Admissibility of DNA Statistical Data: A Proliferation of Misconception

R. Stephen Kramer

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COMMENTS

ADMISSIBILITY OF DNA STATISTICAL DATA: A PROLIFERATION OF MISCONCEPTION

INTRODUCTION

Less than two years ago, DNA[1] evidence[2] was being exalted as the "magic bullet" for courtroom convictions.[3] With statistical probabilities of a random match as high as one in several hundred billion,[4] DNA evidence seemed the ultimate indicator of guilt or innocence.[5] Prosecutors and judges alike rested heavily upon its apparent infallibility.[6] Lauded by some as the "second coming" of the fingerprint,[7] DNA use in the courtroom has been said to be the "single greatest advance in the 'search for truth'. . . since the advent of cross-examination."[8] Prosecutorial use supports such boasts. Over the last six years DNA evidence has been used in more than 500 criminal cases in 49 states.[9]

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1. "DNA" is short for "deoxyribonucleic acid," the chemical compound found in chromosomes within every cell of the human body which contains a nucleus. DNA use for identification purposes is often referred to as DNA identity testing, profiling, fingerprinting, typing or genotyping—all of which concern the characterization of one's genetic makeup. Lorne T. KIRBY, DNA FINGERPRINTING, AN INTRODUCTION 1 (1990).

2. DNA evidence evolves from a process by which a suspect's genetic structure is identified, compared with samples taken from a crime scene, and, if there is a match, subjected to a statistical analysis to determine the frequency of the particular genetic structure (DNA) within the general population. People v. Barney, 8 Cal. App. 4th 798, 805 (1992).

3. Edward Humes, *The DNA Wars*, THE LOS ANGELES MAGAZINE, Nov. 29, 1992, at 23 ("DNA evidence was first presented to the courts and the public: as a magic bullet."); see Jonathan J. Koehler, *DNA Matches and Statistics: Important Questions, Surprising Answers*, JUDICATURE, February-March 1993, at 222 n.1.

4. Current statistical methods can produce odds of up to 1 in 739 billion. Ira Pilchen, *Federal Report and Court Rulings Intensify DNA Evidence Debate*, JUDICATURE, June-June 1992, at 41.

5. *See* Humes, *supra* note 3, at 21 (DNA evidence "[t]outed as an infallible method of identifying criminals, ...") *see also* William C. Thompson & Simon Ford, *DNA Testing: Debate Update*, TRIAL, Apr. 1992, at 52 (DNA testing was "widely hailed as a crime-fighting panacea, capable of infallibly identifying the source of biological samples taken from crime scenes.").

6. Rorie Sherman, *DNA Unraveling*, NAT'L L.J., Feb. 1, 1993, at 1.

7. *See* Lisa Bouwer Hansen, Comment, *Stemming the DNA Tide: A Case for Quality Control Guidelines*, 16 HAMLINE L. REV. 211 n.5 (1992); *see also* Mark D. Stolorow & George W. Clarke, *Forensic DNA Testing: A New Dimension in Criminal Evidence Gains Broad Acceptance*, THE PROSECUTOR, Spring 1992, at 24 ("DNA typing constitutes the most powerful forensic tool since the 19th Century discovery that the fingerprints of no two persons are the same.").

8. People v. Wesley, 533 N.Y.S.2d 643, 644 (N.Y. 1988).

9. George W. Clarke, *DNA Typing: A Scientific Tool Enters the Courtroom*, Women of Conviction, Spring-Summer 1993, at 8.

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In the last year and a half, however, the magic bullet has lost some of its luster. Supreme and appellate courts in several jurisdictions have refused to admit DNA evidence.[10] Specifically, those courts rejected the population frequency data[11] used in conjunction with DNA evidence[12] because the methods used for the statistical calculations are not generally accepted in the scientific community.[13]

Citing a report issued in April 1992 by the National Research Council ("NRC"), several courts found that a legitimate scientific dispute exists between population frequency calculation methods.[14] Some of these courts have suggested that the more conservative statistical calculations offered by the NRC report should be used in place of the numbers generated by the FBI and other labs.[15] Part of this conflict between statistical calculation methods,

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10. *Id.* at 9; Sherman, *supra* note 6, at 1. *See e.g.*, People v. Barney, 8 Cal. App. 4th 798 (1992); People v. Pizarro, 10 Cal. App. 4th 57 (1992); State v. Vandebogart, 616 A.2d 483 (N.H. 1992); Commonwealth v. Lanigan, 596 N.E.2d 311 (Mass. 1992); People v. Atoigue, 1992 WL 245628 (D. Guam App. Div.).

11. Population frequency data refers to the theoretical probability that a randomly selected person from a target population would genetically match the trace evidence as well as the defendant. Koehler, *supra* note 3, at 224. The probability of a DNA match does not refer to the likelihood that the defendant is the source of the trace nor does it indicate the likelihood that the defendant committed the crime. *Id.* It merely assists juries in assessing the probative significance of a DNA match. *Id.*

12. Clarke, *supra* note 9, at 9. The matching of a pair of DNA prints to the exclusion of all other matches is part of the evidence which is supplemented by the probability that such a match would occur. Several courts have concluded that without the probability data, DNA evidence is inadmissible. *See* People v. Barney, 8 Cal. App. 4th 798, 817 (1992) (without a match probability, a match "means nothing."); United States v. Yee, 134 F.R.D. 161, 181 (N.D.Ohio 1991) ("Without the probability assessment the jury does not know what to make of the fact that the patterns match: the jury does not know whether the [matching] pairs are as common as pictures with two eyes, or as unique as the Mona Lisa."); State v. Cauthron, 846 P.2d 502, 516 (Wash. 1993) (finding testimony of a DNA match not helpful to the jury without probability estimates of such a match); *see also* People v. Atoigue, 1992 WL 245628, at *3.

