

**PEOPLE v. KLINGER**

713 N.Y.S.2d 823

N.Y.Co.Ct., 2000

Sept. 5, 2000

Judge Brown

PEOPLE v. MICHAEL KLINGER and RAYMOND KLINGER QDS:76703137—The following constitutes the opinion, decision and order of the court.

An indictment has been filed against the defendant Raymond Klinger accusing him of the Class B felony of Rape in the First Degree, Class B felony of Kidnapping in the Second Degree, Class B felony of Aggravated Sexual Abuse in the First Degree, Class A misdemeanor of Sexual Abuse in the Second Degree, Class B felony of Assault in the First Degree, Class D felony of Assault in the Second Degree (two counts) and the Class D felony of Reckless Endangerment in the First Degree. The indictment also accuses both defendants, Michael Klinger and Raymond Klinger, individually and aiding and abetting and being aided and abetted by each other of the Class E felony of Tampering with Physical Evidence and the Class E felony of Hindering Prosecution in the Second Degree.

By previous order of the Honorable Paul E. Kowtna, this court conducted a Frye hearing on June 6, 2000 and June 13, 2000, to determine the admissibility of mitochondrial DNA evidence at the trial of the above-captioned Indictment.

At the hearing, the court heard testimony from two witnesses, Bruce Budowle, Ph.D., a Senior Scientist with the Federal Bureau of Investigation, and Terry Melton, Ph.D., President of Mitotyping Technologies, LLC.

The court finds that Dr. Budowle and Dr. Melton were credible witnesses.

The court makes the following conclusions of law:

The Court of Appeals has held that "[t]he long recognized rule of *Frye v. United States*, 293 F. 1013, is that expert testimony based on scientific principles or procedures is admissible but only after a principle or procedure has 'gained general acceptance' in its specified field". In *Frye* (supra at 1014) the court stated:

"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*" (emphasis supplied)." (*People v. Wesley*, 83 NY2d 417).

"This Court has noted that the particular procedure need not be 'unanimously indorsed' by the scientific community but must be 'generally acceptable as reliable' (see *People v. Middleton*, 54 NY2d 42, 49). Thus the issue here concerns the acceptance by the relevant scientific community of the reliability of DNA evidence." (*People v. Wesley*, supra at 423).

"Once *Frye* has been satisfied, the question is 'whether the accepted techniques were employed by the experts in this case' (*People v. Wesley*, supra, citing *People v. Middleton*, 54 NY2d at 50). The focus moves from the general reliability of the procedures followed to generate the evidence proffered and whether they establish a foundation for the reception of the evidence at trial. The trial court determines, as a preliminary matter of law, whether

an adequate foundation for the admissibility of this particular evidence has been established." (People v. Wesley, supra at 429).

The first witness was Dr. Bruce Budowle. Dr. Budowle has been employed by the FBI for 17 years and has been a Senior Scientist for the past one and a half to two years. He has a Ph.D. in genetics and a Bachelor's Degree in biology, Dr. Budowle is a member of numerous professional organizations including the American Academy of Forensic Sciences and the International Society of Forensic Genetics. He has published approximately 200-250 articles or materials relating to DNA analysis, nine of those articles regarding mitochondrial DNA (hereinafter "mtDNA"), The majority of these articles were subject to peer review. Dr. Budowle has presented his research and findings to the International Symposium of Human Identification on nine separate occasions. He explained that a symposium is a way to bring the scientific community together so they can exchange ideas. He also serves on numerous journal and editorial boards both in this country and abroad. Dr. Budowle has received numerous honors and awards including the Forensic Scientist of the Year Award. He teaches a course on mtDNA typing for the FBI and for Forensic Institute, which is for national and international students. Dr. Budowle has been qualified on numerous occasions as an expert witness in molecular biology, genetics, population genetics, statistics and forensic science in state, local and federal courts. He stated that he has testified in more than half of the states in this country. Dr. Budowle has also been qualified as an expert on mtDNA in New York, Louisiana, Pennsylvania, Maryland and California.

