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IN THE DISTRICT COURT OF APPEAL
OF FLORIDA
SECOND DISTRICT

JOSEPH MAGALETTI,)
)
 Appellant,)
)
v.)
)
STATE OF FLORIDA,)
)
 Appellee.)
_____)

Case No. 2D01-3074

Opinion filed April 4, 2003.

Appeal from the Circuit Court for Sarasota
County; Nancy K. Donnellan, Judge.

James Marion Moorman, Public Defender,
and James T. Miller, Special Assistant Public
Defender, Bartow, for Appellant.

Charles J. Crist, Jr., Attorney General,
Tallahassee, and Dale E. Tarpley, Assistant
Attorney General, Tampa, for Appellee.

STRINGER, Judge.

Joseph Magaletti challenges his judgment and sentence for the first-degree murder of Kathleen Leonard. He advances four arguments on appeal; we affirm, without discussion, as to three of these but write to address one--the admissibility of identification

evidence in the form of mitochondrial DNA (mtDNA) analysis, an issue of first impression in Florida appellate courts.¹

On March 12, 1995, Kathleen Leonard's employer made a missing person report to the Sarasota County Sheriff's Office after several unexplained absences and being unable to contact Ms. Leonard by phone. Her badly decomposed body was discovered in her apartment on that same day. Upon entering the apartment, investigators found her fully clothed and lying facedown on her bed. Strips of torn towels had been used to strangle her and to bind her hands behind her back. The contents of her purse were dumped out on her living room floor. Credit cards were found inside her wallet but no cash. There were no signs of forced entry. The neck ligature and wrist binding were collected and swept for trace evidence; several hairs were recovered, all of which belonged to the victim, save one. Hair comparison and mtDNA analysis later identified Magaletti as the donor of this single hair, which appeared to have been broken at some point along the shaft rather than having been pulled from its root. Also, Magaletti's fingerprints were found on the inside of the victim's door beneath the door knob.

Prior to trial, Magaletti challenged the admissibility of identification testimony, arguing that the State should not be allowed to introduce evidence of the mtDNA analysis performed on the single hair found in the victim's binding. Specifically, he maintains that mtDNA analysis has been primarily used for genealogical studies and

¹ Magaletti also contends (1) that the State failed to produce sufficient evidence to support his conviction, (2) that the trial court erred in admitting evidence of his cocaine use, and (3) that the trial court erred in admitting evidence of hair comparison.

to identify war remains but has not been widely accepted for use in the area of forensics. Relying on the supreme court's decision in Brim v. State, 695 So. 2d 268 (Fla. 1997), Magaletti argues that the method of statistical calculation used in his case does not satisfy the Frye² test for new or novel scientific evidence. He further argues that the mtDNA results in this case are not reliable due to the limited number of profiles resident in the FBI's national mtDNA database. In response the State contends that it produced sufficient evidence to establish general acceptance under Frye. The State relies on cases from other jurisdictions to argue that disputes concerning the methodological validity of scientific evidence generally go to weight and not the admissibility of evidence. See, e.g., State v. Pappas, 776 A.2d 1091, 1106 (Conn. 2001).

For reasons which will be discussed, we find that the evidence admitted at the Frye hearing conclusively established that the method of mtDNA analysis, as well as the statistical calculations used to determine a rate of exclusion in this case, satisfy Frye.

Admissibility of nucDNA³ Analysis in Florida

In order to test the reliability and determine the admissibility of new or novel scientific evidence, Florida courts adhere to the Frye test. Brim, 695 So. 2d at

² Frye v. United States, 293 F. 1013 (D.C. Cir. 1923).

³ There are essentially two forms of DNA. DNA which resides in the nucleus of cells is termed nuclear DNA (nucDNA). The type of DNA examined in the present case came from organelles found outside of the cell nucleus called mitochondria. This DNA is called mitochondrial DNA (mtDNA). M.M. Holland & T.J. Parsons, Mitochondrial DNA Sequence Analysis – Validation and Use for Forensic Casework, 11 Forensic Science Review 22, 23 (1999).

