UNITED STATES DISTRICT COURT
EASTERN DISTRICT OF MISSOURI
EASTERN DIVISION

UNITED STATES OF AMERICA,	)	
	)	
Plaintiff,	)	
	)	
vs.	)	Case No. S2-4:01CR296 ERW
	)	
KENNETH COLEMAN, et al.,	)	
	)	
Defendants.	)	

MEMORANDUM AND ORDER

This matter is before the Court upon Defendant Andre Worthy's request that the Court hold a Daubert hearing and determine the reliability of expert testimony that the Government intends to offer in the above-styled action regarding mitochondrial DNA analysis [doc. #157].

I. FACTUAL BACKGROUND

In the present case, three defendants, Kenneth Coleman, Orlando Willis, and Andre Worthy, are charged in Count One with conspiring to commit armed robbery of financial institutions between September 1999 and November 2001. Count Two charges Defendants Coleman and Worthy with attempted armed bank robbery on June 2, 2001. In Count Three, Defendants Coleman and Worthy are charged with using, carrying, and brandishing firearms during and in relation to the robbery on June 2, 2001. Defendant Coleman is charged in Count Four with bank robbery on February 22, 2000, and in Count Five with using, carrying, and brandishing a firearm during and in relation to the robbery on February 22, 2000. In Count Six, Defendant Willis is charged with aiding and abetting armed bank robbery from March 2000 through June 2001. It is charged that members of the conspiracy abducted female employees of

financial institutions and forced them to go to the financial institutions while they were closed to remove money from the vaults and ATM machines. This occurred while other members of the conspiracy held the employees' family members hostage, frequently using duct tape and other materials to restrain the victims.

Dr. Terry Melton, President and CEO of Mitotyping Technologies, was asked by the Government to compare a hair sample found on a piece of duct tape used in the robberies with known DNA samples from the three defendants. Using mitochondrial DNA analysis, Dr. Melton concluded that differences existed in the DNA sequences of the unknown hair sample and the known DNA samples from Defendant Coleman and Defendant Willis. Thus, those defendants were excluded as the possible sources of the unknown hair sample. (Tr. p. 53, l. 5-10). As to Defendant Worthy, mitochondrial DNA analysis, according to Dr. Melton, revealed "a perfect match . . . between the hair and the known sample . . . ." (Tr. p. 53, l. 1-4). Using statistical analysis, Dr. Melton concluded that there is a "95 percent chance that 99.93 percent of the people in North America don't have this type." (Tr. p. 54, l. 8- 11). Dr. Melton stated that "Mr. Worthy cannot be excluded as one of a pool of contributors of that hair." (Tr. p. 65, l. 13-14).

In the Motion for Daubert Hearing, Defendant Worthy asserted that forensic identification expert testimony, such as that to be offered Dr. Melton, is "specifically vulnerable to attack" because there has been "little or no testing done to validate the fundamental premises" upon which the expert testimony is based. Accordingly, Defendant Worthy sought a Daubert hearing to determine the reliability of mitochondrial DNA analysis and whether sufficient error rates or objective identification standards have been established for mitochondrial DNA analysis. The Court granted Defendant Worthy's request for a Daubert hearing and heard testimony from Dr.

Melton on February 5, 2002. At the hearing, Defendant Worthy's objection to the mitochondrial DNA testing was more specifically articulated as an objection to the prejudicial effect of illustrating to the jury the inclusive basis for forensic identification, understanding that mitochondrial DNA analysis cannot be used as a unique identifier.

II. DNA ANALYSIS

"DNA is a chemical blueprint of the cell and life." Through DNA, individuals inherit characteristics from their parents. (Tr. p. 10, l. 23-25). DNA is the same in all parts of the body, and it does not change with age. (Tr. p. 12, l. 16-19). It exists in every cell of the body, except red blood cells. (Tr. p. 15, l. 8-10).

A. Nuclear and Mitochondrial DNA

Within a cell, DNA can either be found in the nucleus or in mitochondria. Nuclear DNA, that found in the very center of a cell, is inherited from both parents in the form of chromosomes. (Tr. p. 16, l. 5-6). Nuclear DNA is found in the structure of a double helix, or a "twisted ladder of chemicals." (Tr. p. 11, l. 8-10). If the ladder is untwisted, "what it looks like is a regular ladder with two rails down the sides and rungs." (Tr. p. 11, l. 1-14). The "rungs" of the ladder are composed of four chemical bases known as nucleotides: adenine, cytosine, thymine, and guanine. The chemical bases are generally referred to as A, C, T, and G, respectively. An A is always paired with a T, and a C is always paired with a G on opposite "rails" of the ladder.

