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THE ADMISSION OF DNA EVIDENCE IN STATE AND FEDERAL COURTS

George Bundy Smith and Janet A. Gordon***

INTRODUCTION

IN the past few years DNA evidence has become an important tool in the hands of both prosecutors and defense attorneys. Its value is that it can establish to a virtual certainty the presence or the absence of a defendant at the scene of the crime. This Article discusses DNA evidence, concentrating on the problems that arise for both prosecutors and defense attorneys from its use. The Article begins by discussing what DNA profiling evidence is and why it is useful. Next, it deals with the history of DNA evidence in the courts of the United States over the past ten years. The final section examines trends in DNA evidence.

I. WHAT IS DNA?

Deoxyribonucleic acid[1] ("DNA") is the chemical dispatcher for genetic information. It is found in every cell of the human body, except red blood cells.[2] Each cell contains the same configuration of DNA; that is, DNA is identical in every cell of a person. The important feature of DNA for forensic purposes is that, with the exception of identical twins, no two individuals have the same DNA configuration.

A. *The DNA Structure*

In 1953, James Watson and Francis H.C. Crick, aided by the earlier efforts of scientists such as P. A. Levene, Erwin Chargaff, Rosalind Franklin, and Maurice Wilkins, discovered the structure of the DNA molecule.[3] Wilkins, who studied the DNA molecule by using X-ray crystallography, and Watson and Crick, who constructed DNA models using X-ray data and rules on base composition, received the Nobel Prize for their discoveries in 1962.

Based on the works of these scientists, we now know that a molecule of DNA is shaped like a double helix and resembles a twisted

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1. *See generally* Michael J. Pelczar, Jr. et al., Microbiology: Concepts and Applications 350-400 (1993) (explaining the structure and characteristics of DNA); Lansing M. Prescott et al., Microbiology 193-201, 236-307 (2d ed. 1993) (same).

2. This does not prevent DNA typing of blood since white blood cells contain a nucleus, and, thus, contain DNA.

3. Prescott et al., *supra* note 1, at 7.

ladder.[4] The sides of the ladder—the double strands—are composed of repeated sequences of phosphate and deoxyribose sugar molecules.[5] The steps of the ladder are made of pairs of the following organic bases: adenine (A), cytosine (C), guanine (G), and thymine (T).[6] Due to the chemical composition of these organic bases, adenine will pair only with thymine (A-T or T-A) and cytosine will pair only with guanine (C-G or G-C).[7] This strict complementary pairing means that the order of the bases on one side of a DNA ladder will determine the order on the other side. Because human beings share more biological similarities than differences, our DNA molecules—that is, our base pairing sequencing—are in large part the same. The DNA molecules of each individual consist of approximately 3 billion base pairs, of which only 3 million base pairs differ from one individual to another.[8]

B. *The Organization of DNA in Cells*

The unique, repeating sequence of the base pairs along the double strands of DNA that is responsible for making a particular protein is called a "gene."[9] Each gene is responsible for the production and regulation of a specific cell activity. The order of the four bases—adenine, cytosine, guanine and thymine—within a particular gene determines the function of that gene.[10]

A molecule of DNA contains thousands of genes, which are situated on twenty-three pairs of chromosomes, one-half inherited from either parent. The specific position that a gene occupies is called the "locus."[11] An individual has two genes at each locus, one maternal and one paternal.[12]

Alternative forms of a particular gene are called "alleles."[13] Thus, the gene for the production of eyes may appear in the form of a blue-eyed allele or a green-eyed allele.[14] In chemical terms, the difference in alleles is explained by the difference in the ways the base pairs arrange themselves along the DNA molecule.

An individual who has two identical alleles at a particular locus is said to be homozygous for that particular locus.[15] Stated differently,

4. Pelczar et al., *supra* note 1, at 42-47; Prescott et al., *supra* note 1, at 193-95.
5. Prescott et al., *supra* note 1, at 193.
6. Pelczar et al., *supra* note 1, at 42-43; Prescott et al., *supra note 1, at 193.*
7. Pelczar et al., *supra* note 1, at 43; Prescott et al., *supra* note 1, at 193.
8. *See* National Research Council, The Evaluation of Forensic DNA Evidence 63 (1996) [hereinafter Evaluation of DNA Evidence].
9. Prescott et al., *supra* note 1, at 202.
10. Evaluation of DNA Evidence, *supra* note 8, at 60-63.
11. *Id.* at 13.
12. *Id.* at 14.
13. *Id.*
14. *Id.* at 62-63.
15. *Id.* at 63.

when an individual possesses the same allele at a particular locus on both chromosomes of a pair, then the individual is said to be homozygous for that locus. On the other hand, an individual who has two different alleles at a particular locus is said to be heterozygous for that locus.[16]

An individual's entire complement of DNA is known as the "genome."[17] As stated, the genome of an individual consists of approximately 3 billion base pairs, of which only 3 million base pairs differ from one individual to another. It is the existence of these minor differences in the sequencing of base pairs, known as "polymorphisms," that provide the basis for DNA identification and have great significance for DNA forensic analysis.[18]

The length of each polymorphism is determined by the number of core sequence of base pairs that is repeated many times along the chromosome.[19] The repeat core sequence of base pairs is called a "variable number tandem repeat" ("VNTR").[20] VNTRs are not genes, since they produce no protein.[21] Instead, VNTRs are stretches of DNA in which a short nucleotide sequence is repeated tandemly 20 to 100 times.[22] "The exact number of repeats, and hence the length of the VNTR region, varies from one allele to another, and different [VNTR] alleles can be identified by their lengths."[23]

Much of DNA forensic analysis involves the use of the DNA loci that contain VNTRs.[24] VNTR loci are particularly convenient as markers for human identification because they have a very large number of different alleles.[25] DNA fragments containing the VNTRs can be detected by specially constructed molecular "probes," short segments of single-stranded DNA with a radioactive component that bind to specific DNA sequences.[26]

C. *DNA Replication*

DNA is very precisely copied during its replication, which consists of two-steps: transcription and translation.[27] During transcription, the two strands of the double helix unwind from one another and separate.[28] Thereafter, translation occurs, through complementary base

16. *Id.*
17. *Id.* at 61.
18. *See* National Research Council, DNA Technology in Forensic Science 34-35 (1992) [hereinafter DNA Technology].
19. Evaluation of DNA Evidence, *supra* note 8, at 14-15.
20. *Id.* at 14.
21. *Id.*
22. *Id.*
23. *Id.*
24. *Id.* at 14-15.
25. *Id.*
26. *Id.* at 16.
27. Pelczar et al., *supra* note 1, at 351, 355, 359; Prescott et al., *supra* note 1, at 197.
28. Pelczar et al., *supra* note 1, at 351, 355; Prescott et al., *supra* note 1, at 197, 199.

pairing (e.g., A-T or T-A and C-G or G-C) and the presence of certain enzymes, to form two new progeny strands.[29] Each new strand, containing complementary bases, bonds to the parent strand to form two identical DNA molecules.

