SUPERIOR COURT OF THE DISTRICT OF COLUMBIA
Criminal Division – Felony Branch

UNITED STATES OF AMERICA	**:**	**Criminal No. F-3420-04**
	:	
v.	**:**	**Hon. Robert I. Richter**
	:	
----------	**:**	**Trial: May 31, 2005**

MOTION TO EXCLUDE DNA "INCLUSION" EVIDENCE, EXPERT TESTIMONY, AND FREQUENCY STATISTICS BECAUSE THERE IS NO GENERAL ACCEPTANCE AS TO THE STATISTICAL METHODS OF INTERPRETATION OF DNA EVIDENCE THAT DERIVES FROM A "COLD HIT" IN A DNA DATABASE, WITH POINTS AND AUTHORITIES IN SUPPORT

----------, through undersigned counsel, respectfully moves this Honorable Court, pursuant to *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923), *Dyas v. United States*, 376 A.2d 827 (D.C. 1977), *United States v.* Porter, 618 A.2d 629 (D.C. 1990) ("*Porter II*"),[1] *Daubert v. Merrell Dow Pharm.*, 509 US. 579 (1993), and the Due Process Clause of the Fifth Amendment, to exclude all DNA evidence and testimony from the government's case. Mr. --------- notes that, as the proponent of the scientific evidence, the government bears the burden to prove its evidence is admissible and submits that the government cannot carry its burden. The statistics proffered by the government to explain the significance of the alleged "inclusion" are currently the subject of a raging debate with scientists divided into at least three separate camps calling for three starkly different approaches. *See* Section II, *infra*. The Court of Appeals has made clear that the presentation of a statistical calculation is *required* when admitting DNA evidence. This Court should preclude the government's introduction of DNA evidence in this case until the debate is quelled and a generally accepted approach is developed. Mr. --------- requests a hearing on this

[1] Mr. Berger refers to Judge Kennedy's underlying trial decision, *United States v. Porter*, Crim. No. F-6277-89, 1991 WL 319015 (D.C. Super. Sept. 20, 1991) as "*Porter I*" and the Court of Appeals decision in the case, cited above, as "*Porter II*."

Motion.[2]

Overview

The DNA evidence in this case derives from a novel technique that has not been admitted in any case in the District of Columbia. The sole judge to consider such evidence, the Honorable Rhonda Reid Winston, found it inadmissible. *See United States v. Raymond Jenkins*, No. F-320-00 (the transcript of Judge Winston's ruling is appended hereto as Appendix A).[3] According to the government, Mr. --------- became a suspect upon the "cold hit" of a DNA STR profile purporting to be his in a large databank maintained by the FBI known as the Combined DNA Index System (CODIS).[4] The statistical significance of such a databank search, or "cold hit" is a matter of continuing and strident debate. Because no statistical method is generally accepted for expressing the significance of a cold hit, the government's efforts to introduce any DNA evidence in this case must fail.

Until recently, the DNA STR profiles that have been generated for forensic purposes in this jurisdiction (and, for that matter, nationwide) have exclusively been those that could be characterized as "confirmation matches," in which DNA STR testing has been performed upon a reference sample taken from a suspect who has already been linked to a crime by direct or circumstantial evidence. Mr. ---------'s case presents only the second case in Superior Court to utilize a new type of DNA STR profile "match" – one that was generated as a result of a "cold hit" from the trawling of a large number of DNA profiles maintained in a convicted offender database.

---

[2] The defense notes that discovery requests with the government are ongoing and reserves the right to supplement this Motion upon the receipt of additional discovery.

[3] Counsel is in the process of preparing bound versions of the appendices, which will be delivered to the Court and government counsel as soon as complete. The appendices are divided into two volumes – one includes publications; the other includes affidavits and transcripts.

[4] As discussed, *infra*, CODIS is actually a system amalgamating all of the state databases as well as those of the FBI, the United States Army, and Puerto Rico.

As the primary difference between these kinds of matches is the manner in which a suspect is first identified, it is impossible to convert one type of case into the other (for instance, by simply retesting a reference sample once a "cold hit" has been identified). Instead, the statistical significance of these two kinds of DNA profile matches must be determined differently. On this point, there is broad scientific consensus.

However, the necessary next stop of determining the statistical value of the "cold hit" is buried in scientific controversy: There are at least three different commonly held, and strikingly different and conflicting opinions as to how the statistics associated with DNA profiles generated after a cold hit should be calculated and presented. In short, there is no general acceptance of the scientific significance of the purported cold hit proposed by the government.

As noted, in only one other case in Superior Court has the government prosecuted a cold hit DNA case in which a suspect was identified by the trawling of a crime scene DNA profile through a convicted offender database. In *United States v. Jenkins*, discussed *infra*, Judge Winston held that there does not exist a general consensus in the relevant scientific community on the appropriate method for calculating the significance of a DNA match in a cold hit case.

In addressing the admissibility of DNA evidence in the joint litigation of *United States v. Orlando Roberts*, F-771-01, and *United States v. David Veney*, F-3986-00 ["*Roberts*/*Veney*"],[5] this Court noted that cases where the DNA simply corroborated a complainant's report that she had been

[5] The Court declined to hold a *Frye* hearing in that litigation, instead asking for written pleadings and affidavits from the parties and ultimately denying the motions to exclude on the papers after a colloquy with the parties addressing the issues. As stated in a separate motion, Mr. Berger asks that the Court permit Mr. Berger to adopt the pleadings in the *Roberts*/*Veney* litigation for purposes of this case. Mr. Berger encourages this Court to consider those issues *ab initio*. While a grant of that motion would result in either the exclusion of the evidence or the requirement that the government carry its burden at an evidentiary hearing, a denial of that motion has no consequence on the issues raised here.

sexually assaulted by a named defendant presented a very different situation than cold hit cases where the science itself is the lodestar of the government's evidence against the defendant. In the *Roberts/Veney* litigation, the Court recognized that the debates about the accuracy of the RMP calculated in both the *Roberts* and the *Veney* cases, while of no moment in cases where the suspect had already been identified before DNA testing was done, might very well be problematic in the context of a cold hit case.

Mr. --------- wishes to make clear that the issues presented in this Motion are unique to "cold hit" cases and therefore were not presented before this Court in the *Roberts*/*Veney* litigation. Rather, this Motion – challenging the admissibility of DNA STR evidence in a cold hit case – presents an issue addressed in only one other case in this jurisdiction. Indeed, because the development of convicted offender DNA databases and the trawling of such databases to identify suspects is a recent phenomenon, there are no published opinions from any jurisdiction that address the admissibility of such evidence at trial.

Mr. --------- also wishes to make clear that, as the proponent of the evidence, the government bears the burden to establish that there is a general consensus in the scientific community over how DNA STR matches derived from "cold hits" should be analyzed and presented, and that the government cannot meet its burden in light of the controversy in the relevant scientific community. Mr. --------- is not arguing – for he is not required to – that one approach or another is preferred: The existence of controversy, the lack of consensus alone requires exclusion under *Frye*.

In addition to his *Frye*/*Dyas* claim, Mr. --------- also moves to exclude the DNA evidence on evidentiary grounds. First, in light of the talismanic power of DNA evidence before juries, the admission of the DNA evidence is substantially more prejudicial than it is probative. Additionally, the government will be unable to prove chain of custody concerning the DNA

sample alleged to be Mr. ---------'s that was placed in the convicted offender database and then used for comparison purposes. Thus, under both *Frye*/*Dyas* and the rules of evidence, this Court must exclude the government's proffered DNA evidence.

This pleading will discuss the analytical framework for decision of the issue, the significant debate in the relevant scientific community, and the litigation and holding in the *Jenkins* case before Judge Winston. There currently exist proponents of three different methods of expressing the statistical significance of a DNA "match" where a suspect was originally identified as the result of a database search: (1) the position of the 1992 report of the National Research Council ("NRC I"); (2) the position of the 1996 report of the National Research Counsel ("NRC II"); and (3) the position of Drs. David Balding and Peter Donnelly ("Balding/ Donnelly"). The government, however, argues for a fourth position, an unmodified random match probability – a methodology that carries little favor outside of the law enforcement forensic community.

While there may be consensus at the FBI laboratory, as discussed herein and in the affidavits attached to this motion, there exists a hearty debate among the relevant community of scientists – chief among them statisticians. As statistician after statistician relates, there is a palpable lack of agreement as to which method of calculating a probability statistic is appropriate in a cold hit case:

* Professor Sandy Zabell of Northwestern University, a reviewer of NRC I and a consultant to NRC II, describes "the controversy regarding the use of statistics in assessing the probative value of a matching DNA profile in the case of a database

search." April 4, 2004 Affidavit of Dr. Sandy Zabell, at para. 3.[6]

* Professor Peter Donnelly of Oxford University (U.K.), co-author of *DNA Database Searches and the Legal Consumption of Scientific Evidence*, 97 Mich. L.J. 931 (1999) whose writings are heavily relied on by the government in its Opposition writes about "fundamental disagreements" among statisticians, the "number of research papers addressing this question," and the fact that scientists sit "on each side of the argument." October 3, 2004, Affidavit of Professor Peter Donnelly, attached as Appendix C.

* Professor Terence Speed, Professor of Statistics at the University of California at Berkeley, named by frequent government expert Ranajit Chakraborty as a "famous statistical geneticist" in the *Ida Chase* mtDNA admissibility hearing, *United States v. Ida Chase*, No. F-7330-99 (7/19/04 Tr. 29), describes the state of the current controversy in unequivocal terms: "Despite agreement that cold hit matches require a distinct approach, there is no consensus among statisticians on what that distinct approach should be." September 29, 2004 Affidavit of Dr. Terence Speed at ¶ 10, attached hereto as Appendix D.

