

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

<b>UNITED STATES</b>	:	
	:	<b>Criminal No. F-7330-99</b>
v.	:	<b>Judge Bowers</b>
	:	
<b>--REDACTED--</b>	:	

**MOTION TO EXCLUDE MITOCHONDRIAL DNA “INCLUSION” EVIDENCE, EXPERT TESTIMONY, AND SEQUENCE FREQUENCY STATISTICS**

--REDACTED--, 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), and the Due Process Clause of the Fifth Amendment, to exclude all mitochondrial DNA (mtDNA) evidence and testimony from the government’s case. The methods used by the government in collecting, amplifying, and analyzing such evidence are not generally accepted by the scientific community. To the extent that scientific standards and protocols *do* exist for the handling and analysis of such evidence, the Unit II Laboratory of the Federal Bureau of Investigation (FBI) did not follow such standards. Moreover, the statistics proffered by the government to explain the significance of the alleged “inclusion” are not generally accepted and, in addition, are overly prejudicial because of their potential to mislead and confuse the jury. --REDACTED-- requests a hearing on this motion.<sup>1</sup>

**Overview**

The FBI has just recently begun to use mitochondrial DNA (mtDNA) testing in its criminal

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<sup>1</sup> The defense has sent two letters to the government, one on May 3 and one on May 14, 2002, requesting additional discovery with respect to the mtDNA testing and analysis done in this case. The defense has not yet received the requested material, although AUSA Deborah Sines has represented that such material is forthcoming. --REDACTED-- reserves the right to supplement this motion in light of any further disclosures by the government.

investigations in D.C. Although the D.C. Court of Appeals has held that the scientific procedures for collecting and analyzing *nuclear* DNA are generally accepted by the scientific community and thus admissible under Frye v. United States, 293 F. 1013 (D.C. Cir. 1923), the Court has not yet addressed the admissibility of mtDNA evidence. The differences between nuclear and mtDNA evidence are stark. Unlike nuclear DNA, mtDNA *is not a means of identification*; it can only “exclude” or “fail to exclude” a suspect as the source of an evidence sample. In addition, the amplification and analysis of mtDNA evidence, as well as the interpretation of test results, are mired in controversy and are significantly affected by phenomena such as “heteroplasmy,” high risk of contamination, mutation, and “recombination” that are only beginning to be understood by the scientific community. Moreover, the database used to interpret mtDNA test results is too small, containing only 749 African-American sequences; scientists admit they have much to learn about the statistical meaning of “inclusions” and “exclusions” and when to call one or the other.

--REDACTED-- does not take issue with the general method used for amplification of mtDNA, polymerase chain reaction (PCR). Instead, --REDACTED-- takes issue with the FBI’s use of mtDNA evidence to “include” suspects, including herself, based on FBI interpretive guidelines that are not independent and have not been independently validated or reviewed by peer institutions, do not adequately account for certain scientific phenomena that reputable scientists have publicly acknowledged, and that rely on a database too small and counting method too rough to be statistically sound. In addition, without proof of a proper chain of custody with respect to the hair samples used in the mtDNA analysis in this case, such samples (and the resulting mtDNA evidence) must be excluded. Thus, under both Frye/Dyas and the rules of evidence, this Court must exclude the government’s proffered mtDNA evidence and any testimony based on it.

## 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, see 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 is sufficiently reliable to be “reasonably relied upon” by the expert. United States v. Melton, 597 A.2d 892, 901, 903 (D.C. 1991); see also State v. Scott, 33 S.W.3d 746, 757 (Tenn. 2000) (in mtDNA case, noting that “the underlying facts or data upon which the expert relied must be trustworthy”).

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. 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). 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, 618 A.2d at 635 (citing Jones v. United States, 548 A.2d 35, 41 (D.C. 1988)). Courts also look to the existence of validation studies and peer review of the technology or technique. Id. at 638 n.13; Daubert, 509 U.S. at 584 . 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.” United States v. Porter, 618 A.2d 629, 634 (D.C. 1992) (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 v. Merrell Dow Pharmaceuticals, 509 U.S. 579, 590 n.9 (1993), 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. See also People v. Shreck, 22 P.3d 68, 78 (Colo. 2001) (en banc) (shifting from

Frye to 702 standard and noting that standard for admissibility of DNA expert witness testimony contemplates finding that bases for testimony are reliable).

The D.C. Court of Appeals has also made clear in the context of DNA that the “relevant scientific community” in determining whether a technique has been generally accepted is *not* merely the insulated community of forensic scientists, but the larger community of individuals “whose scientific background and training are sufficient to allow them to comprehend and understand the process and form a judgment about it.” Porter, 618 A.2d at 634. The Court speculated that forensic scientists likely “accept – no qualifier necessary – forensic DNA evidence and believe that the time has come for its use as powerful evidence in criminal trials.” Id. Just as the “relevant scientific community” includes more than merely forensic scientists, the need for validation studies and peer review extends beyond merely forensic laboratories. The Frye/Dyas standard requires more than internal validation studies done by the laboratory researchers themselves, who have personal and professional interests in promoting the legitimacy of the science and its readiness to be used in the lucrative field of forensic casework.

Safeguarding the courtroom from applications of scientific theories that have not sufficiently endured the crucible of peer review to be “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 its almost mysterious quality. 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)).

Several Frye jurisdictions, noting the connection between the Frye inquiry and the need to ensure the reliability of the specific test results relied upon by an expert, have explicitly added a “third prong” to the test for admissibility of DNA evidence that focuses on the adherence to correct scientific procedures in the particular case at hand. Such courts emphasize the special need in DNA cases for including this “third prong” because of the profound impact that DNA evidence has on juries and because DNA testing requires such precision and quality control to ensure accuracy. See, e.g., Spencer v. Murray, 5 F.3d 758 (4th Cir. 1993) (denying habeas relief and noting absence of case-specific errors such as in Castro, below); United States v. Two Bulls, 918 F.2d 56 (8th Cir. 1990), *vacated on other grounds*, 925 F.2d 1127 (8th Cir. 1991) (adopting Castro 3-pronged test because of high potential for prejudice if issue is debated after jury hears DNA evidence); Ex Parte Perry v. State, 586 So.2d 242, 250 (Ala. 1991) (“In this particular case, did the testing laboratory perform generally accepted scientific techniques without error in the performance or interpretation of the tests?”); People v. Axell, 1 Cal. Rptr. 2d 411, 421 (Cal. Ct. App. 1992) (California’s “Kelly/Frye” test includes third prong requiring a showing that “correct scientific procedures were used in the particular case”); Polk v. State, 612 So.2d 381, 390 (Miss. 1992) (adopting test verbatim from Ex Parte Perry); People v. Castro, 545 N.Y.S.2d 985, 987 (N.Y. Sup. Ct. 1989) (“Did the testing laboratory perform the accepted scientific techniques in analyzing the forensic samples in this particular case?”); State v. Ford, 392 S.E.2d 781, 783 (S.C. 1990) (applying Castro and noting defense’s lack of argument as to reliability of particular tests conducted in this case).