271; Hayes v. State, 660 So. 2d 257, 262 (Fla. 1995). Under Frye, the admission of expert testimony concerning a new scientific principle involves a four-step inquiry which requires the trial court to determine whether:

(1) [the] expert testimony will assist the jury in understanding the evidence or in determining a fact in issue; (2) the expert's testimony is based on a scientific principle or discovery that is "sufficiently established to have gained acceptance in the particular field in which it belongs" under the Frye test; and (3) the particular expert witness is qualified to present opinion evidence on the subject in issue. If the answer to the first three questions is in the affirmative, the trial judge may proceed to step four and allow the expert to present an opinion to the jury.

Hayes, 660 So. 2d at 262 (quoting Ramirez v. State, 651 So. 2d 1164, 1166 (Fla. 1995)). In the context of DNA cases, the supreme court has frequently observed that Frye determinations require two levels of analysis. The first involves principles of molecular biology and chemistry and results in a qualitative determination which "simply indicate[s] that two DNA samples look the same." Murray v. State, 692 So. 2d 157, 162 (Fla. 1995); Brim, 695 So. 2d at 269. However, as to this initial inquiry, the supreme court has concluded that "to say that two patterns match, without providing any scientifically valid estimate . . . of the frequency with which such matches might occur by chance, is meaningless." Brim, 695 So. 2d at 270. Therefore, on the second level of analysis, "experts [are required to] provide quantitative, rather than qualitative, estimates of the frequency of an incriminating profile [occurring] in one or more races." Id. This quantitative estimate assists the trier of fact in understanding the probative value or significance of a match, and Florida law requires a separate Frye analysis. Id.

We are guided by the supreme court's analysis in Brim in considering whether the statistical calculations used during the mtDNA analysis in the present case satisfy Frye.

The defendant in Brim challenged his 1993 conviction for several offenses, including two counts of sexual battery. NucDNA evidence was the focus of the State's case, and prior to trial Brim sought to exclude it. Brim alleged that the State's method of calculating frequency was not generally accepted within the relevant scientific community, and he produced evidence of the use of an alternative method. In Brim's 1995 appeal, this court found that the DNA evidence was properly admitted because the Frye standard does not limit the "admissible deductions that can be made from reliable scientific evidence to a single 'generally accepted' deduction or theory." Brim v. State, 654 So. 2d 184, 186 (Fla. 2d DCA 1995). The supreme court later disapproved of this court's decision and held that the statistical presentation of the evidence requires a separate Frye analysis. Brim, 695 So. 2d at 270.

The court noted that the record in Brim established that the scientific community was split as to the proper approach for reporting DNA test results. At that time, the leading authority on DNA analysis, the National Research Council, recommended the use of a "modified ceiling principle" to calculate population frequency. However, the record was not clear as to which statistical method was used in Brim's case or whether that method satisfied Frye. Therefore, the supreme court found it necessary to remand the case for an evidentiary hearing to clarify the exact method of statistical calculation used in that case. Id. at 275.

In contrast, evidence adduced at the Frye hearing below established that the scientific method of mtDNA analysis, as well as the method of statistical calculation

used in the present case, are generally accepted by forensic scientists throughout the country.

MtDNA Analysis in this Case

While the admissibility of mtDNA analysis has been addressed in Florida trial courts as early as 1998,⁴ our appellate courts have not yet weighed in on the issue in light of Frye. This court reviews a trial court's Frye determination de novo. Brim, 695 So. 2d at 274. Under Frye, the trial court in this case had to determine that the basic underlying principles of scientific evidence have been sufficiently tested and accepted by the relevant scientific community. Contrary to the State's assertions, the court was required to treat the Frye inquiry as a question of admissibility, rather than evidentiary weight to be considered by the jury. Id. at 271. As the proponent of mtDNA analysis, the State had the burden of proving general acceptance by a preponderance of the evidence. Id.