The *only* area on which there is substantial agreement is that the government's proposal to provide the jury with an unmodified random match probability is wholly inappropriate and is supported by no one outside of the law enforcement community.

On April 5, 2005, Judge Winston, after reviewing many affidavits and taking testimony,

[6] For convenience, Mr. Berger has adopted many of the affidavits submitted to Judge Winston in the *Jenkins* case. In that case, Dr. Zabell submitted one affidavit with Mr. Jenkins' initial motion and one with Mr. Jenkins' reply to the government's opposition. Both of these affidavits are attached hereto as Appendix B. Dr. Zabell's initial affidavit will hereinafter be referred to as "First Zabell Affidavit." Dr. Zabell's October 4, 2004, affidavit will hereinafter be referred to as "Second Zabell Affidavit."

determined that there is no consensus in the relevant scientific community. Accordingly, Judge Winston ruled that the government did not carry its burden under *Frye* and the DNA evidence derived from the cold hit was inadmissible.

I. ANALYTICAL FRAMEWORK

A. The *Frye*/*Dyas* Framework for Admissibility of Scientific Evidence in D.C.

The D.C. Court of Appeals has set forth three requirements for the admission of expert testimony on a given subject:

> (1) [T]he subject matter must be so distinctively related to some science, profession, business, or occupation as to be beyond the ken of the average layman; (2) the witness must have sufficient skill, knowledge, or experience in that field . . . as to . . . aid the trier in his search for truth; and (3) expert testimony is inadmissible if the state of the pertinent art or scientific knowledge does not permit a reasonable opinion to be asserted even by an expert.

Dyas v. United States, 376 A.2d 827, 832 (D.C. 1977) (citations omitted). This test requires trial courts to find both that the technique relied upon by the expert has gained "general acceptance" in the scientific community, *Ibn-Tamas v. United States*, 407 A.2d 626, 638 n.23 (D.C. 1979) (third prong of *Dyas* requires "general acceptance"), and that the facts or data relied upon by the expert in rendering his or her opinion are sufficiently reliable to be "reasonably relied upon" by the expert. *United States v. Melton*, 597 A.2d 892, 901, 903 (D.C. 1991).

The "general acceptance" requirement of *Dyas* is equivalent to the well-known test of *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923), for admission of novel scientific evidence. *Dyas* and *Frye* require the proponent of the evidence to demonstrate by a preponderance of the evidence that the technology has been generally accepted in the relevant scientific community:

> Just when a scientific principle or discovery crosses the line between the experimental and demonstrable stages is difficult to define. Somewhere in this twilight zone the evidential force of the principle must be recognized, and while courts will go a long way in admitting expert testimony deduced from 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.

Frye, 293 F. at 1014; *see also Yisrael v. State*, 827 So. 2d 1113, 1114 (Fla. Dist. Ct. App. 2002) (proponent has burden to show by preponderance of evidence that scientific method is generally accepted). When determining whether scientific evidence is generally accepted, trial judges do not play the role of scientist and independently determine the validity of a particular science or technique; rather, "*[t]he issue is consensus versus controversy over a particular technique, not its validity. . . . If scientists significant either in number or expertise publicly oppose [a new technique] as unreliable, then that technique does not pass muster under* Frye." *Nixon v. United States*, 728 A.2d 582, 588 (D.C. 1999) (emphasis added). A court "may consider not only expert evidence of record, but also judicial opinions in other jurisdictions, as well as pertinent legal and scientific commentaries." *Porter II*, 618 A.2d at 635 (citing *Jones v. United States*, 548 A.2d 35, 41 (D.C. 1988)). By requiring that the scientific community approve of a technique, the *Frye*/*Dyas* test recognizes the limitations on courts' ability to act as arbiters of scientific disputes: "[T]he court may not resolve a scientific dispute between opponents and proponents of the technique, [and] the very existence of the dispute precludes admission of the testimony." *Id.* at 634 (citation omitted) (alteration in original). "A courtroom is not a research laboratory." *Id.*

Thus, while the federal courts have shifted from *Frye* to a more lenient test based on Federal Rule of Evidence 702 that emphasizes "reliability" based upon "scientific validity" and rejects "general acceptance" as a mandatory requirement, *Daubert*, 509 U.S. at 590 n.9, D.C. has remained true to the "rigid" and "austere" general acceptance standard. *Id.* at 588, 589. On the other hand, because *Dyas* requires that scientific evidence in D.C. be both generally accepted *and* sufficiently reliable to be reasonably relied upon by the testifying expert, trial courts in D.C. maintain a "gatekeeping function" notwithstanding D.C.'s adherence to the *Frye* standard.

Safeguarding the courtroom from applications of scientific theories that are not generally accepted is especially crucial when dealing with evidence such as DNA, which has an aura of infallibility from its coverage in the popular press and from its almost mysterious quality. Where the scientific techniques in question deals with statistics, it is even more important that the Court be certain that the method proposed by the government be the one generally agreed upon by the relevant scientific community. Although statistics are admissible in DNA cases, *see Porter II*, 618 A.2d at 641 n.22, courts have traditionally prohibited the use of statistical evidence to prove a defendant's guilt. In *Brim v. Florida*, 779 So. 2d 427 (Fla. Dist. Ct. App. 2000), the court looked to other courts and scholarly writings to recognize the danger of admitting statistics:

> It should not be overlooked that courts have traditionally prohibited the use of statistical evidence to prove guilt in criminal trials. *See People v. Collins*, 68 Cal.2d 319, 66 Cal. Rptr. 497, 438 P.2d 33 (1968) (noting, "[m]athematics, a veritable sorcerer in our computerized society, while assisting the trier of fact in the search for truth, must not cast a spell over him"); *see also* Laurence H. Tribe, *Trial by Mathematics: Precision and Ritual in the Legal Process*, 84 Harv. L. Rev. 1329, 1377 (Apr. 1971) (concluding that utility of mathematical methods is greatly exaggerated, that the methods inherently conflict with other important values, and thus "the costs of attempting to integrate mathematics into the fact-finding process of a legal trial outweigh the benefits"). Thus, the admissibility of DNA statistical evidence can be viewed as a departure from the general rule.

779 So. 2d at 445 n.47. Accordingly, although in certain circumstances it is proper to admit statistics to explain DNA evidence, the Court must recognize the incredible sway that numbers can have over juries and be extra vigilant in determining their admissibility. Where, as in this case, the prosecution rests almost exclusively on the expert testimony about DNA,[7] it is even

[7] Absolutely no evidence connected Mr. Berger to this offense prior to the cold hit. Even after the cold hit, no direct evidence links Mr. Berger to this sexual assault and robbery but for the fact that he roughly fits a description given by the complaining witness. The complaining witness has never identified Mr. Berger as her assailant. Indeed, the complaining witness has tentatively identified others as her assailant, including at least one person the police had developed as a suspect prior to the cold hit. The police developed at least three people as suspects before focusing on Mr. Berger.

more important that the Court tread carefully regarding the admissibility of some incredibly powerful number. *See Porter II*, 618 A.2d at 631 n.3 (noting that in that case "the evidence is offered to corroborate the identification of Porter as the assailant, and the entire prosecution case does not depend on the expert testimony"). In rejecting expert testimony about lie detector tests, which equally capture the imagination of jurors, the D.C. Court of Appeals noted that "[b]ecause of the authoritative quality which surrounds expert opinion, courts must reject testimony which might be given undue deference by jurors and which could thereby usurp the truthseeking function of the jury." *Proctor v. United States*, 728 A.2d 1246, 1249 (D.C. 1999) (quoting *Smith v. United States*, 389 A.2d 1356, 1359 (D.C. 1978)).

Thus, the government in this case must prove at a *Frye* hearing both that the interpretation and reporting methods used in its cold hit DNA analysis are generally accepted in the scientific community. If the government cannot establish a general consensus, the Court must exclude the DNA evidence. The Court of Appeals has expressly warned that trial courts are only to determine the existence or non-existence of controversy and are not themselves to delve into controversies between scientists. As the Court said in *Porter II*:

> The consensus that will satisfy *Frye* "is that of scientists, not courts," *People v. Reilly*, 196 Cal. App. 3d 1127, 1135, 242 Cal. Rptr. 496, 500 (1987), for "[a] courtroom is not a research laboratory." *United States v. Brown*, 557 F.2d 541, 556 (6th Cir. 1977). Accordingly, "the court may not resolve a scientific dispute between opponents and proponents of the technique, [and] the very existence of the dispute precludes admission of the testimony." *Starr v. Campos*, 134 Ariz. 254, 257, 655 P.2d 794, 797 (1982); *cf. Friend v. Friend*, 609 A.2d 1137, 1139-40 (D.C. 1992) (distinguishing the existence of dispute from the merits of that dispute).

618 A.2d at 634 (alterations in original).

Hence, it is not for this Court to decide which of two – or in this case three or four – different positions is the best. That is precisely what *Frye* prohibits. *See id.* at 631. The reason for this prohibition is that the Court and the lawyers litigating this case are not statisticians or

population geneticists with the training and education necessary to make such a decision. Indeed, the *Porter II* court recognized just that:

> In light of the "abstruse, intensely technical [scientific] standards involved," *Hopkins v. State*, 579 N.E.2d 1297, 1303 (Ind. 1991), courts are well advised not to pick sides in scholarly controversies between eminent scientists about molecular biology or population genetics. As one scholar has observed, "[t]he theory and technology of DNA far surpass everyday knowledge. In fact, only those specifically trained in [relevant scientific disciplines] can even begin to understand the concepts involved." Norman, DNA Fingerprinting: *Is It Ready For Trial*, 45 UNIV. MIAMI L. REV. 243, 243-44 (1990).