II. The Nature of DNA Profiling Evidence

DNA profiling identification tests allow forensic scientists to look at DNA molecules from an individual or a piece of evidence and compare them with DNA samples from other sources.[30] Recently, DNA profiling identification tests have been conducted in laboratories in the United States. Commercial laboratories, such as Lifecodes, Cellmark Diagnostic Corporation, and Cetus Corporation, offer DNA testing.[31] In addition, government laboratories, such as laboratories within the Federal Bureau of Investigation and the Federal Drug Enforcement Administration, also perform DNA testing.

III. The Techniques Used to Develop DNA Profiling Evidence

To develop DNA profiling evidence, forensic scientists use techniques of molecular biology to excise VNTRs from samples of blood, semen or other materials containing fragments of DNA.[32] The forensic scientists then measure the lengths of the VNTRs by examining how far they migrate along the surface of a mixture of gelatinous material, in a certain period of time, when they are subjected to an electric charge.[33]

A. *Restriction Fragment Length Polymorphism Analysis*

The primary technique for developing DNA profiling evidence is restriction fragment length polymorphism analysis ("RFLP") analysis.[34] RFLP analysis, which is referred to in the scientific community as Southern Blot, was developed by Edwin Southern in 1975.[35] RFLP analysis technique detects the specific DNA fragments so that a particular gene may be isolated from a sample of DNA and compared with a known sample of DNA.[36] A brief summary of this procedure follows.

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29. Pelczar et al., *supra* note 1, at 351, 359; Prescott et al., *supra* note 1, at 197-99.

30. U.S. Congress Office of Technology Assessment, *Genetic Witness: Forensic Uses of DNA Tests*, at 3-6, 41-50; Prescott et al., *supra* note 1, at 197.

31. Harlan Levy, And the Blood Cried Out: A Prosecutor's Spellbinding Account of the Power of DNA 52, 138 (1996).

32. David H. Kaye, *DNA Evidence: Probability, Population Genetics, and the Courts*, 7 Harv. J.L. & Tech., 101, 107-08 (1993).

33. *Id.* at 108.

34. This technique is also referred to as VNTR profiling since VNTRs are RFLPs.

35. Prescott et al., *supra* note 1, at 288.

36. *See* People v. Wesley, 633 N.E.2d 451, 459-61 (N.Y. 1994) (outlining the procedure for RFLP analysis).

1. Extraction of DNA

Using chemical enzymes, the DNA to be examined is extracted from the evidentiary sample and then purified.

2. Restriction or Digestion

The extracted DNA is then cut into fragments at specific sites by the use of restrictive enzymes known as restriction endonucleases. The restriction endonucleases recognize certain sequences of base pairs along the DNA, and cut the DNA every time it finds the appropriate sequence to produce RFLPs. The RFLPs produced from an individual will vary with the use of different restriction endonucleases.[37]

3. Gel Electrophoresis

The RFLPs are placed into a semisolid matrix, called an agarose gel, which is then electrically polarized to sort the RFLPs by length so that they can be measured. The RFLPs are placed at the negative end of the electric field. Because DNA is negatively charged, the RFLPs will migrate toward the positive end of the field. The distance traveled will depend on the length of the RFLPs. The longer ones migrate more slowly than, and do not travel as far as, the shorter ones. Fragments of known base pair lengths, called molecular weight markers, are placed in separate lanes to allow the measurement of RFLPs in units of base pairs. Several different samples are run on the same gel, but in different tracks or lanes.[38]

4. Southern Transfer

The sorted RFLPs are chemically split into two separate strands in a process known as "denaturization." Through capillary action, the single strands are then transferred from the agarose gel onto a nylon membrane, known as a nitrocellulose sheet, where they become permanently fixed in their respective positions according to length on the nitrocellulose sheet, which is now known as a "Southern Blot."[39]

5. Hybridization

The Southern Blot is then placed in a solution of genetic probes of known single-stranded segments of DNA which are tagged with a radioactive marker. The radioactive marker attaches to the genetic probes and emits radiation without altering the function of the probes. Each genetic probe is designed to bond, or hybridize, with the single-stranded RFLPs on the Southern Blot that contains the complementary sequence of base pairs (VNTR), to form hybridized polymorphic

37. Prescott et al., *supra* note 1, at 288.
38. *Id.*
39. *Id.* at 288-89.

segments. The radioactive marker is used to determine the position of the genetic probes on the Southern Blot after they hybridize with the single stranded RFLPs.[40] The marker facilitates the visualization of the RFLPs.

6. Autoradiography

Autoradiography is the photographic process that allows us to see the position of the polymorphic DNA segments. The radioactively-marked nylon membrane, with the hybridized polymorphic segments, is then placed against a piece of X-ray film, where the radioactive probes expose the film at their respective locations.[41] After the film is processed, dark bands, which resemble bar codes on grocery items, appear on the X-ray film where the radioactive probes have bonded to the RFLPs, producing the "DNA print."[42] The DNA print is then examined to determine the length of the DNA fragments containing a specific sequence of base pairs. The position of each dark band indicates the location of a polymorphic segment on the blot. The location of the polymorphic segment indicates the length of the DNA fragment that contains the specific sequence of base pairs. The length of the DNA fragments is measured by how far they traveled through the gel.[43] The length of the DNA fragments containing the specific sequence of base pairs will vary from person to person. The dark bands on the DNA prints are then studied to determine if a match exists between a known sample (*e.g.*, from a crime suspect) and an unknown sample (*e.g.*, from a crime scene or victim).[44]

B. *Polymerase Chain Reaction*

Increasingly, another technique for DNA testing, polymerase chain reaction ("PCR") analysis,[45] has received overwhelming acceptance in the scientific community and the courts.[46] PCR analysis takes advantage of the reproductive nature of DNA, and allows a forensic scientist to produce multiple copies from a single test sample of DNA in a process similar to the one by which DNA duplicates itself normally.[47]

The PCR technique was invented by Kary Mullis during his employment at a California genetics company named Cetus Corporation, and earned him the 1993 Noble Prize for Chemistry.[48] PCR analysis was

40. *Id.*
41. *Id.*
42. *See* DNA Technology, *supra* note 18, at 38-39.
43. Prescott et al., *supra* note 1, at 288-89.
44. *See* DNA Technology, *supra* note 18, at 38-39.
45. *See* Pelczar et al., *supra* note 1, at 357.
46. *See* People v. Morales, 643 N.Y.S.2d 217, 218-19 (App. Div. 1996).
47. Kamrin T. MacKnight, *The Polymerase Chain Reaction (PCR): The Second Generation of DNA Analysis Methods Takes the Stand*, 9 Santa Clara Computer & High Tech. L.J. 287, 304 (1993).
48. Levy, *supra* note 31, at 137-38.

first used in a criminal identification by another California scientist named Dr. Edward Blake.[49]

The three-step PCR technique involves the denaturization, annealing and extension of the DNA sample, and results in the true replication or amplification of the original DNA sample.[50] A segment of double-stranded DNA, containing a target sequence (a nucleotide sequence containing the gene of interest) is extracted from the test sample.[51] The target sequence then undergoes denaturization, during which the DNA is heated to separate the two strands.[52] In the annealing phase, two kinds of primers—short synthetic pieces of DNA—are added to the target sequence.[53] Each primer has a nucleotide sequence that is complementary to a particular region at the end of the gene to be amplified.[54] The mixture of primers and DNA is then cooled, and the primers bind to the gene.[55]

At the end of the PCR cycle, two copies of the gene are formed from each initial copy. The PCR cycle may be repeated as often as necessary to obtain the desired amount of a target sample of DNA. Once the desired amount of DNA is obtained using the PCR method, the analysis of the DNA proceeds in essentially the same way as with RFLP analysis.

