Page 513
584 A.2d 513
STATE of Delaware
v.
Steven B. PENNELL, Defendant.
Superior Court of Delaware,
New Castle County.
Submitted: Sept. 20, 1989.
Decided: Sept. 25, 1989.
Reargued After Further Hearing: Nov. 6, 1989.
Decided: Nov. 6, 1989.

Upon defendant's motion in limine to exclude DNA identification evidence. GRANTED in part. DENIED in part.

Page 514
Upon defendant's motion for mistrial. DENIED.

Peter N. Letang, and Kathleen M. Jennings, Deputy Attys. Gen., Dept. of Justice, Wilmington, for State of Del.

Eugene J. Maurer, Jr., and Elizabeth Barnes, pro hac vice, Wilmington, for defendant.

OPINION

GEBELEIN, Judge.

This case arises from a series of murders of young females during 1987-88. In particular, the defendant is charged with 3 counts of First Degree Murder relating to the deaths of Catherine DiMauro, Shirley Ellis, and Michelle Gordon. Due to the "serial" nature of these murders this case achieved a high degree of publicity. Likewise, law enforcement agencies established a joint task force to investigate these crimes as well as other deaths and disappearances which occurred in the same area during the same general time frame.

During the course of these investigations the defendant was identified as a suspect. After extensive surveillance, the defendant was arrested and charged with three counts of First Degree Murder. Pursuant to a search warrant defendant's van was searched and a piece of carpet and carpet backing was seized from the rear floor area of the van. On those articles a stain was identified as that of blood. These two articles were submitted to Cellmark Diagnostics, a division of ICI Americas Inc., hereinafter "Cellmark", for comparison to known blood samples of the decedents through a DNA analysis.

On December 1, 1988, Cellmark reported that the stains "matched the DNA banding pattern" of the known blood of Catherine DiMauro. Subsequently, on March 27, 1989, Cellmark opined that the "frequency" of the DNA banding patterns of Catherine DiMauro is approximately "one in 180 billion" in the caucasian population. Defendant has filed a motion in limine to exclude this evidence from the trial in this case.

No court in this jurisdiction has determined the admissibility of this type of DNA analysis in a criminal case where such evidence has been challenged by the defense. The Court has conducted extensive pretrial hearings on this matter and has further had the record supplemented by extensive videotape depositions of defense experts and prosecution rebuttal expert testimony.

The parties have briefed the issues involved with regard to the admissibility of this type of evidence. This is the Court's opinion on defendant's motion in limine.

HEARINGS

This Court heard testimony on behalf of the State from: Dr. David E. Housman, Professor at Massachusetts Institute of Technology, and staff member at the Center for Cancer Research, MIT, accepted as an expert in molecular biology, and molecular genetics; Dr. Robin Cotton, manager of research and development, Cellmark, accepted as an expert in molecular biology and biochemistry; Dr. Lisa Forman, Cellmark, accepted as an expert in population genetics; Karen Rubenstein, staff molecular biologist, Cellmark, (individual who performed the analysis in this case); Dr. David Goldman, Chief, Section on Genetic Studies at NIAAA, accepted as an expert in human genetics; and Dr. Edward Ratledge, Director, Center for Demography, University of Delaware, accepted as an expert in demographics. Testifying by deposition for the defense were: Dr. Laurence Mueller, Associate Professor, University of California, Irvine, accepted as an expert in ecology and population genetics; Dr. Simon Ford, Associate Professor, University of California, Irvine, accepted as an expert in genetics, biochemistry and molecular genetics; Dr. William Thompson, Associate Professor, University of California, Irvine, accepted as an expert in psychology, social science surveys, and social ecology.

All of those who testified have educational qualifications and employment experiences that qualify them as experts in their chosen aras of study. D.R.E. Rule 702.

Upon conclusion of the live testimony in this case and after reviewing the video

Page 515

taped deposition testimony and exhibits, the Court must rule on the admissibility of the results of this DNA analysis.