13. *See* Commonwealth v. Lanigan, 596 N.E.2d 311, 316 (Mass. 1992); State v. Vandebogart, 616 A.2d 483, 494-95; People v. Barney, 8 Cal. App. 4th 798, 811-14 (1992); State v. Bible, 858 P.2d 1152, 1188-89 (Ariz. 1993); People v. Atoigue, 1992 WL 245628 (D.Guam App.Div.). Additionally, Courts have excluded DNA evidence, with its spectacular statistics and unimaginable probabilities obtained from the population frequency data has been held inadmissible due to its intimidating effect upon juries. *See* State v. Schwartz, 447 N.W.2d 422, 428 (Minn. 1989) (holding DNA population frequency data inadmissible since jurors, when confronted with technology as complex as DNA typing, may give undue weight and deference to DNA statistical evidence); *see also* Koehler, *supra* note 3, at 229 n.24.

14. *See Breadmore*, 596 N.E.2d at 316; *Vandebogart*, 616 A.2d at 494-95; *Barney*, 8 Cal. App. 4th at 811-14; *Bible*, 858 P.2d 1152, 1188-89 (Ariz. 1993); *Atoigue*, 1992 WL 245628 (D.Guam App.Div.).

15. Sherman, *supra* note 6, at 30. The method used by the FBI and many commercial laboratories is known as the "multiplication rule" which, as noted earlier, can produce odds of a DNA match as high as 1 in 739 billion. Pilchen, *supra* note 4, at 41. The method endorsed by the NRC report—which envisions the possibility that matches within ethnic groups may occur with greater frequency—produces more conservative numbers through modified calculations. DNA Technology in Forensic Science, National Research Council (U.S.), National Academy of Sciences, 1992, at 80-86 [hereinafter DNA Technology]. A DNA calculation method is termed 'conservative' if the estimated probability of a DNA match is, on average, larger than the actual one so that any weight placed on the estimate would favor the suspect. *Id.* at 78. Thus, overestimating a particular genetic type's frequency in a target population would make the

stems from the NRC's report itself. The NRC report, written by a 12-member committee of scientific and legal experts over a two-year period, was originally hoped to end any debate on the admissibility of DNA evidence. However, the report was unclear in its message. While it endorses the use of DNA evidence in general, it raises concerns about the statistical assumptions necessary for the admission of DNA evidence.[16]

Since courts have traditionally deferred to pronouncements from the National Academy of Sciences, the NRC report has consistently been cited in judicial opinions.[17] Perhaps due to the complex nature of DNA evidence, the reaction to the report's proposals have been subject to various interpretations by the courts.[18]

Part I of this Comment provides a brief introduction to the theories behind DNA evidence and how it can be used as evidence in the court room. Part II examines the latest series of challenges opponents have levied against DNA evidence focusing specifically on the population statistical evidence. In addition, this section presents a comprehensive analysis of the population substructuring theory. Part III gives an overview of the case law regarding these latest attacks starting with a brief description of the various admissibility standards for scientific evidence and ending with a perspective on the California experience. Part IV examines two implications affecting the future admissibility of DNA evidence. First, the section proposes that courts realize that a conservative consensus among scientists is currently possible. Second, the section analyzes a major breakdown in the argument of some DNA critics who influenced the NRC report.

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estimate conservative. *Id.*

16. Regarding the technology behind DNA analysis, the report concluded that the principles underlying DNA identification are sound and further admissibility hearings on such technology were unnecessary. DNA Technology, *supra* note 15, at 144.

17. Sherman, *supra* note 6, at 30. The National Academy of Sciences is a branch of the National Academy of Sciences.

18. *See* Commonwealth v. Lanigan, 596 N.E.2d 311, 316 (Mass. 1992) (holding DNA evidence inadmissible due to a significant debate among scientists over statistical data); State v. Vandebogart, 616 A.2d 483, 494-95 (N.H. 1992) (remanded to determine whether a conservative estimate—as recommended by the NRC Report—can be generally accepted); State v. Pierce 597 N.E.2d 107, 115 (Ohio 1992) (holding DNA population frequency data admissible because the court must let the jury weigh the evidence, make credibility determinations, and determine the facts); People v. Wesley, 589 N.Y.S.2d 197, 201 (N.Y. 1992) (DNA population frequency data admissible and any attacks are matters of weight for jury consideration); U.S. v. Porter, 618 A.2d 629 (D.C. App. 1992) (holding DNA population frequency data inadmissible due to controversy surrounding assumptions upon which the calculations were made). In California particularly, the NRC report has added fuel to the controversy of the admissibility of DNA evidence. *See* People v. Barney, 8 Cal. App. 4th 798, 819 (1992) (finding disagreement among scientists "significant in both number and expertise" and subsequently holding the population frequency data inadmissible); People v. Pizarro, 10 Cal. App. 4th 57, 77-83 (1992) (trial court decision reversed and remanded after a review of the NRC's recommendations). On the federal level, see United States v. Yee, 134 F.R.D. 161 (N.D. Ohio 1991).

I. THE THEORY OF DNA TYPING

A. Deoxyribonucleic Acid (DNA)

DNA is the chemical dispatcher of genetic information, essentially the "blueprint" of life.[19] DNA is composed of two parallel strands of repeated sequences of phosphate and sugar which are coiled into a double helix.[20] These strands are linked together like rungs on a ladder by a series of molecules called nucleotide bases.[21] Each rung consists of two bases forming what are called "base pairs."[22] There are four of these bases,[23] which by combination, create about 3.3 billion base pairs per set of chromosomes.[24] Except for reproductive cells, the sequence of these base pairs is identical in every cell in the human body which has a nucleus.[25] Each base pair sequence has its own position, or locus, on a chromosome.[26] Each particular sequence of base pairs is called an allele and occupies its own locus on the chromosome.[27] Of the 3.3 billion base pairs, 99.9 percent of the sequences (or alleles) are identical in every person.[28] The remaining base pairs, about 3.3 million molecule combinations, are different for all individuals—except identical twins.[29] A locus located on one of these variable sections is said to be a polymorphic locus.[30] The alleles located at such loci have base pairs that repeat varying number of times.[31] Because of this variation, no two

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19. Clarke, *supra* note 9, at 6. Every human cell with a nucleus contains a set of chromosomes and each chromosome contains thousands of genes, each of which occupies a particular location on the chromosome. *Barney*, 8 Cal. App. 4th at 805. The molecular component of the genes and the chromosome is DNA. *Id.* DNA serves as a blueprint for assembling amino acids into proteins and more importantly for identity testing, it serves as a template for cell reproduction. KIRBY, *supra* note 1, at 11; *see generally* Office of Technology Assessment, Genetic Witness: Forensic Uses of DNA Tests (1990) [hereinafter Genetic Witness].