Id. at 638 n.14 (alterations in original).

The logic of the *Porter II* court is especially sound in this instance. Any methodology may upon explanation by an effective presenter appear to make sense to a layperson. However, the "hard-wired human tendency to process information according to heuristics[8] [can], under certain conditions, predictably lead even extremely intelligent people confidently to the wrong result." D. Michael Risinger & Jeffrey L. Loop, *Three Card Monte, Monty Hall, Modus Operandi and "Offender Profiling": Some Lessons of Modern Cognitive Science For The Law Of Evidence*, 24 Cardozo L. Rev. 193, 199-200 (2002).

An example of such a statistical situation is the so-called "Monty Hall problem." The problem is as follows: Assume three doors and a prize behind each one. You pick door number one. Before showing you what is behind door number one, the host tells you he will show you what is behind one of the two remaining doors, but not the door with the prize. The host opens door two and shows you that the prize is not behind door two. The host asks you if you want to keep door number one, or if you want to switch to door number three. Almost all non-

[8] Heuristics" is defined as "built-in recipes for dealing quickly with a general class of problems from input information." D. Michael Risinger & Jeffrey L. Loop, *Three Card Monte, Monty Hall, Modus Operandi and "Offender Profiling": Some Lessons of Modern Cognitive Science For The Law Of Evidence*, 24 Cardozo L. Rev. 193, 196 (2002).

statisticians would opine that the odds are now 50-50 that the prize is behind door one or door three. Statisticians, however, would advise to switch and pick door number three. Why? "[B]ecause the odds of the prize being behind door 3 are actually two out of three." *Id*. Undersigned counsel respectfully submits that many, if not most, laypersons (including judges, lawyers, and jurors) could be convinced by an effective presenter that the answer was indeed that the odds are 50-50, especially since the "human instinct . . . to believe that the odds of winning are now 50- 50 between doors 1 and 3 (and that therefore you might as well stick with door 1) is amazingly powerful." *Id*. at 201-02; *see generally* Sworn Affidavit of Dr. Keith Devlin, at 2-3, 6-7 (March 24, 2005) (discussing difficulty of non-mathematicians and statisticians to comprehend statistics: "Based on my 35 years of teaching mathematics, writing about it for experts and for laypersons, broadcasting about it, and receiving letters and emails from people from many walks of life, my belief is that many people, maybe even the majority, fundamentally DO NOT UNDERSTAND how probabilities work, even in the case of very simple examples.") (appended with curriculum vitae as Appendix E). This is why *Porter* and *Frye* dictate that the Court not choose sides but, rather, wait until the scientific community reaches consensus.

As discussed below, because of the raging controversy about the significance of a DNA cold hit and its effect on any subsequent comparisons and the lack of reliable information concerning the process that led to the cold hit in this case, the government cannot successfully show either general acceptance or reliability sufficient to pass muster under *Frye*/*Dyas*.

B. Forensic DNA Evidence is Inadmissible Without Accompanying Probability Statistics to Explain the Statistical Significance of a Match to Provide to the Jury.

As Judge Kennedy explained in *Porter I*, the accuracy of the statistical expression of the significance of a reported "match" is "at the very core of DNA evidence" and goes to admissibility

of the DNA evidence, not merely weight:

> It is the proclaimed ability to tell a jury that the odds of a coincidental match is one in thirty million, more than twice the number of African American men in the United States, which makes it so potentially compelling. No matter what qualifiers precede the statistical expression one in thirty million, this is tantamount to saying that Porter was the donor of the questioned specimen, that he, in effect, left his fingerprint.

United States v. Porter, No. F-6272-89, 1991 WL 319015 at *26 (D.C. Super. Ct. Sept. 20, 1991). Judge Kennedy further explained that complex statistical issues should be resolved before trial as admissibility issues rather than through cross-examination or competing experts, because juries will naturally gravitate toward numbers and the "bottom line":

> It is almost certain that jurors would simply "jump" to the bottom line numbers without giving any meaningful consideration to any dispute over the principles, which underlie the methodology used to generate those numbers. To permit the fancy of jurors to operate in this manner is the antithesis of "due process."

Id. at *27. The D.C. Court of Appeals agreed with Judge Kennedy, noting that such probability issues are subject to a *Frye* challenge:

> "Since a match between two DNA samples means little without data on probability, 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 *Kelly*/*Frye*." Axel, *supra*, 235 Cal. App. 3d at 866-67. "[W]e would not permit the admission of test results showing a DNA match (a positive result) without telling the jury anything about the likelihood of that match occurring." *Curnin*, *supra*, 409 Mass. at 222 n.7. Since the probability of a coincidental match is an essential part of the DNA evidence, and since there is no consensus as to the accuracy of the FBI's calculation, we decline to hold that the defense objections to *that precise calculation* go only to its weight.

Porter II, 618 A.2d at 640 (alteration in original). Thus, the government's "underlying method of arriving at th[e] calculation" of the likelihood of the match occurring is a proper focus of a *Frye* inquiry. *Id*.

C. History of CODIS, ----------'s Inclusion, and Report of Cold Hit in this Case.

The cold hit in this case arose from a search of the FBI's Combined DNA Index System Program (CODIS). *See* http://www.fbi.gov/hq/lab/codis/index1.htm. CODIS connects electronically the convicted offender databases of every state, the United States Army, the FBI, and Puerto Rico. *See* http://www.fbi.gov/hq/lab/codis/partstates.htm. This enables federal, state, and local crime labs to exchange and compare DNA profiles electronically. CODIS began as a pilot program in 1990 serving fourteen state and local laboratories. The DNA Identification Act of 1994 formalized the FBI's authority to establish a national DNA index for law enforcement purposes. CODIS is a distributed database with three hierarchical levels (or tiers) – local, state, and national. The FBI's National DNA Index System (NDIS) is the highest level in the CODIS hierarchy and allows CODIS laboratories to exchange and compare DNA on a national level. All DNA profiles originate at the local level (LDIS) then flow to the state (SDIS) and national (NDIS) levels. *See* http://www.fbi.gov/hq/lab/codis/national.htm. As of February 2005, there are 2,176,610 convicted offender profiles in NDIS.[9] *See* http://www.fbi.gov/hq/lab/codis/clickmap.htm.

As the administrator of the program, the FBI has taken steps to ensure uniformity among the jurisdictions in how they administer their individual database programs. Among the FBI's prescriptions was the setting of a core group of 13 genetic loci (known as the CODIS loci) that should always be tested regardless of the jurisdiction.

In this case, the DNA cold hit occurred after the Park Police sent evidence samples to the FBI for analysis and comparison to the CODIS databases. On August 14, 2003, United States Park

[9] The defense is currently unaware how many profiles were in the CODIS database in May 2004. Mr. Berger has made a request that the government provide this information.

Police Commander Michael Fogarty wrote the FBI and asked that it conduct DNA analysis on certain items of evidence. Commander Fogarty requested that if any DNA was recovered (that did not match the complaining witness) that the FBI compare the profile to the available offender database. *See* Letter from Michael Fogarty, United States Park Police Commander (Aug. 14, 2003). On January 15, 2003, the FBI advised the Park Police that a DNA profile had been recovered from an evidence sample and that this profile could be entered into CODIS. *See* Affidavit In Support of An Arrest Warrant (May 27, 2004). On May 20, 2004, the FBI informed the Park Police that the profile had been entered into CODIS and identified a cold hit DNA profile in its database that "matched" the profile generated from the crime scene evidence. *Id*. As the government stated in its Notice of Government's Intent to Admit Other Crimes, Wrongs, and Acts Evidence, "Almost a year [after the sexual assault], the Combined DNA Indexing System (CODIS) identified a match between evidence collected from the complainant and her previously unknown assailant. That DNA match was for ----------." Because of the risk of a coincidental match, the FBI qualified the significance of the cold hit, stating that new DNA would have to be obtained from the suspect to confirm the CODIS hit. USPP Supplemental Incident Record (May 20, 2004).

Following the cold hit, the government then sought and obtained an arrest warrant for Mr. ---------. After his arrest, the government obtained an order for the production of a new sample of Mr. ---------'s blood and delivered his blood sample to the Federal Bureau of Investigation ("FBI"). The FBI analyzed Mr. ---------'s blood for his DNA types across 13 different loci – the same loci that the FBI used to generate the profile in its database – and determined that the probability of finding Mr. ---------'s 13-loci DNA profile at random in the African-American population (also known as the random match probability or RMP) is 1 in 15,040,000,000,000,000, and that based upon that result of this 13-loci comparison, the FBI concluded that Mr. --------- is the sole contributor to the

evidentiary blood samples to a reasonable degree of scientific certainty. From the discovery provided to date, it is Mr. ---------'s understanding that the government will seek to admit this testimony at Mr. ---------' trial.

II. THE DNA EVIDENCE DOES NOT MEET THE *FRYE*/*DYAS* TEST BECAUSE THE INTERPRETION OF SUCH EVIDENCE, WHEN DERIVED FROM A COLD HIT OF A DNA DATABASE TRAWL, IS MIRED IN CONTROVERSY.

