

SUPREME COURT OF GEORGIA

Caldwell v. State, 260 Ga. 278

393 S.E.2d 436 (1990) · No. S90A0463 · Decided July 3, 1990

SUMMARY

The Supreme Court of Georgia reviews a capital case on pretrial review and addresses the admissibility of forensic DNA identification evidence, including laboratory procedures, match determination, and population-statistics calculations. The court also upholds consensual searches of the defendant's apartment and truck and rejects challenges concerning discovery of recordings and an opposing expert's scientific report. The DNA evidence ruling is affirmed except that the State may not use Lifecodes' claimed identity probability based on an unestablished Hardy-Weinberg equilibrium assumption, although more conservative figures may be used.

OPINION

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HUNT, J.

260 Ga. 278 (1990)

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CALDWELL

v. THE STATE. S90A0463. Supreme Court of Georgia. Decided July 3, 1990. Jimmy D. Berry, Bruce S. Harvey, for appellant. Thomas J. Charron, District Attorney, Debra H. Bernes, Nancy I. Jordan, Jack E. Mallard, Assistant District Attorney, Michael J. Bowers, Attorney General, C. A. Benjamin Woolf, for appellee. HUNT, Justice. This case, in which the prosecutor seeks a death penalty, is here on pre-trial review under OCGA §§ 17-10-35.1 and -35.2.

1. The defendant moved the trial court to prohibit the introduction of DNA identification evidence. Between May 8, 1989, and October 31, 1989, the trial court heard evidence, including six experts called by the state and four experts called by the defense. Ultimately, the trial court denied the motion, concluding that the relevant scientific principles and techniques are valid and that the laboratory procedures in this case were performed in a scientifically acceptable manner, "thereby obtaining sufficiently reliable results within a reasonable degree of scientific certainty so as to be admissible in evidence."

The admissibility of DNA identification evidence is an issue of *279 first impression in this court.

[1] There are at present three private, forprofit laboratories equipped to conduct forensic DNA identification, two of which Lifecodes and Cellmark use essentially the same process. Lifecodes conducted the DNA tests in this case. Considerable testimony was presented in this case about the methodology used by Lifecodes (which in many respects is standard in all DNA research plant,

animal or human), about its protocol and standards, and about its population statistics and probability calculations. The defendant's quarrel with DNA identification is not with the science on which it is based, nor with the general scientific acceptability of the techniques used to generate an "autoradiograph." The defendant's concerns essentially are Lifecodes' quality control, the manner in which it declares a "match," and in its probability calculations. (a) It would be helpful at this point to review relevant principles of genetics and cellular biology. We set forth a "brief genetic and biological primer" from *People v. Wesley*, 533 NYS2d 643 (Co. Ct. 1988): A cell is the basic unit of all living organisms including animals, plants, insects, and people. The human body has more than 10 trillion cells. A cell has two main parts the nucleus and the cytoplasm. The nucleus contains two important types of structures: chromosomes and nucleoli. The cytoplasm is all the material inside the cell membrane outside the nucleus. The nucleus contains the cell's genetic program, a master plan that controls almost everything the cell does. It sends instructions to cytoplasm, which is the cell's chemical "factory," to take amino acids and build proteins to construct an arm, a leg, a head, and ultimately a total, functioning human body. A chromosome is composed mainly of DNA and associated proteins and stores and transmits genetic information. In each human cell there are 46 chromosomes, arranged in pairs of 22 plus two sex chromosomes (represented by X for female and Y for male). DNA is an abbreviation for deoxyribonucleic acid, its chemical structure. It is a molecule that carries the body's genetic information. It is contained in every cell with a nucleus in every living organism.

*280 In 1953, James Watson, an American scientist, and Francis Crick, a British scientist, working together at Cambridge University in England, discovered the chemical and spatial structure of the DNA molecule. It was a "double helix" in which two chains of nucleotides, running in opposite directions, are held together between pairs of bases reminiscent of the rungs of a ladder, and coiled like a spring. It looks like a twisted rope ladder or a spiral staircase. Wherever their derivation human, animal or vegetable all DNA molecules have this shape.