PCR analysis has some proven advantages over RFLP testing.[56] First, this technique requires very little DNA in the evidence sample, and forensic scientists can increase substantially a small sample of DNA.[57] Second, forensic scientists can perform PCR analysis within twenty-four hours, whereas RFLP analysis may take several weeks. Third, PCR analysis does not require the use of radioactive materials.

There are also some disadvantages to using PCR analysis. For example, any procedure that uses PCR methodology is susceptible to error caused by contamination, leading to amplification of the wrong DNA.[58] In addition, most of the markers used in PCR based typing have fewer alleles than VNTRs.[59] This means that more loci are required to produce the same amount of information about the likelihood that two persons share a profile.[60] Furthermore, some of these loci are associated with functional genes, which means that they may have been subject to natural selection, possibly leading to greater dif-

49. *Id.* at 139.
50. Evaluation of DNA Evidence, *supra* note 8, at 69-70.
51. *Id.*
52. *Id.*
53. *Id.*
54. *Id.*
55. *Id.*
56. Levy, *supra* note 31, at 140.
57. *Id.*
58. Evaluation of DNA Evidence, *supra* note 8, at 71.
59. *Id.*
60. *Id.*

ferences among population subgroups than among VNTRs.[61] However, these disadvantages may be minimized with the proper choice of markers and procedures.[62]

In the years since its invention, the PCR technique has been substantially improved, thereby increasing the significance of the technique. The initial PCR technique, the DQ alpha test, was first marketed commercially in 1990.[63] It was followed over the next several years by a series of additional techniques, each of which relied on copying different genetic material through PCR and then analyzing it.[64] These additional techniques are known as the D1S80 test, the polymarker test and the short tandem repeats ("STR") test.[65] The results achieved from the STR test have been compared to those achieved from RFLP analysis.[66]

IV. Statistical Analysis of DNA Profiling Evidence

Once PCR or RFLP analysis is completed, forensic scientists then perform statistical analysis to determine the source of the DNA sample. Statistical analysis of DNA profiling evidence involves three steps: (1) the analysis of a known sample (e.g., a sample from a crime scene) and an unknown sample (e.g., a sample from a crime suspect) to determine whether there is a match; (2) the determination of the statistical significance of the match; that is, the likelihood that a random person would match the same bands as those matched between the crime scene and the crime suspect; and (3) the determination of the frequency of the occurrence of each matched band in the general population.[67]

When forensic scientists declare that a DNA match exists, the scientists are not stating unequivocally that a crime suspect is the source of an unknown sample of DNA.[68] Nor are they describing the probability that the crime suspect may be the source of the unknown sample; that is the "source probability."[69] Instead, the scientists are merely assessing the theoretical likelihood that a randomly selected person from the general population or a certain subsection of the population would match the known sample from the crime scene and the unknown sample from the crime suspect; that is the "random sample

61. *Id.*
62. *Id.*
63. *See id.* at 71-72.
64. *See id.* at 72.
65. *Id.* at 70-72.
66. *Id.* at 70-71.
67. DNA Technology, supra note 18, at 74.
68. *See* Jonathan J. Koehler, *DNA Matches and Statistics: Important Questions, Surprising Answers*, 76 Judicature 222, 224 (1993).
69. *Id.*

probability."[70] The scientists are asserting that the crime suspect cannot be excluded as a possible source.[71]

A. *Determination of a DNA "Match"*

Forensic laboratories declare a match between a known and an unknown sample of DNA when two conditions are met: (1) the sizes and number of the detected RFLPs in the known and unknown samples have migrated the same distance on the gel; and (2) computerized measurements confirm that the difference in migration distances is less than the permissible degree of error.[72] The observed differences seen in repeated measurements of DNA fragments of the same length define the "match window;" that is, "the range within which two bands can be declared to match."[73]

If a match is declared, forensic scientists then estimate the statistical significance of that match; that is, the relative frequency with which a match would occur in a sample population.[74] Furthermore, if a match is found between a known sample of DNA taken from a crime scene and a large percentage of the sample population, then the match does not significantly incriminate a particular suspect.[75] In addition, even if a correct population frequency can be found, there is a risk that it will be interpreted as a probability that someone other than the suspect is the source of the evidence sample.[76]

B. *Determination of the Statistical Significance of a Match*

The statistical significance of a match is determined by a two-step process.[77] An initial determination is made regarding the probability of each matching band being present in a random population sample.[78] Thereafter, the overall probability of having all of the same matching bands—the independence of the matching bands—is calculated.[79]

1. Probability of Presence of Matching Band in Random Sample

The standard method of estimating the probability of matching bands in a random sample of DNA profiling evidence utilizes theoretical models based on "population genetics."[80] The objective of popula-

70. *Id.*
71. *Id.*
72. *See* Kaye, *supra* note 32, at 110.
73. *Id.* at 110-11.
74. *Id.* at 104.
75. *Id.* at 117.
76. *Id.* at 117-18.
77. *See* DNA Technology, *supra* note 18, at 4-5.
78. *See id.* at 4.
79. *See id.* at 5.
80. Sue Rosenthal, *My Brother's Keeper: A Challenge to the Probative Value of DNA Fingerprinting*, 23 Am. J. Crim. L. 195, 200 (1995).

tion genetics is "to determine the frequency with which a given genetic pattern will occur in the general population."[81]

One recommended procedure for performing population genetics is to sample people in the relevant population, analyze their DNA, and report the number of people in the population sample who match the crime sample.[82] To accomplish this, forensic scientists must establish a DNA data bank from a sample of the population and estimate the frequency of a specific DNA pattern within that population sample.[83] In most states, this is done by collecting DNA samples from convicted criminals. However, population genetics is limited by the size of the DNA data bank and is susceptible to error.[84]

As a general principle, the forensic matching rule must be precise and objective in order to properly calculate the proportion of individuals with matching alleles in the population databank.[85] Furthermore, the same rule must be applied to count all of the frequencies in the population databank in order to adequately determine the proportion of random individuals that would have been declared a match in the forensic context.[86]