At the Frye hearing in this case, the State produced the testimony of Meghan Clement, technical director for the Forensic Identity Department of Laboratory Corporation of America (Labcorp). The State also introduced an article which discusses the use of mtDNA profiling in forensic investigations: M.M. Holland & T.J. Parsons, Mitochondrial DNA Sequence Analysis – Validation and Use for Forensic Casework, 11 Forensic Science Review 22 (1999). Ms. Clement was familiar with Holland and

⁴ See State v. Crow, No. 96-1156 *4 (Fla. 18th Cir. Ct. May 14, 1998) (finding mtDNA analysis inadmissible because the “database from which the experts wish to refer is insufficient to provide reliable statistical conclusions,” also finding that the counting method of quantitative analysis used for mtDNA test results “fails to provide a meaningful comparison to assist, rather than confuse, the jury”).

Parsons' article and testified that it has been peer reviewed and is considered authoritative in the field of mtDNA profiling. These commentators note that "mtDNA analysis has become a validated,⁵ robust, reliable, and well established forensic DNA profiling system." Id. at 23.

MtDNA analysis has two primary advantages over nucDNA: mtDNA requires smaller samples than are necessary for nucDNA analysis, and small amounts of mtDNA sufficient for analysis may be recovered from highly degraded samples which are old or have been exposed to extreme conditions, e.g., heat or cold. Because nucDNA is not present in the human hair shaft, only in the follicle, mtDNA analysis is the method used in cases such as this where there is no root or follicle tissue attached to the subject hair. Id. Ms. Clement testified that mtDNA analysis is widely used in forensics and has been accepted as reliable by the Federal Bureau of Investigation (FBI), the Armed Forces Institute of Pathology, and medical examiners' labs in New York and Illinois. Internationally, mtDNA analysis is being used in Sweden, Germany, and the United Kingdom. Ms. Clement further testified that a uniform process of mtDNA analysis has been validated for use in Labcorp facilities. This testimony, which was corroborated by Holland and Parsons' article, established general use of mtDNA analysis in the area of forensic science.

⁵ Validation studies are conducted during the development of a new procedure or technology in order to facilitate uniformity, monitor consistency, and to ensure that results are reproducible. The Technical Working Group on DNA Analysis Methods (TWGDAM), sponsored by the Federal Bureau of Investigation, has developed guidelines for the validation of DNA profiling systems, including mtDNA analysis. M. M. Holland & T.J. Parsons, Mitochondrial DNA Sequence Analysis – Validation and Use for Forensic Casework, 11 Forensic Science Review 22, 34 (1999).

After responding to the State's questions regarding the history and present use of mtDNA analysis, Ms. Clements gave a step-by-step description of the process. The preliminary steps of nucDNA and mtDNA analysis (extraction, replication, and sequencing) are essentially identical with the exception of the source of the genetic material. These methodologies have been scientifically validated and used by researchers in nucDNA analysis since the 1970s and 1980s. The Florida Supreme Court first declared evidence of nucDNA analysis admissible in the trial courts of this state in Hayes v. State, 660 So. 2d 257 (Fla. 1995).

Once the preliminary steps have been completed, a technician may then compare the unknown sample to the known sample to determine whether there is a match. If there is a match, the matching sequence is then compared to profiles in the FBI's mtDNA database to determine whether the sequence appears in the database, and a simple "counting method" is used to indicate the number of times the sequence appears in the database. There are presently 4142 profiles in the FBI's mtDNA database. For example, if the subject sequence appears in the database twice, the lab will report that two matches were observed out of 4142 profiles currently in the database. Because mtDNA is maternally inherited and because all matrilineal decedents will share the same mtDNA, traditional random match probability used in nucDNA analysis cannot be calculated. Instead, the counting method is used, and a ninety-five percent confidence interval is applied. If, as in this case, the matching sequence derived from the mtDNA analysis is not found in the FBI database, an exclusionary rate is calculated to say that "X" percent of the population may be excluded as potential donors of the unknown sample.

