merely makes a match "more probative"). Rather than directing courts to apply *Frye* to the government's proposed formula to determine if it reliably estimates the chance of a coincidental match, the opinion appears to mandate admission of cold hit match evidence whenever accompanied by a formula deemed "relevant" by the court purporting to explain the significance of the match. Slip op. at 20 ("What is and is not relevant is not appropriately decided by scientists and statisticians."). Put differently, the division improperly dismisses the need to seek guidance from the scientific community in determining whether the government's proposed formula accurately estimates the chance of a coincidental match, suggesting that the only question for the scientific community is whether, once the government has chosen a particular formula, it has correctly applied the

significance of a match by calculating the "odds of finding a matching pattern at random or by coincidence"). But in a "cold hit" case, both the division and the government acknowledge that, because the match is the non-random result of a database trawl, the RMP alone no longer accurately reflects the chance that the cold hit match is coincidental. *See* discussion *infra*.

formula by plugging in the right numbers.⁷ In the division's view, the former question is one of mere "relevance," rather than competing "methodologies" subject to *Frye*, and thus bears no inherent connection to the views of the scientific community.⁸

The division's characterization of this central scientific inquiry as one of "relevance" rather than "methodology" is without precedent. Such an approach improperly disregards scientific opinion in the first stage of the inquiry – what statistical formula most accurately estimates the chance of a coincidental cold hit match – and arbitrarily limits scientific inquiry to whether the government has correctly applied the formula of its choosing. *Porter* indicates that "relevance" is not sufficient to admit DNA match evidence or a statistic purporting to explain the significance of that evidence; rather, under *Porter*, a match is admissible only if accompanied by the answer to a specific question: What is the probability that the match is coincidental? In turn, whether the government's proposed formula accurately estimates this probability is a question of admissibility subject to the strictures of *Frye*. In replacing *Porter's* *Frye*-based standard for admitting match statistics with a mere "relevance" test, the division does not explain how a trial court could determine whether a statistical formula is "potentially relevant" or an "independently significant statistical calculation," Slip op. at 14-15, except by looking to the scientific community to determine whether the formula accurately estimates the chance that the cold hit is coincidental, the very information that makes the match evidence probative to begin with.

⁷ See Slip op. at 15 ("[T]here is no controversy in the relevant scientific community as to the accuracy of the various formulas. . . . [T]he math that underlies the calculations is not being questioned. Each approach to expressing significance of a cold hit DNA match accurately answers the question it seeks to address."); *id.* at 18 ("There still exists controversy as to the appropriateness of the use of the rarity statistic . . . in a cold hit DNA match. This debate, however, still does not address the mathematics or methodology of the various computations. The argument . . . is to the relevancy of the statistics, not the soundness of the calculation.").

⁸ See Slip op. at 14 ("At the heart of this debate is a disagreement over the competing questions to be asked, not the methodologies used to answer those questions.").

It cannot be the case that *Porter* – after taking pains to emphasize the centrality of the probability of a coincidental match to the admissibility of DNA evidence – intended for courts to determine which statistic accurately estimates the chance of a coincidental match without looking to the scientific community for guidance. Indeed, the very premise of *Frye* is that the admission of novel scientific evidence should rest on its general acceptance in the relevant scientific community rather than a court’s determination that it is reliable: “In light of the abstruse, intensely technical [scientific] standards involved, courts are well advised not to pick sides in scholarly controversies between eminent scientists about molecular biology or population genetics.” *Porter II*, 618 A.2d at 638 n.14 (alteration in original) (internal citations and quotation marks omitted). Moreover, it is the very province of the science of statistics to explain, using probabilities, how to draw correct mathematical inferences from a given set of data.⁹ A trial court does not abdicate its legal responsibilities by seeking guidance from the scientific community as to how to accurately estimate the chance of a coincidental match; rather, a trial court abdicates its duties under *Porter* by failing to seek such guidance.