The long threads that make up the sides of the DNA ladder are made up of alternating units of phosphate and sugar called deoxyribose. The "rungs" of the "ladder" are made up of four compounds called bases. These bases are adenine, cytosine, guanine, and thymine (abbreviated A, C, G, and T). They are attached to the sugar units of the ladder's side pieces. Each rung consists of two bases: A-T, T-A, C-G, or G-C, held together by hydrogen bonds, a weak form of chemical bond. No other combination is possible because only the A-T and C-G pairs are chemically attracted to each other; that is, A can only link with T, and C can only link with G. (See Figure 1 ... [next page.]) The order of the bases in one strand of the DNA ladder determines the order of the bases in the other strand. For example, if the bases in one strand of the ladder are ACTAGT, the bases in the opposite strand would be TGATCA. Each rung on the DNA ladder is known as a "base sequence," or a "base pair," and constitutes a bit of information. There are approximately 3 billion bits of information, or base sequences, in a molecule of DNA that is, the genetic code in the nucleus of each cell of the human body consists of approximately 3 billion bits of information.

The DNA molecule is tightly coiled within the nucleus of a cell like a ball of yarn. Unraveled, a molecule of DNA is approximately six feet in length. A sequence of three bases on the DNA molecule is known as a codon. Groups of codons form genes. A gene is a unit of inheritance composed of a segment of DNA and carrying coded information associated with a specific function. It contains a certain number of base pairs in a certain order. The instructions for making specific proteins from the 20 amino acids contained in a cell are carried by specific genes. The genetic code lies in the order of the bases in the DNA molecule, organized in genes. This order of bases is

*281 *282 passed on from one generation of cells to the next and from one generation of an organism to the next. It causes a rhinoceros to give birth to a rhinoceros and not to an ant.

Every human being inherits half of its genes from each of its parents. It is the order of the base sequences, organized in genes, that determines all of the characteristics of a living organism the color of our eyes, the shape of our ears, and thousands of other traits. Within the DNA in the nucleus of every cell in the human body is all the genetic information needed to form another human body. Each gene is a continuous segment of DNA along the molecule and is located at a specific site, known as a locus, upon a specific chromosome. Genes may be of different lengths and follow one another along the DNA molecule. Each gene differs from the next because the sequence or order of base pairs in one gene is not identical to the following one. There is no restriction on which base pair must necessarily follow another. The only restriction is that an A base (adenine) on one strand of the DNA molecule must connect with, and only with, a T base (thymine) on the other strand, and a C base (cytosine) on one strand must connect with, and only with, a G base (guanine) on the other strand.... The discovery of the structure of DNA by Watson and Crick, recognized as one of the major scientific events of the Twentieth Century, caused an explosion in biochemistry, molecular biology and related sciences, and the technology thereof. Among its vast biological implications are mindboggling applications to medical diagnostics and forensic identification. Now knowing the structure of DNA, and its immutable rules, and knowing that genetic information and instructions are transmitted by varying sequences of matched base pairs, molecular scientists were able to decipher much of the genetic codes. In 1970 there was isolated the first enzyme, known as a restriction endonuclease, or restriction enzyme, that cuts DNA molecules at specific sites. A flood of other restriction enzymes were thereafter identified and used to segment the strands of the DNA molecule.... Other major developments in DNA technology occurred, leading to enhanced methods of sequencing or fragmenting DNA and enabling the examination of specific fragment lengths of the DNA molecule. DNA researchers were soon able to identify and map the location on the chromosomes of many genes and alleles (alternative forms of genes, as, for example, alternative genes

*283 that determine eye color pursuant to Mendelian rules of inheritance). Every two years a prestigious group of international scientists meets in a body known as the Human Gene Mapping Conference, receives applications for the acceptance, mapping, and publication of gene sites

newly-discovered since the last meeting of said body. The Human Gene Mapping Conference, is uniformly recognized by the scientific community as the official registrar of gene sites....

The Human Gene Mapping Conference assigns a locus for every gene site accepted by it. A locus is the specific position occupied by a particular gene or alternative forms of a gene on a chromosome.... Long segments of DNA are the same from person to person. These are the genes whose functions are known to build the necessary organs that characterize the organism it controls in a human being, a head, lungs, a heart, limbs, and the like. However, certain areas of the DNA are highly variable from one person to another. These areas are called polymorphisms. These areas contain what is called "anonymous sequences" or "junk DNA" by reason of the fact that their function is not clearly understood.... Because of these polymorphic regions, the DNA from no two people, outside of identical twins, contains the same sequential pattern. DNA ... forensic identification, involves essentially six steps, all the scientific principles and technology of which have gained general acceptance in the scientific field in which they belong:

(1) EXTRACTION OF DNA. The DNA is chemically extracted from the submitted evidentiary sample semen found in the victim, blood, hair, or any other tissue thought to originate from the perpetrator of the crime and purified.