The order of the chemical bases is what provides the informational content of the DNA. For example, down one side of the nuclear DNA ladder, there will be a "long string of three billion base pairs." (Tr. p. 17, l. 16-17). The sequence, for instance A,C,G,T,C,G,A,C . . . , is analogized to a phone number. "[I]f you take the order of these letters and you mix them up, it's

not your phone number anymore, it's the phone number of someone else." (Tr. p. 11, l. 1-4). With the exception of identical twins, "everyone could be considered unique with respect to their nuclear DNA." (Tr. p. 12, l. 22-25).

DNA is also found in mitochondria. Mitochondria are "little peanut-shaped organelles" contained in the cytoplasm surrounding the nucleus. (Tr. p. 16, l. 14-18). Accordingly, mitochondrial DNA analysis can be used on material without a nucleus, such as a bone sample or a piece of hair without a root segment. It can also be used on unknown samples degraded by environmental factors or time. Thus, it provides forensic scientists with an alternative procedure when an unknown sample cannot be analyzed by nuclear DNA analysis.

Mitochondrial DNA is inherited only from the mother. Any one cell contains hundreds to thousands of mitochondria, (Tr. p. 17, l. 4-5), and "every mitochondrion has ten to a hundred mitochondrial DNA molecules." (Tr. p. 16, l. 25 - p. 17, l. 1). The mitochondrial DNA is a double helix structure; the exact same structure as nuclear DNA. However, the mitochondrial DNA molecules are "in the shape of a circle" as opposed to a long "twisted ladder." (Tr. p. 17, l. 1-2). As with nuclear DNA, if the double helix structure of the mitochondrial DNA is stretched out, the "exact order of As, Ts, Cs, and Gs in the mitochondrial DNA molecules of one person" can be determined. However, in nuclear DNA, there are three billion base pairs of nucleotides, where in the smaller, circular mitochondrial DNA, there are only approximately sixteen and a half thousand nucleotide bases. (Tr. p. 17, l. 13-20; Exh. 4). Thus, the double helix structure is much smaller in mitochondrial DNA as opposed to nuclear DNA.

The present case raises the question of whether the use of mitochondrial DNA in DNA analysis, rather than the use of nuclear DNA, is reliable, and whether the proffered mitochondrial

DNA analysis shall be admitted into evidence. DNA analysis using mitochondrial DNA has had little judicial scrutiny.

B. DNA Analysis Procedure

With both nuclear and mitochondrial DNA analysis, a four step process is followed. The first step is extraction. During extraction, the DNA sample is purified from any other substances contained in the sample. The second step is polymerase chain reaction ("PCR") amplification, which makes copies of the DNA for analysis. Third, sequencing is accomplished to identify the order of the As, Cs, Ts, and Gs contained in the sample. The same analysis – extraction, amplification, and sequencing – is completed on both the known and unknown samples, adhering to certain safeguards to prevent contamination of the unknown sample. (Exh. 9). Finally, the sequencing of the unknown sample is compared to the sequencing of a known sample. (Tr. p. 25, l. 4 - p. 30 l., 12; Exh. 6-7).

The laboratory analysis steps for mitochondrial DNA are exactly the same as the steps used for nuclear DNA analysis, except that the resulting comparison differs. With nuclear DNA analysis, the sequence of three billion pairs of As, Ts, Cs, and Gs is compared, and "source attribution" is possible. Thus, the nuclear DNA of a known donor can be compared to "an unknown sample of human cell tissue to determine if the known donor is in fact the source of the unknown sample" because the pattern is "virtually unique." (Tr. p. 13, l. 9-16). Nuclear DNA analysis been in existence as a forensic identification technique for approximately fifteen years and "has experienced general acceptance for a long time within courts." (Tr. p. 19, l. 17-20).