Because the cold hit derived from a trawl of the CODIS database, the proper statistical interpretation of its results are critical. The relevant scientific community of statisticians, mathematicians, and population geneticists is divided as to the proper statistical approach to take in database search cases and as to the statistical affect on the random match probability number offered at trial when the defendant was initially identified through a DNA database cold hit. In simplest terms, some statisticians believe that the random match probability statistic *overestimates* the probability of inclusion when identification follows a cold hit and divide into two separate camps as to how to correct the overestimation, while others believe the exact opposite, that the random match probability statistic *underestimates* the probability of inclusion in such circumstances. *No* scientist outside the community of government-employed forensic scientists agrees with the government's proposal to simply place before the jury the random match probability as one does in more traditional DNA confirmation cases like *Orlando Roberts*. Rather, the scientific community generally agrees that a cold hit case must always be treated differently statistically because cold hit cases are fundamentally different than "confirmation" cases. Because of the controversy over how significant DNA evidence is in a cold hit case, the government cannot carry its burden under *Frye*/*Dyas*, and this Court must exclude all DNA evidence at trial.

A. The Scientific Community Generally Agrees that Cold Hit Cases Must Always Be Treated Differently in Explaining the Significance of the DNA Evidence Because Cold Hit Cases Are Fundamentally Different than Confirmation Cases.

A cold hit case must be treated differently than a confirmation case. This is due to the fundamental difference in how a coincidental match could have come to light. In any case where DNA analysis is present, there in one relevant question: What is the significance, as expressed in a statistical manner, of the fact that a suspect's DNA profile matches the profile of an evidence sample at a given number of loci? The "random match probability" (RMP) that the government seeks to put before the jury does not answer this question in the context of a case where the suspect was first arrived at by virtue of a database search. Rather, the RMP calculates the chances that an unrelated[10] randomly selected person would happen to match the evidence profile. This is an appropriate calculation in a confirmation case because, for the defendant to be innocent, the government's suspect just happened to also match the evidence DNA profile. This calculation does not appropriately address the significance of the match, however, when the very reason the government suspects the person is because he was found to match the evidence profile after authorities had trawled through millions of people to find it. No amount of subsequent retesting can ever convert this situation back into a confirmation case.

Consider for example a case where an eyewitness describes her attacker but the attack left her blind and unable to engage in an identification procedure. A suspect is nonetheless developed based upon, say, suspicious actions near the crime scene. If the victim describes her attacker very precisely, naming eight unusual visible characteristics (*e.g.*, male, 5'10" tall, 160 pounds, 30s,

[10] All DNA statistical calculations rely on the *assumption* that no relative of the defendant could be the evidence sample donor. *See* David J. Balding, *Errors and Misunderstandings in the Second NRC Report*, 37 Jurimetrics J. 469, 473 (1997) (appended).

black, facial hair, no glasses, and dark clothing), and the suspect matches every one of them, then the probative value of this match is great. If the circumstances of making him the suspect were just unfortunate coincidences and he is innocent, one would ask, "But what are the chances a randomly selected person just happens to share the eight distinctive visible characteristics as the assailant?" This is the form of question that is relevant in a confirmation case.

Suppose instead that no leads were developed after the attack. Inspired by the detail in the description, the police start looking through DMV photographs. Eventually, after looking through many thousands, they come across a person who matches all eight characteristics. In this instance it would not be appropriate to ask "What are the chances a randomly selected person would just happen to share the eight distinctive visible characteristics as the assailant?" because the new suspect was not randomly selected. Rather, he was selected for the very reason that he shared those traits. Common sense shares the lesson of statistics that if one looks through thousands of samples for something rare, one is more likely to come across it than if you look at only one. "[T]he argument is essentially the same as for a lottery; if P is the probability of winning with one ticket, the probability of winning with N tickets is NP." Newton E. Morton, *The Forensic DNA Endgame*, 37 Jurimetrics J. 477, 499 (1997) (appended); *see also* Dr. Keith Devlin Affidavit, *supra*, at 4-5 (discussing lottery analogy).[11]

Scientists unanimously acknowledge this difference between a cold hit case and a confirmation case.

[T]he more extensive was your search, the less impressed I am. The reason is that

[11] This example also illustrates why retesting cannot convert a cold hit case into a confirmation case. No matter how may times one asks the victim to describe the same eight traits or how many times one looks at the suspect's features, they will still be the same. Likewise, the reason the person is being suspected will always be the same – because he was searched for based on those very traits.

> among many comparisons, it is unsurprising that one of them will, "by chance," display results that, on their own, might be regarded as significant. In this setting, the effect of the search is to weaken evidential strength. This phenomenon is widely understood by scientists. Indeed, conveying the idea to the general public is often regarded as a major challenge in advancing the public understanding of science.

David J. Balding, *Errors and Misunderstandings in the Second NRC Report*, 37 Jurimetrics J. 469, 471 (1997) (appended).

The National Research Council of the National Academy of Sciences has twice issued "blue ribbon" reports that deal with DNA evidence, including DNA evidence derived from cold hits. As to the stark difference between confirmation and cold hit cases, the NRC reports agree. "The distinction between finding a match between an evidence sample and a suspect sample and finding a match between an evidence sample and one of many entries in a DNA profile database is important. The chance of finding a match in the second case is considerably higher." National Research Council, DNA Technology in Forensic Science 124 (Nat'l Acad. Press 1992) ("NRC I") (selected portions appended). "There is an important difference between [the situation where a suspect is first identified by evidence other than DNA] and one in which the suspect is initially identified by searching a database to find a DNA profile match that [was] left at a crime scene. In the latter case, the calculation of a match probability or LR should take into account the search process." National Research Counsel, The Evaluation of Forensic DNA Evidence 134 (Nat'l Acad. Press 1996) ("NRC II") (selected portions appended); *see also id.* at 161 ("If the suspect is identified through a DNA database search, the interpretation of the match probability and likelihood ratio . . . should be modified."). The DNA Advisory Board (DAB), which was led by the FBI, also agrees that cold hit cases are qualitatively different than confirmation cases and, because "the probability of identifying a DNA profile by chance increases with the size of the database[,] this chance event must be taken into account when evaluating value of the matching profile found by a database search." 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. Communications 1, 5 (July 2000) (appended).

The reason that scientists pay particular attention to cold hits is because, as in the blinded-witness example above, when an individual is identified through a database trawl, there is the very real danger that an innocent person, who coincidentally shares an identical profile at the evidence loci, will be caught up in the net. There have been too many examples of two persons sharing genetic profiles on low-number loci comparisons (out of tens of thousands of possible loci) to fail to account for the unfortunate reality that database searches can lead to false matches and can generate inflated probability statistics. *See, e.g.*, Kathry Troyer *et al.*, *A Nine STR Locus Match Between Two Apparently Unrelated Individuals Using AmpF/STR Profiler Plus and Cofiler*, presented at 12th International Symposium on DNA Identification (Phoenix, Ariz. 2001) (appended) (reporting 9-location DNA profile match between two unrelated individuals (one white, one black) in state DNA database); Department of Justice, National Institute of Justice, The Future of Forensic DNA Testing 25 n.13 (Nov. 2000) (reporting ten 6-location DNA profile matches in New Zealand database of 10,907 records in which eight matches were brothers and two matches were unrelated persons); Richard Willing, *Mismatch Calls DNA Tests into Question*, USA Today (Feb. 8, 2000), at 3A (reporting instance of false match involving 6-location DNA search in UK database) (appended); *cf.* Keith Moor, *Experts Dispute DNA Claims in Leskie Case*, Herald Sun (Dec. 11, 2003) (appended), available at http://www.newstest.com.au (10-loci match was either coincidental as opined by Australian crime lab director or result of contamination).

Notwithstanding that all experts agree that the statistics are different in cold hit cases, the remaining debate is about what method should be used to report those statistics. And here, there is

no agreement.[12]

B. The Position Espoused By The Scientists In NRC I (1992) And Espoused By A Number Of Scientists Today Is That The Loci Used In The Database Search Should Not Be Part Of A Random Match Probability Calculation.

The first method to deal with this problem was promulgated in 1992 by the first body of experts appointed to the Committee on DNA Science by the National Research Council (NRC I).[13] This panel concluded that selection bias invalidates the use of searched profiles at trial:

> The distinction between finding a match between an evidence sample and a suspect sample and finding a match between an evidence sample and one of many entries in a DNA profile databank is important. The chance of finding a match in the second case is considerably higher, because one does not start with a single hypothesis to test (i.e., that the evidence was left by a particular suspect) but instead fishes through the databank, trying out many hypotheses. . . .
>
> When a match is obtained between an evidence sample and a databank entry, the match should be confirmed by testing with additional loci. The initial match should be used as probable cause to obtain a blood sample from the suspect, but only the statistical frequency associated with the additional loci should be presented at trial (to prevent the selection bias that is inherent in searching a databank). Forensic DNA typing laboratories should recognize that they will require additional loci beyond those used in the databank to prove a case against a suspect.

NRC I at 124.

The primary criticism leveled against this approach, and recognized by NRC I itself, *id.*, is that, out of concern that the database match was purely coincidental such that an innocent person might get charged with an offense, NRC I elects to not use all the information available to determine identity. Rather, some loci are used solely for the database trawl and are subsequently discarded if the analyst goes on to compare the cold hit person's genetic profile to that of the crime

---

[12] In an attempt to help clarify the distinctions among the three separate approaches, Mr. Berger has obtained sworn declarations from Dr. Sandy L. Zabell, Professor in the Departments of Mathematics and Statistics at Northwestern University. Dr. Zabell's declarations use examples to walk through the differing statistical approaches and are provided, along with his curriculum vitae, in the Appendix.