(2) FRAGMENTATION BY RESTRICTION ENZYMES. The DNA is then cut into fragments. The "molecular scissors" used to cut the DNA are called restriction endonucleases, or restriction enzymes enzymes that cleave the DNA molecule at specific base sequences; routinely, a restriction enzyme will cut everyone's DNA in the same places, resulting in same-size fragment lengths however, in every person's DNA, variable lengths of repetitive "junk DNA" periodically turn up. In those areas the cut points get shifted, resulting in fragments of varying lengths.

(3) GEL ELECTROPHORESIS. The fragments of DNA are then subjected to a technique widely accepted by the scientific *284 community, and much used particularly by molecular biologists, known as "gel electrophoresis"; the purpose of this process is to arrange or line up the fragments of DNA according to length, for later comparative purposes. The process of gel electrophoresis essentially consists of placing the DNA fragments on an electrically charged flat gelatin surface containing agarose gel, a thick jello-like substance, full of holes; at one end of this surface is a positively charged electric pole and at the other end a negatively charged pole; because DNA carries a negative charge, and because opposite electrical charges attract, the DNA fragments will travel from the negatively charged end toward the positively charged end; the distance the fragments travel depends on their length the larger fragments, being bulkier than the shorter fragments, find it more difficult to worm their way through the holes in the agarose gel, and will not travel as fast or as far, remaining closer to the negative pole, while the shorter fragments will arrange themselves closer to the positive pole. The result is an orderly arrangement of the DNA fragments along parallel lines.

(4) SOUTHERN BLOTTING.[2] The double-stranded DNA fragments are then chemically split apart into two strands, leaving their chemical bases (A, C, G and T) separated like open zipper

teeth; the fragment pattern is then transferred from the wobbly surface of the agarose gel onto a... nylon membrane... This procedure is known as Southern Blotting, after Dr. E. H. Southern, who reported the process in 1975.

(5) HYBRIDIZATION. To identify the aspects of the DNA pattern unique to each individual, "probes," developed in the laboratory by the use of recombinant DNA technology, are applied to the ... [nylon] membrane. These probes are tagged with a radioactive marker substance and are designed to seek out a pre-determined locus in a polymorphic (highly variable) region of the DNA. Upon finding a DNA fragment that carries all or part of its complementary base sequence, the probe will bind to the fragment. The marker component of the probe will cause the probebound fragments to "light up," allowing easy identification of their positions in the fragment pattern. To enhance the power of identity, Lifecodes uses four probes in its "DNA

*285 PRINT IDENTIFICATION TEST."

(6) AUTORADIOGRAPH. The excess probe is then washed away and the ... [nylon membrane] is placed against a piece of X-ray film and exposed for several days. When the film is processed, black bands appear where the radioactive probes stuck to the fragments. All of the four probes used by Lifecodes produce an average of two dark bands on a white column, looking much like the bar codes found on food packages in supermarkets. This is known as an autoradiograph, which term is often shortened to autorad.

All of the procedures hereinabove constituting DNA Fingerprinting are recognized as reliable and have gained general acceptance in the scientific community in which they belong. When comparing two DNA fragment patterns, such as one produced from an unknown biological evidentiary sample e.g., a semen specimen retrieved from a rape victim and one from the known blood sample of the suspected rapist one simply looks to see where the probe "landed" on the two patterns. Because of polymorphisms in the chromosomal loci to which the probe is directed, it is highly unlikely that the probe will find its complementary code on fragments of equal length in the DNA specimens of two people. If the known and unknown biological specimens are from the same person, one can expect to find the probe on fragments of identical length and, consequently, in identical positions on the two patterns.[3] [Footnotes supplied.] *People v. Wesley*, supra, 533 NYS2d at 645-60. (b) In many states, the test for admissibility of novel scientific evidence is whether the "scientific principle or discovery" supporting the evidence is "sufficiently established to have gained general acceptance in the particular field in which it belongs." *Frye v. United States*, 293 F 1013, 1014 (DC Cir. 1923). This is not the test in Georgia. In *Harper v. State*, 249 Ga. 519, 525 (1) (292 SE2d 389) (1982), we concluded: the Frye rule of "counting heads" in the scientific community is not an appropriate way to determine the admissibility of a scientific procedure.... We hold that it is proper for the trial judge to decide whether the procedure or technique

*286 in question has reached a scientific stage of verifiable certainty, or in the words of Professor Irving Younger, whether the procedure "rests upon the laws of nature." The trial court may make

this determination from evidence presented to it at trial by the parties; in this regard expert testimony may be of value. Or the trial court may base its determination on exhibits, treatises or the rationale of cases in other jurisdictions. [Cits.] The significant point is that the trial court makes this determination based on the evidence available to him rather than by simply calculating the consensus in the scientific community.