THE LEGAL STANDARD FOR ADMISSIBILITY

New or novel scientific evidence in Delaware must be determined to be admissible under the Delaware Uniform Rules of Evidence. The Supreme Court of Delaware has determined that the so-called "Frye" test, see Frye v. United States, D.C.Cir., 293 F. 1013 (1923), is no longer the sole test for admissibility of scientific evidence in Delaware. Santiago v. State, Del.Supr., 510 A.2d 488, 489 (1986); Fensterer v. State, Del.Supr., 493 A.2d 959, 962 n. 3 (1985) rev'd other grounds, 474 U.S. 15, 106 S.Ct. 292, 88 L.Ed.2d 15 (1985); Whalen v. State, Del.Supr., 434 A.2d 1346, 1354 (1981). In particular, the Court has held that a duly qualified expert may offer his opinion based upon tests or processes if those tests are those reasonably relied upon by experts in the particular field in forming opinions or inferences upon the subject. Santiago, supra at 489, D.R.E., Rule 703.

Basically then, this Court's analysis must determine first, that the expert being offered is qualified; second, that the evidence offered is otherwise admissible, relevant and reliable; third, that the bases for the opinion are those reasonably relied upon by experts in the field, fourth, that the specialized knowledge being offered will assist the trier-of-fact in understanding the evidence or to determine a fact in issue; and finally, whether such evidence would create unfair prejudice, confusion of the issues, or misleading of the jury. D.R.E., Rule 403.

Defendant argues that in this particular area of scientific evidence, the Frye test should be used, rather than the more relaxed standard under the Rules of Evidence. This Court cannot agree. The Supreme Court has determined that Frye alone does not govern the introduction of scientific evidence. Santiago, supra. It should be noted however, that the basic principles underlying Frye are protected by the current standard that opinions may be based on information, tests or processes which are reasonably relied upon by experts in the field. The Frye court had noted:

... 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, supra at 1014.

The basic difference, therefore, is that the State must establish only that the tests or processes used are "reasonably relied upon by experts in the field" rather than "generally accepted by experts in the field" as the third step of the Court's analysis.

In this case, it is clear, and the Court finds, that the experts offered by the State are qualified in the area of DNA analysis. Likewise, it is clear to the Court that the offered testimony would assist the trier-of-fact in determining a fact in issue, i.e. the presence of Catherine DiMauro's blood in the defendant's van. It is clear also that an opinion that the blood in the van matched that of one of the victims, if based upon reasonably accepted facts, tests or processes, would be relevant and admissible in this case. Thus, the focus of this Court's inquiry must be:

1.) Are the tests, processes, etc. followed by Cellmark in this case, those reasonably relied upon by experts in the fields of molecular biology and human genetics?

2.) Is the evidence offered by the State reliable?

3.) Will the evidence offered by the State create unfair prejudice, confusion of the issues, or mislead the trier-of-fact?

DNA ANALYSIS

Before the Court can begin the analysis of the legal principles involved, it is necessary to set out a brief introduction to the basic theory underlying such analysis.

DNA, deoxyribonucleic acid, is the fundamental or basic material which determines the genetic properties of all living things.

Page 516

Different characteristics of different life forms are caused by differences in the molecular composition of their DNA.

Every human nucleated cell contains DNA. The DNA in each cell in a particular human being is identical. Thus, DNA from skin, blood, semen or other parts of the same human body will be identical. In an exceedingly appropriate visual analogy the New York Supreme Court described the DNA molecule as follows:

DNA is composed of a long double helix, which looks like a spiral staircase. The backbone of this molecule (i.e., the handrails and balustrade of the staircase) consists of repeated sequences of phosphate and deoxyribose sugar. Attached to the sugar links in the backbone are four types of organic bases: Adenine (A), Guanine (G), Cytosine (C) and Thymine (T). The steps of the staircase are formed by pairs of these bases, (hereinafter, "base

pairs"). People v. Castro, N.Y.Supr., [144 Misc.2d 956] 545 N.Y.S.2d 985 (opinion of J.S.C. Sheindlin, August 14, 1989. p. 9).

As noted by the Castro Court, there are approximately three billion of these base pairs in each DNA molecule. The order or sequence of these base pairs is what determines genetic traits of an individual life form. Each human being with the exception of identical twins will have some difference in the sequence of these base pairs. Identical twins, because they originate from a single sperm cell's union with a single egg, will have an identical DNA molecule.

Within the human genetic molecule there are several million locations or sites where the base pairs may differ, i.e., be arranged in a different sequence. One of these areas where the base pairs are arranged differently is called a polymorphic sequence or segment. These polymorphic segments are the parts of the DNA chain that are used for analysis or identification.