Predicating admissibility of mtDNA evidence not only on the scientific community’s acceptance of the science involved but also on the laboratory’s adherence to generally accepted procedures in the particular case is crucial to avoid prejudicing the jury with unreliable or confusing DNA evidence:

Because DNA evidence is so new and the resulting prejudice to the defendant is sufficiently great, it is imperative that the court satisfy itself that there exists a sufficient foundational basis as to the overall admissibility of the evidence. This must be done before the government exposes the jury to the lab results. If the court has explored only scientific acceptability and the reliability of acceptable testing procedures in camera, and then, at trial the government fails to show that the lab tests did conform to reliable procedures, the court would have to exclude the evidence for lack of foundation. In doing so, the resulting prejudice to the defendant would be obvious. Notwithstanding the fact that an objection is sustained and the evidence excluded, aside from valuable trial time wasted, the jury would be exposed to prejudicial proofs and left to speculate as to why the defendant opposed the ultimate result.

Two Bulls, 918 F.2d at 60.

Thus, the government in this case must prove at a Frye hearing both that the collection, amplification, and interpretation methods used in its mtDNA analysis are generally accepted in the scientific community *and* that the FBI adhered to such generally accepted procedures in this case. As discussed below, because of the infancy of forensic mtDNA casework and the lack of independent review of the FBI's procedures and statistical methodology, the government cannot successfully show either general acceptance or reliability sufficient to pass muster under Frye/Dyas.

## **B. The Science of Mitochondrial DNA – An Introduction**

To understand the concept of mitochondrial DNA, it is helpful first to understand the broader concept of DNA. The D.C. Court of Appeals articulately explained, in layman's terms, the definition of DNA and the nature of forensic DNA analysis in United States v. Porter:

DNA is sometimes called the blueprint of life. It contains the chemical instructions for all of life's processes, as well as the "genetic code" that defines who we are, what we look like, and where our talents lie. With the exception of identical twins, no two people have the same DNA. . . . In recent years, forensic technologies have been developed for removing the DNA from human cells discovered at crime scenes and for comparing the evidentiary sample with the suspect's DNA.

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Embedded within the nucleus of virtually every cell of each human being's body are forty-six rod-shaped chromosomes. Half of these chromosomes are inherited from

one's mother and half are inherited from one's father. Each chromosome has the shape of a twisted ladder or spiral staircase. The "banisters" of this staircase are made of phosphates and sugars, while the "steps" or "rungs" consist of "base pairs," or pairs of amino acids bound together.

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Located at specific sites, or "loci," along each chromosome are large groups of base pairs known as "alleles," or "genes." Over 99% of these genes are identical among all human beings. . . . The remaining genes – known as "polymorphic" genes because they vary in form from person to person . . . account for our unique characteristics as individuals. Many polymorphic genes are known to have definite functions: some are responsible for the color of our hair . . . . Other polymorphic genes, however, appear to have no function whatever. These "junk DNA" segments, which typically consist of varying lengths of repeating sequences of base pairs, form the basis for the DNA identification evidence at issue in this case.

618 A.2d at 632.

The DNA at issue in Porter was *nuclear* DNA, meaning the DNA bundled up into chromosomes that are located exclusively in the nucleus of each human cell. Recently, scientists have discovered that tiny particles found in cells (but outside the nucleus) called "mitochondria" also contain DNA.<sup>2</sup> Unlike the nuclear DNA strand, which contains approximately 3 million base pairs, the human mtDNA "genome" consists of only 16,569 base pairs.<sup>3</sup> In that sequence, two "hypervariable" regions exist – typically referred to as HV1 and HV2<sup>4</sup> – within a larger "control region" of non-coding or "junk" mtDNA.<sup>5</sup> These regions, because they are allegedly highly

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<sup>2</sup> National Research Council, *The Evaluation of Forensic DNA Evidence* 72-73 (1996) [hereinafter NRC (1996)].

<sup>3</sup> Thomas J. Parsons & Michael D. Coble, Increasing the Forensic Discrimination of Mitochondrial DNA Testing through Analysis of the Entire Mitochondrial DNA Genome, 42 *Croatian Med. J.* 304, 304 (2001) [hereinafter Parsons & Coble (2001)].

<sup>4</sup> Scientists know very little about the region outside HV1 and HV2. The Armed Forces DNA Identification Laboratory is in the process of attempting to map the entire mtDNA genome "in order to identify sites that . . . alleviate the problem of low discriminatory power when common HV1/HV2 types are encountered." Parsons & Coble (2001), at 305.

<sup>5</sup> In the context of mtDNA, "junk" mtDNA might more accurately be described as "DNA whose function is yet unknown," given that the mtDNA genome has not yet been mapped and mtDNA analysis is still in its infancy. Even in the context of the better-understood nuclear DNA, a recent study showed that the nuclear DNA genome contains much less "junk" DNA than

variable within the human population, are the only regions used in mtDNA forensic testing. Together, HV1 and HV2 make up only about 610 bases.<sup>6</sup>

The transmission of mitochondria is usually only from mother to child;<sup>7</sup> all children of one woman will, theoretically, have identical mitochondrial DNA profiles.<sup>8</sup>

Unlike the nuclear DNA genome, only two “copies” of which exists in each cell, there are 500-2000 copies of mitochondria in any given cell.<sup>9</sup> Because of its abundance, mtDNA will survive in even highly degraded forensic samples such as hair, bones, fingernails, and saliva.<sup>10</sup> Once the mtDNA is collected, it is amplified using the same technique – polymerase chain reaction (PCR) – as is currently used in nuclear DNA analysis. The amount of amplification cycles needed to test a mtDNA sample, however, far exceeds the number required in nuclear DNA analysis; according to the government’s proffered expert in this case, over thirty cycles are required. See Constance Fisher et al., Mitochondrial DNA: Today and Tomorrow, presented at the Eleventh Int’l Symposium on Human Identification (2000) [hereinafter Fisher, et al. (2000)]. This increase in amplification leads to a high risk of contamination. See discussion infra at II.D.