The preferred method for estimating the probability of matching bands in a random sample of DNA profiling is referred to as the "product rule" method.[87] This method utilizes theoretical models to allow for a statement of numerical significance that can go beyond the size of the sample population.[88]

The product rule method involves determining the statistical frequency of each independent allele in a DNA sample.[89] These calculations are performed by using probabilities derived from previously constructed data bases to determine the probability with which a number of independent alleles will occur simultaneously.[90] After the individual frequencies of the alleles are determined, they are multiplied together to determine the likelihood of a match for the entire pattern.[91]

The validity of the product rule is based on two assumptions: (1) that the underlying figures to be multiplied together are themselves correct, and (2) that the figures are not dependent on one another.[92]

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81. *Id.*
82. *See* Kaye, *supra* note 32, at 119.
83. *See* DNA Technology, *supra* note 18, at 76.
84. *See* Rosenthal, *supra* note 80, at 200.
85. *See* DNA Technology, *supra* note 18, at 78.
86. *Id.*
87. *See* Rosenthal, *supra* note 80, at 200.
88. *Id.* at 200-01.
89. *Id.*
90. *See* United States v. Jakobetz, 955 F.2d 786, 799 (2d Cir. 1992); Margann Bennett, Comment, *Admissibility Issues of Forensic DNA Evidence*, 44 U. Kan. L. Rev. 141, 150-51 (1995).
91. *See* Rosenthal, *supra* note 80, at 201.
92. *Id.*

Stated differently, the product rule is based on the assumption that the population does not contain subpopulations with distinct allele frequencies—that each individual's alleles constitute statistically independent random selections from a common gene pool.[93] Two alleles are independent if the occurrence of one is not associated with the occurrence of the other.[94]

Applying the product rule assumptions, forensic scientists employ the forensic matching rule to calculate the population frequency of a genotype.[95] First, forensic scientists examine a random sample of the population and count the frequency of matching alleles.[96] This step requires only the selection of a sample that is truly random with reference to the genetic type.[97] Second, the scientists calculate the frequency of the genotype at each locus.[98] The genotype frequency is calculated by simply multiplying the two allele frequencies.[99] Third, the scientists calculate the frequency of the complete multilocus genotype.[100] The frequency of a complete genotype is calculated by multiplying the genotype frequencies at all the loci.[101] The calculation assumes that there is no correlation between genotypes at different loci.[102] The absence of such correlation is called "linkage equilibrium."[103]

As stated, the validity of the product rule depends on the absence of population substructure because only then are the different alleles statistically uncorrelated with one another. The key question underlying the use of the product rule is whether the random population samples used "have a significant substructure for the loci used for forensic typing."[104] For example, population genetic studies show some substructure within racial groups.[105]

> In a population that contains groups with characteristic allele frequencies, knowledge of one allele in a person's genotype might carry some information about the group to which the person belongs, and this in turn alters the statistical expectation for the other alleles in the genotype. . . . The true genotype frequency is thus higher than would be predicted by applying the multiplication rule and using the average frequency in the entire population.[106]

93. *See* DNA Technology, *supra* note 18, at 77.
94. *See* Kaye, *supra* note 32, at n. 93.
95. *See* DNA Technology, *supra* note 18, at 76-77.
96. *Id.* at 77.
97. *Id.*
98. *Id.* at 78.
99. *Id.*
100. *Id.* at 78-79.
101. *Id.* at 78.
102. *Id.*
103. *Id.*
104. *Id.* at 79.
105. *Id.*
106. *Id.*

Furthermore, the possibility of a population substructure, subgroups within the population which affect analysis, undermines the assumption of independence.[107]

Because it is impossible or impractical to draw a large enough population to test calculated frequencies for a particular DNA profile much below 1 in 1000, there is not a sufficient body of empirical data on which to base a claim that such frequency calculations are reliable or valid per se.[108] The assumption of independence must be strictly scrutinized and estimation procedures appropriately adjusted.[109]

Professor Thomas Caskey, a Baylor College scientist, has suggested a solution to the obstacles presented by population substructure, and this solution has largely been adapted by forensic scientists.[110] This solution, the ceiling principle, uses the maximum frequency of allele occurrences to produce the most conservative estimate for a match with a crime suspect.[111]

The ceiling principle requires the sampling of various population subgroups to determine whether some alleles occur more frequently in some subgroups than in the general population. In applying the ceiling principle, random samples of DNA from homogeneous ethnic subgroups are collected, and the highest frequency for each allele in the crime sample, with respect to all of the subgroups, is selected.[112] These frequencies are then multiplied to produce genotype frequencies.[113]

2. Independence of the Matching Bands

Forensic scientists use three methods to assess the independence of matches in a DNA sample.[114] The first method is based on the Hardy-Weinberg Equilibrium ("HWE") assumption, which is named after G. H. Hardy, a British mathematician, and Wilhelm Weinberg, a German physician.[115] HWE depends on a truly random population with a thoroughly mixed gene pool, and assumes the independence of the two alleles inherited from each parent at the same locus.[116] "When there is no correlation between the two parental alleles, the locus is said to be in [HWE]."[117]

In the second method, forensic scientists determine whether the matched bands in a DNA sample occur in the absence of a linkage

107. *Id.*
108. *Id.* at 74.
109. *Id.* at 91-93.
110. *See* Rosenthal, *supra* note 80, at 204-05.
111. *Id.*
112. *See* Kaye, *supra* note 32, at 134.
113. *Id.*
114. *See* Bennett, *supra* note 90, at 151.
115. *See* Evaluation of DNA Evidence, *supra* note 8, at 90-91.
116. *See* Bennett, *supra* note 90, at 151.
117. DNA Technology, *supra* note 18, at 78.

disequilibrium.[118] As indicated, a linkage disequilibrium occurs when "two or more probes bind to adjacent locations on a human DNA molecule."[119] To avoid a linkage disequilibrium, scientists use probes "which identify widely dispersed VNTR locations in the human genome."[120]

In the third method, scientists determine "whether certain bands or patterns of bands occur more frequently within subpopulations of a larger racial or ethnic population."[121] If the scientists discover the existence of subgroups, then they will determine whether the frequency of alleles are more likely to occur among different racial or ethnic subpopulations.[122]

C. *Validity and Reliability of DNA Profiling Evidence*

In addition to determining the existence of a match in DNA analysis, forensic scientists must also determine whether the technique used to produce the match is valid and produces reliable results. A technique is valid if it produces accurate results; that is, if it correctly identifies true matches and non-matches.[123] A technique is reliable if it produces the same results time and again.[124] In the case of DNA forensic evidence, evidentiary reliability will be based upon scientific validity.[125]

D. *Common Problems with the Validity and Reliability of DNA Profiling Evidence*

The major problems affecting the validity and reliability of DNA profiling evidence stem from an inadequate population database, the presence of substructures in the population, and the inadequacy of laboratory standards and techniques. As a general principle, the relevant population should consist of all people who might have been the source of the evidence sample.[126] In most instances, such population would consist of people from many ethnic groups.[127]

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118. *Id.*

119. *See* Bennett, *supra* note 90, at 151.