The human DNA molecule will be divided into 46 sections called chromosomes. Each human being obtains 22 of these chromosomes from each parent and the remaining two chromosomes are sex-typing chromosomes. The 44 chromosomes received by a human from his/her parents are arranged in pairs. The 22 pairs contain one chromosome from each parent. Each of these chromosomes has thousands of genes and each gene is located at a particular site on the chromosome. Each gene or segment of the DNA molecule that produces a trait is called an allele. Each of these alleles may be composed of up to 10,000 or more base pairs. (1,000 base pairs being a kilobase.) It is these alleles that are used to determine the unique identity of a DNA molecule.

In DNA identification analysis a process is followed where the DNA chain is broken into small segments by use of restriction enzymes. The enzymes basically eat through the DNA molecule at certain identifiable locations or sites. Created by this process are restricted fragment length polymorphisms or "RFLPs".

The fragments created by use of restriction enzymes are then segregated by length by a process of agarose gel electrophoresis. Basically, the fragments are placed in a gel which is electrically polarized. The fragments will migrate through the gel attracted by the positive electricity at one end. The fragments will migrate at a different speed depending upon the length of the fragment because of the difficulty of longer fragments proceeding through the maze of the gel. After a certain period of time, the electrical polarization is stopped and the DNA is fixed.

At this point the DNA in the gel is incubated, sodium hydroxide is added to the gel and the DNA strands become "unzipped." Actually, the base pairs are separated all along the segment of DNA trapped in the gel. These segments are then transferred to a nylon membrane by a blotting process. Paper towels are stacked on top of the nylon membrane which in turn is on top of the gel. The moisture is wicked up into the towels and the nylon membrane catches the unzipped DNA segments. A probe, i.e., an unzipped DNA segment of a known length and sequence that has been irradiated, is added to the nylon membrane by soaking it in a solution

Page 517

containing the probes. The probes will bond with a like segment of DNA. The membrane then has x-ray film placed on it and a photograph is made of the irradiated DNA segments, i.e. an autorad. Bands will show up on the autorad indicating which length DNA segments have been identified.

To this stage in the process the principles of DNA identification, i.e., the tests, procedures and underlying theory are all generally accepted in genetic research. No one contests that every individual, except identical twins, has a different DNA chain. Thus, if the entire chain were analyzed, there is no doubt a positive identification could be made. That is to say a DNA fingerprint would exist. Likewise, there is no serious scientific dispute over the principle that segments can be created by use of restriction enzymes, and that the length of those fragments can be measured with some degree of accuracy. The bonding of an irradiated segment with another segment is a routine practice in genetic research. Finally, the production of an x-ray image from the radiated segments, an autorad, is an accepted practice in the scientific community.

The questions arise, however, as to the interpretation of the autorads, the standards used to determine a match, the number of probes necessary to obtain a true identification, the statistical probabilities of a population sample and, of course, the actual reliability of the procedures used in a particular testing laboratory.

THE TEST RESULTS

Cellmark purports to match DNA samples within a statistical probability by measuring the length of particular alleles or segments in the DNA samples compared. If both samples have the same photographic imprint as to the eight or less alleles measured by the probes, then a match is declared. Cellmark then looks at its data base for DNA from the same racial group to determine the frequencies at which those eight or less alleles occur in the population generally. If, for example, the allele measured was the genetic determinant for eye color and the allele was for blue eyes, its probability of occurrence in the caucasian data base would be much higher than an allele for violet or green

eyes. That particular allele would not be particularly helpful in identification as its occurrence would be fairly common.

For a test to be reliable, two basic conditions must be met: 1.) the alleles that are tested for must not be the result of linkage disequilibrium; and 2.) the data base population must be in or approach Hardy-Weinberg equilibrium.

The first condition is met by seeking alleles from different chromosomes. This increases the probability that the segments measured occurred randomly, rather than being the product of one parent's genetic contribution.

Hardy-Weinberg equilibrium assumes that allele frequencies in the population will remain constant from generation to generation so long as there is random mating in the population. Of course, small deviations from Hardy-Weinberg equilibrium exist in human communities for a number of reasons, including the fact that human mating is not, in its truest sense, random.