Even if this Court were to agree that the choice of the “best” statistic is committed to the trial court’s discretion, the court’s exercise of that discretion must at least be informed by scientific authority, if not grounded in scientific consensus pursuant to *Frye*. Here, in choosing what it deems the “best” statistic under its newly created “relevance” test, the division endorses a formula for producing a match statistic – the RMP alone, unmodified by the additional fact of the database search – that is universally recognized as an *inaccurate* estimate of the chance of a

⁹ See, e.g., *In re Estate of Marcos Human Rights Litigation*, 910 F. Supp. 1460, 1465 (D. Haw. 1995) (statistics “uses mathematical equations to infer the probability of events occurring or not occurring”); Michael O. Finkelstein & Bruce Levin, *Statistics for Lawyers* 1 (2d ed. 2001) (statistics is involved with “describing data and drawing inferences from them”); Webster’s Collegiate Dictionary 1149 (10th ed. 1999) (“Statistics: 1) a branch of mathematics dealing with the collection, analysis, interpretation, and presentation of masses of numerical data”).

coincidental match. The division concedes this point, Slip op. at 7 (“The government . . . concedes that in a cold hit case, the [RMP] no longer accurately represents the probability of finding a matching profile by chance.”), mirroring the opinions of the government’s own two witnesses¹⁰ and the rest of the scientific community.¹¹

The division’s choice of the RMP alone as the “best express[ion]” of the significance of a cold hit match in any cold hit case is further contradicted by the division’s concession that a *different* match statistic – the “database match probability” (DMP) – more accurately represents the chance of finding a cold hit match by coincidence. Slip op. at 7 (because “the fact that many profiles have been searched increases the probability of finding a match,” the “‘database match probability’ more accurately represents the chance of finding a cold hit match.”).¹² The DMP is equal to the RMP multiplied by the size of the database. By mathematically accounting for the fact that numerous profiles have been compared in a database search, this figure alerts the jury that the discovery of the match may not be particularly surprising, and is far less significant – typically by several orders of magnitude – than if the match were random. It is for this reason that the National Research Council advocated use of the DMP to express the significance of a cold hit match, stating that the RMP alone is inaccurate: “If the only reason that the person becomes a suspect is that his DNA profile turned up in a database, the calculations *must* be

¹⁰ Slip op. at 8 n.12 (noting the opinion of government witness and well-respected population geneticist Dr. Ranajit Chakraborty that “presentation of rarity alone in a cold hit case does not provide the complete picture.”); Tr. 3/28/05 at 122 (government witness Dr. Bieber testifying that scientists “don’t use [the RMP] to reflect the significance of a confirmatory and a DNA data base match. They don’t actually use it to reflect the significance of anything but to reflect the expected frequency of finding such a profile in an unrelated person”).

¹¹ See Br. of Appellee at 26-28 (noting the opinions of the DNA Advisory Board, the NRC I and II committees, and numerous individual scientists that were credited by the trial court).

¹² Although the DMP does not precisely calculate the probability that the cold hit was obtained by chance, it at least accounts for the fact that many profiles have been searched and thus comes closest to expressing the statistical significance of the match, as defined by *Porter*.

modified” by “multiply[ing] the [random] match probability by the size of the database searched.” National Research Council, *The Evaluation of Forensic DNA Evidence* 32-33 (1996) (emphasis added).

Notwithstanding these concessions, the division later shifts its position and asserts, without explanation or authority, that the RMP is “always relevant” because it “best expresse[s]” the “[t]he likelihood that the suspect is the actual source.” Slip op. at 20. In addition to contradicting the division’s own earlier statements to the contrary, this assertion contradicts its own remand order to the trial court in this case. While claiming that its holding is a “limited one,” Slip op. at 20, the division strips discretion from trial courts to decide whether a particular statistical formula is relevant by declaring that the RMP alone is “always relevant,” thus requiring trial courts in all future cold hit cases to allow the government to present its match evidence accompanied by a match statistic that is universally rejected by the scientific community as an inaccurate estimate of the chance that a cold hit is coincidental.