[13] The panel of experts that generated NRC I included Drs. Mary-Claire King, Richard Lempert, Eric Lander, Ruth Macklin, Thomass Marr, Victor McKusick, and Phillip Reilly.

scene evidence. So, for example, if the database search that generated the cold hit used 10 particular loci, those same 10 loci could not be used for the subsequent comparison between the cold hit suspect's profile and the crime scene evidence profile. Rather, the forensic laboratory should use additional, different loci in making its comparison. Depending on the number and specifics of the additional loci used, this procedure could dramatically reduce the government's random match probability calculations by a number of magnitudes. As the NRC II report recognized, however, the problems associated with the NRC I approach will become less as "STRs and other systems with many loci become more widely used." NRC II at 32.

DNA forensic laboratories have the core 13 CODIS loci – and another 8 loci, at their disposal for forensic DNA identification. *See* http://www.promega.com/techserv/apps/hmid, http://www.promega.com/geneticidproc/ussymp7proc/ab60.html (together listing 21 separate loci, plus an additional loci to determine gender, that can be forensically tested).[14] Given the abundant number of genetic markers available at the present time, even as some scholars have criticized and proposed alternatives to this approach, *see infra* Parts II.C and II.D, NRC I's approach currently enjoys a number of followers.

For example, Newton E. Morton, Professor, Human Genetics, University of Southhampton opined in a 1997 peer-reviewed article in Jurimetrics: "As recognized by NRC I, the best solution is

---

[14] The 13 CODIS loci are: CSF1PO, FGA, TH01, TPOX, vWA, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, and D21S11. Powerplex 16 also includes Penta D & Penta E (and Amelogenin, the gender-determinative locus). Powerplex ES includes SE33. All of this information can be cited to http://www.promega.com/techserv/apps/hmnid/. In addition, the published protocol for the Geneprint Fluorescent STR System (known as Silver STR) lists the additional loci as F13A01, FESFPS, F13B, HPRTB, LPL The cite is: http://www.promega.com/geneticidproc/ussymp7proc/ab60.html.

to confirm a match by a panel of markers independent of the ones used in trawling in the database. This evidence is free of ascertainment bias, and the corresponding likelihood ratio can be presented as evidence without indicating that the defendant was identified through a criminal database." Morton, *supra*, at 489. Writing separately in that volume of Jurimetics, Dr. Richard Lempert, who served on the committee that produced NRC I, affirmed his belief that NRC I best presented the manner in which to report cold hit DNA statistics. Richard Lempert, *After the DNA Wars: Skirmishing With NRC II*, 37 Jurimetrics J. 439, 461-62 (1997) (appended); *see also* Aidan Sudbury, *Comment to David J. Balding & Peter Donnelly, Inference in Forensic Identification*, 158 J. Royal Stat. Socy. A, Par 1, 21, 48-49 (1995) (appended) (agreeing with substance of NRC I).

Furthermore, several other experts who are currently involved in the interpretation of forensic DNA evidence endorse NRC I's method. Dr. Laurence Mueller, a professor in the Ecology & Evolutionary Biology Department at the University of California-Irvine who frequently testifies about forensic DNA, opines: "This approach can both take advantage of a genetic database as an investigative tool and yield probative evidence that can be evaluated by the same statistical techniques used in standard cases. There exist today a sufficient number of genetic markers to allow the creation of a useful database and the production of probative forensic evidence." Sworn Declaration of Dr. Laurence D. Mueller, at 3-4, para. 12 (Apr. 2, 2004) (appended with curriculum vitae as Appendix F). Professor Dan Krane, a professor in the Department of Biological Sciences at Wright State University who has conducted his own analyses of population databases, believes that NRC I's approach is the only way to "consistently generate conservative statistics that still reflect the power of DNA typing methodologies." Sworn Declaration of Dr. Dan E. Krane, at 5, para. 8 (April, 2, 2004) (appended with curriculum vitae as Appendix G). Additionally, Lab Director Marc Taylor, whose DNA lab work contributed to the dismissal of charges against Kobe Bryant,

supports the NRC I approach where practicable. *See* Affidavit of [DNA Lab Director and Forensic Scientist] Marc Taylor at ¶ 12 (October 4, 2004) (attached as Appendix H). Further, Dr. Krane testified in *State v. Robinson*, about five other forensic DNA experts (Dr. Bill Shields, Dr. Ron Ostrowski, Dr. Ted Kessis, Dr. Simon Ford, and Dr. Steve Leadon), who advocate the NRC I approach. *See* Excerpted Transcript of January 21, 2003, Direct Examination Testimony, *State v. Robinson*, No. 00F06871 (Jan. 21, 2003), at 1645-47 (full direct examination transcript is provided for the Court's review) (attached as Appendix I).

Indeed, at the hearing on this issue in the *Jenkins* case, one of the two experts called by the government, Dr. Ranajit Chakraborty testified that although he believes that the NRC I approach generally would not work because all loci of the evidence profile are used in the database search in order to increase discrimination, a situation where there were other loci available for testing would be acceptable to him and he believed would be acceptable to any court.[15] Additionally, another expert on whom the government relied in *Jenkins*, James Crow – Chairperson of NRC II – wrote an article in which he recognized the fact that established scholars believe in the NRC I method and that it is the appropriate method to use in cold hit cases: "With the increasing number of STR loci this is no longer so impractical. Morton in particular advocates going back to the NRC1 recommendation. He thinks the ascertainment procedure should not be ignored. It is clear, I think, that the NRC1 recommendation is unbiased." James F. Crow, *1996 NAS Report: Another Look* (1998), Promega Ninth International Symposium on Human Identification 1998, at 112 [hereinafter "*1998 NAS Article*"], available at http://www.promega.com/geneticidproc/ussymp9proc/content/24.pdf, (appended).

[15] The transcript of the testimony in this hearing is currently on order and can be provided to the Court once it is obtained by the Public Defender Service.

C. The Position Espoused By The Scientists In NRC II, A Report That The Government Relied Heavily Upon In *Roberts*/*Veney*, Is That In A Database Search Case The Random Match Probability Should Always Be Modified By Multiplying It By The Number Of Persons Searched In The Database.

By 1996, as the use of DNA databases was gaining in practice, some scientists developed a different view as to how DNA evidence in cold hit cases should be interpreted, though they continued to recognize that cold hit cases were different than the typical forensic DNA case. This approach was set forth in the NRC II report. "A special circumstance arises when the suspect is identified not by an eyewitness or by circumstantial evidence but rather by a search through a large DNA database. If the only reason that the person becomes a suspect is that his DNA profile turned up in a database, *the calculations must be modified*." NRC II at 32 (emphasis added). NRC II discussed two approaches. These scholars believe that a cold hit match is less significant than a single DNA match since as a statistical matter the chance of finding a match to a particular evidence DNA profile increases as it is compared to more people. Thus, for example, finding that a single person chosen at random is left-handed is somewhat unusual but finding at least one left-handed person in a sample of 1000 is not at all surprising. The committee in NRC II offered a method different from that of NRC I to account for the risk of a coincidental match in a large database: "Multiply the match probability by the size of the database searched. This is the procedure we recommend." *Id.*

The proponents of this method believe that the NRC I approach is too conservative because while it is "a sound procedure," "it wastes information, and if too many loci are used for identification of the suspect, not enough might be left for an adequate subsequent analysis." *Id.* Their alternative method differs from NRC I in three ways: 1) no testing is performed at additional loci; 2) genetic markers used in the original database search are included in the statistical calculations, and 3) the size of the database being searched (N) is taken into consideration.

The group of scientists who adhere to NRC II believes that the larger the searched database, the less significant the DNA identification of a suspect identified from the database. For them a DNA "match" arrived at by a database search is not as significant as a "match" where the suspect was identified through other means. So, for example, under the NRC II approach, if the RMP is 1 in 1,000,000, and the number of profiles in the database is 100,000, the corrected RMP would be 1 in 10. As shown by the example, the match probability presented to the jury can be reduced significantly under the NRC II approach.

While most scientists acknowledge the continuing accuracy of the NRC I view, many have espoused a preference for the view set forth by NRC II. *See, e.g.*, Bernie Devlin, *The Evidentiary Value of a DNA Database Search*, 56 Biometrics 1276 (Dec. 2000) (appended); Anders Stockmarr, *Likelihood Ratios for Evaluating DNA Evidence When the Suspect is Found Through a Database Search*, 55 Biometrics 671 (Sept. 1999) (appended). After greatly considering the arguments of all sides, the DNA Advisory Board also endorsed the NRC II methodology for the presentation of DNA evidence derived from a cold hit: "[W]e continue to endorse the recommendation of the NRC II Report for the evaluation of DNA evidence from a database search." *See* 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 Foren. Sci. Comm. slip op. at 8 (July 2000), available at http.//ww.fbi.gov/hq/lab/fsc/backissu/july2000/dnastat.htm.

The NRC II approach was immediately and virulently attacked by a third group of scholars, discussed *infra* in Part II.D., who take the polar opposite position and believe that the larger the searched database, the more significant is the DNA identification of a suspect identified from the database. Notwithstanding those attacks, statisticians and other supporters of NRC II have stood

their ground and reaffirmed the correctness of their position and the incorrectness of that of their opponents. *See, e.g.*, Anders Stockmarr, *Likelihood Ratios for Evaluating DNA Evidence When the Suspect is Found Through a Database Search*, 55 Biometrics 671 (Sept. 1999) (appended); Anders Stockmarr, *Reply to Comment on Stockmarr's "Likelihood Rations for Evaluating DNA Evidence When the Suspect is Found Through a Database Search*, 57 Biometrics 978 (Sept. 2001) (appended); Anders Stockmarr, Reply to *Ewett Letter to the Editor of Biometrics*, 56 Biometrics 1275 (Dec. 2000) (appended); Bernie Devlin, *The Evidentiary Value of a DNA Database Search*, 56 Biometrics 1276 (Dec. 2000) (appended).