If the population is in Hardy-Weinberg equilibrium, a probability that a DNA with eight identified rare alleles will occur is determined by multiplication of the eight individual probabilities, e.g., 1/a X 1/b X 1/c X 1/d X 1/e X 1/f X 1/g X 1/h. It is easy to see that if the probability of each of these alleles occurring is but 1 in 10, the probability of all eight appearing in the same individual is 1 in 108 or 1 in a hundred million. If but two of the alleles occur only in 1 of a hundred individuals, the resulting probability of all eight alleles matching becomes one in ten billion. It is easy to see just how powerful this identification tool is and what a tremendous impact it could have on a jury.

In this case the defense has offered expert testimony to challenge the reliability of Cellmark's procedures and the underlying probabilities or frequencies in the population of the alleles measured on account of

Page 518
an alleged Hardy-Weinberg disequilibrium in the caucasian data base.

The challenge mounted as to Cellmark's data base is convincing on the surface. In particular, using Cellmark's probes there is an unusually high incidence of homozygosity. A homozygote is an individual who has inherited the same allele (or same length allele) from both parents. Thus, when a probe is used to measure the allele present at a specific locus, only one band will occur on the autorad indicating the presence of only one length allele at that geno locus for that individual. The percentage of expected homozygotes in the population for any loci tested may be calculated. The frequency of homozygotes found in Cellmark's data base at several loci significantly exceeds the expected frequencies. If the incidence of homozygosity far exceeds the expected frequency of that condition, then clearly the data base population is not in Hardy-Weinberg equilibrium. If that is the case, then Cellmark's use of probability statistics is not based upon reliable scientific assumptions.

The testimony of Drs. Forman and Goldman, however, explain to a great degree the reason for the original high occurrence of homozygosity in Cellmark's data base. In particular, the use of a 20 cm gel has apparently permitted the shortest length alleles to migrate off the gel prior to the electroporesis being stopped. Thus, where the one allele was extremely small, it would not appear on the autorad and the individual would appear to be a homozygote. Cellmark is in the process of retesting its data base with a 15 cm gel test 1 and preliminary results testified to, indicated a much lower level of homozygosity than previously indicated. These results do not prove absolute Hardy-Weinberg equilibrium, but approach that condition more closely.

Defendant also challenges the binning processes used by Cellmark in determining the allele frequency in the general population (data base). In particular, Cellmark uses a "resolution unit" to determine a match between known and unknown DNA samples. When the test is done on one gel as in this case, if the bands appear to be within one resolution unit a match is declared. If the tests are run on two gels, then Cellmark uses two resolution units to declare a match. In determining the frequency of the allele in the data base population, Cellmark uses the same resolution unit test as used on the forensic sample, i.e., if the tested DNA was on one gel, they apply one resolution unit to the data base; if the test was on two gels, they apply two resolution units to the data base. Dr. Forman testified that this seemed logically consistent. Defense argues, and the Court agrees, that this is not a proper measurement of the frequency of alleles in the data base population when applied to a case involving a single gel test. 2 Simply put, the data base was generated using different gels. For Cellmark to positively claim a match on a forensic test performed on two gels and yet to exclude that occurrence in the data base frequency for the population produces an unjustifiably low rate of occurrence in the community. The bin or frequency at which an allele occurs in the population must be calculated using the widest range Cellmark would use to declare a match on any individual test, that is, by two resolution units. This would, of course, change the frequencies calculated in this case.

Defendant further contends that there are additional aspects of Cellmark's procedures that lead to unreliable results. In particular, the defense points to a false positive result obtained by Cellmark on a blind study performed for the California Crime Laboratory. While such a result is clearly impossible if the principles underlying DNA

fingerprinting are correct (absent human error), this false positive does not invalidate the process. In the blind study performed by Cellmark, apparently blood

Page 519
samples were mixed causing the false positive. This error is certainly good cross-examination material, but it does not invalidate the generally accepted principles of DNA individuality and matching procedures.

Likewise, challenges as to the use of particular concentrations of restriction enzymes or kinds of enzymes and the failure to heat markers while raising questions of accuracy of the exact tests performed, do not invalidate the procedures used by Cellmark. These arguments are best addressed to the trier-of-fact and go to the weight of Cellmark's opinion.