20. Genetic Witness, *supra* note 19, at 3; D.H. Kaye, *The Admissibility of DNA Testing*, 13 CARDOZO L. REV. 353, 353 (1991).

21. Kaye, *supra* note 20, at 353.

22. *Barney*, 8 Cal. App. 4th at 805.

23. These bases are known as adenine, thymine, cytosine and guanine and are commonly referred by their abbreviations A, C, G, and T. KIRBY, *supra* note 1, at 12.

24. Genetic Witness, *supra* note 19, at 3.

25. Clarke, *supra* note 9, at 6.

26. KIRBY, *supra* note 1, at 334.

27. People v. Axell, 235 Cal. App. 3d 836, 845-46 (1991).

28. Genetic Witness, *supra* note 19, at 3-4. The repeated duplication of these DNA strands is known as "tandem repeat." KIRBY, *supra* note 1, at 341. These portions of DNA which are identical in all people are responsible for shared traits such as arms and legs. People v. Barney, 8 Cal. App. 4th 798, 806 (1992).

29. *Barney*, 8 Cal. App. 4th at 806.

30. *Id.*

31. *Id.* Alleles that are composed of a variable number of tandem repeats, i.e., the base pairs repeat for varying numbers of times, are known as "variable number tandem repeats" or "VNTR." KIRBY, *supra* note 1, at 342. These portions of DNA are responsible for a person's individual traits. People v. Axell, 235 Cal. App. 3d 836, 845 (1991)

human beings have identical sequences of all base pairs.[32] It is this tiny amount of variation in human DNA sequences that allows forensic scientists to use DNA evidence to identify a particular person.[33]

B. DNA Detection Methods

Although there are several methods to detect DNA variations, the most common procedure is known as restriction fragment length polymorphism (RFLP) analysis.[34] Basically, the RFLP analysis consists of extracting DNA from biological evidence,[35] breaking the DNA strands into fragments with a restriction enzyme,[36] and pouring the fragments into an electrified gel, which displays the fragments according to size. The fragments are then transferred to a nylon membrane through a process which maintains the order of the fragments in the gel.[37] A "probe"[38] is eventually added to the membrane which bonds with DNA fragments sharing the same base pair sequences which creates a radioactive tag for that specific fragment.[39] Next, the membrane is exposed to X-ray film and the radioactive tags appear as a band on the film, similar to a barcode.[40] This enables one to measure the fragments which contain varying sections and identify the specific alleles.[41] Since the DNA strands for a particular person will always fragment in the

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32. *Axell*, 235 Cal. App. 3d at 845. Because the length of the alleles formed from the repeats varies from person to person, individual identification can be achieved by measuring the allele lengths at various loci. *Id.* at 845-46.

33. Clarke, *supra* note 9, at 6. Because the probability of two people having the same VNTR is low, the examination of a person's VNTR over several loci reduces the probability of a random match. KIRBY, *supra* note 1, at 2. It is the small probability (up to 1 in 739 billion) of such a match that "identifies" the individual with the DNA print.

34. Genetic Witness, *supra* note 19, at 4. Another common method for DNA identification is polymerase chain reaction ("PCR"). The great advantage of PCR over RFLP is that it can identify a DNA type from a sample with 1,000 times less DNA than required for RFLP analysis. *Id.* at 69. PCR starts off procedurally similar to RFLP where cells are extracted of their DNA. William C. Thompson & Simon Ford, *DNA Typing: Acceptance and Weight of the New Genetic Identification Tests*, 75 VA. L. REV. 45, 76. (1989). Yet, it differs in that the tiny amounts of DNA are then "amplified" or reproduced millions of times before being spotted on to the nylon membrane. *Id.* at 76-77.

35. Since all cells in the body share the same DNA, tissue from any part of the body (hair, blood, skin, or semen) can be used for DNA identity testing. KIRBY, *supra* note 1, at 14.

36. Restriction enzymes cut the DNA strands into fragments at specific locations along the base pair sequences. *Id.* at 338. A different enzyme usually cuts the strand at a different location. *Id.*

37. Thompson & Ford, *supra* note 34, at 71.

38. A probe is a recorded sequence of bases which is radioactively tagged enabling it to be traced once it is added to the DNA fragments. *Id.* at 71-72.

39. *Id.*

40. *Id.* at 74.

41. Hansen, *supra* note 7, at 216. This process or step is known as "matching" and consists of comparing DNA patterns produced by the processing with DNA patterns of biological material found at the crime scene.

same place (with the same restriction enzyme), an individual can be identified based on the varying lengths of his or her DNA fragments.[42]

C. Population Frequencies and the Multiplication Rule

Once a conclusive DNA print has been obtained, two possible outcomes exist depending on whether the DNA print matches the sample, (i.e. the suspect's blood).[43] If the print does not match the sample, then the evidence may be declared exculpatory.[44] If it does match the sample, then it must be determined what the likelihood is that such a match occurs by chance and that the suspect is not linked to the sample.[45] To establish this, it is necessary to estimate the frequency within the population of allele distribution at each of several loci.[46] Since obtaining enough empirical data on which to calculate a frequency is largely impossible (due to the necessary size of such a database), population geneticists must make the assumption that each particular allele match within a locus is independent from the other loci.[47] Because each pair of matching alleles is assumed to be statistically independent,[48] the frequencies (or odds) of each match are multiplied together to come up with a probability for the entire DNA pattern.[49] This

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42. Thompson & Ford, *supra* note 34, at 67-68.

43. Ranajit Chakraborty & Kenneth Kidd, *The Utility of DNA Typing in Forensic Work*, 254 SCIENCE 1735, 1735 (1991).

44. *Id.* ("No population genetic issues arise in interpreting this outcome."); *see* DNA Technology, *supra* note 15, at 75 (a "nonmatch" or "exclusion" is sufficient proof that the two samples came from different origins).