The comparison process for mitochondrial DNA analysis involves two areas of the mitochondrial DNA structure, referred to as HV1 and HV2. These areas, referred to as the

control region, are comprised of 1100 nucleotide bases and demonstrate high levels of sequencing variation among different individuals. Dr. Melton opined that it is "very, very unlikely that any two people will have the same order of their As, Ts, Cs, and Gs" in the control region of mitochondrial DNA. (Tr. p. 17, l. 4-8). Mitochondrial DNA is not a "unique identifier," however, because any other persons "in that same maternal lineage will have the same type." (Tr. p. 66, l. 20-22; Tr. p. 22, l. 23-25). It is also possible that two people seemingly "unrelated by maternal lineage" will have the same mitochondrial DNA because the maternal lineage may go back further than known and there is a remote possibility of small mutational changes. (Tr. p. 23, l. 6-15).

In mitochondrial DNA analysis, the sequence of the known and unknown samples are lined-up next to each other and compared. If there is not "perfect symmetry between the As, Ts, Gs, and Cs," in the control region, the known sample is excluded as being the source of the unknown sample. (Tr. p. 31, l. 4-6). If, instead, "there is a common base at every position, then we will be able to say this person cannot be excluded as the contributor of that hair . . . ." (Tr. p. 30, l. 5-9).

After determining that a sample cannot be excluded, a statistical analysis is performed to determine the frequency the sequence is likely to exist in the population. Although mitochondrial DNA is "not a unique identifier" like nuclear DNA, (Tr. p. 31, l. 22-23), by relying on a database of types and statistics, it has been determined that "the chance of choosing any one type at random is very low. So if we see a particular type, we know that it's very unlikely . . . that it would be highly unlikely to go out in the population and pick someone with that type." (Tr. p. 32, l. 2-7).

The statistical analysis is based upon an FBI database of 783 nucleotides, representing 4,142 people. The database is used to determine the "estimated frequency of this particular type that we've observed in some defined group." (Tr. p. 33, l. 4-6). The "upper-bound frequency" is an estimate of "how many times we're likely to see a particular frequency in the population at large." (Tr. p. 69, l. 8-16). The validity of the test, to some extent, depends upon the number of observed samples in the database; "as the database grows, that upper-bound frequency shrinks." (Tr. p. 69, l. 21-22).

The FBI database is not limited to ethnicity. It contains observed samples from Caucasians, Asians, African-Americans, and other ethnic groups. Dr. Melton opined that because the characteristics of an unknown sample cannot be assumed, it would be improper to use a database limited by ethnicity. The frequency of the existence in the general population must be determined, rather than the frequency in any given racial group. (Tr. p. 73, l. 16-17; Tr. p. 74, l. 1-8).

Accordingly, through the comparison stage of mitochondrial DNA analysis, a known sample may be positively excluded or included as the possible source of the unknown sample. A sample is included if the data – the sequence of As, Ts, Cs, and Gs – reveals an exact match. If it is included, a statistical analysis reveals what percent of the population would have the same sequence.

In the present case, the unknown hair sample found on the duct tape used in the armed robbery was not susceptible to nuclear DNA analysis. Dr. Melton conducted mitochondrial DNA analysis of the unknown hair sample in accordance with the above detailed procedures. (Exh. 14). He concluded that there were eleven differences between the unknown sample and the

known sample from Defendant Coleman, and seventeen difference between the unknown sample and the known sample from Defendant Willis. Therefore, Defendants Coleman and Willis were excluded as possible sources of the unknown hair sample. (Tr. p. 53, l. 5-10). With regard to Defendant Worthy, Dr. Melton concluded that there was an exact sequencing match of As, Ts, Cs, and Gs, and Defendant Worthy could not be excluded. (Tr. p. 53, l. 1-4). Using the FBI database, Dr. Melton's statistical analysis revealed that there is a "95 percent chance that 99.93 percent of the people in North America don't have this type." Accordingly, Dr. Melton testified that "at the most," seven out of 10,000 people would be expected to have that exact sequence of As, Ts, C, and Gs. (Tr. p. 54, l. 12-14). The Government intends to present this evidence at trial.

III. APPLICATION OF DAUBERT

Federal Rule of Civil Procedure 702 provides:

> If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise, if (1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles or methods, and (3) the witness has applied the principles and methods reliably to the facts of the case.

Fed. R. Civ. P. 702. To admit scientific expert testimony, the Court must find that the proposed testimony constitutes (1) scientific knowledge and that (2) it will assist the trier of fact to understand the evidence. Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579 (1993).