Unlike in nuclear DNA analysis, where an individual’s forensic DNA profile consists of that person’s allelic combination (from both mother and father) at each of thirteen loci used by the FBI in its analysis, a person’s mtDNA profile merely consists of that person’s HV1/HV2 sequence within the single linked mtDNA molecule. In other words, mtDNA “is a single genetic locus.”

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scientists had assumed. See Andrew Pollack, Citing RNA, Studies Suggest a Much Deeper Gene Pool, N.Y. Times, May 4, 2002, at A10.

<sup>6</sup> Id.

<sup>7</sup> See J.L. Elson et al., Analysis of European mtDNAs for Recombination, 68 Am. J. Hum. Genet. 000, 000 (2001) [hereinafter Elson et al. (2001)].

<sup>8</sup> In some cases, a small amount of “paternal leakage” may occur, causing a child to have some mitochondria passed down from the father. See discussion infra at II.A.

<sup>9</sup> Parsons & Coble (2001), at 304.

<sup>10</sup> Id.

Department of Justice, Mitochondrial DNA Analysis at the FBI Laboratory, Forensic Science Communications (July 1999) [hereinafter 1999 DOJ Report].

Whereas the probability of a random person having the nuclear DNA profile of the evidence sample is calculated using the “product rule” (multiplying the probabilities of each of the thirteen allelic combinations together), which typically generates “random match probabilities” of one in 3 billion and the like, the probability of a random person have the same mtDNA profile is determined by estimating the frequency of that person’s sequence in a relevant human population. Put simply, mtDNA typing “*does not provide definitive identification.*”<sup>11</sup> Indeed, even government laboratory researchers acknowledge the reality that “there is an appreciable chance for a random match in the population” in mtDNA testing.<sup>12</sup> Thus, the most that can be said about a suspect after mtDNA testing is that he is “*excluded*” or “*not excluded*” as the source of the evidence sample.

Any lay person studying allelic ladders and seeing the vast number of possibilities for nuclear DNA combinations at various loci will be astonished at the lack of diversity in mtDNA sequences among humans. For example, two randomly selected Caucasian individuals will have, on average, only eight base-pair differences in their mtDNA control region sequences. Tomasz Grzybowski, Extremely High Levels of Human Mitochondrial DNA Heteroplasmy in Single Hair Roots, 21 Electrophoresis 548, 551 (2000) [hereinafter Grzybowski]. In addition, certain mtDNA sequence “types” are quite common, accounting for nearly 7% of the U.S. Caucasian population. Parsons & Coble (2001), at 305. Indeed, of the 602 different African-American mtDNA profiles in the FBI database,<sup>13</sup> 37% occur at least twice. Fisher et al. (2000) at 3.<sup>14</sup>

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<sup>11</sup> Id.

<sup>12</sup> Id.

<sup>13</sup> Although the FBI database contains 794 African-Americans’ profiles, many of those individuals have the same sequence. Thus, only 602 unique African-American sequences are listed in the database.

Mitochondrial DNA testing is in its infancy; as of 2001, “[i]nvestigators in the United States [were] still learning about the availability of mtDNA testing.” Terry Melton & Kimberlyn Nelson, Forensic Mitochondrial DNA Analysis: Two Years of Commercial Casework Experience in the United States, 42 *Croatian Med. J.* 298, 301 (2001) [hereinafter Melton & Nelson (2001)]. Although mtDNA testing can prove useful to historical research and human remains identification from a list of known sources, neither the state of the interpretive guidelines nor the procedures followed by the FBI is advanced enough to be considered generally accepted by the scientific community for purposes of forensic casework.

**II. THE mtDNA EVIDENCE DOES NOT MEET THE FRYE/DYAS TEST BECAUSE SEVERAL BASIC ASSUMPTIONS UNDERLYING mtDNA ANALYSIS AND INTERPRETATION ARE MIRED IN CONTROVERSY AND NOT WELL UNDERSTOOD.**

The science of mtDNA is relatively new and rapidly evolving. Several key points of contention with respect to basic assumptions about mtDNA still remain among forensic scientists. Although the state of the science may one day soon be sufficiently stable to warrant use of mtDNA in criminal trials, it is not yet close.

**A. Paternal Leakage**

Until very recently, scientists assumed that mtDNA was inherited solely from one’s mother. In 1999, a group of British scientists from Sussex University found signs of “recombination,” or mixing between maternal and paternal mtDNA, in offspring. Adam Eyre-Walker, Noel Smith, &

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<sup>14</sup> A person’s mtDNA “profile” consists of a list of locations at which that person’s sequence differs from a reference sequence. By convention, scientists use as a reference the first complete published mtDNA sequence, named the “Anderson sequence” after the author of a 1981 study. 1999 DOJ Report, at 2.

John Maynard Smith, How Clonal Are Human Mitochondria?, 26 Proc. Royal Soc’y London 477 (1999) [hereinafter Eyre-Walker et al. (1999)]. The explanation for this recombination, also called “paternal leakage,” is *still* unknown; the assumption has been that no physical contact occurs between maternal and paternal mtDNA during the fertilization process. Indeed, three FBI scientists presented proposed mtDNA interpretation guidelines at a 1999 conference working on the assumption that “[t]here does not appear to be any recombination at the mtDNA.” Bruce Budowle, Joseph A. DiZinno, & Mark R. Wilson, Interpretation Guidelines for Mitochondrial DNA Sequencing, *presented at the Tenth Annual Int’l Symposium on Human Identification* (1999) [hereinafter FBI Guidelines]. The government’s proffered expert in this case, Constance Fisher, has posited that mtDNA is entirely maternally inherited and “treated as a single locus due to the lack of recombination.” Constance L. Fisher et al., Mitochondrial DNA: Today and Tomorrow, *presented at the Eleventh Annual Int’l Symposium on Human Identification*, at 1 (2000) [hereinafter Fisher et al. (2000)].