120. *Id.*

121. *Id.* at 152; *see also* DNA Technology, *supra* note 18, at 79 (noting that "a person who has one allele that is common among Italians is more likely to be of Italian descent").

122. *See* Bennett, *supra* note 90, at 152.

123. *See* Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 591 (1993). DNA forensic analysis is considered valid if there are credible grounds to support the results of such analysis.

124. *Id.* at 590-91 & n.9 (stating that evidentiary reliability in DNA forensic analysis refers to trustworthiness).

125. *See id.*

126. *See* Kaye, *supra* note 32, at 138-39.

127. *Id.* at 139.

The most powerful criticism of DNA forensic evidence concerns population substructures; that is, "the presence of subgroups with varying DNA patterns that tend to mate among themselves."[128] The existence of population substructures negates the assumption of the independence of alleles at a specific locus, and calls into question the validity of genotype frequencies across loci.[129]

Other problems that may affect the validity and reliability of DNA forensic evidence include inadequate laboratory standards and techniques—such as an insufficient DNA sample size, deterioration of the DNA sample, contamination of DNA Sample, improper test procedures, false inclusion (false positive identification), and false negative results.[130]

V. STANDARDS USED TO DETERMINE THE ADMISSIBILITY OF DNA EVIDENCE

A. *The Standard Used by Most States*

Most states have now accepted DNA profiling evidence as admissible.[131] In determining the standard of admissibility, most states use the standard announced in *Frye v. United States*.[132] The *Frye* rule admits expert testimony based on scientific principles or procedures only after it has "gained general acceptance" in its specified field.[133] The *Frye* court refused to admit a lie detector test.[134] Specifically, the *Frye* court rejected evidence that a person's truthfulness could be determined by a study of systolic blood pressure.[135]

The *Frye* rule 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 specific field.[136] In *Frye*, the defendant, James Alphonzo Frye, appealed from a conviction, after a jury trial, for murder in the second degree.[137] Before the trial, the defendant took a systolic blood pressure deception test. During the trial, defense counsel offered expert testimony as to the results of the test. The trial court refused to accept the testimony, the defendant was convicted, and the conviction was appealed.[138] The appeals court

128. *Id.* at 127-28.
129. *Id.* at 128.
130. *See* DNA Technology, *supra* note 18, at 88-89.
131. *See* Aviam Soifer & Miriam Wugmeister, *Mapping and Matching DNA: Several Legal Complications of "Accurate" Classifications*, 22 Hastings Const. L.Q. 1, 21 (1994) (citing Office of Technology Assessment, U.S. Congress, Genetic Witness: Forensic Uses of DNA 157 (1990)).
132. 293 F. 1013 (D.C. Cir. 1923).
133. Id. at 1014.
134. *Id.*
135. *Id.*
136. *Id.*
137. *Id.* at 1013.
138. *Id.* at 1014.

affirmed the conviction, concluding that the systolic blood pressure deception test had not yet gained such standing and scientific recognition among physiological and psychological authorities as would justify the courts in admitting expert testimony deduced from the discovery, development, and experiments thus far made.[139] 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 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.[140]

Applying the *Frye* analysis to DNA testing would require: (1) the acceptance in the scientific community of the theory that DNA testing can produce reliable results; and (2) the general acceptance in the scientific community of techniques which can produce reliable results in DNA identification.[141]

From time to time the *Frye* standard has been criticized.[142] One critique is that it does not assess the reliability of the particular evidence at issue. This may be an unwarranted criticism. How does particular evidence gain acceptance in the scientific community unless it is reliable?[143] On the other hand, in New York, in determining whether new scientific evidence should be accepted, a court must conclude that the relevant scientific community accepts that evidence as reliable.[144]

B. *The Federal Standard*

The *Frye* standard of admissibility is no longer acceptable in the federal courts.[145] In 1993, the Supreme Court of the United States

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139. *Id.*

140. *Id.* at 1014.

141. It should be noted that in *People v. Castro*, a Supreme Court in New York State (the Supreme Court is a trial court in New York State) added a third part to the *Frye* analysis; that is, did the testing laboratory perform accepted scientific techniques when it analyzed forensic examples in that particular case. 545 N.Y.S.2d 985, 987 (Sup. Ct. 1989). This third part to the *Frye* test was rejected by the New York State Court of Appeals, the highest court in New York State when it distinguished *Castro* in *People v Wesley*. 633 N.E.2d 451 (N.Y. 1994).

142. Paul C. Giannelli, *The Admissibility of Novel Scientific Evidence:* Frye v. United States, *a Half-Century Later*, 80 Colum. L. Rev. 1197 (1980); *see also* State v. Vandebogart, 616 A.2d 483, 488-90 (N.H. 1992) (describing criticisms of and alternatives to the two prong *Frye* test).

143. *See* United States v. Jakobetz, 747 F. Supp. 250, 254 (D. Vt. 1990), *aff'd*, 955 F.2d 786 (2d Cir.), *cert. denied*, 506 U.S. 834 (1992); *Vandebogart*, 616 A.2d at 489-90.

144. People v. Middleton, 429 N.E.2d 100, 103 (N.Y. 1981).

145. Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 587-88 (1993).

determined that the *Frye* standard had been superseded by the Federal Rules of Evidence and, specifically, Rule 702.[146]

In *Daubert v. Merrell Dow Pharmaceuticals, Inc.*,[147] the United States Supreme Court held that Rule 702 superseded *Frye's* "general acceptance" test and provided the standard for admitting expert scientific evidence in a federal trial.[148] In *Daubert*, two minor children and their parents sought to recover damages for birth defects which were allegedly caused by the mother's prenatal ingestion of Bendectin, a prescription anti-nausea drug marketed by the defendant.[149] After extensive discovery, the defendant moved for summary judgment, asserting that Bendectin does not cause birth defects in humans, and the plaintiffs would not be able to produce admissible evidence that it does. To support its position, defendant submitted an affidavit from a well-credentialed expert, stating that his review of all of the literature on Bendectin revealed nothing to indicate that Bendectin was capable of causing birth defects in humans.[150]

The issue before the Supreme Court was the standard for admitting expert scientific testimony in a federal trial. In vacating the decision of the Court of Appeals and remanding the case for further proceedings, the Supreme Court held that Rule 702 was the appropriate standard.[151]

Rule 702 provides: "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise."[152] Thus, Rule 702 permits the introduction of new scientific evidence if it will aid the factfinder in understanding the evidence or determining a fact in issue.