45. Chakraborty & Kidd, *supra* note 43, at 1735. A DNA print "cannot be interpreted with regard to inclusion until the population frequencies of the patterns have been established." DNA Technology, *supra* note 15, at 75.

46. DNA Technology, *supra* note 15, at 75. Population estimates could be accomplished through an actual counting method which involves counting the occurrences in a random sample of a certain population and then applying classical statistical formulas, however, due to a lack of such empirical data, DNA analysis uses theoretical assumptions based on population genetics. *Id.* at 76.

47. *Id.* at 77. The multiplication rule cannot be used accurately where the factors (alleles) are not independent. In population genetics, the independence of allele frequencies is shown by the existence of Hardy-Weinberg equilibrium. KIRBY, *supra* note 1, at 169. Hardy-Weinberg law states that in a large random mating population, where no disturbances by outside influences such as mutation, migration, or selection exist, the allele frequencies at specific loci remain constant from generation to generation. *Id.*

48. Independence means that the occurrence of A does not affect the estimate B. KIRBY, *supra* note 1, at 165. Thus, the frequency of a particular allele at one locus does not influence the estimate of an allele frequency at another locus. The probability that each will occur together is simply the product of each allele's probability, i.e., the frequency of an allele at locus A multiplied by the frequency of an allele at locus B yields the frequency, or probability that the alleles will occur together.

49. For example, one VNTR sequence may occur in 1 in 50 people. Another may occur in 1 in 100 people and another in 1 in 14 people. Multiplying the odds of all three or more such sequences generates extremely small probabilities of a match, such as 1 in 100,000 to 1 in several billion. Increasing the probability can be done by adding another locus to the calculation. DNA Technology, *supra* note 15, at 76; Humes, *supra* note 3, at 54, 56.

statistical procedure is know as the "multiplication rule"[50] and the lower the frequency it produces, the more certainty is associated with an individual's DNA identification. However, independence of an allele match within a locus carries with it the assumption that population frequency data is sampled from a common gene pool.[51] The validity of the multiplication rule's results depends on the absence of any subpopulations[52] within the gene pool of the general population.[53]

II. THE SCIENTIFIC ATTACK: POPULATION SUBGROUPS

Scientific questioning of the population frequency data began prior to the NRC report.[54] In December 1991, a critical article written by two population geneticists, Dr. Richard C. Lewontin of Harvard University and Dr. Daniel L. Hartl of Washington University, appeared in the journal *Science*.[55] This article disputed the validity of the assumptions used in conjunction with the multiplication rule to support DNA frequency estimates.[56] Appearing in the same issue of *Science*, however, a rebuttal article by Dr. Chakraborty and Dr. Kenneth Kidd of Yale University explicitly challenged the charges made by Lewontin and Hartl.[57]

A. The Lewontin and Hartl Challenge

The article by Lewontin and Hartl extends beyond former areas of DNA debate, such as the reliability of the tests or validity of DNA matches. Instead, they attack the huge probabilities and statistics underlying the population frequency data necessary for the admission of DNA evidence.[58] Specifically, they question whether the multiplication rule actually yields a "valid and reliable estimate of the probability of matching between 'random'

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50. *See generally* DNA Technology, *supra* note 15, at 76-77.

51. *Id.* at 77. A freely mixing population allows a homogenous distribution of genes from which all members more or less share the same genetic make-up. *Id.* at 81-82; Huber, *Battling Chromosomes: Fighting "DNA Fingerprinting" Evidence*, ARMY LAW., June 1993, at 39.

52. Subpopulations, like Italians, for instance, are ethnic groups that share a more common gene pool than the general population due to intermarriage within the group. The existence of such subgroups within the general population it is argued may affect the accuracy of the multiplication rule. DNA Technology, *supra* note 15, at 79.

53. *Id.*

54. Clark, *supra* note 9, at 9.

55. *See* Richard C. Lewontin & Daniel L. Hartl, *Population Genetics in Forensic DNA Typing*, 254 SCIENCE 1745 (1991).

56. *Id.* at 1746-1749.

57. Clarke, *supra* note 9, at 9; Chakraborty & Kidd, *supra* note 43, at 1735.

58. Lewontin & Hartl, *supra* note 58, at 1749 ("As currently calculated, the [population frequency] estimates may be in error, possibly by two or more orders of magnitude. . . Hence, probability estimates like 1 in 738,000,000,000,000, however they are calculated, are terribly misleading . . . .").

individuals."[59] The problem with the multiplication rule, the authors argue, is the assumption that population frequencies of DNA sequences with each locus are independent.[60] Current methods for estimating population frequencies assume that Caucasians, Blacks, and Hispanics are homogeneous populations[61] undergoing random mating.[62] Such an assumption, Lewontin and Hartl claim however, is unjustified because it ignores "a considerable body of evidence" indicating genetically diverse subpopulations exist within these larger populations.[63]

They allege that within large population groups, such as Caucasians or Hispanics, subpopulations exist with significantly different allele frequencies from other subgroups within the same population.[64] For example, the article contends that there is "on average, one-third more genetic variation among Irish, Spanish, Italians, Slavs, Swedes, and other subpopulations, than there is, on the average between Europeans, Asians, Africans, Amerinds, and Oceanians."[65] Genetic variation among such subgroups, concluded Lewontin & Hartl, will likely be maintained, even in the U.S., because such subgroups tend to intermarry rather than forming a "biological melting pot."[66] Accordingly, Lewontin and Hartl question whether it is legitimate to use such reference populations for allele frequency estimations and whether it is legitimate to multiply these frequencies to estimate the probability of a DNA match.[67]

They contend that because "Caucasian" Americans share ancestry from many genetically diverse European subgroups, a single "Caucasian" reference database for estimating the probabilities of a DNA match is misleading.[68] Rather, to produce accurate probabilities each subgroup must have its own reference database which is computed separately from the larger population frequencies.[69] Consequently, multiplying frequencies across several loci (according to the multiplication rule) is inappropriate.[70] Since

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59. *Id.* at 1746.

60. *Id.*

61. Single pooled reference population databases, such as "Caucasians," are used to estimate allele frequencies of each individual VNTR. *Id.* at 1747.