The evidence in this case clearly demonstrates that the DNA identification techniques used in this case are based on sound scientific theory and that, if proper procedures are followed, analysis of clean, undegraded samples of sufficiently high molecular weight DNA can produce reliable results. There is no real dispute about this. The dispute centers on the techniques and procedures followed (or not followed) by Lifecodes in this case. Initially, then, we need to decide whether such concerns go merely to weight or whether they implicate admissibility also. We recognize that, while the DNA identification procedures and technology used in this case have been widely used in laboratories for years in experimental and diagnostic settings, the transfer of this technology to a forensic setting is comparatively recent. As noted previously, there are three private laboratories in this country doing forensic DNA analysis. One of them uses procedures entirely different from those explained above (and the record in this case does not explain what those procedures are). The other two use essentially the same technology, but their protocols are different, and they use different restriction enzymes and different probes. The FBI has recently set up its own forensic DNA lab, using still different restriction enzymes and probes. One consequence of this is that the database generated by each system for use in probability analysis is unusable by the other laboratories. In other respects, there may be disagreements at present about, for example, what is a match. Because of "band shift," two lanes of identical samples may not run exactly the same, raising questions such as: How much variation can exist before a match is not a match? What tests, if any, should be run to determine whether a difference in the pattern on two lanes of an autoradiograph is due to band shift? In light of the novelty of the use of DNA analysis in forensics, the complexity of the tests, and the present lack of national standards governing such tests, we conclude the trial court was correct when it determined not just whether the general scientific principles and *287 techniques involved are valid and capable of producing reliable results, but also whether Lifecodes substantially performed the scientific procedures in an acceptable manner. Compare *Minnesota v. Schwartz*, 447 NW2d 422, 428 (Minn. 1989); *People v. Castro*, 545 NYS2d 985 (Supp. 1989). We believe this approach is consistent with *Harper v. State*, supra, 249 Ga. at 524-526. (c) This does not mean that the trial court must exclude novel scientific evidence unless convinced there is no possibility of error. No procedures are infallible. If, for example, a sample was accidentally mislabelled, and the laboratory compared two samples from the same source believing it was comparing a sample of evidence with a sample from the defendant, the result would be a false match. Or, if the laboratory mistakenly or carelessly added sample material from the defendant to the evidentiary sample, and the evidentiary sample was very degraded leaving no bands on the autoradiograph, the bands from the defendant's sample in

evidence lane would match the bands in the lane assigned the defendant's sample, and, again, a false match would occur. Obviously, a laboratory needs to take precautions at all stages of its testing procedures. The defendant's experts testified about various ways that errors conceivably could occur, including mislabelling and cross-mixing of samples, bacterial contamination, less than perfect chemical preparations, and so forth. We agree with the trial court's assessment that Lifecodes' protocol is adequate to meet these concerns. More significant were criticisms about: (1) the manner in which a match was declared; (2) Lifecodes' failure (initially) to test for band shift; and (3) the probability estimates. (d) Samples from the same person will not run at exactly the same speed every time. The buffer, the agarose gel and the salt solution are all manufactured and can vary minutely between one batch and the next. Moreover, the gel may not be absolutely consistent across its length, and the lanes into which the samples are poured can have minor variations and imperfections which can affect speed from one lane to the next. The result is called band shift: The banding patterns of two different samples containing the same DNA may not line up exactly they will be close, but not exact. A match can nevertheless be called if the bands are in essentially the same place within a permissible degree of error. The matches in this case were initially declared by visual means. Lifecodes contended that a visual observation was adequate to declare a match, and that it was not necessary to run further tests to document that any difference was due to band shift rather than different DNA. Some band non-alignment was noted and ascribed to band shift, but no tests were run to establish band shift. However, possibly in response to the decision in *People v. Castro*, supra, 545 *288 NYS2d 985 (which involved a Lifecodes DNA analysis), as well as criticisms by defense experts in the initial hearings in this case, Lifecodes decided to run a test in this case to determine band shift. There are two ways to test for band shift. First, a mixed-lane sample can be run. Here, a part of the known sample and the evidence sample are run in the same lane. If only two bands appear,[4] the DNA is the same. Of course, a mixed lane cannot be run after the evidence sample is used up. Lifecodes took the alternate route, and rehybridized the membrane with a non-polymorphic (or monomorphic) probe. A non-polymorphic probe will attach to DNA which everyone has, and so samples from different people should generate identical banding patterns. Since the non-polymorphic probe is run on the same nylon membrane which generated the previous autoradiographs,[5] the lanes in the autoradiograph derived from running the non-polymorphic probe can be compared to previous ones, and the differences from one lane to the next can be compared. Dr. McElfresh from Lifecodes testified that the results of the test confirmed the presence of band shift and confirmed his previous testimony interpreting the autoradiographs. Agreeing with him on this count were Dr. Wyatt W. Anderson, Alumni Foundation Distinguished Professor of Genetics, member of the National Academy of Sciences and former President of the American Genetic Association; Dr. Sidney R. Kushner, head of the Department of Genetics at the University of Georgia; and Dr. Martin L. Tracey, Professor of Biology at Florida International University in Miami, Florida. These witnesses agreed that visual observation of the autoradiograph, when coupled with the