The *Daubert* Court stated:

> "General acceptance" is not a necessary precondition to the admissibility of scientific evidence under the Federal Rules of Evidence, but the Rules of Evidence— especially Rule 702—do assign to the trial judge the task of ensuring that an expert's testimony both rests on a reliable foundation and is relevant to the task at hand. Pertinent evidence based on scientifically valid principles will satisfy those demands.[153]

146. *Id.*
147. *Id.*
148. *Id.* at 587-88.
149. *Id.* at 582.
150. *Id.*
151. *Id.* at 597.
152. Fed. R. Evid. 702
153. *Daubert*, 509 U.S. at 597.

The case was remanded to the Court of Appeals for further proceedings.[154] Since the decision, several federal Circuit Courts of Appeal have applied *Daubert* in approving the RFLP technique[155] and the PCR technique.[156]

VI. DNA Evidence in New York and Other States

A. *The New York Standard for Admitting DNA Evidence*

In *People v. Wesley*[157] the New York State Court of Appeals, the highest court in New York State, determined that DNA profiling evidence was admissible in New York State courts.[158] In doing so the Court concluded (1) that DNA evidence should be considered using the *Frye* standard, (2) that using the *Frye* standard, DNA evidence had been shown to be generally accepted among scientists as reliable, and (3) that no issue had been raised concerning the statistical probabilities of the evidence or the foundation used prior to its admission.[159]

Defendant Wesley was convicted of the rape and murder of a seventy-nine year old woman.[160] Both the deceased and the defendant had been clients of an organization known as the Albany City Hostel which served persons who were developmentally disabled.[161] Defendant became a suspect because a routine check of defendant's apartment by a member of the Albany City Hostel found a bloodstained T-shirt with gray and white hairs, bloodstained underwear, and bloodstained sweatpants.[162]

As stated in the opinion, evidence of defendant's guilt was strong even without the DNA profiling evidence.[163] It included the bloody clothes, several conflicting statements, and fibers both on the victim and defendant.[164]

When the case reached the Court of Appeals by permission to appeal by one of the seven judges, the conviction had already been af-

154. *Id.* at 598. On remand, the Court of Appeals for the Ninth Circuit, using the *Daubert* standard, held that the scientific testimony was not admissible to prove that Bendectin caused birth defects. Daubert v. Merrell Dow Pharmaceuticals, Inc., 43 F.3d 1311, 1322 (9th Cir. 1995).

155. United States v. Davis, 40 F.3d 1069, 1072 & n.4 (10th Cir. 1994); United States v. Chischilly, 30 F.3d 1144, 1153 (9th Cir. 1994); United States v. Martinez, 3 F.3d 1191 (8th Cir. 1993).

156. United States v. Hicks, 103 F.3d 837, 846-47 (9th Cir. 1996); United States v. Beasley, 102 F.3d 1440, 1447 (8th Cir. 1996).

157. 633 N.E.2d 451 (N.Y. 1994).

158. *Id.* at 455.

159. *Id.* at 455-56.

160. The conviction was for murder in the second degree, rape in the first degree, attempted sodomy in the first degree and burglary in the second degree. *Id.* at 453.

161. *Id.*

162. *Id.*

163. *Id.*

164. *Id.*

firmed by an intermediate appellate court. The introduction of the DNA profiling evidence was the major issue before the Court of Appeals.[165]

In order to determine whether DNA profiling evidence was generally acceptable and reliable, a hearing was held by the trial court. Following that hearing, the trial court found such DNA evidence both generally accepted by the relevant scientific community and accepted as reliable by that community in 1988, the date of the trial of the *Wesley* action.[166] During the hearing, several persons, after giving their credentials as authorities in the field, testified to the reliability and acceptance of DNA profiling evidence.[167]

It should be noted that while all five judges[168] who determined the *Wesley* case in the New York State Court of Appeals agreed that DNA profiling evidence was generally acceptable as of the date of the appeal and that no new *Frye* hearing was necessary in future cases, there was disagreement on whether the prosecution had proved the general acceptance of the DNA evidence in the *Wesley* case. While three judges of the Court concluded that DNA profiling evidence was generally acceptable at the time of the hearing in 1988, the two-person concurrence concluded otherwise.[169] The concurrence found the admission of DNA evidence harmless error because of the wealth of other evidence of the defendant's guilt.[170]

B. *The Acceptance of DNA Evidence by Other States*

Using the *Frye* standard, a number of the highest state courts have concluded that the RFLP technique is generally accepted by the relevant scientific community and have admitted DNA evidence.[171] A number of states now admit DNA evidence by using the *Daubert* standard.[172] Other states, using the *Frye* standard,[173] or the *Daubert* stan-

165. *Id.* at 452.

166. *Id.* at 455.

167. *Id.*

168. Two of the seven judges on the Court were recused in the case. *Id.* at 468.

169. *Id.* at 461 (Kaye, C.J., concurring).

170. *Id.*

171. Arizona v. Bible, 858 P.2d 1152, 1183 (Ariz. 1993); Fishback v. Colorado, 851 P.2d 884, 890 (Colo. 1993); Minnesota v. Schwartz, 447 N.W.2d 422, 424-25 (Minn. 1989); State v. Vandebogart, 616 A.2d 483 (N.H. 1992); South Carolina v. Ford, 392 S.E.2d 781, 784 (S.C. 1990) (admitting RFLP analysis evidence and test results under both the *Frye* standard and a less restrictive standard found in South Carolina v. Jones, 259 S.E.2d 120 (S.C. 1979)).

172. Mitchell v. Kentucky, 908 S.W.2d 100 (Ky. 1995); Louisiana v. Quatrevingt, 670 So. 2d 197 (La. 1996).

173. Kansas v. Hill, 895 P.2d 1238 (Kan. 1995); New York v. Morales, 643 N.Y.S.2d 217 (N.Y. App. Div. 1996).

dard,[174] or an evidentiary standard[175] have admitted the PCR technique of DNA evidence.

Minnesota v. Schwartz[176] was one of the earliest DNA cases to reach a state's highest court.[177] There the defendant was indicted for the stabbing death of a woman on May 27, 1988. Pursuant to a search warrant, the police took a pair of bloody blue jeans and a bloody shirt from the defendant's residence.[178] DNA analysis confirmed that the victim's blood was on both the blue jeans and the shirt.[179] The frequency of the bonding pattern of the deceased in the Caucasian population was approximately one in thirty-three billion.[180]

The Supreme Court answered the three questions which had been certified to it. First, it concluded that the *Frye* standard was applicable to the case.[181] Second, it concluded that DNA evidence was admissible.[182] Third, the Minnesota Supreme Court placed a limitation on the introduction of DNA evidence in Minnesota.[183] The court concluded that there should be a limitation on the use of statistical evidence in the case. In so holding the Court relied on *Minnesota v. Joon Kyu Kim*,[184] *Minnesota v. Boyd*,[185] and *Minnesota v. Carlson*.[186] In *Kim*, a case involving an allegation of rape, the Minnesota Supreme Court upheld the suppression of testimony by an expert of the statistical frequency with which the defendant's blood type occurred in the population.[187] The court expressed the opinion that such statistical evidence could be prejudicial to the defendant.[188]