FINDINGS

In reviewing the extensive evidence offered, the Court makes the following findings:

1. DNA identification procedures are based upon generally accepted scientific principles in that restriction fragment length polymorphism technology is accepted in the field of human genetic research.

2. The use of four probes of the type used by Cellmark can give a basis for an opinion of a positive identification of DNA or matching of DNA to a known sample.

3. The calculation of frequencies of genotypes (alleles of a particular length) through use of a proper data base can be useful in expressing an opinion as to a positive match of DNA samples.

4. The probability of the occurrence of DNA with certain alleles may be calculated by the multiplication method from a data base of the size of Cellmark's if:

a. The data base can be demonstrated to be in Hardy-Weinberg equilibrium or substantially in Hardy-Weinberg equilibrium; or

b. If appropriate corrections are made to the probabilities to reflect the effect of such Hardy-Weinberg disequilibrium.

5. The danger of misleading a jury, confusing the issues, or of creating undue prejudice to the defendant is extremely great when probabilities in the nature of 1 in 100 billion are expressed. Thus, such probabilities should only be expressed if they are soundly grounded in statistics generated from assumptions that are not subject to serious dispute.

6. Cellmark's binning procedure for determining the frequency of a certain size allele in the data base (and hence in the population at large) is too restrictive in the light of its policy of declaring a positive match for a forensic sample obtained by use of a two-gel comparison that would lie outside of the bin defined for data base frequency for one-gel comparisons. The result of this procedure is a lower frequency for a given allele in the data base than would be proper using generally accepted scientific principles.

7. Clearly, standards for DNA identification procedures should be developed. The suggestions of Dr. Eric Lander in a paper presented to the Banbury Conference entitled, "Population Genetic Considerations in the Forensic Use of DNA Fingerprinting" deserve serious consideration. In particular, the Court notes that the use of more than four probes could well lead to general acceptance of "DNA fingerprinting" by the scientific community and the Courts.

CONCLUSION

In conclusion, the Court finds that Cellmark's procedures in matching DNA samples are based upon tests and procedures generally relied upon by experts in the field. Their opinion, therefore, that the samples analyzed matched the blood sample from Catherine DiMauro is admissible at this trial.

The statistical probabilities, or frequencies of DNA with like characteristics being found in the population as developed by Cellmark, have not been demonstrated to be reliable based upon the evidence adduced to this point to the extent that such large numbers should be expressed to the jury with their potential for an extremely prejudicial effect. The danger of prejudice at this time outweighs the probative value of approximate figures based upon a data base not yet established to be in substantial conformity with Hardy-Weinberg equilibrium

Page 520
or corrected in a scientifically accepted way; and not yet corrected to reflect the use of a two-resolution unit standard for determining data base frequencies. Should the ongoing research at Cellmark resolve these deficiencies, the Court would reconsider the issue of testimony as to probability statistics. This would only be done after a further voir dire on this issue.

OPINION AFTER FURTHER HEARING AND ARGUMENT

During the course of the trial of this First Degree Murder case, the State has moved to reopen the evidentiary hearing on defendant's motion in limine. The Court granted the State's motion to reopen the hearing on this issue recognizing the rapidly changing state of knowledge and experience in DNA identification technology.

Dr. Lisa Forman, testified upon voir dire, as to the current testing protocols and procedures at Cellmark, as well as to the further statistical analysis of its data base. Significantly, Cellmark has basically created a new data base upon which it relies to generate population probabilities. The original data base of over 600 individuals accumulated from blood banks, paternity cases and forensic cases has been discarded in favor of a smaller data base, approximately 250 individuals, selected primarily from blood bank samples. 3

This new data base was being completed during the proceedings in this case, and initial statistics from this base were introduced in the early September testimony before the Court. Those statistics showed a deviation from Hardy-Weinberg expectations for apparent homozygotes in the population sample with regard to several of the probes used. It was this deviation, that in part led to the Court's exclusion of probability statistics. To use probability multiplication to obtain a purported frequency in the population for a number of alleles assumes randomness of allele occurrence or in other words that the population or data base be in substantial conformity with Hardy-Weinberg expectations.