As early as 1989, Dr. Budowle co-wrote a chapter of a book describing mtDNA as a possible genetic tool. In October of 1993, he co-wrote one of the first guidelines for the use of mtDNA sequencing in forensic science. In 1995, he co-wrote a peer review journal describing the procedure that was developed at the FBI for the extraction, amplification and sequencing of mtDNA from human hair shafts. Also, in 1995, a peer review article was co-written by him on the validation of the aforesaid procedures for their application to case work. An article was also co-written by Dr. Budowle, which was published in 1997, that described a phenomenon observed in mtDNA called heteroplasmy. Dr. Budowle also co-wrote a peer review article for publication where a mtDNA study was done with crab lice. He determined that this study was a valuable way of looking at the DNA environment to determine whether its analysis produces a reliable result. In 1999, he co-wrote a peer review journal article describing some of the population data from a portion of the data bases that demonstrates, by inference, the rarity of the mtDNA type among unrelated individuals. Finally, Dr. Budowle is on the DNA Commission of the International Society for Forensic Genetics. He was one of 13 members of the DNA Commission who published an editorial which contained guidelines for typing mtDNA.

Dr. Budowle testified as to the specific composition of mtDNA and the procedures used for its profiling. DNA contains the information that allows us to be what we are, to wit, eye color and hair color. It also defines out species. Under a microscope, it resembles a spiral staircase, and while stretched out, it is described as resembling a railroad track. All DNA codes consist of a four letter alphabet ( A, T, C and G) which make up "all the words of life". Whenever A is found at the top of the strand , you will find T at the bottom of the strand. Whenever T is found at the top of the strand, you will find A at the bottom of the strand. The same phenomena occurs when C is found at the top of the strand, G will be found at the bottom of the strand. Finally, whenever G is found at the top of the strand, C will be found at the bottom of the strand. DNA always finds its complement very efficiently under protocol conditions. the nuclear DNA in a human being is over 3 billion letters long.

There are two types of DNA found in a cell, nuclear DNA and mtDNA. The DNA that resides in the nucleus of the cell is called nuclear DNA. The use of nuclear DNA as a forensic tool has been found scientifically reliable by the general scientific community for more than a decade. (see gen. People v. Wesley, 83 NY2d 417). In the human cell, there is another

chromosome of DNA which is found outside the nucleus and resides in the organelle called the mitochondrion. Each mitochondrion contains 8 or 10 chromosomes. As a result, you find a greater quantity of mtDNA to work with as compared to nuclear DNA. MtDNA is much heartier than nuclear DNA. For example, old bones and teeth that have been exposed to the environment may still have sufficient quantity for mtDNA typing where nuclear DNA typing would fail to give a result,

There are, however, differences between the two types of DNA. First, in nuclear DNA, you inherit half from your mother and half from your father. In mtDNA, you inherit all of it from your mother. Second, instead of being billions of letters long, the mtDNA strand is 16,569 letters long. Further, mtDNA is circular rather than linear. Dr. Budowle opined that the circular strands may actually protect the mtDNA from being degraded.

Dr. Budowle testified that the entire mtDNA sequence was defined approximately twenty years ago. Within the mtDNA, the noncoding region is examined for forensic purposes. Within the noncoding region, there are two regions—Hypervariable-1 (HV-1) and Hypervariable-2 (HV-2). Each of these regions are about 300 letters in code in length and contain sequence information which vary amongst different individuals. Dr. Budowle testified that, by reading this sequence, the technician can generate patterns of profiles to compare from reference samples to evidence samples to determine whether an individual can be excluded from the source of the sample.

The analysis of DNA is a multi-step procedure including extraction, amplification and sequencing. The first step is the extraction process, which is the removal of the proteins so the technician is left with the DNA. The sample is put into a glass dish homogenizer, ground up and the chemicals are added to remove the protein from the sample. As a result of this process, the DNA remains.