Recombination of mtDNA, if corroborated by further studies, could shatter the most basic assumption used by scientists in interpreting mtDNA test results. The lack of consensus in the scientific community about the existence of recombination, the rate of its occurrence, and the effect of recombination on the use of mtDNA as a tool for identification purposes in criminal cases precludes a finding under Frye/Dyas that mtDNA analysis is sufficiently established to allow the government to secure convictions based on alleged “inclusions.”

In any event, Elson et al. (2001) notes that the existence and prevalence of “biparental recombination” is a “persistent question” in the forensic community. Id. (noting a number of challenges to Eyre-Walker’s work, and a number of rebuttals to those challenges); see also Mitchell Holland & Thomas Parsons, Mitochondrial DNA Sequence Analysis – Validation and Use for

Forensic Casework, 11 Forensic Science Review 22 (1999) [hereinafter Holland & Parsons (1999)] (general rule is maternal inheritance but nothing that “the mechanism for elimination of paternal mtDNA is not fully elucidated, nor known to be absolute in terms of extremely low level persistence”). Elson’s conclusion strikes at the heart of the reason for many court’s adherence to the Frye test: “This [recombination] issue is thus unresolved at the present time, and it is in need of further analysis and critical evaluation.” Id.

## **B. Heteroplasmy**

Nuclear DNA is “homoplasmic,” meaning that an individual’s DNA sequence is identical from cell to cell throughout his or her entire body. In contrast, mtDNA is “heteroplasmic,” meaning that an individual’s mtDNA sequence may be different in a bone cell than in a hair cell. See Melton & Nelson (2001), at 300. In other words, *one* individual can simultaneously have *two* or more mtDNA profiles. There exists both *length* and *site* heteroplasmy; length heteroplasmy is a base-pair difference in two of a person’s mtDNA sequences; site heteroplasmy is when two bases appear at one position in an otherwise unmixed sequence. Id. Such a phenomenon has profound implications for forensic mtDNA testing; if the samples being tested all reflect merely one of several mtDNA profiles in the sample’s source, a perceived inclusion or exclusion could be illusory. For example, the FBI currently considers a one-base-pair mismatch to be a “match” and not an exclusion due to the possibility of undetected heteroplasmy.

Heteroplasmy is an especially significant factor in a case such as --REDACTED--’s case, involving a comparison between hair (the crime scene sample) and blood (the sample taken from --REDACTED-- post-arrest). Heteroplasmy is “incomparably more frequent in hair than in other tissues.” Tomasz Grzybowski, Extremely High Levels of Human Mitochondrial DNA Heteroplasmy in Single Hair Roots, 21 Electrophoresis 548, 550 (2000) [hereinafter Grzybowski

(2000)]. Additionally, the existence of heteroplasmy calls into question the legitimacy of the mtDNA database statistics, as only one profile from each individual is listed in the database. Were the database to account for heteroplasmy, a particular profile may be much more common than originally thought.

Scientists differ in their estimates of the percentage of the human population exhibiting heteroplasmy. While some estimates are between 8 and 10%, others are much higher. Researchers conducting a two-year study of commercial casework at Mitotyping Technologies found a 9.7% rate of site heteroplasmy in hair samples, as well as 110 instances of length heteroplasmy. See Melton & Nelson at 300. Researchers Cassandra Calloway and Rebecca Reynolds of Roche Molecular Systems, examining the level and frequency of heteroplasmy in various tissue samples and age groups, found a heteroplasmy rate of 51.2%.<sup>15</sup> Forensic Medicine Institute researcher Tomasz Grzybowski found heteroplasmy in 13 individuals in a 35-subject study, with 7 individuals exhibiting heteroplasmy at more than one location and one individual at *six* locations. Grzybowski (2000) at 550. Scientists from the Forensic Science Service in London and the Institute of Legal Medicine in Spain, in response to Grzybowski's study, acknowledged that "it is clear that mtDNA heteroplasmy exists at an appreciable frequency." Gillian Tully & Maviky Lareu, Controversies over Heteroplasmy, 22 *Electrophoresis* 180 (2001). Jennie Grover and Mitchell Holland of the Armed Forces DNA Identification Laboratory presented a study concluding that *all* humans are heteroplasmic to some degree.<sup>16</sup> This high rate of heteroplasmy suggests that additional mtDNA testing of criminal suspects may produce results excluding them as the source of an evidence

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<sup>15</sup> See Cassandra Calloway & Rebecca Reynolds, Characterization of Heteroplasmy Across Various Tissue Types and Age Groups, presented at the Tenth Annual International Symposium on Human Identification, September 29, 1999.

<sup>16</sup> See Jennie C. Grover, Mitchell Holland, and Marie-Gaelle Le Roux, An International Study on the Detection of Heteroplasmy in Mitochondrial DNA, presented at the Tenth Annual International Symposium on Human Identification, September 29, 1999.

sample or, alternatively, that testing of another individual would produce a match.

Scientists still do not know whether heteroplasmy exists within individual mitochondria, in different mitochondria in the same cell, or in different mitochondria in different cells within the same tissue. See Kazumasa Sekiguchi, Kentaro Kasai, & Barbara Levin, Human Mitochondrial DNA Heteroplasmic Variation Among Thirteen Maternally Related Family Members, NIST and the National Research Institute of Police Science, Kashiwa-shi, Chiba, Japan (1999). Some scientists have suggested that heteroplasmy changes during a person's lifetime. See Gillian Tully, et al., Control Region Heteroplasmic Differences Between Fetal and Adult Mitochondrial DNA, *presented at Mitochondria: Genetics, Health, and Disease* (Dec. 2, 1998) (finding 30.2% heteroplasmy rate, 52.4% in adults and 9.1% in fetuses, and suggesting that heteroplasmy “may be an ongoing process throughout life.”).

Dr. Grzybowski explained the significance of heteroplasmy to forensic mtDNA analysis:

[E]xtremely high levels of heteroplasmy in single hairs have important implications for the forensic interpretation of mtDNA sequence data. Since there is no sequence homogeneity between hair and other tissues, reference hair will always be required to identify evidentiary hair samples. Moreover, due to the differential level of heteroplasmy observed from hair to hair, *more reference samples should be analyzed before a final conclusion can be reached*.

Gryzybowski (2000) at 552 (emphasis added). Dr. Grzybowski noted that “relatively little information exists on [heteroplasmy’s] biological meaning.” Id. Heteroplasmy “can be difficult to distinguish from ‘background’ in sequencing data,” and “newer and ‘cleaner’” technologies are being developed to deal with the problem. Holland & Parsons (1999), at 25.