D. A Third Set Of Scholars Rejects The Classical Statistics Methodologies Of The Two NRC Reports And Argues That Using A Statistical Method Known As The Likelihood Ratio Approach, Evidence Of Probability Is Stronger, Not Weaker, When The Suspect Is Identified From A Database Trawl.

The third group of scientists is comprised of individual scientists who have published peer-reviewed papers in which they argue that a cold hit should actually be given *more, not less*, weight than a match found in a confirmation case. *See, e.g.*, David J. Balding & Peter Donnelly, *Evaluating DNA Profile Evidence When the Suspect is Identified Through a Database Search*, 41 J. Forensic Sci. 603 (July 1996) (appended) ("[W]e argue that in a situation in which exactly one matching individual is found from a database search, the strength of the DNA evidence against that individual is *not* reduced relative to [a confirmation case]. In fact, in the database search case, under reasonable assumptions, the DNA evidence will be slightly stronger than in the probable cause setting."). Their position is based on the thinking that not only has the defendant been found to match the evidence, but also many more individuals have been found not to match. *Id.* at 605. To these scientists, in confirmation cases where only a single match is found during the course of DNA testing, there is at least still a formal possibility that one or more untested people may also match the evidence, and that possibility becomes increasingly less likely as the database used for a cold hit

becomes larger.[16]

> These scientists reject the "classical statistics" orientation of NRC I and NRC II:
>
> [Classical statisticians] grew up to facilitate objective inferences from data. Classical statisticians try to avoid subjective judgments, seeking instead to determine what conclusion can be drawn solely on the basis of frequency of observation. [Our] Bayesian approach – updating the odds assigned to a given proposition in light of evidence subsequently received – is thus unacceptable to classical statisticians because it depends on the subjective assignment of odds in the absence of objectively measurable data. . . .
>
> . . .
>
> It is considered bad science to trawl data, looking for surprising results and then proclaiming that the data proves a proposition that would likely lead to such results. . ..

Peter Donnelly & Richard D. Friedman, *DNA Database Searches and the Legal Consumption of Scientific Evidence*, 97 Mich. L. Rev. 931, 966-68 (Feb. 1999) (appended). These scientists reject the random match probability calculation, whether corrected or not. They believe that such a statistic does not accurately indicate the significance of the match. Instead, they rely solely upon the determination of a likelihood ratio. Their form of statistical analysis, known as "Bayesian," requires making statistical assumptions as to the prior odds for an individual. They present a powerful statistical argument that has yet to gain currency in United States courts.

The method of the Balding/Donnelly school differs from NRC I's approach in three ways: 1) no testing is performed at additional loci; 2) genetic markers used in the original database search

---

[16] For a selection of relevant publications, each appended, see David J. Balding, *The DNA Database Search Controversy*, 58 Biometrics 241 (March 2002); David J. Balding, *Errors and Misunderstandings in the Second NRC Report*, *supra*; David J. Balding & Peter Donnelly, *Inference in Forensic Identification*, 158 J. Royal Statistical Socy., Series A (21 (1995); A.P. Dawid, *Comment on Stockmarr's "Likelihood Ratios for Evaluating DNA Evidence When the Suspect is Found Through a Database* Search, 57 Biometrics 976 (2001); A.P. Dawid & J Mortera, *Coherent Analysis of Forensic Identification* Evidence, 58 J. Royal Statistical Socy., Series B, 425 (1996); Ian W. Evett et al., *Letter to the Editor of Biometrics*, 65 Biometrics 1274 (Dec. 2000); Ian W. Evett & Bruce S. Weir, Interpreting DNA Evidence: Statistical Genetics for Forensic Scientists 219-22 (Sinauer Assocs. 1998); and Michael O. Finkelstein & Bruce Levin, *On the Probative Value of Evidence from a Screening Search*, 43 Jurimetrics J. 265 (Spring 2003).

are included in the statistical calculations; and 3) the size of the database being searched (N) is taken into consideration. Their method also differs from the NRC II's approach in one, extremely fundamental way: to this group of experts, the effect of the database size on the significance of a match is precisely the opposite – large databases generate the most damning statistics for a defendant while, in the NRC II approach, the larger the database the less damning the statistics become to a defendant. Thus, the second and third approaches are diametrically opposed – in scientific theory and in practical consequences – with respect for implications of the size of the database that is searched.[17]

Notably, this Balding/Donnelly view was considered but expressly rejected by NRC II. *See* NRC II at 164; *see also* Donnelly Affidavit at 3-4. Moreover, this approach, while still in current favor with statisticians and population geneticists, has *never* been accepted in any court in the United States – neither the Balding/Donnelly analysis in the context of cold hit evidence, nor, for that matter, the Bayesian reasoning that underpins the analysis in any context. *See* 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)*, *supra* at 8 ("Bayesian logic has not been considered by the U.S. criminal legal system for DNA analysis.").

The Balding/Donnelly argument is, however, a strong voice critical of the NRC II method and is significantly indicative of the very real and stark disagreement among statisticians over what approach is proper in this sort of case. As Dr. Donnelly himself points out, "Since the

[17] The NRC II school of thought does not dispute that when databases get very large in size, the correction espoused by NRC II to account for database comparison becomes inappropriate. In fact, the NRC II report itself recognized that its proposal "assumes that the database, although perhaps large, is nevertheless a small fraction of the population." NRC II at 32.

publication of NRCII, there have been a number of other research papers addressing this question. There have been authors on each side of the argument: those endorsing the recommendation of NRC II, and those agreeing with the position I have just described [the Balding/Donnelly approach]." Donnelly Affidavit at 5.

E. There is Bitter, Irreconcilable Conflict and Controversy Among the Three Groups.

The disagreement among the relevant experts is open and unresolved. In the March 2004 issue of *Law, Probability and Risk*, scientists published an article that noted the "serious controversy about the strength of DNA evidence when a suspect is identified through a database search; this discussion was statistical and philosophical in nature . . . . One of the main practical problems seems to be the question of how to report the DNA evidence to judges and jurors, since it seems that they are easily misled by the (numerical) statements of the forensic or statistical expert." *See* Ronald Meester & Marjan Sjerps, *Why the Effect of Prior Odds Should Accompany the Likelihood Ratio When Reporting DNA Evidence*, 3 Law, Prob. & Risk, 51, slip op. at 1-2 (2004) (appended). While Meester and Sjerps argued that the proper approach is to apply Bayesian reasoning like Drs. Donnelly and Balding, *id.* invited comments on their article were aggressively opposed. *See* David Balding, *Comment on: Why the Effect of Prior Odds Should Accompany the Likelihood Ratio When Reporting DNA Evidence*, 3 Law, Prob. & Risk 63 (2004) (appended); A.P. Dawid, *Which Likelihood Ratio? Comment on: Why the Effect of Prior Odds Should Accompany the Likelihood Ratio When Reporting DNA Evidence, By Ronald Meester and Marjan Sjerps*, 3 Law, Prob. & Risk 65 (2004) (appended); Christopher M. Triggers & John S. Buckleton, *Comment on: Why the Effect of Prior Odds Should Accompany the Likelihood Ratio When Reporting DNA Evidence*, 3 Law, Prob. & Risk 73 (2004) (appended); Ronald Meester & Marjan Sjerps, *Response to Dawid, Balding, Triggs, and Buckleton*, 3 Law, Prob. & Risk 83

(2004) (appended). Other journals too are publishing on this controversy. *See, e.g.*, Samuel Lindsey, Ralph Hertwig & Gerd Gigerenzer, *Communicating Statistical DNA Evidence*, 43 Jurimetrics J. 147, 148-50 (2003) (appended); Ronald Meester & Marjan Sjerps, *The Evidential Value in the DNA Database Search Controversy and the Two-Stain Problem*, 59 Biometrics 727 (2003) (appended).

In 2002, Professor Balding even published an article titled, "The DNA Database Search Controversy," Balding, *The DNA Database Search Controversy*, 58 Biometrics 241 (March 2002). That article opens, "[M]any of the statistical issues are now largely resolved. One of the areas where consensus remains incomplete concerns the effect of database searches on evidential strength." *Id.* at 241; *see* also *id.* at 243, 244 (further reporting on "controversy" among statisticians). Thus, as demonstrated above, in 2000, Biometrics published a bitter back-and-forth, provided in the Appendix, between Drs. Sensabaugh and Bernie Devlin's supporting NRC II on the one hand and Drs. Evett, Foreman, and Weir, quoting Drs. Balding and Donnelly's counterapproach, on the other. Similarly, in 1997, Jurimetrics published a collection of articles disagreeing with one another on the proper meaning of this evidence, and those articles too are included in the Appendix.

The experts are not mincing words in their disagreement. This has been a particularly bitter dispute that has involved language not normally found in scientific literature. Dr. Balding refers his readers to Dr. Stockmarr's 1999 Biometrics article to observe the "flaws" in NRC II's reasoning and calls Dr. Devlin's support of NRC II "flawed" with reasoning that has "no bearing on the issues" and with an approach that "makes little sense." Balding, *The DNA Database Search Controversy*, *supra*, at 243.