The next step is amplification which is accomplished by a procedure known as Polymerase Chain Reaction ("PCR") which is a procedure that has been employed for approximately fifteen years. During this procedure, the technician, while using chemicals, heats the double stranded molecule to 95 degrees centigrade in order to separate it into single strands, each with their own letter code. These shorter pieces of DNA, called primers, are typically 20-30 letters long. The temperature is then reduced and DNA will again come together and bind at about 55 or 60 degrees centigrade. The result is that the technician has now made a copy from the original mtDNA sample. This process is repeated 36 times for hair samples and 32 times for blood samples, The only difference between the PCR procedure for mtDNA and for nuclear DNA is the actual sequence of a primer. Although the basic chemicals and the primer are generally the same, the difference is that the sequence of the primer "has to be one that recognizes whatever it is designed to copy".

The next step of the analysis is the sequencing step. This process generates a whole series of classes of fragments of DNA that permits the technician to actually read the sequence. As a result of sequencing, the technician read the actual array that exists in a DNA molecule.

The technician next uses a process called electrophoresis. Electrophoresis, which has been around for approximately one hundred years, is a procedure by which any object which has an electric charge is placed into an electronic field. The object will migrate to its complement, either the positive or negative electrode. For example, since DNA is negatively charged, it would migrate towards the positive electrode. Moreover, fragments of different sizes will migrate at different rates, i.e. smaller fragments will migrate faster than larger fragments. The smaller fragments will gravitate to the bottom of the field and larger fragments will gravitate toward the top of the field.

Dr. Budowle further testified that in order to read the sequence of letters, the technician uses a technology called fluorescent tagging. In fluorescent tagging, each letter is assigned a different color. By use of a laser, energy activates the fluorescent tags so that they will emit their light. As the DNA molecules migrate past the laser, they give off low light and the color of that light can be recorded. By a process similar to a bar code on a supermarket package, interpretations are made by both the use of a computer and the human eye.

Three controls are used in PCR sequencing—one positive control and two negative controls. Positive controls are a sample of a known type that is taken through the complete process. The sequence, as a result, would have to come up with the right answer and, if not, it suggests that something went wrong. Positive controls are monitored to see if it gives the right answer. Two negative controls are also used and are monitored to see how much background or contamination DNA is present which might impact on the technician's ability to achieve reliable results. Low levels of contamination are not of a great concern. Only high level contamination could effect the interpretations of analysis.

Numerous controls and practices are used to minimize contamination. Technicians use gloves, masks and work in separated, dedicated areas. There are hoods in the dedicated area so that the technician does not breathe into the samples. In addition, the technicians wear lab coats and use separate rooms. Further, the technicians use devices called pipettes that draw up small quantities of solutions. These pipettes contain aerosol resistant barriers that block contaminants from entering. Ultraviolet radiation is used to decontaminate the contaminants.

Dr. Budowle also testified that one could argue that contamination is the cause of heteroplasmy. Heteroplasmy occurs when an individual carries more than one type of detectable DNA type. If one letter is different, the technician will call that result inconclusive and the test would be redone with a different sample to see if the particular heteroplasmy site is demonstrating itself. If it does, then it would be considered a match. If not, that test is considered inconclusive. If two or more letters are different, the technicians will exclude that result. Although the explanation for this result may be low level heteroplasmy, the technician would rather falsely exclude someone than falsely include someone.

The technicians use the mtDNA database which includes more than four thousand typed individuals (approximately 4,360 human mtDNA sequences). Numerous laboratories in the world contribute to this database, called SWGDAM, which is updated every six months. This database consists of general population groups of Caucasians, African-Americans, Hispanics and Asians. The groups are further broken down into geographic areas or ethnic origin.

After sequencing, the technician analyzes the array of the setup of the base pairs. The methodology and principles of this analysis are the same for nuclear DNA and mtDNA. With both types, the technicians examine the different kinds of patterns to determine whether or not they match up.

The evidence sample is matched to the reference samples using a methodology called the counting method. The counting method is a statement of fact which finds how many times a sequence is observed. Basically, the technician compares the evidentiary sample to the reference samples and determines how many times it occurs out of these four thousand people. For example, if you type four thousand people and you never have seen a certain result before, that result would have some significance. A difference between nuclear DNA and mtDNA is that with nuclear DNA, it is not necessary to use the counting method to predict the degree to which a profile is common or rare. With nuclear DNA, the markers are independent of each other, while, in mtDNA, the letters each act as one marker since they

are all linked together. Therefore, the counting method is used to predict how common a particular profile is in mtDNA.