Notwithstanding the significance of heteroplasmy to forensic DNA typing, no standards currently exist for accurately detecting or interpreting heteroplasmy in mtDNA testing. According to the National Institute of Standards and Technology (NIST), standards for quality control and for determining the presence of heteroplasmy in forensic testing are still under development. See Lois

Tully, Frederick Schwartz, & Barbara Levin, Development of a Heteroplasmic Mitochondria DNA Standard Reference Material for Detection of Heteroplasmy and Low Frequency Mutations, NIST, Gaithersburg, MD, 1999. Researchers at the Mitotyping Technologies commercial laboratory noted in 2001 that a laboratory’s ability to detect heteroplasmy “is, of course, reliant on the sensitivity of instrumentation and may also be dependent on the particular chemistry used for sequencing. Therefore, . . . different laboratories may have different abilities to detect site heteroplasmy.” Melton & Nelson at 302. To date, the government in --REDACTED--’s case has not explained the FBI Unit II Laboratory’s method for detecting heteroplasmy or proven that such a method is generally accepted in the scientific community. Without such information, this Court cannot certify the FBI’s mtDNA testing procedures under the Frye/Dyas standard.

### **C. Mutation Rate**

Unlike an individual’s nuclear DNA profile, which remains constant throughout an individual’s lifetime, an individual’s mtDNA sequence(s) can mutate, or change, over time. The prevalence and frequency of such mutation is the subject of much controversy in the scientific community. The FBI’s proposed interpretation guidelines for mtDNA analysis note the existence of “mutational hotspots residing within the mtDNA genome.” Bruce Budowle, Joseph A. DiZinno, & Mark R. Wilson, Interpretation Guidelines for Mitochondrial DNA Sequencing, presented at the Tenth Annual Int’l Symposium on Human Identification, at 3 (1999) [hereinafter FBI Guidelines]. But as Elson et al. (2001) observe, “there is considerable debate over the rate of human mtDNA divergence.” Id. at 000. The continuing scientific debate over mutational rate and its impact on forensic testing underscores the lack of general acceptance in the scientific community over the accuracy of the interpretation of mtDNA test results. Consequently, the mtDNA evidence in this

case must be excluded pursuant to Frye/Dyas.

#### **D. High Rates of Contamination in mtDNA Analysis**

Mitochondrial DNA testing presents a higher risk for contamination than nuclear DNA testing because of the need for many more stages of PCR amplification. To conduct mtDNA analysis, technicians must make very small amounts of DNA visible, which entails amplifying a sample  $10^{20}$  times more than in PCR amplification of nuclear DNA. The risk of contamination when amplifying to such a degree is highly troubling:

The most critical potential source of error in mtDNA sequencing is contamination. If more than one individual's DNA is extracted and amplified, the sequencing results will reflect this mixture. In extreme cases the contaminating DNA can greatly exceed the DNA from the donor, and thereby yield a false positive result.

Mark Wilson, Bruce Budolwe, & Mitchell Holland, Guidelines for the Use of Mitochondrial DNA Sequencing in Forensic Science (1993). To address the issue, the FBI has established a "contamination ratio" of 10:1, meaning that the FBI considers one part contamination per 10 parts mtDNA sample to be acceptable. See Fisher et al. (2000), at 2. The FBI arrived at this figure through a single test of five samples, a size consistent with a 35% laboratory error rate. See Mark Wilson et al., Extraction, PCR Amplification and Sequencing of Mitochondrial DNA from Human Hair Shafts, 18 BioTechniques 662 (1995). Wilson and Dr. Budolwe, both researchers in the FBI's laboratory division, have conceded that the FBI's method of assessing acceptable contamination rates in the laboratory is one that is not utilized by any other DNA testing laboratory in the world. Dr. William Shields, a DNA researcher at the State University of New York in Syracuse, has testified that the FBI has insufficient data to permit the use of the 10:1 contamination ratio.

A commercial laboratory, Mitotyping Technologies of Pennsylvania, recently conducted a two-year study over thousands of trials to determine the effect of heteroplasmy, contamination, and

other factors on laboratory test results. See Terry Melton & Kimberlyn Nelson, Forensic Mitochondrial DNA Analysis: Two Years of Commercial Casework Experience in the United States, 42 *Croatian Med. J.* 298 (2001). With respect to contamination, the researchers found the presence of contaminants in 2.4% of cases. Id. At 300. The source of the contaminated DNA was not laboratory staff; the researchers determined the contaminants came from a source outside of the laboratory. Id. In at least two cases, the contamination affected the interpretation of results. Id.

The significantly skewing effect that contamination and over-amplification can have on mtDNA testing results is evident from scientists' critiques of a study conducted on heteroplasmy rates in hair samples. Forensic Medicine Institute researcher Tomasz Grzybowski conducted a study showing extremely high rates of heteroplasmy in hair samples, including at locations along the mtDNA sequence where heteroplasmy had never been seen in the mtDNA database used by the FBI. See Grzybowski (2000) at 550. In turn, scientists at the FBI laboratory in D.C. and at George Washington University took issue with Dr. Grzybowski's study, claiming that the results were unreliable because of likely contamination and an "excessive number of amplification cycles." Bruce Budowle, Marc W. Allard, & Mark R. Wilson, Critique of Interpretation of High Levels of Heteroplasmy in the Human Mitochondrial DNA Hypervariable Region I from Hair, 126 *Forensic Sci. Int'l* 30, 30 (2002) [hereinafter Budowle et al. (2002)] (suggesting that Grzybowski's "odd" results might be due to additional amplification cycles and large quantity of template DNA); Gillian Tully & Maviky Lareu, Controversies over Heteroplasmy, 22 *Electrophoresis* 180 (2001) (acknowledging that heteroplasmy "may be the true explanation" for Grzybowski's results but that further studies and quality control measures are necessary).

Budowle et al. also suggest that Grzybowski's results could have been caused by accidental amplification of a "nuclear pseudogene," a gene found on the nuclear genome; researchers "have

mapped a nuclear pseudogene to chromosome 11 that corresponds to the human mtDNA control region.” Budowle et al. (2002) at 32. When the pseudogene is amplified instead of the mtDNA sequence, which is apparently an understandable mistake, the results are compromised; indeed, Budowle et al. declare that amplification of such pseudogenes “should be considered before relying on data generated with as many PCR cycles as employed by Grzybowski.” Id.