In *Arizona v. Bible*,[189] the Supreme Court of Arizona found DNA evidence admissible using the *Frye* standard.[190] It concluded, however, that the probability calculations used by the Cellmark Laboratory and based upon the product rule were not generally accepted in the relevant scientific community and should have been excluded.[191]

174. South Dakota v. Moeller, 548 N.W.2d 465 (S.D. 1996).
175. Oregon v. Lyons, 924 P.2d 802 (Or. 1996); Spencer v. Virginia, 393 S.E.2d 609 (Va. 1990).
176. 447 N.W.2d 422 (Minn. 1989).
177. *Id.* at 423.
178. *Id.*
179. *Id.* at 423-24.
180. *Id.* at 424.
181. *Id.* at 424-26.
182. *Id.* at 427-28.
183. *Id.* at 428.
184. 398 N.W.2d 544 (Minn. 1987).
185. 331 N.W.2d 480 (Minn. 1983).
186. 267 N.W.2d 170 (Minn. 1978).
187. 398 N.W.2d at 548.
188. *Id.*
189. 858 P.2d 1152 (Ariz. 1993).
190. *Id.* at 1189.
191. *Id.* at 1188-89.

Nevertheless, it found other evidence overwhelming and confirmed the conviction for murder and related crimes.[192]

Some states use their own evidentiary statutes or rules to determine the admissibility of DNA evidence. For example, in Delaware, the Supreme Court noted that the *Frye* standard was inapplicable.[193] Instead, the Delaware Rules of Evidence were applicable.[194] Using those Rules, the Supreme Court of Delaware upheld the five-step test used by the trial court for determining the admission of DNA evidence:

> 1) that the expert witness was qualified; 2) that the evidence offered was otherwise admissible, relevant and reliable; 3) that the bases for the opinion are those "reasonably relied upon by experts in the field;" 4) that the specialized knowledge being offered will assist the trier of fact to understand the evidence or determine a fact in issue and (5) [that the] evidence would create unfair prejudice, confuse the issues or mislead the jury.[195]

In Ohio, an evidence standard is also used, with DNA evidence being admissible if it is "relevant and will assist the trier of fact in understanding evidence presented or in determining a fact in issue."[196]

Another method for the introduction of DNA evidence has been adopted in Maryland and some other states. Maryland has passed legislation that requires the admission of DNA evidence.[197] The legislature has thus mandated court admission of this evidence. The Court of Appeals of Maryland, the State's highest court, upheld the DNA legislation in *Armstead v. Maryland*.[198] There, the defendant was accused of the rape and sodomy of a woman on January 29, 1991 in Howard County, Maryland. The victim picked his photograph from a photo array and identified him in court as the perpetrator. A neighbor also identified him as a person who fled from the scene of the incident. When arrested on the evening of the incident, defendant was wearing a leather jacket matching one which the victim described.[199]

The DNA evidence indicated a match between defendant's blood and semen which had been taken from the victim. The RFLP method of testing was used. Both the product rule and the ceiling principle were used in explaining the statistical information to the jury. The testimony of the product rule calculation indicated that the chances of a match between the DNA of the defendant and the DNA in the se-

192. *Id.* at 1193.
193. Nelson v. Delaware, 628 A.2d 69, 73-74 (Del. 1993).
194. *Id.* at 74.
195. *Id.* (citations omitted).
196. Ohio v. Pierce, 597 N.E.2d 107, 112 (Ohio 1992).
197. Md. Code Ann., Cts. & Jud. Proc. § 10-915 (1995).
198. 673 A.2d 221 (Md. 1996).
199. *Id.* at 223.

men taken from the victim was one in 480 million.[200] The ceiling principle calculation indicated that the odds were one in 800,000.[201]

Following his conviction of first degree rape, first degree sexual offense, perverted practices, assault, burglary, and attempted robbery, defendant was sentenced to two consecutive life terms in prison plus twenty years.[202] The Court of Special Appeals affirmed the convictions. Following this affirmance, the Court of Appeals granted certiorari.[203]

Section 10-915, the statute challenged by the defendant, provided that "[i]n any criminal proceeding, the evidence of a DNA profile is admissible to prove or disprove the identity of any person."[204] It defined "DNA profile" to mean "an analysis that utilizes the restriction fragment length polymorphism analysis of DNA resulting in the identification of an individual's patterned chemical structure of genetic information."[205] Sections 10-915(b)(1) and (b)(2) provide for at least forty-five days notice that DNA evidence will be offered in evidence and for discovery of the procedure and results of the DNA testing.[206] Finally, while section 10-915 does not specifically provide for the in-

200. *Id.* at 225.
201. *Id.*
202. *Id.*
203. *Id.*
204. Md. Code Ann., § 10-915(b).
205. *Id.* § 10-915(a)(3).
206. Section 10-915 provides, in pertinent part,

> (a) Definitions . . . (2) "Deoxyribonucleic acid (DNA)" means the molecules in all cellular forms that contain genetic information in a patterned chemical structure of each individual. (3) "DNA profile" means an analysis that utilizes the restriction fragment length polymorphism analysis of DNA resulting in the identification of an individual's patterned chemical structure of genetic information.
>
> (b) Purposes.—In any criminal proceeding, the evidence of a DNA profile is admissible to prove or disprove the identity of any person.

Id.

The only condition the statute imposes on admission of DNA evidence relates to a discovery requirement, viz, information the proponent of the DNA evidence must provide to the opponent on request. *Id.* § 10-915(b)(1)-(b)(2).

Sections 10-915(b)(1) and (b)(2) of the statute provide that DNA profile evidence is admissible if the proponent:

> (1) Notifies in writing the other party or parties by mail at least 45 days before any criminal proceeding; and
>
> (2) Provides, if requested in writing, the other party or parties at least 30 days before any criminal proceeding with:
>
> (i) Duplicates of the actual autoradiographs generated;
>
> (ii) The laboratory protocols and procedures;
>
> (iii) The identification of each probe utilized;
>
> (iv) A statement describing the methodology of measuring fragment size and match criteria; and
>
> (v) A statement setting forth the allele frequency and genotype data for the appropriate data base utilized.