Even the FBI recognizes the dispute noting that, with neither camp's view clearly superior –

or – inferior to that of the other, "we are left with an interesting dilemma." DAB, *Statistical and Population Genetics Issues*, *supra*, at 7. In discussing the battle between the NRC II camp and the Balding/Donnelly camp, the DNA Advisory Board wrote: "Both camps appear to present rigorous arguments to support their positions. Indeed, the proper treatment superficially appears to rest in the details of arcane mathematics. . . . Curiously, the mathematics underlying both approaches is correct, despite the apparently divergent answers. It is the *foundations of the formulations that differ, and they differ substantially*." *Id.* at 6-7 (emphasis added). As Professor Crow pointed out in his 1998 article summarizing the debate: "These are not numerically unimportant disagreements, for the differences among various procedures can be several orders of magnitude." Crow, *1998 NAS Article*, *supra* at 112.

The question for this Court is not which of the three divergent positions is the correct one. *Porter II*, 618 A.2d at 634. The question is whether the government is able to prove that there is general acceptance as to any one of them. *Id.* There clearly is not, and the government should therefore be precluded from admission of the DNA evidence in Mr. ---------'s trial.

Though statistics are difficult and sometimes counter-intuitive, statisticians can reach total agreement on issues where intelligent non-statisticians would believe something completely contradictory, such as the Monty Hall problem discussed above. *See* Affidavit of Dr. Keith Devlin, *supra*. In that problem, all statisticians agree that the answer is to switch doors, thus giving 2/3 chance, even though instinct says that one has a 50-50 chance after learning that door 2 is empty. Statisticians just have not yet arrived at this point of agreement with respect to DNA cold hits.

Because there is no general consensus in the relevant scientific community, the Court has no choice but to exclude the evidence. This jurisdiction's adherence to the *Frye* standard

"retards somewhat the admission of proof based on new methods of scientific investigation by requiring that they attain sufficient currency and status." *United States v. Addison*, 162 U.S. App. D.C. 199, 201, 498 F.2d 741, 743 (1974), *quoted with approval in Porter II*, 618 A.2d at 633. Although the *Frye* test has a "built-in cultural lag," *Porter I*, 1991 WL 319015, at *14, this cost is "outweighed by the benefits of a standard which 'assures that those most qualified to assess the general validity of a scientific method will have the determinative voice." *Id*. (*quoting Addison*, 162 U.S. App. D.C. at 202, 498 F.2d at 744).

In the end, the government's proposed scientific methodology is just too new at this time. *See* Speed Affidavit at ¶ 10. There cannot be three or four possible answers to the ultimate question and still adhere to the dictates of *Frye*. *See Porter II*, 618 A.2d at 631. Thus, the Court cannot admit this evidence until there is *an* answer. As it presently stands, this debate between and among statisticians and population geneticists is beyond the understanding of a jury. At some future date, perhaps there will be an NRC III report reflecting a general consensus among the relevant scientific community, and then the government will be able to introduce a statistic derived from an established method showing the probability of a coincidental match in a case where the defendant was initially identified through a cold hit. Today, however, the government cannot show that there is such a consensus. Once the Court discerns "a lack of general scientific acceptance – which in this instance is palpable – [the Court has] no choice but to exclude the 'bottom line' expression of statistical significance in its current form." *People v. Barney, et al.*, 8 Cal. App. 4th 798, 819, 10 Cal.Rptr.2d 731, 743 (1st Dist.1992), *quoted in Porter II*, 618 A.2d at 639.

F. The Failure To Take Into Account The Mathematical Possibility That A False Positive Contributed To The "Cold Hit" Of Mr. ---------'s Profile In The CODIS Database Requires Exclusion Of The DNA Evidence.

In "cold hit" cases in which the DNA match itself makes the defendant a suspect, often, like here, there is little or no other evidence against the defendant. The absence of other evidence makes the DNA evidence, and the proper statistical presentation of that evidence, all the more important. Scientists across the board acknowledge the possibility of handling or laboratory error leading to a false positive match, *see, e.g.*, Balding, *Errors and Misunderstandings in the Second NRC Report*, *supra*, at 475.[18] "Anything is possible, counsel," as some witnesses like to say. That possibility must be mathematically measured to maximize accuracy and ensure fairness in the presentation of the DNA evidence.

The question of how the probability of a false positive affects the value of DNA evidence was raised in an article by that name in the Journal of Forensic Science last year. *See* William C. Thompson, *et al.*, *How the Probability of a False Positive Affects the Value of DNA Evidence*, 48 J. Forensic Sci. 1 (Jan. 2003) (appended). There, the authors noted that

---

[18] A number of commentators have long expressed that consideration of error rates is crucial to an accurate determination of the probability that the report of a match signals that the defendant is actually the source of the DNA:

> Although a precise probability cannot be associated with the chance of laboratory error, error rates in other types of forensic laboratory tests and the results in the few blind proficiency tests done to date suggest that false positive error rates in DNA tests must be many orders of magnitude higher than the random DNA match probabilities often given juries.

Lempert, *After the DNA Wars: Skirmishing with NRC II*, *supra*, at 446-47. *See also* Jonathan J. Koehler, *On Conveying the Probative Value of DNA Evidence: Frequencies, Likelihood Ratios, and Error Rates*, 67 U. Colo. L. Rev. 859, 869 (1996) (appended); William C. Thompson, *Accepting Lower Standards: The National Research Council's Second Report on Forensic DNA Evidence*, 37 Jurimetrics J. 405, 419-21 (1997) (appended) (noting need for error rate estimation to limit random match probability before it reaches jury).

> [t]he potential for false positives may be a particularly important consideration when evaluating DNA evidence in trawl cases where the prior probability that any particular suspect is the source of an evidentiary sample is very low. In such cases, a key issue is whether the DNA match is sufficiently probative to create a high posterior probability that the suspect is the source despite the low prior probability. The results reported in Table 1 suggest that the probability of a false positive may be a critical factor in determining whether the DNA evidence is indeed strong enough.

Id. at 6. The authors then go on to use an example to show how circumstances under which even low false positive probabilities are of concern.

> Consider, for example, the hypothetical cases reported in Table 1 in which the prior odds that the suspect is the source of an evidentiary sample are 1 in a thousand and the random match probability is 1 in a billion. If the probability of a false positive is zero, then the posterior odds are a million to one in favor of the suspect being the source, which certainly seems high enough to justify confidence in that conclusion. In other words, the DNA evidence has more than enough probative value to make up for the low prior probability. However, if the false positive probability is even 1 in 10,000, the posterior odds in favor of the suspect being the source are reduced drastically to only 10:1. *It is very important for those evaluating DNA evidence to understand that a false positive probability on the order of 1 in 10,000, which may seem low enough to be "safe," may nevertheless undermine that, when combined with a low prior probability, there is still room for doubt about whether the suspect is the source of the matching sample.*

Id. (emphasis added).

It is of course difficult to determine the false positive rate, though 1 in 10,000 does not seem grossly off, and, barring the ability to develop the database cold hit error rate factually (say, by determining the quality of the lab work and the clarity of the results of the VDFS and the private laboratories like Bode with which it contracts), that seems an appropriate estimation.

III. THE ONLY OTHER JUDGE IN D.C. SUPERIOR COURT TO CONSIDER THIS ISSUE HAS RULED THAT THERE IS NO GENERAL CONSENSUS IN THE RELEVANT SCIENTIFIC COMMUNITY AND THAT THE DNA EVIDENCE IS THUS INADMISSIBLE.

The Honorable Rhonda Reid Winston recently ruled on this exact issue in the case of *United States v. Raymond Jenkins,* No. F-320-00. In *Jenkins,* the defendant was identified as a suspect in a

murder case after the government submitted a DNA profile from an evidence sample for comparison to the convicted offender database maintained by the State of Virginia. At the time of the search, Virginia maintained convicted offender profiles at only eight genetic locations ("loci"). Following a match at eight loci, the government obtained a warrant for blood and saliva from Mr. Jenkins. With this new DNA sample in hand, the government obtained a 13-loci profile, which it then matched to the evidence sample at all thirteen loci.

The government sought to provide the jury with the unmodified RMP for all thirteen loci. This resulted in a probability of 1/10,750,000,000,000,000 in the African American population. In response to a defense motion to preclude the introduction of the unmodified RMP, the government offered to present the jury with both the RMP and the statistic recommended by NRC II – the RMP multiplied by the number of people in the database, sometimes referred to as the Database Match Probability or DMP.

Judge Winston considered the articles and affidavits that are submitted herewith as well as affidavits and articles submitted by the government. Judge Winston also heard testimony from two government experts – Drs. Frederick R. Bieber and Ranajit Chakraborty – and one defense expert – Dr. Dan E. Krane. After hearing argument and considering all of the evidence and testimony, Judge Winston held that there is no general consensus in the relevant scientific community.

Judge Winston did find that she believes the NRC II method to be scientifically sound. (4/5/05 Tr. 18). Judge Winston recognized, however,

> I'm reminded of what *Porter* holds, it's not what the Court believes, and I'm not to choose sides or to decided whether this group of people disagree with the NRC II approach or DAB approach are less worthy of belief than the individuals who espouse the view that RMP and DMP should be reported, and so I do believe that there still is a controversy about whether the DAB/NRC II approach is generally accepted.

Id. at 18. Accordingly, Judge Winston found that there did exist controversy: "And it's not a

manufactured controversy, it's not an insignificant one because there are esteemed members of the community on, I would say, both sides but on all the several sides of this issue." *Id*. at 22.[19] Thus, Judge Winston held that the DNA evidence was inadmissible.[20]

Mr. --------- submits that Judge Winston's ruling is legally sound and based on a thorough review and consideration of the different positions of experts in the relevant scientific community. Accordingly, Mr. --------- respectfully requests that this Court adopt the holding of Judge Winston in *Jenkins* and exclude the DNA evidence in this case.