results of the band-shift test, can justify declaring a match, and did so in this case. It may be concluded that declaring a match by visual observation is scientifically acceptable at least where, as here, the visual observation is confirmed by a scientifically acceptable test for determining band shift. (e) Once a "match" is declared, its significance is determined by statistical analysis, applying theories of population genetics: The population geneticist determines the frequency with which a specific allele occurs within a given human racial *289 group. In the case of a common allele, for example the Rh positive blood types, the frequency of occurrences in the human population is quite large. Thus, if both DNA samples show the Rh positive allele, the population geneticist can say only that both samples could have come from any person, male or female, who is part of the majority of the human population. In the case of the Rh negative allele, the population geneticist can say that the allele is somewhat rarer and that the samples come from a minority of the human population. In the case of alleles that occur in the anonymous or polymorphic section of the genome the likelihood that the samples will match is much smaller. This reduced likelihood of matches is what gives DNA identification technology its value for forensic purposes. *People v. Castro*, supra, 545 NYS2d at 992. The defendant complains of Lifecodes' use of a "double integral Gaussian weighted average" in its calculations. We need not consider this complaint, as Lifecodes subsequently revised its calculations using a "straight binning method," which the defendant does not complain about. He does complain that Lifecodes' statistical calculations assume the relevant population is in Hardy-Weinberg equilibrium[6] and that for each of the relevant alleles, the population is in linkage equilibrium. See *People v. Castro*, supra, 545 NYS2d at 992-93. There was testimony in this case (by state's witnesses) that these assumptions are not unreasonable. However, none of the state's witnesses had studied Lifecodes' database to determine whether the relevant population is in Hardy-Weinberg equilibrium. Only a defense witness attempted to make that determination. Dr. Jung Choi, molecular geneticist, member of the faculty at the Georgia Institute of Technology and consultant to the U. S. Army Criminal Investigation Laboratory, testified that he had analyzed Lifecodes' databases and concluded that the populations were not in Hardy-Weinberg equilibrium. This testimony essentially is undisputed, and seriously calls into question Lifecodes' claimed power of identity one in twenty-four million for the defendant's DNA identification. However, as has been noted, "[c]onservative or reduced calculations may ... correct ... Hardy-Weinberg deviation problems." *People v. Castro*, supra, 545 NYS2d at 993. Dr. Anderson testified (for the state) that Lifecodes' calculations *290 were based on a number of assumptions, which Dr. Anderson characterized as "not unreasonable." However, Dr. Anderson testified, a more conservative approach is simply to use the database itself, and not "any population theory" to generate frequencies of "individuals" from frequencies of "patterns." His "conservative" power of identity was one in approximately 250,000. Although in a future case the state may establish scientifically that the populations represented in Lifecodes' (or some other laboratory's) databases are in Hardy-Weinberg equilibrium, we conclude the state has not done so in this case. Thus, the state should not be

permitted to use Lifecodes' enormous claimed power of identity based on its "assumption" that the relevant population is in Hardy-Weinberg equilibrium. The state may, however, use the more conservative figures Dr. Anderson calculated. Compare *People v. Wesley*, supra, 533 NYS2d at 659 (reducing "overall claimed mean power of identity ... to eliminate any possible Hardy-Weinberg disequilibrium"). (f) It should be noted that the defense was well-assisted by experts on the issue of admissibility of DNA identification evidence, and that Lifecodes' testing procedures, data and results were disclosed to the defense. Compare *Minnesota v. Schwartz*, supra, 447 NW2d at 429 (II) (DNA test results not admissible where Cellmark laboratory failed to make its testing data and results available to the defense). (g) In all respects save that of the population statistics, the trial court's order is affirmed.