With regard to Magaletti's objections to the number of profiles in the FBI database (4142), Ms. Clement testified that this number, albeit limited, does not affect the validity of test results. Her testimony is consistent with Holland and Parsons' observations. See Holland & Parsons, Mitochondrial DNA Sequence Analysis, 11 Forensic Sci. Rev. at 32. Their article, which was published in 1999, indicates that the database was even more limited at that time and contained only 1657 profiles. Id. at 29. In spite of this limited number of profiles in the database at that time, these commentators describe mtDNA analysis as a "robust" and "reliable" method of DNA profiling. Id. at 23. Moreover, they note that the counting method is the only method of analysis reported in the United States. Id. at 31. And, while they acknowledge that labs in the United States report the results of mtDNA analysis using the counting method exclusively, they suggest that when used by itself, this is "a poor method of estimating the frequency of rare⁶ mtDNA types." Id. at 30. They also note, however, that the reliability of results is increased by going beyond the counting method to provide a more valid statement regarding frequency. Id. at 32. This may be done by applying a ninety-five percent confidence interval based on the number of times a sequence occurs in the database. Id. at 32.

Consistent with the authors' suggestions, Ms. Clement testified that the results in the present case were obtained by use of this statistical methodology. And, by applying a ninety-five percent confidence interval, the mtDNA analysis conducted in this case determined an exclusionary rate of 99.93 percent. In other words, the results

⁶ There was no testimony characterizing Magaletti's mtDNA sequence as rare.

indicate that 99.93 percent of people randomly selected would not match the unknown hair sample found in the victim's bindings. By providing an explanation of the analytical process which resulted in the genetic match between the hair found in the victim's bindings and Magaletti's hair, and then going further to explain the statistical significance of the match, the expert testimony provided in this case assisted the jury in determining a critical fact issue—identity. See Hayes, 660 So. 2d at 262.

Unlike the method of statistical calculation challenged in Brim, the State established that the counting method is the only method of reporting used by analysts in the United States. As the supreme court noted in Brim, "general acceptance" under the Frye standard can be established if use of a technique is supported by a clear majority of the community. 695 So. 2d at 272. Having established that the counting method is used exclusively in this country, the State amply satisfied its burden of proving general acceptance by a preponderance of the evidence. Furthermore, in view of Ms. Clement's testimony and Holland and Parsons' commentary on the method used to calculate an exclusionary rate, the State also established general acceptance of the statistical methodology used in this case.

For the foregoing reasons, we find that the trial court properly admitted evidence of mtDNA analysis in this case.⁷

⁷ In determining the admissibility of mtDNA analysis in the present case, we join several jurisdictions which have accepted this method of identification as a reliable forensic tool to assist in identifying and excluding suspects during criminal investigations and trials. See, e.g., People v. Klinger, 713 N.Y.S.2d 823 (N.Y. Co. Ct. 2000); State v. Smith, 100 Wash. App. 1064 (Wash. Ct. App.), review denied, 16 P.3d 1237 (Wash. 2000). MtDNA analysis has likewise been deemed admissible in jurisdictions which adhere to the federal standard pronounced in Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579 (1993), wherein the court held that Federal Rule of

Affirmed.

SALCINES and DAVIS, JJ., Concur.

Evidence 702 supersedes Frye. See Fed. R. Evid. 702 (enumerating criteria for determining the admissibility of scientific evidence based on reliability rather than general acceptance within the scientific community); State v. Pappas, 776 A.2d 1091 (Conn. 2001); State v. Hammons, 2002 WL 484645 (Del. Super. Ct. Mar. 28, 2002); State v. Scott, 1999 WL 547460 (Tenn. Crim. App. July 28, 1999), reversed in part on other grounds, 33 S.W.3d 746 (Tenn. 2000) (reversing for new trial based on trial court's failure to approve DNA expert assistance for the defense).