Dr. Forman testified that Cellmark had run 15 cm gel tests upon the new smaller data base, but had not thoroughly analyzed them prior to the initial testimony in this case. The 15 cm gel is one produced by conducting electrophoresis for a shorter period of time, thereby catching more of the shorter length alleles on or in the gel when the electrical charge was stopped. The 15 cm gel, therefore, according to Cellmark's theory would when read in conjunction with the 20 cm gel show a smaller percentage of "apparent one banded individuals" or homozygotes. The test results appear to bear out this theory with respect to three probes; the number of "apparent" homozygotes as a percentage of the population dropped substantially when both gels were analyzed.

Dr. Forman further testified that three of the four probes when run on both 20 cm and 15 cm gels produced a percentage of homozygotes in the population that would approach or be in substantial conformity with Hardy-Weinberg expectations as calculated by her. When cross-examined upon the statistical basis for her expectation calculations, Dr. Forman produced no notes or calculations. She explained that these calculations were done on her computer and were discarded due to the lack of a functioning printer. Dr. Forman also testified that the statistical compilation of the population data base allele frequency calculations for two probes was not yet available in printed or written form.

Finally, Dr. Forman testified that Cellmark's protocol for data base frequencies had been amended to provide for a wider bin for occurrence of specific alleles in the population. Basically, Cellmark has expanded the bin size to two resolution units for population frequencies where a forensic match has been declared on a one-gel test; and to three resolution units where the forensic match came from a two-gel test.

At the conclusion of this testimony, the defense objected to any modification of the Court's previous decision, but presented no

Page 521

evidence other than through cross-examination. The defendant further objected that he was being denied due process of law in that he had no access to calculations as to how Hardy-Weinberg expectations were determined; and that the defendant had not been supplied with the calculations of allele frequencies as to two of the four probes used by Cellmark with respect to 15 cm gel tests and the frequency of perceived homozygosity.

The Court ruled tentatively that statistical evidence could be admitted upon the record as it now existed based upon the assumption that the new data base approached or was in substantial conformity with Hardy-Weinberg expectations. Further, the Court noted that Cellmark's new protocol used in calculating the frequencies in this case specifically addressed the anomaly observed in its initial opinion, see p. 518 supra.

The Court's ruling, however, was made contingent on the prosecution supplying defendant with the calculations used to determine Hardy-Weinberg expectations; and the calculations of frequencies of allele occurrence as to the two additional probes. Further, the Court noted that before these statistics could be admitted, defendant would have to be provided with the opportunity to challenge these calculations on voir dire; and that the State's expert witnesses would be available for recall on this issue.

On November 3, 1989 the Minnesota Supreme Court issued an Opinion in Hennepin County, State of Minnesota v. Thomas R. Schwartz, Minn., 447 N.W.2d 422 (1989) (C.J. Popovich). The Court provided counsel with a copy of the opinion and invited their comments on the issues raised by that opinion in which the Minnesota Court found that Cellmark's "test results lack foundational adequacy and, without more, are thus inadmissible." Schwartz, 447 N.W.2d at 428. Defendant argues that Schwartz is directly on point and should be persuasive to this

Court; and that further, a mistrial is required to cure any prejudice caused by the introduction of DNA test results in this case. The prosecution disagrees.

The Court has analyzed Schwartz as it applies to this case. The Minnesota Court is bound by Minnesota Rules of Evidence and case law to apply the so-called "Frye" test to scientific evidence. Frye v. United States, supra. As noted, supra at p. 515, the Frye test is not controlling Delaware law. In Schwartz, the Court notes that Cellmark's statistical analysis are not done in a manner that meets certain guidelines recently established by certain elements of the scientific community, in particular the F.B.I., the California Association of Crime Lab Directors, and the Technical Working Group on DNA Analysis Methods (TWGDAM). There has been little testimony about any such standards during the extensive pre-trial and trial hearings on DNA in this case. While these standards may be extremely helpful in determining a level of acceptability of a procedure in the scientific community under the Frye test, they are much less helpful in a case such as this where it is conceded by all parties that the "technology" used to perform the comparison of blood samples is generally accepted, relied upon and used by the scientific community. In particular, as noted by the Schwartz Court:

It is undisputed that RFLP analysis is routinely performed and generally accepted for research and diagnostic purposes within many scientific disciplines. Schwartz, supra, 447 N.W.2d at 425.

Thus, this Court concludes that Cellmark is performing a procedure that is generally accepted and used within the scientific community. The individuals who have testified from Cellmark, clearly qualify as experts in the areas of microbiology and/or population genetics. They are, therefore, competent to offer their opinion as to the results of the DNA test.