2. Shortly after 3:00 p. m. on August 16, 1988, Kay Caldwell (the defendant's wife) called the police to report that her children had been stabbed. The police arrived minutes later and were invited into the apartment by Mrs. Caldwell. They found 12-year-old Sara Caldwell lying on the bed, stabbed to death, and 10-year-old Ben Caldwell lying in the bathroom floor, seriously injured, but still alive. Police searched the apartment, looking for evidence until 10:00 p. m. that evening, and continued searching the next day. The defendant and his wife did not remain in the apartment after the murder, and stayed with relatives. The defendant disappeared on August 20, and an arrest warrant was issued August 23, 1988.

The police did not obtain a written consent to search until August 21, 1988. Eight months later, Mrs. Caldwell signed a consent to search purportedly ratifying all police searches of her apartment on or after August 16, 1988. The defendant concedes Kay Caldwell "initially ... consented to and in fact requested that the police enter her home." However, he objects to the "scope and intensity" of the search. Relying on *Mincey v. Arizona*, 437 U. S. 385 (98 SC 2408, 57 LE2d 290) (1978), he argues that there is no crime-scene exception to the warrant requirement, *291 and that while exigent circumstances justified the initial entry by police into the Caldwell apartment and a limited search for a killer or victims on the premises, the search here went well beyond that justified by the exigencies of the situation. Our answer is that the searches here were not based on "exigent-circumstances"; they were based on Kay Caldwell's consent. Kay Caldwell (the sole lessee on the apartment) called the police because her children had been stabbed, and she wanted the police to investigate the crime. She invited them into her home, and then left, entrusting it to the police. Her later written consents to search confirm her intent. The police obtained the defendant's clothes and a key by consent. Later, his truck was searched after having been abandoned by the defendant in some woods one-half mile from the expressway in Gilmer County. See *Williams v. State*, 171 Ga. App. 546 (2) (320 SE2d 389) (1984). Consensual searches do not violate the Fourth Amendment. The trial court properly denied the defendant's motion to suppress.

3. The court did not err by denying the defendant's motion to require the state to produce "any and all" audio and video recordings of interviews with state's witnesses. *Boatright v. State*, 192 Ga. App. 112 (2) (385 SE2d 298) (1989).

4. Contrary to the defendant's contention, we have held that the state is entitled to obtain a copy of a written scientific report by a defendant's expert, just as the defendant is entitled to obtain a copy of a written scientific report by a state's expert. *Sabel v. State*, 248 Ga. 10, 18 (6) (282 SE2d 61) (1981); OCGA § 17-7-211. Moreover, the defendant's expert may be called as a witness by the state. *Ibid.*; *Weakley v. State*, 259 Ga. 205 (2) (378 SE2d 688) (1989).

5. Except as noted in Division (1) (e) and (g), *supra*, the trial court's orders at issue on this appeal are affirmed.

Judgment affirmed in part, reversed in part. All the Justices concur.

NOTES

[1] DNA (deoxyribonucleic acid) is an organic substance found in the chromosomes in the nucleus of a cell. It provides the genetic code which determines a person's characteristics. Research laboratories have been conducting DNA analyses for years. The forensic use of DNA analysis, however, is of quite recent origin.

[2] While some sources describe the initial 6 steps as "Southern Blotting," any difference in nomenclature does not affect the outcome of this decision.

[3] Compare *People v. Castro*, 545 NYS2d 985 (Supp. 1989), which also describes DNA identification evidence. That opinion includes a footnote which serves as a bibliography for further reading in this area. *People v. Castro*, *supra* at 990, n. 3.

[4] This assumes (1) that a single-locus probe is being used, and (2) that there is no homozygosity at the locus being probed.

[5] Each time a different probe is run, the old probe is chemically washed off, the new probe is hybridized to the samples on the membrane, and a new autoradiograph is made. Theoretically, a membrane could be rehybridized indefinitely. There was testimony, however, that in practice each wash takes off some of the sample as well as the probe, so that eventually the remaining sample will be too small to generate a readable autoradiograph.

[6] In 1908, Dr. Hardy and Dr. Weinberg formulated a binomial equation used to calculate the frequency of an allele in a population from sample population data. This equation is valid only if there is random mating in the population, if there is no inbreeding, if there is no mutation, and if the population is effectively infinite.