Id.

troduction of population genetics statistics, the statute would permit the introduction of both the product rule and the ceiling principle.[207]

VII. Trends in the Admission of DNA Evidence

A. *Acceptance of Statistical Information*

As stated previously, one of the major problems in the use of DNA profiling evidence has been the use of statistics. While there may be a match between the DNA of a defendant and the DNA found at a crime scene, this is not the end of the story. The issue still remains of just how many other persons in the population could have the same match as that of the defendant. It is clear that most states require statistical evidence with the admission of DNA evidence.[208] In *Nelson v. Delaware*[209] the Supreme Court of Delaware stated: "We hold that DNA matching evidence is inadmissible in the absence of a statistical interpretation of the significance of the declared match. Accordingly, admission of only one of these components without the other renders *all* of the DNA evidence inadmissible."[210] Some courts have rejected challenges to the admission of DNA statistical evidence.[211] Some courts, while agreeing that DNA profiling evidence is admissible, have rejected the attempt to introduce statistics.[212]

One of the main criticisms of the statistical evidence is that not enough account is taken of possible differences in the genetic makeup of subpopulations such as African-Americans or Latinos.[213] One study stresses that among the white European population in America, subpopulations show little variance from the overall population.[214] The same study indicates considerable differences between the genetic makeup of different racial groups.[215]

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207. Armstead v. Maryland, 673 A.2d 221, 240-43 (Md. 1996).
208. *See* Nelson v. Delaware, 628 A.2d 69, 75 (Del. 1993).
209. *Id.*
210. *Id.* at 75.
211. Lindsey v. Colorado, 892 P.2d 281 (Colo. 1995); Hawaii v. Montalbo, 828 P.2d 1274 (Haw. 1992); Idaho v. Faught, 908 P.2d 566 (Idaho 1995); State v. Morel, 676 A.2d 1347 (R.I. 1996); South Dakota v. Schweitzer, 533 N.W.2d 156 (S.D. 1995).
212. Arizona v. Bible, 858 P.2d 1152 (Ariz. 1993); Connecticut v. Sivri, 646 A.2d 169 (Conn. 1994) (remanding case for further deliberations on population frequency calculations); Massachusetts v. Curnin, 565 N.E.2d 440 (Mass. 1991) (concluding that results of DNA testing were improperly admitted because of absence of general acceptance or inherent rationality of the process used); Nebraska v. Carter, 524 N.W.2d 763 (Neb. 1994) (limiting evidence on statistical frequency to two racial groups when the racial group of the perpetrator was unknown was prejudicial); State v. Vandebogart, 616 A.2d 483 (N.H. 1992) (remanding case for a new trial since statistical technique used by the FBI in estimating population frequencies was not generally accepted by the relevant scientific community); Washington v. Cauthron, 846 P.2d 502 (Wash. 1993) (ordering new trial because of the absence of probability statistics).
213. DNA Technology, *supra* note 18, at 11-15.
214. Evaluation of DNA Evidence, *supra* note 8, at 151-54.
215. *Id.*

An effort was made to meet the criticism of the statistical calculations in a study completed in 1992. The study is known as *DNA Technology in Forensic Science*.[216] It was funded by several federal agencies and one private foundation.[217] One of the main conclusions of that study was the recommendation that the ceiling principle be used to account for population substructure.[218]

The 1992 study did not resolve the issue of statistics. Consequently, a new study was undertaken. Known as *The Evaluation of Forensic DNA Evidence*, it was completed in 1996.[219] It concluded that the use of the ceiling principle is unnecessary.[220] It also endorsed the product rule.[221] Thus, according to some experts, some of the problems surrounding the use of statistics have been dealt with and apparently resolved.

B. *Legislation*

A second trend has been toward the adoption of legislation. Sometimes that legislation goes to the approval of the admission of DNA evidence itself. The Maryland legislation discussed above is a case in point. Similar legislation has been passed in other states such as Alaska, Delaware, Indiana and Virginia. The legislation takes a variety of forms.

The Alaska statute permits the introduction of DNA evidence "to prove or disprove any relevant fact" and states specifically that general acceptance in the relevant scientific community is not necessary.[222] The Delaware statute permits the introduction of a RFLP analysis "to prove or disprove the identity of any person."[223] Both the Indiana Statute and the Minnesota Statute provide that DNA evidence is admissible without expert testimony.[224]

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216. DNA Technology, *supra* note 67. The study was published by the National Academy Press in Washington, D.C. in 1992.

217. *Id.* at ii. The Federal Bureau of Investigation, the National Institutes of Health National Center for Genome Research, the National Institute of Justice, the National Science Foundation, the State Justice Institute and the Alfred P. Sloan Foundation. *Id.*

218. *Id.* at 82-85.

219. Evaluation of DNA Evidence, *supra* note 8.

220. *Id.* at 156-59.

221. *Id.* at 5.

222. Alaska Stat. § 12.45.035(a) (Michie 1996). The statute reads as follows:

> In a criminal action or proceeding, evidence of a DNA profile is admissible to prove or disprove any relevant fact, if the court finds that the technique underlying the evidence is scientifically valid. The admission of the DNA profile does not require a finding of general acceptance in the relevant scientific community of DNA profile evidence.

Id.

223. Del. Code Ann. tit. 11, § 3515 (1995).

224. Ind. Code Ann. § 35-37-4-13 (Michie 1994); Minn. Stat. Ann. §§ 634.25-634.26 (West Supp. 1997).

Other legislation deals with the adequacy of laboratories. A proper foundation is necessary to admit DNA evidence. That foundation must show that the laboratory conducting the DNA tests used proper procedures. Most often when there are challenges to the particular procedures used by the laboratory, the DNA evidence is not excluded. The particular challenges go to the weight of the evidence but not to its admissibility.[225]

New York State has adopted legislation which requires the accreditation of laboratories.[226] New York and other states have established DNA databanks using the blood or saliva of persons convicted of crimes.[227] A number of other states have begun addressing the issues raised by the use of DNA evidence. Such issues included the proper licensing of laboratories which perform DNA testing, preservation of DNA-related evidence and the privacy issues involved in the establishment of DNA data banks.

CONCLUSION

DNA evidence is a powerful tool for both the prosecutor and the defense attorney. It is strong evidence of the probability that a person was present or absent at a crime scene. While the acceptance by courts of the validity of DNA evidence now seems universal, there may still be problems with the foundation for the admission of such evidence because of inadequate laboratory procedures or because the statistical information is flawed. Whatever the problems, DNA evidence should continue to have a profound effect on criminal litigation for years to come. Finally, it should always be remembered that DNA testing does not prove conclusively that a particular person committed a crime. The basis of DNA testing is to indicate the probability that a person with the defendant's genetic makeup committed a crime.

Because DNA evidence may aid both prosecutors and defendants, an issue arises as to the duty to preserve DNA-related evidence over a number of years. While there is no universal rule of preservation, this is an issue that should be addressed by both courts and legislatures.

225. Washington v. Kalakosky, 852 P.2d 1064, 1073 (1993); Ohio v. Pierce, 597 N.E.2d 107, 115 (1992).

226. 1994 N.Y. Laws § 737-1; N.Y. Exec. Law § 995-b (McKinney 1996).

227. N.Y. Exec. Law § 995-c (McKinney 1996); Fla. Stat. ch. 948.03 (1996); Haw. Rev. Stat. § 706-603 (1993); Ohio Rev. Code Ann. § 109.57.3 (Anderson Supp. 1996).