In addition to the contamination occurring in the amplification process, the FBI’s method of washing hair samples for mtDNA testing exacerbates the contamination problem. According to Dr. Shields, the FBI’s method has been *rejected* by other independent laboratories and is no longer used because other laboratories found it to be insufficient in removing contaminants, such as mtDNA from foreign sources that could be transferred to the hair during collection, storage, or analysis.

The debate in the scientific community concerning the acceptable level of contamination in mtDNA analysis is far from over. The absence of any independently determined standards other than the self-serving 10:1 ratio used by the FBI cannot satisfy the generally acceptance standard of Frye/Dyas.

### **III. THE mtDNA EVIDENCE MUST BE EXCLUDED BECAUSE THE FBI UNIT II LABORATORY DID NOT FOLLOW THE CORRECT SCIENTIFIC PROCEDURES IN *THIS* CASE.**

As noted above, both because the basis of an expert’s testimony must be sufficiently reliable to be “reasonably relied upon” under Dyas and because DNA evidence is sufficiently prejudicial to require a “third prong” under Frye to ensure quality control in testing results, the government must prove that the mtDNA analysis and interpretation *in this case* was both sufficiently trustworthy and adhered to generally accepted scientific principles and procedures.

In this case, the FBI Unit II laboratory appears to have failed to meet several generally

accepted standards. First, it failed to preserve a portion of the mtDNA sample for duplicate testing. The 1996 NRC Report acknowledged that laboratory error can never be completely eliminated in DNA testing and, thus, “evidence material should be separated into two or more portions, with one or more portions reserved for possible duplicate tests. *Only an independent retest can satisfactorily resolve doubts as to the possibility that the first test was in error.*” 1996 NRC Report at 25 (emphasis added).<sup>17</sup>

Second, according to molecular biologist and DNA expert Dr. Theodore Kessis, with whom the defense has consulted on this case, there are troubling amounts of contamination in the reagent blank runs in the data provided by the government in this case. As discussed above, such contamination can often skew results of mtDNA testing and should undercut confidence in the reliability of the results in this case.

Because much of the discovery requested as necessary in this case to the defense’s independent evaluation of the mtDNA has not yet been provided, --REDACTED-- does not have sufficient material to expose all the ways in which the FBI Unit II laboratory may have failed to take into account phenomena such as heteroplasmy, mutation, contamination, possible material relatives as sources, and other relevant factors. --REDACTED-- expects that, at the Frye/Dyas hearing in this case, and after the defense expert is able to better evaluate all the data once it has been provided, she will have more instances to show the Court of the FBI’s failure to adequately follow generally accepted procedures for collecting, amplifying, analyzing, and interpreting the mtDNA test results.

#### **IV. THE LACK OF INDEPENDENT VALIDATION STUDIES OF THE FBI’S METHOD OF ANALYZING mtDNA AND INDEPENDENT GUIDELINES TO GOVERN THE FBI’S mtDNA SEQUENCING INDICATE THAT mtDNA TYPING**

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<sup>17</sup> The NRC also notes that, in PCR-based tests, laboratories should always be able to reserve sufficient material for such independent confirmatory tests. 1996 NRC Report at 25.

**HAS NOT REACHED GENERAL ACCEPTANCE IN THE SCIENTIFIC COMMUNITY.**

Even if the D.C. Court of Appeals and the U.S. Supreme Court had not explicitly mentioned independent validation studies and peer review as hallmarks of general acceptance, common sense (as well as a loss of innocence in the wake of Enron, Arthur Anderson and recent reports of lack of accountability at the FBI) dictates that the work of institutions such as the Federal Bureau of Investigation requires *external* validation to be established as legitimate in the scientific community, especially with respect to a field as new and little understood as mitochondrial DNA. Indeed, forensic laboratories like the FBI that have a vested interest in solving crimes quickly and maintaining funding from one year to the next are the *last* institutions that should be governed solely by internally developed standards.

The only published guidelines for interpreting mtDNA testing results come from the FBI itself. See Bruce Budowle, Joseph A. DiZinno, & Mark R. Wilson, Interpretation Guidelines for Mitochondrial DNA Sequencing, *presented at the Tenth Annual Int'l Symposium on Human Identification* (1999) [hereinafter FBI Guidelines]. The FBI exclusively looks to these internally-developed guidelines in determining how to read mtDNA test results. See 1999 DOJ Report at 5. The guidelines themselves note that they do not cover some cases, and that such cases “generally can be interpreted within the ‘spirit’ of the guidelines.” Id. at 3.

In addition, the lack of independent validation studies and blind proficiency tests approving the FBI’s methods of collecting, amplifying, and interpreting mtDNA evidence belies the notion that mtDNA science, and more specifically the FBI’s methods of amplification, interpretation of results, and statistical analysis, are “generally accepted” in the scientific community. Although the 1996 NRC Report recommends that proficiency tests of forensic DNA laboratories be blind, 1996 NRC Report at 79, none of the proficiency tests done on the FBI Unit II mtDNA laboratory has

been blind. 1999 DOJ Report at 7.

The only published validation study on mtDNA analysis is Holland & Parsons (1999), who note that the TWGDAM (now SWGDAM) guidelines “can be used to evaluate whether mtDNA analysis of biological evidence has been properly validated.” Id. at 35. The “validation” that Holland & Parsons perform, however, is merely to explain that the PCR amplification process is similar to that used in nuclear DNA and is routine and scientifically sound.<sup>18</sup> Id. at 35. Holland & Parsons do claim, in the abstract, that contamination can be controlled and need not disrupt interpretation, but do not explain which laboratories successfully control contamination, and only discuss contamination in the context of historical research uses of the science, not forensic casework. See id. at 36. Indeed, they claim that, “given the sensitive nature of mtDNA analysis, an analytical strategy should be developed for dealing with the occurrence of PCR amplification in reagent controls.” Id. at 37. Apparently, such strategies have not yet been developed. Holland & Parsons do not discuss whether the effects of mutation rates, heteroplasmy, recombination, and contamination make forensic casework using mtDNA too risky until the science matures.