The Court, however, maintains its concern that the population frequency of the occurrence of any specific allele in the data base must be shown to rest upon sound scientific analysis or principles. While the testimony from Cellmark's experts resolved one of the specific concerns raised

Page 522

by the Court, i.e., the binning procedure, it has also raised other concerns.

In particular, the Court notes from the testimony of Dr. Cotton, it was developed that any two scientists may well measure (estimate from measurements on the autorad) the exact length of an allele to be different from that estimate of another scientist. This difference would not necessarily impact upon the declaration of a match in a forensic case since purportedly the scientist would be consistent in the manner in which he or she takes measurements. The Court notes that at this time Cellmark is using bioimaging technology that uses computer scanning to measure the autorad bands for purposes of inputing the allele lengths into the population data base. This eliminates to a greater degree the possibility of human difference in the data entry. It does not remove that problem, however, as it is conceded by Cellmark that the bioimager cannot read all autorads, and it is incapable of discerning an imperfection on the autorad from a band. When this occurs the placement of the location of the band and, hence, the estimate of allele lengths is accomplished by concensus of three scientists, who together read the autorad and agree upon an estimated length.

Since Cellmark's data base is small, approximately 250 people, the misidentification of a small number of allele lengths could substantially alter the frequency calculated from that data base.

As this Court has previously noted, the impact of statistical testimony upon a jury can be overwhelming. This is especially true when the statistics involved speak in numbers such as one in one hundred million and above. The Court does not adopt the position of the Schwartz Court that this type of population frequency statistical analysis would never be proper. See, State v. Joon Kyu Kim, Minn., 398 N.W.2d 544 (1987) and Tribe, Trial by Mathematics: Precision and Ritual in the Legal Process, 84 Harv.L.Rev. 1329 (1971); but see, Finkelstein & Fairley, A Comment on "Trial by Mathematics", 84 Harv.L.Rev. 1801. In this case, however, the State has failed to demonstrate a degree of reliability necessary to admit such statistical probabilities. See, Evidence: Admission of Mathematical Probability Statistics Held Erroneous for Want of Demonstration of Validity, 1967 Duke L.Jour. 665. The potential prejudicial effects of frequency probabilities clearly outweighs their probative value unless or until there is a measure of scientific certainty to those probabilities. In an appropriate case this type of statistical evidence may be acceptable; but, upon the record developed in this case, it has not been demonstrated to rest on a sound scientific basis.

Finally, the Court notes that to this point defendant has not been supplied with the calculations performed to estimate Hardy-Weinberg expectations for the probes used. Likewise, the statistical input relating to the frequencies of alleles as to two probes is likewise unavailable. On this basis alone the Court would exclude this testimony. In a case such as this where an independent test upon the DNA samples cannot be conducted due to destruction of the samples, due process requires that the defendant have access to these types of information to prepare and conduct his cross-examination. 4

The defendant seeks a mistrial based upon the fact that a prosecution witness blurted out the probabilities arrived at in this case. The Court finds that the introduction of that evidence was not the result of a tactical decision by the State; but rather came as the witness attempted to explain his answer. The actual testimony did not address in any way what the statistics meant; nor did it suggest that any one number had been arrived at in this case. In fact, the testimony was purely conditional as to what the statistical frequencies could or would be. The statistics, however, should be stricken from evidence

Page 523

and not referred to by counsel in argument. The Court will give an instruction to the jury on this matter clarifying that there is no statistical probability evidence in this case.

For the foregoing reasons, the State's motion to modify the Court's ruling is DENIED. The defendant's motion for a mistrial is DENIED.

IT IS SO ORDERED.

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1 Actually, the difference in the test being run is that for a 15 cm gel test the electrophoresis is run for a shorter length of time, capturing more alleles on the gel, but allowing for the longer alleles to bunch together.

2 The tests in this case were single gel matches.

3 The stated reasons for this modification of data base included the elimination of mother-father combinations, the procurement of more information on the persons included, etc.

4 The State just prior to argument on this issue indicated that it now did not intend to use the statistical frequency evidence. That statement does not make the issue moot as trial tactics change; and the Court's oral modification of its decision remained the law of this case until it is withdrawn by this decision.