The passage of Rule 702 superceded the courts' previous "general acceptance" standard for the admittance of scientific evidence, as articulated in Frye v. United States, 293 F. 1013 (D.C. Cir. 1923). In Daubert, the United States Supreme Court described Rule 702 as a "flexible" inquiry, "tied to the facts of a particular case." Daubert, 509 U.S. at 595. Consistent

with Rule 702, scientific evidence must be reliable and relevant before being admitted, and to qualify as scientific knowledge, it must be "derived by the scientific method," "be supported by appropriate validation," and "assist the trier of fact." Id.

In reviewing proffered scientific or other specialized testimony, a court looks at the conclusions of the expert to assure that they are logical, but may not evaluate the weight of the expert testimony. Nat'l Bank of Commerce v. Assoc. Milk Prod., Inc., 191 F.3d 858, 862 (8th Cir. 1999); General Electric Co. v. Joiner, 522 U.S. 136 (1997). Courts consider, among other possible factors: (1) whether the technique or theory can be and has been tested; (2) whether the technique or theory has been subjected to peer review and publication; (3) the known or potential rate of error for the technique or theory and the existence and maintenance of standards for controlling the technique or theory's operation; and (4) whether the technique, theory, or opinion has been generally accepted by the scientific community. Daubert, 509 U.S. at 593 (identifying the list of factors but stating that the list of factors is not a "definitive checklist or test"). A district court acts as a "'gatekeeper' for the admission of novel scientific evidence." United States v. Boswell, 270 F.3d 1200, 1204 (8th Cir. 2001) (finding "sufficient evidence that the district court was justified in permitting the admission of PCR test results of swine DNA").

The Court notes that the Eighth Circuit has "taken judicial notice of the reliability of the general theory and techniques of DNA profiling . . . ." United States v. Beasley, 102 F.3d 1440, 1445 (8th Cir. 1996). In United States v. Martinez, 3 F.3d 1191 (8th Cir. 1993), the Eighth Circuit took judicial notice of the use of the restriction fragment length polymorphism ("RFLP") procedure. Martinez, 3 F.3d at 1197. The RFLP procedure requires a large sample of DNA and "can result in statistical 'matches' of a sample to a particular individual." See United States v.

Hicks, 103 F.3d 837, 844 n.7 (9th Cir. 1996). In United States v. Beasley, the Court determined that the polymerase chain reaction ("PCR") method of DNA typing is "sufficiently well established to permit the courts of this circuit to take judicial notice of it in future cases." Beasley, 102 F.3d at 1447. PCR testing is an amplification technique that can be used on small or degraded DNA samples. It is "generally not used to establish a statistical 'match' between a sample and an individual, but rather, is used as a technique to exclude certain individuals as possible contributors to a particular sample." See Hicks, 103 F.3d at 844.

Although judicial notice has been taken of DNA profiling, it is not "automatically admissible under Daubert." See Martinez, 3 F.3d at 1197. A court may "further inquire into whether the expert properly performed the techniques" and "new techniques" may require a Daubert hearing to determine reliability. Id. "In every case, of course, the reliability of the proffered test results may be challenged by showing that a scientifically sound methodology has been undercut by sloppy handling of the samples, failure to properly train those performing the testing, failure to follow the appropriate protocols, and the like." Beasley, 102 F.3d at 1448.

Dr. Melton testified that the process used for mitochondrial DNA analysis is the same process used for nuclear DNA analysis. The "same machine, same basic principles, size [and] separation" are used for mitochondrial and nuclear DNA analysis. Additionally, "[s]tudies have been done to determine the validity of the process . . . ." (Tr. p. 49, l. 17-20). The Mitotyping Technologies lab completed "six weeks of validation studies before starting casework in early 1999 . . . " and "sequencing itself is used in thousands of labs around the world for sequencing DNA." (Tr. p. 49, l. 17 - p. 50, l. 9). When performing analyses in the lab, "every conclusion receives the review and interpretation of two individuals." (Tr. p. 8, l. 15 -18).