Approving the use of mtDNA analysis for assisting in researching evolutionary tracts or identifying human remains from a known set of possible sources is a far cry from approving its use in forensic casework, where the difference between an “exclusion” and a “failure to exclude” is often one base, and can thus be profoundly affected by even small amounts of contamination with an exogenous source, ambiguous heteroplasmy, or other phenomenon. That these factors are not fully understood underscores the need to wait until the science of forensic mtDNA analysis matures

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<sup>18</sup> As the D.C. Court of Appeals has held, the issue under Frye is not merely whether the overarching scientific theory is generally accepted, but whether “the pertinent scientific community generally accepts the ability of the FBI’s protocol and procedures to ... provide a scientifically acceptable estimate of the relative rarity of the particular pattern in the [relevant] population.” Porter, 618 A.2d at 634 n.8 (discussing nuclear DNA).

before allowing the government to use mtDNA evidence against its citizens in criminal trials.

The acute need for validation studies, and the relative infancy of mtDNA forensic casework, is also evident in the lack of quality control over mtDNA databases. Although Holland & Parsons (1999) cite the sharing between laboratories of sequencing data as a step in the right direction, *id.* at 37, another article written by FBI laboratory researchers notes that the international standard forensic mtDNA database currently being developed suffers from many transcription errors, and is of dubious quality because data gleaned from public sources has not been confirmed as accurate. Kevin W. P. Miller & Bruce Budowle, A Compendium of Human Mitochondrial DNA Control Region: Development of an International Standard Forensic Database, 42 *Croatian Med. J.* 315, 316 (2001) [hereinafter Miller & Budowle (2001)]. The developers of the database “recommend the use of published sequence data for investigative or research purposes only and not for the assignment of weight regarding forensic matches.” *Id.* at 316. Thus, other scientists agree that a stricter standard for maturity of the science should apply when contemplating application of mtDNA science to *forensic casework*, rather than historical research or remains identification from a finite list of sources.

Three months ago, the Minnesota Court of Appeals held that the trial court erred in admitting expert testimony on nuclear DNA evidence because of the lack of independent validation studies and peer review over the FBI laboratory’s procedures. See State v. Traylor, 641 N.W.2d 335, 341 (Minn. Ct. App. 2002). The court noted that the FBI should be accountable under independent standards and not merely its own internal guidelines and protocols: “The supreme court has clearly and unequivocally adopted the TWGDAM guidelines and the guarantees of reliability contained therein – not merely whatever guidelines may currently serve as the official standards of the FBI.” *Id.* Until independent guidelines for interpreting mtDNA testing results exist, the FBI’s

guidelines and consequent interpretations and conclusions cannot be considered “generally accepted” by the scientific community.

**V. THE SMALL SIZE OF THE FBI mtDNA DATABASE RENDERS ANY ESTIMATE OF SEQUENCE FREQUENCY INSUFFICIENTLY RELIABLE AND, THEREFORE, SUCH STATISTICS SHOULD BE EXCLUDED ON BOTH FRYE/DYAS AND PREJUDICE GROUNDS.**

If the mtDNA profile from a crime scene sample and a suspect’s sample match sufficiently that the suspect is deemed by the FBI to be “included,” the crime scene sample may, indeed, have come from the suspect. Alternatively, the inclusion might represent a coincidental match between two persons who happen to share the profile. To assess the probability of such a coincidental match, and thus give meaning to the FBI’s claim of “inclusion,” the government must also provide statistics as to the frequency of the profile in the relevant human population.

Ideally, the FBI would determine such figures by examining the mtDNA profiles of every person on Earth that was alive when the crime occurred. Because such figures are impossible to come by, the FBI relies on a smaller database of known profiles to estimate frequencies. In mtDNA analysis, the FBI uses a database developed by the FBI-initiated Scientific Working Group on DNA Analysis Methods (SWGAM), which contains only about 2,400 sequences from 4,142 individuals. Fisher et al. (2000), at 3; 1999 DOJ Report at 6. *Of those 4,142, only 794 are African-American, like --REDACTED--.* *Id.* The NRC Report notes that a database of “a few hundred persons” is necessary even to have “some statistical accuracy.” 1996 Report at 34 (emphasis added).

Because the mtDNA database is so small, the FBI cannot state that mtDNA testing produced a “match” between the suspect’s sample and the evidence sample. Instead, the most that can be said is that the suspect is not excluded – hence, is “included” – as a possible source of the mtDNA.

Even researchers at the Armed Forces DNA Identification Laboratory admit that “the significance of mtDNA typing when previously unobserved types are encountered is currently database-limited.” Parsons & Coble (2001), at 305; see also Holland & Parsons (1999), at 30 (“[T]he strength of mtDNA evidence is limited by the size of the current databases.”); State v. Scott, 33 S.W.3d 746, 757 (Tenn. 2000) (noting that small size of FBI mtDNA database is “due to the relative infancy of forensic mtDNA analysis”). As Fisher et al. (2000) observed, “the number of individuals who must be sequenced to reach the limit of mtDNA diversity is unknown.” Id. at 3.

Moreover, the African-American mtDNA sequences in the FBI database have a frequency distribution that shows five distinct “haplogroups,” or “clusters of closely related mtDNA lineages.” Parsons & Coble (2001), at 306. Individuals within such “haplogroups” have very similar sequences, often diverging by only a base pair. Id. Given that heteroplasmy and other forces often skew results to show a one-base-pair difference, such similarities have grave consequences for the reliability of a report of a supposed “inclusion” or “exclusion.”

In mtDNA analysis, the FBI’s current practice is to use a “counting method” to determine sequence frequencies. See Budowle et al., FBI Guidelines, at 2; Fisher et al. (2000) at 3; 1999 DOJ Report at 6; Holland & Parsons (1999) at 31-32. Instead of reporting that a certain percentage of the population shares a particular profile, the FBI checks the database for the mtDNA sequence in the evidence sample and reports that the sequence was found “X” number of times in the database. One question that arises in this method is whether and how to account for heteroplasmy – whether one- or two- base differences should still be considered an inclusion.<sup>19</sup> Heteroplasmy, mutation, and

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<sup>19</sup> Additionally, the FBI often conducts a search of the SWGDAM mtDNA database using “indeterminate bases,” where an “N” is listed instead of one of the four possible nucleotides – A, C, G, or T. Presumably, this “wild card” slot increases the chance that a suspect will be “included” as a possible source, even if the sequences only line up because of such indeterminate bases. See 1999 DOJ Report, at 6.

contamination also affect the “likelihood ratio” – or ratio of the probability of the evidence given that the suspect is the source to the probability of the evidence given that the source is an unknown, unrelated person – that is used to explain to the jury the import of a failure to exclude. See Holland & Parsons (1999), at 32 (heteroplasmy, mutation, contamination, and laboratory error can drive down probability of evidence given that suspect is source, which would otherwise be  $p=1$ ).