Next, the technician can go further by calculating a confidence level based upon a statistical formula established early in the twentieth century. The lab, in essence, would calculate a confidence interval around the estimated frequency based on the size of the database. This formula is based upon bell-shaped distribution theories that have been in existence since the mid-eighteenth century. A confidence level, based upon a statistical analysis, creates an upper bound to the benefit of the accused, and then provides that they have confidence that the frequency is no higher than this amount, Dr. Budowle is not aware of any peer review article that disagrees with this method of calculation.

MtDNA research began at the FBI in 1992 and testing commenced in 1996. Numerous procedures and protocols were developed that were subject to peer review. Moreover, validation studies for mtDNA have been published and subject to peer review. Apparently, there have been no peer review articles that disagree with the FBI validation studies. Rather, more articles were written in the scientific community using the same procedures.

Further, protocols are subject to validation studies. The protocols of the different labs are quite similar. Some labs, like Mitotyping Technologies, use the FBI protocols and make minor adjustments. Some labs use the FBI protocols without change and others create their own in the same fashion as did the FBI.

There are approximately a half dozen labs in the United States that conduct mtDNA analysis. Two of those labs are non-commercial—the FBI lab and the Armed Forces Institute of Pathology. There are over 50 labs in Europe that do mtDNA analysis. MtDNA is also used in anthropology, in identifying war remains, in clinical diagnosis to exonerate subjects and repatriating children that have been separated from their families.

Dr. Budowle testified that the testing procedures used for mtDNA profiling, i.e., extraction, the ability to quantitate and the PCR method, are the same as those used for nuclear DNA profiling. "The reliability of the PCR method for nuclear DNA has gained general acceptance in the scientific community." (People v. Lin, 267 AD2d 256; see also People v. Morales, 227 AD2d 648; People v. Garcia, 190 AD2d 749). It is only in the typing where there is a slight divergence between these two types of DNA.

Over 1,000 articles have been written with respect to mtDNA. Dr. Budowle testified that it is "a well-described genetic marker." Numerous validation studies were published and subject to peer review. Dr. Budowle also stated that the use of mtDNA for forensic identity testing is based upon universally accepted techniques and has been subject to peer review. Dr. Budowle testified that he knew of no peer review articles that state the aforesaid process, as testified to, is not a scientifically reliable process. He testified that the underlying principles of mtDNA are generally accepted by the relevant scientific community. Further, the statistical formulas used in determining whether a profile is rare or common are acceptable in the scientific community. Moreover, he knew of no peer review articles that state that this application of statistics is not a reliable interpretation of mtDNA. Further, Dr. Budowle testified that mtDNA is scientifically reliable even though the heteroplasmy exists. He does not believe that the existence of heteroplasmy makes it "an unreliable issue." He also does not consider contamination to be a problem as long as it is monitored and the proper controls are used. Further, the lab keeps an inventory of the sequences of all the people in the laboratory which would be a source of possible contamination.

Dr. Terry Melton has been working with mtDNA since 1991. She has a Ph.D. from Penn State University in genetics. She has performed hundreds of DNA analyses and thousands of PCR amplifications. She testified that her lab exclusively performs mtDNA analysis. One high profile analysis that she was involved with was the claim of Anna Anderson that she

was the remaining living child of the Romanov family. By the use of mtDNA, it was determined that she was not the Grand Duchess Anastasia. Dr. Melton has been employed for the past two years by Mitotyping Technologies, a commercial laboratory in Pennsylvania, which conducts mtDNA analysis. She has been studying and working with mtDNA for approximately nine years. Dr. Melton is a member of Sigma Xi, a research society, and a provisional member of the Academy of Forensic Sciences and she has published approximately eleven articles in the area of mtDNA. Dr. Melton has published numerous papers which were subject to peer review. One of the areas in which she has been published is the examination of population variations using mtDNA as a forensic marker. She was an invited speaker at numerous conferences including the American Academy of Forensic Sciences and the National Institute of Justice for the First International Conference on Forensic Human Identification. Dr. Melton has testified as an expert in the fields of genetics, PCR and mtDNA in the state and federal courts in five states.