Mitochondrial DNA analysis has received peer review since 1991. (Tr. p. 58, l. 4). Dr. Melton stated that there have been dozens, if not hundreds, of peer-reviewed articles on forensic mitochondrial DNA. (Tr. p. 55, l. 17-20). Several articles were presented to the Court demonstrating publication of the technique used in mitochondrial DNA analysis. (Exh. 10-13). It is further noted that Emory University maintains a website listing peer-reviewed articles on mitochondrial DNA. Of particular interest, the article Validation of Mitochondrial DNA Sequencing for Forensic Casework Analysis concludes that "automated DNA sequencing of amplified mtDNA [mitochondrial DNA] products from hair shafts and other tissues is a valid and reliable method of forensic human identity testing." Mark R. Wilson, et al., Validation of Mitochondrial DNA Sequencing for Forensic Casework Analysis, 108 J. of Legal Medicine 68 (1995). Another article, titled Mitochondrial DNA Sequence Analysis and authored by M.M. Holland and T.J. Parsons of the Armed Forces DNA Identification Laboratory, concludes that mitochondrial DNA "has been performed routinely for at least seven years, with a proven track record of utility and reliability. . . . the forensic scientific community has amassed a vast base of experience in mtDNA [mitochondrial DNA] identity testing, in many laboratories worldwide." They further conclude that "mtDNA sequence analysis is robust and 'validated.'" M.M. Holland & T.J. Parsons, Mitochondrial DNA Sequence Analysis, 11 Forensic Science Review 1, 41 (June 1999).

According to Dr. Melton's testimony, certain testing is performed to determine lab error in mitochondrial DNA testing. Guidelines, written by the American Society of Crime Laboratories/ Laboratory Accreditation Board (ASCLD/LAB), require proficiency tests twice a year, by an outside agency. (Tr. p. 58, l. 20-24). Dr. Melton's lab has "gone through seven

rounds" of proficiency testing. The seventh is in progress, but on the previous six, the lab was 100 percent accurate. (Tr. p. 59, l. 6-22). The lab also has exchanged some forty samples with the FBI as part of its validation studies, and it has had 100 percent accuracy. (Tr. p. 59, l. 25 - p. 60, l. 8). Dr. Melton opined that there is no potential for error in terms of the ultimate statistical conclusions reached as they are based upon calculable probability.

Dr. Melton opined that mitochondrial DNA analysis is "generally accepted within the scientific community, particularly the forensic scientific community." (Tr. p. 55, l. 7-11). Dr. Melton is aware of no scientists who question the validity of mitochondrial DNA analysis. (Tr. p. 55, l. 12-14). Mitochondrial DNA analysis has been in existence since 1981. (Tr. p. 58, l. 10-11). The Armed Forces has been using the process to identify remains of soldiers since 1993, (Tr. p. 58, l. 7), and the FBI has used the process since 1995, (Tr. p. 58, l. 2). Other practical uses for mitochondrial DNA analysis include: the Human Genome Project; the study of human evolutionary history; identification of the victims of the World Trade Center attacks; and identification of historical remains such as the remains of Jessie James' and "Wild Bill" Longley. In addition, it is used by the Forensic Science Service in England. (Tr. p. 55, l. 24 - p. 57, l. 7).

Based on the foregoing, it is clear to the Court that mitochondrial DNA analysis constitutes scientific knowledge, and the Court believes that mitochondrial DNA analysis is a reliable method, based upon reliable principles. Dr. Melton's testimony will be helpful to the jury in deciding the issues presented in the present case. There is no assertion that Dr. Melton, or the Mitotyping Technologies lab, did not follow the procedures properly. Thus, any objection to Dr. Melton's testimony that there has been minimal testing to validate the fundamental premises upon which the mitochondrial DNA identification is made, that there is insufficient peer review

and publication scrutiny of mitochondrial DNA analysis, that there is a lack of error rates or objective identification standards for the mitochondrial DNA analysis procedures, and that there is no general scientific acceptance by the scientific community of the techniques, theories, or opinions regarding mitochondrial DNA analysis is overruled.

IV. FEDERAL RULE OF EVIDENCE 403

Defendant Worthy has also objected to Dr. Melton's testimony based on the prejudicial effect of Dr. Melton's characterization of an "exact match" between the nucleotide sequence of the known and unknown samples.[1] Defendant Worthy correctly states that mitochondrial DNA is not a unique identifier even though the sequence of As, Cs, Ts, and Gs in a known and unknown sample may result in an exact match, and that the jury could easily, but inappropriately, draw the conclusion that the unknown hair sample found in the duct tape is hair from Defendant Worthy.