62. *Id.* at 1746; "Random mating," in the sense used here, means that individuals do not choose a mate based directly on physical or genetic characteristics. *Id.*

63. *Id.*

64. *Id.*

65. *Id.* at 1747.

66. *Id.*; Leslie Roberts, *Fight Erupts Over DNA Fingerprinting*, 254 SCIENCE 1721, 1723 (1991). According to Lewontin and Hartl, genetic substructure within mixed populations can also exist if immigrants to the conglomerate population carried over the genetic differentiation of their ancestors or if only a few generations have passed since the mixing. Lewontin & Hartl, *supra* note 58, at 1747. In addition, their data indicated that all three conditions occur with the Caucasian, Black, and Hispanic populations within the U.S. *Id.*

67. Lewontin & Hartl, *supra* note 58, at 1747.

68. *Id.* at 1748.

69. *Id.*

70. *Id.*

the subpopulations allegedly have different allele frequencies, they require separate multiplication within each subgroup.[71]   Thus, the minuscule probability estimates under the multiplication rule are "terribly misleading" and "unreliable," claim Lewontin and Hartl, because the labs have not taken into account the effect of population substructuring.[72] Based on these observations, Lewontin and Hartl concluded that use of DNA typing in the courtroom must wait until extensive study of population subgroups is completed.[73]

B. The Chakraborty and Kidd Rebuttal

In their article, Chakraborty and Kidd specifically refute the conclusions of Lewontin and Hartl.[74]   Although they admit substructuring may exist within the general population, Chakraborty and Kidd concluded that the effect of any subpopulation has a negligible effect on DNA typing probabilities.[75]   No matter what the mating habits of a particular group are, each group generally shares the same genetic patterns of the larger population because of the "gene exchange" that has occurred since the beginning of evolution.[76] Specifically, the Chakraborty and Kidd article urges the reader "not to be misled regarding nonrandom mating and the genetic consequences of the substructure in human populations."[77]

As a basis for their attack, Chakraborty and Kidd challenge the "demographic studies" which were used by Lewontin and Hartl to support their claim that genetic variation stays within the individual subgroups.[78] Chakraborty and Kidd argue that "population genetic theory shows that even a small amount of gene migration across ethnic and religious boundaries will quickly homogenize populations."[79]   When Lewontin's theory is applied to subgroups, Chakraborty and Kidd find that most genetic differences are still found between individuals within the subgroups rather than between the

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71. *Id.*

72. *Id.* at 1749; The fear is that courtroom prejudice might occur where a VNTR combination that is very rare in the reference population may in actuality be very common within the suspect's particular subgroup which increases the chance of him or her being incorrectly identified as the criminal. Roberts, *supra* note 66, at 1723.

73. Lewontin & Hartl, *supra* note 58, at 1749-50. The authors did acknowledge that DNA typing was probably one of the most powerful innovations in forensic science since the development of fingerprinting. *Id.* at 1746.

74. Chakraborty & Kidd, *supra* note 43, at 1736-39.

75. *Id.* at 1738.

76. *Id.*

77. *Id.* at 1737.

78. *Id.*; *see* Lewontin & Hartl, *supra* note 58, at 1747.

79. Chakraborty & Kidd, *supra* note 43, at 1737. Small gene migration, such as marriages outside a 10 mile radius or marriages of mixed ethnicity, are enough to cause substantial homogenization within only two or three generations. *Id.*

subgroups themselves.[80]   Accordingly, this demonstrates the biological diversity of individuals, even "in extremely subdivided groups."[81]

Furthermore, Chakraborty and Kidd state that even if such genetic differences do exist and do affect the statistical estimates, the current testing procedures are conservative enough to compensate for their effect on the multiplication rule.[82]   Their article notes that an technique known as "binning" obtains valid but conservative estimates for DNA profile probabilities.[83]   Essentially, the binning method (which is used by the FBI) takes alleles that are of similar size, but are too difficult to distinguish from one another, and pools them into the same bin.[84]   This creates a standard base-pair length which factors out any measurement error.[85]   The total allele frequencies within the bin appear in a data base composed of persons of a given race.[86]   As a result, population substructure is not needed in the frequency calculations because the "binned allele frequencies" are basically unbiased estimates of the averages of any underlying subgroups within the general population.[87]

C. The NRC Response

After a two year study, the NRC released its report, *DNA Technology in Forensic Science*.[88] Published four months after the *Science* articles, the NRC report specifically considered the population substructuring theory.[89] The committee spent months analyzing this subject and found considerable debate among population geneticists regarding the existence and effect of substructuring.[90] The report noted that there are some population geneticists that believe "the absence of substructure cannot be assumed, but must be proved empirically."[91] The report also found that other population

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80. *Id.*

81. *Id.*

82. *Id.* at 1735-36.

83. *Id.* The same procedure is used for blood groups and proteins. *Id.* at 1735.

84. *Id.* Bins are a defined range of DNA base pairs lengths which are classed according to measurement error and size standards. *Id.* The FBI, for example, determines a match if two fragments differ in base-pair length by less than 2.5%. People v. Barney, 8 Cal. App. 4th 798, 809 (1992).

85. Chakraborty & Kidd, *supra* note 43, at 1735.

86. People v. Barney, 8 Cal. App. 4th 798, 809 (1992). Such a data base is created by obtaining DNA pattern bands for each racial group (i.e., Caucasian, Black, and Hispanic), and then processing the pattern for each member assigning the bands to appropriate bins and then calculating the frequency of occurrence within the data base for the bands assigned to a given bin. *Id.*

87. Chakraborty & Kidd, *supra* note 43, at 1736.

88. *See* DNA Technology, *supra* note 15.

89. DNA Technology, *supra* note 15, at 79.

90. *See Id.* at 79, 91-95; *see also* Roberts, *supra* note 66, at 1723.