This “counting method” is not used in any other scientific discipline and has not been subject to peer review or any published study supporting its use. Holland & Parsons (1999) note that the counting method is controversial in courts and that its interpretive guidance is limited because the number of observations of a sequence in the FBI database cannot reliably be used as a means for estimating the frequency of a profile in the population. Holland & Parsons (1999), at 31. Dr. William Shields of the State University of New York at Syracuse has testified that the counting method produces statistically indefensible results.<sup>20</sup> Dr. Shields has noted that the danger in permitting testimony as to rarity of a sequence in the population leaves the jury believing that mtDNA typing is similar to other DNA that can discriminate among individuals and allow the reporting of a “match.” According to Dr. Shields, the scientific community has not yet reached agreement on the statistical method that should be used to interpret mtDNA test results. Dr. Shields also questions the FBI’s decision not to include in their calculations those sequences in the database that differ from the evidence sample by one base.

At least one court has ruled that the results of a comparative test of mtDNA samples did not meet the Frye standard and was inadmissible because of questions about the statistical methods involved. See State of Florida v. James Deward Crow, No. 96-1156-CFA (Fla. Cir. Ct., Seminole Cty. 1998). In Crow, the trial court ruled that the FBI mtDNA database was too small to render

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<sup>20</sup> See, e.g., State v. Bolin, No. SC95775 (Fla. 2001).

statistically sound conclusions. The trial court further found that the “counting method” failed to provide meaningful comparison to assist, rather than confuse, the jury. The court thus excluded all mtDNA from Crow’s trial.

The argument that probability calculations go to the weight of DNA evidence and not its admissibility was foreclosed by the D.C. Court of Appeals in Porter. The Court recognized that “it is the probability feature which is at the very core of the DNA evidence. . . . [T]he underlying method of arriving at that calculation must pass muster under [Frye].” 618 A.2d at 640. The Porter Court agreed with the defense that the government’s calculation in that case of the probability of a coincidental match was based on a controversial “fixed bin” statistical method that had not gained general acceptance. Id. The Court remanded to the trial judge to determine a more conservative estimate of the random match probability based on generally accepted methods. Id. at 642. Here, there is considerable controversy surrounding both the small size of the mtDNA database, the “counting method” used by the FBI, and the effect of heteroplasmy and its questionable treatment by the FBI in deciding what to call an “exclusion” versus a “failure to exclude.” Because of this controversy, this Court should not allow the government to introduce evidence that --REDACTED--’s mtDNA sequence “matched” or “cannot be excluded as a source of” the mtDNA evidence samples.

Moreover, independent of this Court’s Frye/Dyas inquiry, this Court should exclude the mtDNA statistical evidence as overly prejudicial. If the prejudicial effect of admitting evidence substantially outweighs its probative value, it should be excluded. Johnson v. United States, 683 A.2d 1087, 1100 (D.C. 1996). When a lay person hears the word “DNA,” he or she does not distinguish between nuclear DNA and mitochondrial DNA. Indeed, neither did undersigned counsel until many conferences and late-night seminars on DNA technology over the past few

months. The minute a juror hears that there is “DNA evidence” against the defendant, the government’s case is given a veneer of legitimacy and infallibility that does not correspond to the probative value of the mtDNA. As stated above, mtDNA is not a means of identification; it can only, at most, “exclude” or “fail to exclude” a suspect as the source of the evidence sample. Given the limited probative value of such evidence, and its incredible power nevertheless to mesmerize jurors, this Court should exclude such evidence and any expert testimony regarding it on prejudice grounds.

Even if a laboratory could theoretically perform mtDNA testing reliably and not be affected by the above-mentioned points of contention, the fact that scientists do not fully understand such phenomena and their effect on forensic testing underscores the embryonic nature of mtDNA analysis. Only after further peer review, research on heteroplasmy, mutation, and paternal leakage, and further development of the database to a statistically sound size can mtDNA analysis hope to be generally accepted in the scientific community. In turn, only upon such general acceptance can mtDNA test results be admitted against a defendant at a criminal trial. In this case, therefore, the government’s proffered mtDNA evidence must be excluded.

**VI. THE MITOCHONDRIAL DNA EVIDENCE IN THIS CASE MUST BE EXCLUDED BECAUSE THE GOVERNMENT CANNOT ESTABLISH A PROPER CHAIN OF CUSTODY SUFFICIENT TO AUTHENTICATE THE HAIR SAMPLES USED IN THE mtDNA ANALYSIS.**

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 were

improperly admitted where there was “missing a necessary link in the chain of identification” to show that the specimen tested was the 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 State v. Scott, the Tennessee Supreme Court found the government’s proffered mtDNA 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.

33 S.W.3d 746, 760-61 (Tenn. 2000). Thus, the fact that this Court might know that the FBI handled the hair samples in this case is insufficient to establish chain of custody; the government must show each link in the chain to establish a sufficient chain of custody for this Court to admit the mtDNA evidence from the hair samples in this case.<sup>21</sup> Moreover, establishing a chain of custody is especially crucial in admitting scientific evidence that, like mtDNA, is “hypersensitive to contamination.” Id. at 761 n.13. Without such a showing, the mtDNA evidence is inadmissible

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<sup>21</sup> The government also must establish such a chain of custody with respect to samples taken from substances or tissues other than hair, including --REDACTED--’s blood or the blood of any co-defendant.

under Rule 901.

### **CONCLUSION**

“Mitochondrial genetics and mtDNA evolution” are “complex system[s] that [are] not yet fully understood.” Elson et al. (2001) at 000. 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 mtDNA evidence must be sufficiently reliable to reasonably form the basis for the government’s DNA expert’s testimony. mtDNA 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 --REDACTED--. For the foregoing reasons, and for such other reasons that may appear to this Court at a hearing on this Motion, --REDACTED-- respectfully requests that this Court exclude all mtDNA evidence from this case.

Respectfully submitted,

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**CERTIFICATE OF SERVICE**

I hereby certify that a copy of the foregoing Motion to Exclude mtDNA Inclusion Evidence has been served, by hand, upon AUSA Deborah Sines, United States Attorney's Office, Felony Division, 555 4th Street, N.W., Washington, D.C. 20530, on this 7th day of June, 2002.

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ANDREA ROTH