Like Dr. Budowle, Dr. Melton explained the procedures and protocols that her lab follows in order to prevent contamination and maintain the integrity of the achieved results. In order to prevent heteroplasmy, the technician makes sure that the negative controls are free of contamination. Her lab uses two types of negative controls, one which goes with the sample from the moment of extraction through the complete process. The other one is used for PCR amplification. The latter control will tell the technician if contamination exists. She also testified that both the French and the Italians have created their own databases. If you totaled the databases from around the world, the sequences would be close to eight thousand. Further, like Dr. Budowle, Dr. Melton uses a standard statistical formula used by the scientific community in order to obtain a confidence interval.

Dr. Melton testified that she is unaware of any peer review articles in disagreement with the method used by her lab with respect to the analysis and interpretation of mtDNA. She testified that there is no process for mtDNA analysis that is not generally accepted as a valid scientific procedure. The whole process has been subject to peer review. Further, the statistical formula for mtDNA is generally accepted by the scientific community. Dr. Melton testified that there were no peer review articles stating that this statistical formula or method was not a reliable interpretation of the mtDNA database. She also testified that counting method, the confidence interval approach and the likelihood calculation are each equally valid.

With respect to the database, Dr. Melton testified that, as it grows in size, the frequency estimates for individual mtDNA profiles will become more and more refined leading to increasingly reliable population frequency calculations. Based upon the statistical methodology, the results create a confidence interval of either 95 or 99 percent. The 95 percent confidence interval is standard for most people, while the 99 percent confidence interval is slightly more conservative. Moreover, the database can wily show an estimate since every person in the world cannot be typed. Further, the database as it is presently constituted is sufficient to provide reliable population frequency estimates. The statistical result of the confidence interval is that the lab is confident that the true frequency in the population falls somewhere within that range. So, in a 95 percent confidence interval, there is only an uncertainty of 5 percent.

Dr. Melton testified that, in her opinion, the underlying principles of mtDNA, the principles of mtDNA analysis and the statistical methods as applied to mtDNA are generally accepted as reliable in the scientific community.

Apparently the use of mtDNA as a forensic tool and its general acceptance as reliable in the scientific community is one of first impression in this state. This court's research reveals only one unreported case in New York County Supreme Court which deals with the reliability in the scientific community of mtDNA. On May 11, 2000, in the case of People v. Edmund Ko, Justice Harold Beeler rendered an oral decision on the record after a Frye

Hearing with respect to the reliability of mtDNA in the scientific community. Like this case, he discussed his concerns with respect to contamination and heteroplasmy which he found should be subject to the dictates of cross-examination. Justice Beeler did not invalidate the procedures of mtDNA testing and the reliability of this procedure. His determination was that heteroplasmy has to be considered and factored in when making the ultimate interpretation of the issues, involved. Further, he found the counting method to be appropriate and that it would assist the jury to a certain extent. He held open the possibility of the use of population statistics after the court had received additional testimony. Justice Beeler gave great credence to Dr. Budowle's testimony, who was one of the witnesses in the case before him, and determined that his testimony reflects the pulse of the scientific community in this area.

MtDNA has been found scientifically reliable in other jurisdictions. In the case of *United States of America v. Douglas Turns*, United States District Court Judge James L. Graham (Southern District of Ohio-Eastern division January 24, 2000) found that MtDNA testing satisfied the standard set forth in *Daubert v Merrell Dow Pharmaceuticals*, 509 U.S. 579 which requires the trial court to determine whether the reasoning or methodology underlying the testimony is scientifically valid and can be applied to the facts in issue. Judge Graham found that the significant difference between mtDNA and nuclear DNA is that mtDNA has significantly fewer numbers of base pairs in the DNA helix, He found that the statistical analysis is based upon a formula which is apparently recognized in the scientific community and used in a variety of scientific contexts. Judge Graham determined that this statistical method is an acceptable and reliable estimate of probability.