91. DNA Technology, *supra* note 15, at 80. Specifically, the report cited Lewontin and Hartl. *See Id.* at 95 n.10.

geneticists, "while recognizing the possibility or likelihood of population substructure, conclude that the evidence to date suggests that the effect on estimates of genotype frequencies are minimal."[92]

After consideration of numerous scientific data, including both *Science* articles, however, the committee could find no evidence based on current empirical data to support the proposition that subpopulations have any effect on the calculation of population frequencies.[93] In spite of this conclusion, the committee chose to "assume for the sake of discussion that population substructure may exist" and may significantly affect frequency calculations.[94] With this assumption in mind, the report recommended its own conservative number method for estimating population frequencies.[95] The NRC's method sought a calculation method "so conservative as to ensure that there would be no serious scientific argument that the evidence could be said to *overstate* the case against a defendant."[96]

Although the NRC report endorsed the multiplication rule, it modified the calculations.[97] To keep estimates conservative—even with substructuring—the allele frequencies used in the calculations must exceed the allele frequencies in the subpopulations.[98] To accomplish this goal, the report proposed a "ceiling principle" whereby a ceiling frequency is determined for each allele at each locus.[99] This ceiling represents the upper bound for the allele frequency independent of the individual's ethnicity. In order to determine ceiling frequencies the NRC report recommended that 100 persons from each of 15-20 population subgroups should be sampled for allele frequency variation.[100] The highest allele frequency found in any of the 15-20 subpopulations or 5%, whichever is greater, should be used as the frequency for that particular allele.[101] The resulting frequencies then may be multiplied pursuant to the multiplication rule.[102] Until such sampling and estimates are completed, the NRC report recommended temporary adjust-

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92. *Id.* Specifically, the report cited Chakraborty and Kidd. *See id.* at 96 n.12.

93. *Id.*

94. *Id.*

95. *Id.* at 82-86.

96. Eric S. Lander, *DNA Fingerprinting: The NRC Report* (Letter), 260 SCIENCE 1221 (1993). The NRC report stated, "Our recommendations represent an attempt to lay a firm foundation for DNA typing that will be able to support the increasing weight that will be placed on such evidence in the coming years." DNA Technology, *supra* note 15, at 93.

97. DNA Technology, *supra* note 15, at 82.

98. *Id.*

99. *Id.*

100. *Id.* at 83.

101. *Id.* Since subpopulation frequencies may "drift" more than the general population, a conservative allele frequency can be achieved by using a bound of 5% even if the observed frequency is 1%. *Id.* at 84.

102. *Id.* at 82.

ments of current data to achieve more conservative frequency esti-mates.[103]

III. JUDICIAL REACTION

A. Admissibility Standards

The NRC's report has had a wide impact on the admissibility of DNA evidence.[104]   The admissibility of new or novel scientific techniques, such as DNA typing, is generally governed in most jurisdictions by one of two standards.[105]   Courts have used either the *"Frye* standard" or the "relevan-cy standard" when deciding whether novel scientific evidence will be admit-ted.[106]

1. The *Frye*-Test

The majority of state and federal courts have used the standard set forth in *Frye v. United States*[107] as the basis for the admission of scientific evidence.[108]   Under the *Frye*-test, the scientific technique employed must be "sufficiently established to have gained general acceptance in the particular field in which it belongs."[109]   Since judges are not qualified to decide who is right in a scientific debate, *Frye* merely requires them to decide whether a legitimate debate exists in the scientific community.[110]

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103. *Id.* at 91. This temporary method requires testing laboratories to determine if a sample matches any previously tested DNA type in the lab's databank. *Id.* If no match occurs, then the lab should report the size of the database in order to illustrate to jurors its rarity in the population. *Id.* at 92.   In addition, the laboratory should determine an "interim ceiling" frequency by modifying the ceiling principle with a higher bound of 10% instead of 5% for each allele frequency (provided that population studies have been completed on at least three major races.) *Id.* The 10% higher boundary merely reflects the uncertainty surrounding the effect of substructuring on frequency estimates. *Id.*

104. Sherman, *supra* note 6, at 30.

105. John T. Sylvester & John H. Stafford, *Judicial Acceptance of DNA Profiling*, FBI Law Enforcement Bulletin, July 1991, at 26, 26.

106. *Id.*

107. 293 F. 1013 (D.C. Cir. 1923)

108. Stolorow & Clarke, *supra* note 7, at 18.

109. Frye, 293 F. at 1014.

110. The technique or procedure used in a given case is usually not at issue under the *Frye*-test since such questioning is reserved for the jury which may weigh the evidence according to how correctly the testing procedures were applied. Sylvester & Stafford, *supra* note 105, at 26-27.

2. The Relevancy Standard

As an alternative to the *Frye*-test, federal courts and several state courts have turned to the relevancy standard.[111] Under the relevancy standard, which is based on the Federal Rules of Evidence,[112] the court must consider whether the relevance, the probativeness, the materiality, and reliability of the proffered evidence outweigh its potential to either mislead the jury or unfairly prejudice the defendant.[113] Whether the technique is "generally accepted" in the scientific community is merely a factor in determining its admissibility.[114]

3. The Reliability Requirement

Both standards have been expanded in some states and in federal courts with an additional "reliability" requirement.[115] The reliability requirement asks whether the correct scientific techniques have been applied in the testing process.[116] On the state court level, one of the first DNA cases to use this new requirement in conjunction with the *Frye*-test was *People v. Castro*.[117] The *Castro* court felt that DNA evidence presented special problems of reliability which required adding another layer to the already conservative *Frye*-test.[118] The *Castro* court enunciated a three prong test for the admissibility of DNA evidence.[119] The first two prongs of the test were

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111. *See* Daubert v. Merrell Dow Pharmaceuticals, Inc., 113 S. Ct. 2786 (1993); *see also* State v. Pierce, 597 N.E.2d 107 (Ohio 1992); Kelly v. State, 824 S.W.2d 568 (Tex. Crim. App. 1992).

112. *See* Fed. R. Evid. 401-403, 702-704.

113. Stephanie B. Goldberg, *A New Day for DNA?*, ABA JOURNAL, Apr. 1992, at 84, 84. *See* United States v. Williams, 583 F.2d 1194 (2d Cir. 1978), *cert. denied*, 439 U.S. 1117 (1979). States that have adopted the relevancy standard include Arkansas, Delaware, Florida, Georgia, Iowa, Louisiana, Maine, Montana, North Carolina, Ohio, Oregon, South Carolina, Texas, and Virginia. Clarke, *supra* note 9, at 8.