On cross-examination at the February 5, 2002 hearing, counsel inquired of Dr. Melton: "And your conclusion that the two samples are identical match – are an identical match could easily be misunderstood by someone without any follow-up explanation or without any training that this sample, unknown sample came from the person?" Dr. Melton responded: "Well, not if I had anything to do with it, but I suppose you're right." Counsel further stated: "[A] person who was not trained looking at this match could reasonably conclude, without the benefit of [] training and knowledge, that the person who produced this unknown sample was Mr. Worthy, correct?" Dr. Melton replied that "[t]he conclusion of the report is very general. . . . So the

[1] The objection as to the prejudicial effect of the evidence was not discussed under the Court's Daubert analysis as the Court believes that the objection goes to the weight of the evidence, as opposed to whether the scientific evidence is admissible as a reliable method under Rule 702. See Nat'l Bank of Commerce, 191 F.3d at 862. The objection is more appropriately analyzed under Federal Rule of Evidence 403.

answer to your question is yes. . . ." (Tr. p. 90, l. 19-24).

Federal Rule of Evidence 403 allows for the exclusion of evidence otherwise relevant if "its probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury . . . ." Fed. R. Evid. 403. Pursuant to Rule 403, a balancing test is employed to compare the probative value and prejudicial effect of the evidence. If the court determines that the evidence creates a danger of unfair prejudice, the court balances the relative probative value and prejudicial effect of any evidentiary alternatives. See United States v. Becht, 267 F.3d 767, 772 n.7 (8th Cir. 2001) (citing Old Chief v. United States, 519 U.S. 172, 182-83 (1997)).

The mitochondrial DNA evidence in the present case is clearly probative of the source of the hair found in the duct tape used in the robberies to which Defendant Worthy is charged. The Court notes the potential prejudice that may result from illustrating the "exact match" data without further explanation due to the obvious inference the jury may draw that the match of As, Cs, Ts, and Gs in the mitochondrial DNA molecules of the known and unknown samples conclusively determines that the hair found on the duct tape is Mr. Worthy's hair. However, Dr. Melton was very clear in both his direct examination and his cross-examination that an exact mitochondrial DNA match only leads to the conclusion that the sample cannot be excluded; it does not conclusively determine that the matched individual is the only potential match in the population. (Tr. p. 65, l. 9 - p. 66, l. 15).

Dr. Melton explained that mitochondrial DNA analysis is a two-step process: first, the known sample is deemed excluded or included, and second, if it is included, it is subject to a statistical analysis to determine the frequency with which it is likely to exist in the population.

Dr. Melton's conclusion will not be proffered to prove that "upon a reasonable degree of scientific certainty, the hair that's in the unknown sample is the hair of Mr. Worthy." (Tr. p. 66, l. 6-10). His conclusion at the former hearing was that Mr. Worthy cannot be excluded as the source of the hair sample. The following testimony was given upon cross-examination:

Q: You ended by concluding that there was a high degree of likelihood that the DNA found in the hair and in the unidentified sample was the DNA of Mr. Worthy, correct?

A. No, our conclusion is that Mr. Worthy cannot be excluded as one of a pool of contributors of that hair.

Q: Didn't I hear you say, in response to Mr. Holtshouser's question, that there is a 95 percent chance that 99.93 percent of the people in North America don't have the sequence associated with Mr. Worthy?

A: That's not the same as saying that it's likely to be his or that it is his; it's just telling you what percent of the population cannot be – could not have his type.

Q: Okay. So I mistook your statement for a conclusion that the hair – the questioned hair actually belonged to Mr. Worthy. You can't tell me that and you're not telling me that, correct?

A: I would never tell you that, no.

Q: Okay. And it cannot be established by any means, any scientific means currently available to you by this mitochondrial DNA, correct?

A: That's correct.

(Tr. p. 65, l. 9 - p. 66, l. 5).

Thus, as the Daubert hearing demonstrated, effective cross-examination alleviates the concern of unfair prejudice arising from a premature conclusion by a jury that a person may be unequivocally identified by mitochondrial DNA testing. Therefore, the Court concludes that any prejudice is not unfair and does not outweigh the probative value of the mitochondrial DNA analysis. The evidence shall not be excluded under Rule 403.

Accordingly,

IT IS HEREBY ORDERED that Defendant Andre Worthy's request to exclude Dr. Terry Melton's expert testimony concerning mitochondrial DNA analysis is **DENIED**.

Dated this 15th day of February, 2002.

/s/ E. Richard Webber
E. RICHARD WEBBER
UNITED STATES DISTRICT JUDGE