What may have led the division to improperly bypass *Frye* and assert that the RMP is “always relevant” without first seeking guidance from the scientific community is the fact that, in Mr. Jenkins’ case, the RMP and DMP were both extremely low probabilities – 1 in 26 quintillion and 1 in 260 trillion, respectively – and, thus, the choice among statistical formulas, while yielding numbers that differ by orders of magnitude, did not seem to dramatically change the significance of the match. *See, e.g.*, Slip op. at 8 (the “rarity statistic is a more significant number than database match probability when one tests at thirteen individual loci,” thus yielding an extremely small RMP). But the question before the trial court and the division was one of *methodology*; that is, whether the government’s proposed statistical formula is the most accurate means of estimating the chance that a cold hit match is coincidental. The size of the RMP and

DMP bears no relation to whether either formula accurately estimates the chance of a coincidental match. At most, the size of the numbers in a particular case merely minimizes the extent to which the jury will be misled by being presented with the RMP alone. But future cold hit cases in Superior Court will inevitably involve match statistics much larger than those here, particularly when degraded samples, partial profiles, or mixed samples are involved. In such cases, the RMP alone as an estimate of the chance of a coincidental cold hit match could be wrong by orders of magnitude.¹³

While the division notes that the government has offered to introduce the DMP in its case in chief if ordered by the trial court, and that the government has no “objection” to introduction of both numbers, Slip op. at 9 n.13, 11-12, the opinion as written does not require the government to introduce the DMP, or any other information besides the RMP, in its case in chief. The government may certainly reference the RMP as part of the formula used to calculate the DMP, but it should not be allowed to present to the jury the RMP *alone*, unmodified to account for the effect of the size of the database, as a supposedly accurate and complete calculation of the chance that the cold hit match was coincidental.

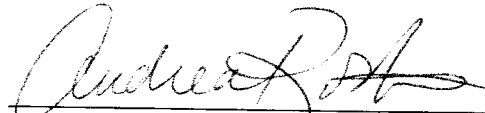
In setting the standard for all future cold hit cases in this jurisdiction, including currently pending Superior Court cases in which a “cold hit” is the only evidence against the defendant,¹⁴ the division should have followed *Porter* and *Frye* and looked to the scientific community to determine whether the government’s formula correctly estimates the information needed by the

¹³ For example, if the RMP in this case had been 1 in 1 million, and the Virginia database of approximately 100,000 individuals were searched, the DMP would have been approximately 1 in 10. If the jury were only given the RMP alone – 1 in 1 million – as the match statistic purporting to express the chance of a coincidental match, the jury would have a grossly misleading and incomplete picture of the true significance of the match. Such relatively large RMPs are common. *See, e.g., United States v. Roberts*, DCCA No. 03-CF-853 (reporting a RMP of 1 in 410,000 based on a mixed sample).

¹⁴ *See, e.g., United States v. William Rue*, Super. Ct. Crim. No. F-3817-05 (Christian, Erik, J.).

jury to assess the probative value of the match: the probability that the match is coincidental. If it had done so, the division would have had no choice but to reject the government's proposal to introduce the RMP by itself as an ostensibly accurate estimate of the chance of a coincidental cold hit. Further, the division should have followed the *Porter* Court's lead and required the government to present its match evidence using a more conservative formula agreed upon by the scientific community, whether it be the "confirmatory loci" method endorsed by Mr. Jenkins or the DMP approach endorsed by NRC II and the vast majority of the scientific community.

Respectfully submitted,



James Klein, Bar No. 252 999

Alice Wang, Bar No. 495 098

Andrea Roth, Bar No. 466 690

PUBLIC DEFENDER SERVICE

633 Indiana Avenue, NW


Washington, DC 20004

(202) 628-1200

Counsel for Appellee Raymond A. Jenkins

CERTIFICATE OF SERVICE

I hereby certify that a copy of the foregoing Petition for Rehearing or Rehearing *En Banc* has been served, by hand, upon Roy W. McLeese III, Esq., Chief, Appellate Division, Office of the United States Attorney, 555 Fourth Street NW, Room 8104, Washington, D.C. 20530, this 9th day of January, 2006.



Andrea Roth