114. Sylvester & Stafford, *supra* note 105, at 27.

115. Goldberg, *supra* note 113, at 84; *see, e.g.*, People v. Castro, 545 N.Y.S.2d 985 (N.Y.S. 1989); United States v. Jakobetz, 955 F.2d 786, 796 (2d Cir. 1992); *see also infra* text accompanying notes 151-156.

116. Goldberg, *supra* note 113, at 84; *see, e.g.*, People v. Castro, 545 N.Y.S.2d 985, 986 (N.Y. Sup. Ct. 1989); State v. Schwartz, 447 N.W.2d 422, 426 (Minn. 1989); *Caldwell v. State*, 393 S.E.2d 436, 441-42 (Ga. 1990); United States v. Two Bulls, 918 F.2d 56, 60-61 (8th Cir. 1990), *reh'g granted, vacated en banc*, 925 F.2d 1127 (8th Cir. 1991); *Jakobetz*, 955 F.2d at 796; *see also* People v. Kelly, 549 P.2d 1240 (Cal. 1976).

117. 545 N.Y.S.2d 985 (N.Y. Sup. Ct. 1989).

118. *Id.* at 987. The court was of the view that by focusing attention on the general acceptance issue, the *Frye*-test overlooked significant problems in the use of a particular technique. *Id.* Because DNA typing is so complex, the court felt that even if it passed the *Frye*-test, it was still insufficient to present it to a jury without a preliminary hearing regarding the procedures used. *Id.*

119. *Id.*

from *Frye*,[120] but the third prong was concerned with whether the testing laboratory had performed the accepted scientific techniques in analyzing the forensic samples in the particular case.[121]   Applying the three prong test, the *Castro* court had no problem finding general acceptance of DNA evidence under the first two prongs.[122] It was at the third inquiry, however, that the court held the DNA evidence inadmissible because the private laboratory had not applied the generally accepted technique for DNA typing.[123]

On the federal level, the Eighth Circuit followed the *Castro* decision and added the reliability requirement to the *Frye*-test in *United States v. Two Bulls*.[124]   The court justified the addition to the *Frye*-test because of the novelty of DNA evidence and the prejudice to the defendant.[125]   The *Two Bulls* court found the added requirement to be "a sufficient foundational basis as to the overall admissibility of the evidence."[126]

The more liberal relevancy standard was also subjected to the reliability requirement in *United States v. Jakobetz*.[127]   Citing both *Two Bulls* and *Castro*, the Second Circuit did not find the challenges of DNA evidence so special "as to require a new standard of admissibility."[128]   Although the trial court should inquire as to whether the proper scientific techniques were properly performed, the *Jakobetz* court, in contrast to *Castro*, concluded that this issue should go to the weight rather than the admissibility of the evidence.[129]   Adopting a standard of relevance and reliability, the circuit court held that despite the complex, confusing, and novel evidence, "the jury must retain its fact-finding function."[130]

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120. Prong one asks if there is a theory which is generally accepted in the scientific community which supports the conclusion that DNA forensic testing can produce reliable results. *Id.* Prong two asks whether the techniques that currently exist are capable of producing reliable results. *Id.*

121. *Id.*

122. *Id.* at 988-90.

123. *Id.* at 995-99.   Ironically, after the judge's exclusion of the DNA evidence, the defendant decided to plead guilty and he subsequently admitted that the blood found on his watch from which the DNA was taken was that of the victim. Stolorow & Clarke, *supra*, note 7, at 18-19. Other states courts have followed the *Castro* precedent and applied a similar "reliability" requirement. *See* State v. Schwartz, 447 N.W.2d 422 (Minn. 1989); Caldwell v. State, 393 S.E.2d 436 (Ga. 1990).

124. 918 F.2d 56 (8th Cir. 1990).

125. *Id.* at 60.

126. *Id.* Although the appeal was dismissed when the appellant died, the *Two Bulls* court ultimately adopted the three part test laid in *Castro*. *Id.* at 61.

127. 955 F.2d 786 (2d Cir. 1992).

128. *Id.* at 796.

129. *Id.* at 800.

130. *Id.* at 796.   For the standards implicit in the relevancy test adopted in *Jacobetz see* United States v. Williams, 583 F.2d 1194, 1198 (2d Cir. 1978).

4. *Daubert v. Merrell Dow Pharmaceuticals, Inc.*

Recently, on June 28, 1993, the United States Supreme Court in *Daubert v. Merrell Dow Pharmaceuticals, Inc.*[131] held that the *Frye* standard of admissibility does not govern trials conducted in federal courts.[132] Instead, *Frye*'s "general acceptance" test was superseded by the Federal Rules of Evidence and, in particular, by the more liberal admissibility standard of Federal Rule of Evidence 702, which permits the admission of expert testimony pertaining to "scientific, technical, or other specialized knowledge[.]"[133] The "general acceptance" standard, wrote Justice Blackmun for the court, would be contrary to the "liberal thrust" of the rules.[134] Rule 702's requirement, stated Blackmun, that an expert's testimony pertain to "scientific knowledge" establishes a standard of evidentiary reliability.[135] In addition, the Court found that Rule 702's requirement that expert testimony "assist the trier of fact to understand the evidence or to determine a fact in issue" addresses the relevancy of such evidence.[136] In order to satisfy this condition, the proponent of the testimony must demonstrate that the evidence supports "a valid scientific connection to the pertinent inquiry."[137] The Court also noted that "[v]igorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of proof are the traditional and appropriate means of attacking shaky but admissible evidence."[138]

Daubert's effect on the admissibility of DNA evidence was examined by the Eighth Circuit in *United States v. Martinez.*[139] The Eighth Circuit noted that the Second Circuit in *Jakobetz* employed a reliability approach under Rule 702 similar to that used in *Daubert.*[140] The court in *Martinez* concluded that the Second Circuit's determinations as to the general theory

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131. 125 L.Ed.2d 469 (1993).

132. *Id.* at 480.

133. *Id.* (quoting Fed. R. Evid. 702).

134. *Id.*

135. *Id.* at 480-81. In order to assess the reliability of novel scientific evidence under Rule 702, the Court instructed courts to look at (1) whether the scientific knowledge being presented has been tested or whether its underlying theory can be falsified; (2) whether it has been subject to peer review and publication; (3) what the technique's known rate of error is; and (4) whether the technique is generally accepted in the relevant community. *Id.* at 482-83.