IV. THIS COURT SHOULD EXCLUDE THE DNA EVIDENCE BECAUSE ITS PROBATIVE VALUE IS SUBSTANTIALLY OUTWEIGHED BY ITS PREJUDICIAL EFFECT.

Even should this Court conclude that the government has met its burden of admissibility under the *Frye*/*Dyas* inquiry, Mr. --------- submits that the DNA evidence should nonetheless be excluded because its probative value is substantially outweighed by the potential for prejudice. *Johnson v. United States*, 683 A.2d 1087, 1100 (D.C. 1996) (en banc).

As explained in Section II.C, the government's random match probability calculation –

---

[19] In her ruling, Judge Winston made specific reference to several paragraphs in John Buckleton, Christopher Triggs, & Simon Walsh, eds., *Forensic DNA Evidence Interpretation*, "DNA Intelligence Databases," at 464-65 (CRC Press 2005) (appended). The excerpt from this book, published in 2005, recognizes and highlights the controversy that exists. Dr. Buckleton is the preeminent forensic scientist in New Zealand and is widely respected on DNA forensic issues. Dr. Triggs is a forensic statistician. Dr. Walsh is a forensic biologist.

[20] The government is taking an interlocutory appeal of Judge Winston's ruling. It is worthy of note that Judge Winston provided the government with an opportunity to adopt the NRC I approach as one on which there is general consensus even if it is considered excessively conservative. *Id*. at 23. The government declined this offer and argued that there is no consensus on any of the approaches. *Id*. at 23-24. Rather, the government asserted solely that "as long as DAB approach is sound, statistically and scientifically, regardless of whatever discussions are going on in the scientific community, under *Porter* it can be admitted and should be admitted." *Id*. at 24.

inaccurately expressed as "to a reasonable degree of scientific certainty" – has minimal probative value. As NRC I committee member Dr. Richard Lempert explains, the RMP's probative value is always limited by a larger error rate and failure to include such an error leads to jury confusion:

> A scientists who testifies that false positive error never happens does not address the question the jury needs answered – namely, how likely is it that a match would be reported if the evidence DNA was not the suspect's. Moreover, she risks misleading or confusing the jury because she uses language in a specialized way that invites misinterpretation.

Lempert, *After the DNA Wars*, supra, at 442. Dr. Lempert explains the limited probative value of the RMP alone:

> Although a precise probability cannot be associated with the chance of laboratory error, error rates in other types of forensic laboratory tests and the results in the few blind proficiency tests done to date suggest that false positive error rates in DNA tests must be many orders of magnitude higher than the random DNA match probabilities often given juries. If so, the probative value of a DNA match is always limited by the chance of false positive error.

Id. at 447. Presenting the jury with two numbers, both the RMP and the laboratory's estimated false positive rate, does not solve the prejudice problem, because jurors "may tend to see the probative value of the evidence as somewhere between the two probabilities rather than treating the chance of a false positive report as limiting the probative value of the reported match." *Id.*

On the other hand, the power of the DNA evidence to mislead and confuse the jury is great. It is no surprise that jurors, most of whom do not have a background in mathematics, often "have poor intuitions when it comes to reasoning with statistics in general and forensic science statistics in particular." Jonathan J. Koehler, *The Psychology of Numbers in the Courtroom: How to Make DNA-Match Statistics Seem Impressive or Insufficient*, 74 S. Cal. L. Rev. 1275, 1279 (2001) (appended); *see also* Sworn Affidavit of Dr. Keith Devlin (discussing inability of most people to comprehend probabilities). In empirical studies, jurors tend to determine the probative value of DNA evidence based solely on the probability of a "match by chance," whether or not other factors

minimize the diagnostic value of the RMP in a given case. Koehler, *supra*, at 1280. This is a case in point of the so-called "exemplar cue theory," well known in psychological literature, holding that people will view the probability of an event as inversely proportional to the ease with which alternative examples are cued in their mind. *Id.* Studies have shown that if the target of a DNA match is a particular suspect, examples of coincidental matches are less likely to be "cued" in the juror's mind, and "jurors will be more likely to treat small DNA matches as conclusive proof of identity." *Id.* at 1282. In several experiments from 1998 involving mock jurors, jurors were several times more likely to convict when given an RMP as compared to the phrase "the probability that the suspect would match the blood sample if he were not their source is [X]." *Id.* at 1288.

In their analysis of the risk of errors to "cold hit" identification, Professor Thompson and his colleagues noted that jurors' ability to understand the potential for false positives does not translate into an ability to assess the statistical significance of error:

> Even if jurors understand the various ways in which a false positive might occur, it requires a leap of faith to conclude that they will therefore be able to determine accurately, based on common sense, whether, for example, the probability of such an error in a particular case is 1 in 100 or 1 in 10,000. . . . To rely on jurors' common sense to produce accurate estimates when experts cannot agree seems unduly optimistic.

Thompson et al., *supra*, at 2-3. *See also* Jonathan J. Koehler, *On Conveying the Probative Value of DNA Evidence: Frequencies, Likelihood Ratios, and Error Rates*, 67 U. Colo. L. Rev. 859 (1996) (appended); Jonathan J. Koehler, *The Random Match Probability in DNA Evidence: Irrelevant and Prejudicial?*, 35 Jurimetrics J. 201, 212 (1995) (appended). Accordingly, this Court should exclude the DNA evidence because the prejudicial effect of the evidence substantially outweighs its probative value.

V. THE "COLD HIT" DNA EVIDENCE IN THIS CASE MUST BE EXCLUDED BECAUSE THE GOVERNMENT CANNOT ESTABLISH A PROPER CHAIN OF CUSTODY SUFFICIENT TO AUTHENTICATE THAT THE SAMPLE REPORTEDLY TO BE ----------'S IN THE CODIS DATABASE WAS IN FACT HIS AND WAS PROPERLY ACCOUNTED FOR FROM THE TIME OF HIS BLOOD'S SEIZURE, THROUGH THE ANALYSIS OF HIS BLOOD FOR A PROFILE, TO THE INCLUSION OF THAT PROFILE IN THE DATABASE.

This jurisdiction has adopted Federal Rule of Evidence 901, requiring that evidence be properly authenticated, meaning reliably identified as being what it purports to be, before being admitted. Specifically, a missing link in the chain of custody that calls into question the identity of the evidence is a bar to admission. *See, e.g.*, *Turney v. United States*, 626 A.2d 872, 873 (D.C. 1993); *Novak v. District of Columbia*, 160 F.2d 588, 589 (D.C. Cir. 1947) (urinalysis records improperly admitted where there was "missing a necessary link in the chain of identification" to show specimen tested was defendant's urine); *cf.* D.C. Code § 16-2343.01(a)(2) (requiring proof of chain of custody to admit paternity testing results using Human Leukocyte Antigen (HLA) test)).

Specifically with respect to DNA evidence, several courts have held that gaps in the chain of custody or evidence of contamination in a sample are reasons to exclude such evidence. *See, e.g.*, *Smith v. Deppish*, 807 P.2d 144, 159 (Kan. 1991) (DNA test results may be inadmissible based on relevance, prejudice, chain of custody, or contamination issues). In addition, the Tennessee Supreme Court found the government's proffered DNA evidence to be inadmissible due to the government's failure to prove chain of custody with respect to the hair samples:

> We agree with the appellant that the trial court erred in finding that the hair samples were properly authenticated. The hairs were not identified by a witness with knowledge that the mounted hair samples were the same hairs as the ones originally taken from the victim. Further, we can find no evidence whatsoever to show how the hairs came to be mounted on the slides. We also can find no evidence to show who mounted the hairs on the slides or whether the hairs were mounted in a manner sufficiently free of contamination or alteration. Although the hairs were apparently mounted . . . by someone at the FBI, no one was able to establish this important "link" in the chain of custody.

State v. Scott, 33 S.W.3d 746, 760-61 (Tenn. 2000). Here, this Court knows absolutely nothing about the chain of custody as to Mr. ---------'s alleged DNA sample that was included in the CODIS database. At a pretrial hearing, the government must show each link in the chain to establish a sufficient chain of custody for this Court to admit the DNA evidence from the cold hit in this case. Moreover, establishing a chain of custody is especially crucial in admitting scientific evidence that, like DNA, is "hypersensitive to contamination." *Id.* at 761 n.13. Without such a showing, the DNA evidence is inadmissible under Rule 901.

Conclusion

The concern of the *Frye* test is that courts not supplant scientists in determining the validity of scientific methods; a technique must be sufficiently tested and stable before it is introduced in a courtroom and used to take away a citizen's physical liberty. Additionally, under *Dyas*, the cold hit DNA evidence must be sufficiently reliable to reasonably form the basis for the government's DNA expert's testimony. Cold hit DNA evidence is not now at the point of general acceptance in the scientific community, the government's interpretation of the test results are not sufficiently reliable, and the evidence would severely prejudice Mr. ---------.

WHEREFORE, For the foregoing reasons, and for such other reasons that may appear to this Court at a hearing on this Motion, Mr. --------- respectfully requests that this Court exclude all DNA evidence from this case.

Respectfully submitted,

_____

Ronald Horton
Eric K. Klein
Counsel for ----------

Public Defender Service
for the District of Columbia
633 Indiana Avenue, N.W.
Washington, D.C. 20004
(202) 628-1200

CERTIFICATE OF SERVICE

I hereby certify that a copy of the foregoing Motion and accompanying Memorandum of Points and Authorities has been served this 21st day of April 2005, by fax, without appendices (305-0652), by hand, with appendices, upon Kimya Jones, Esq., United States Attorney's Office for the District of Columbia, 555 Fourth Street, N.W., Washington, D.C. 20530.

_____

Eric K. Klein