The Tennessee Criminal Appeal Court in the case of *State of Tennessee v. Randall Scott*, 1999 WL 547460, which follows the Daubert rule, determined that it was not error to admit mtDNA without a hearing. Further, in Tennessee, the applicable case law does not require a finding of scientific reliability. (See also *State of Tennessee v. Paul William Ware*, 1999 WL 235592).

In the case of *People v. Kevin Carter Holtzer* (Circuit Court State of Michigan, June 10, 1999) Judge Thomas Power determined, after an evidentiary hearing, that mtDNA has achieved general scientific acceptance for reliability as required by the Davis-Frye standard. In South Carolina, the High Court found no error by the admittance of mtDNA (See *State v. Donney S. Council*, 335 S.C. 1, 515 S.E. 2d 508) according to its standard. The standard used by the courts of South Carolina is whether the evidence will assist the trier of facts, whether the expert is qualified and whether the underlying science is reliable. Further, the probative value must outweigh any prejudicial effect. The Court of Appeals of North Carolina also found no error by the admittance by the trial court of mtDNA (See *State v. Lamont ClaxtonUnderwood*, 134 N.C. App, 533, 518 S.E.2d 231). In North Carolina, a scientific method is admissible at trial if it is scientifically reliable and these courts do not exclusively adhere to the Frye standard. Rather, the courts in North Carolina follow the facts as outlined by the United States Supreme Court in *Daubert* when determining whether scientific evidence is reliable, to wit: 1) whether the theory or technique can be or has been tested, 2) whether the theory has been subject to peer review, 3) whether the theory has been submitted to the scrutiny of the scientific community, 4) the known or potential rate of error, and 5) the general acceptance in the relevant scientific community.

MtDNA has been found admissible in the state of Maryland in that it has been determined to be generally accepted in the relevant scientific community (*State v. Scotland Eugene Williams*, Circuit Court for Anne Arundel County, Maryland, Judge Pamela L. North, May 6, 1998; affirmed Court of Special Appeal of Maryland, April 12, 2000). Further, the courts of the Commonwealth of Pennsylvania have determined that mtDNA has gained general acceptance in the relevant scientific community pursuant to a Frye standard. (See *Commonwealth v. Andrew Dillon*, January 30, 1998, Court of Common Pleas of Lackawana

County; Commonwealth v. Patricia Lynne Rorrer, January 20, 1998, Court of Common Pleas of Lehigh County, affirmed Superior Court of Pennsylvania, October 22, 1999). Likewise, a judge in California has found that the mtDNA process is generally acceptable in the applicable scientific community. (People v. Christian Guillermo Torres, September 21, 1999, Superior Court of California for the County of Orange).

The court finds that the credible evidence adduced at the hearing established that mtDNA analysis and interpretations are generally accepted as reliable in the scientific community and that the procedures followed in this case establish a foundation for admission of such evidence. The evidence has sufficiently established that the analyses and interpretations of mtDNA has gained general acceptance in the community of scientists that work in this field. The existence of contamination and heteroplasmy do not affect the reliability of the scientific procedure and these issues, which are subject to cross-examination at the time of trial, do not invalidate the procedures of mtDNA testing. Although both Dr. Budowle and Dr. Melton testified that mtDNA can not be the unique identifier that nuclear DNA can achieve, this conclusion, however, does not invalidate the accuracy of the procedure and whether it is acceptable in the relevant scientific community.

This court finds that many of the procedures used in analyzing mtDNA are the same as those used in analyzing nuclear DNA. Further, the statistical methods used by the technician in creating the upper bounds of the confidence interval are basic statistical methods that have been found generally accepted in the relevant scientific community. Moreover, mtDNA procedures have been subject to peer review and Dr. Budowle testified that he knew of no peer review articles that state that the aforesaid process and statistical methods were not scientifically reliable. In addition, Dr. Melton testified that the whole process has been subject to peer review and that she is unaware of any peer review articles in disagreement with the methods used by her lab with respect to analysis, interpretation and use of the statistical formulas.

Therefore, the court will permit the People to present expert testimony at trial regarding the mtDNA analysis and the results determined therefrom.

The foregoing constitutes the opinion, decision and order of the court.