136. *Id.* at 481 (quoting Fed. R. Evid. 702). According to *Daubert*, before scientific expert testimony can be admitted, the trial court must conclude, under Federal Rule of Evidence 104(a) that the proposed testimony constitutes (1) scientific knowledge that (2) will assist the jury to understand or determine a fact in issue. *Id.* at 482. The subject of the testimony does not have to be a known certainty, but "in order to qualify as 'scientific knowledge,' an inference or assertion must be derived by the scientific method." *Id.* at 481.

137. *Id.* at 482.

138. *Id.* at 484. Recommending that courts respect the differing functions of judge and jury, the Court also noted that the focus of the inquiry "must be solely upon the principles and methodology, not on the conclusions that they generate." *Id.*

139. 3 F.3d 1191 (8th Cir. 1993).

140. *Id.* at 1197.

and techniques of DNA evidence were valid under *Daubert*.[141] The Eighth Circuit then inquired into whether the Supreme Court created a reliability requirement in its *Daubert* opinion.[142] The *Martinez* court found that the reliability inquiry[143] set forth in *Daubert* mandates a preliminary hearing to determine if the expert properly performed the scientific procedure.[144] The court determined that such a hearing suggests that the inquiry goes beyond merely the reliability of the abstract principles or methodologies.[145] According to *Martinez*, *Daubert* requires the trial court to determine if the expert applied a reliable technique in the particular case.[146] The Eighth Circuit emphasized, however, that this inquiry was "a flexible one . . . [and] not every error in the application of a particular methodology should warrant exclusion." Apparently inferring that this reliability requirement goes more to the weight of the evidence than to its admissibility, the circuit court stated that any alleged deficiencies in the techniques used provide a basis for exclusion of the evidence only if "'a reliable methodology was so altered . . . as to skew the methodology itself . . .'"[147]

With this adoption of the relevancy standard, DNA evidence will likely have less trouble with admissibility in federal courts. The *Frye* test, which has been used in both federal and state courts, has represented a major obstacle for the admission of DNA population frequency data.[143] It remains to be seen whether state courts will adopt the *Daubert* relevancy standard over a *Frye* related standard. Although *Daubert* does not necessarily apply to state courts, its persuasive force is strengthened in that many states have modeled their rules of evidence after the federal rules.[149]

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141. *Id.*

142. *Id.* The court noted both the *Castro* and the *Jakobetz* reliability requirement and that *Castro*'s requirement went to the admissibility of the evidence whereas *Jakobetz*'s reliability requirement went to the weight of the evidence. *Id.*

143. *See supra* note 144.

144. *Id.* at 1197-98.

145. *Id.* at 1198.

146. *Id.*

147. *Id.*

148. For a criticism of the *Frye*-test *see* Jason D. Altman, Comment, *Admissibility of Forensic DNA Profiling Evidence: A Movement Away From Frye v. United States and a Step Toward the Federal Rules of Evidence: United States v. Jakobetz, 955 F.2d 786 (2d Cir. 1992), cert. denied, 113 S. Ct. 104 (1992)*, 44 WASH. U.J. URB. & CONTEMP. L. 211, n.27 (1993).

149. A few state courts have specifically commented on the *Daubert* rationale. In August 1993, the Arizona Supreme Court considered the *Daubert* standard, but declined to use it and opted for the *Frye*-test instead. State v. Bible, 858 P.2d 1152, 1183 (Ariz. 1993) ("We leave *Daubert* for another day and, in accordance with Arizona precedent—old and new—apply *Frye*[.]"); *see* Springfield v. State, 1993 WL 362357 *9 (Wyo.) (adopting the *Daubert* rationale as similar to its relevancy standard); *see also* Nelson v. State, 628 A.2d 69, 74 n.7 (Del. 1993) (state's relevancy standard modeled after the Federal Rules).

B. Judicial Acceptance

1. DNA Theory & Technology

The underlying principles and theory behind DNA technology have been generally accepted for several years within both the scientific community and the judicial system.[150] Attacks on the testing process, such as subjective interpretation of band matches or the absence of standardization and proper proficiency testing have frequently been used to show a lack of general acceptance.[151] Yet, such claims, analyzed under either the *Frye*-test or a relevancy related test, have been rejected in twenty-nine states and one federal circuit court.[152] In addition, the Office of Technology Assessment of the United States Congress ("OTA") and the NRC have both endorsed the reliability of RFLP typing. Over three years ago the OTA stated that "forensic uses of DNA tests are both reliable and valid when properly performed and analyzed by skilled personnel."[153] The OTA went on to report that questions about DNA technology or its theory are "red herrings that do the courts and the public a disservice."[154] In April of 1992, the NRC released its report, *DNA Technology in Forensic Science*, which endorsed forensic uses of DNA typing technologies, specifically RFLP analysis.[155]

2. DNA Population Frequency Data

While the prevalent case law and the recommendations from both the OTA and the NRC support the general acceptance of DNA technology, the NRC report's discussion of substructuring has had a confusing effect on the

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150. Genetic Witness, *supra* note 20, at 7-8; DNA Technology, *supra* note 15, at 144-145, 149; People v. Axell, 235 Cal. App. 3d 836, 856 ("DNA fingerprinting involve[s] scientific principles and technology all of which have gained general acceptance in the scientific field in which they belong."). Extensive case law in several other states also supports the admission of DNA evidence. *See e.g.*, Snowden v. State, 574 So. 2d 960 (Ala. App. 1990); Swanson v. State, 823 S.W.2d 812 (Ark. 1992); Toranzo v. State, 608 So. 2d 83 (Fla. Dist. Ct. App. 1992), *review dismissed,* State v. Toranzo, 613 So. 2d 9 (Fla. 1993); Caldwell v. State, 393 S.E.2d 436 (Ga. 1990); State v. Montalbo, 828 P.2d 1274 (Haw. 1992); People v. Miles, 577 N.E.2d 477 (Ill. 1991); Woodcox v. State, 591 N.E.2d 1019 (Ind. 1992); State v. Brown, 470 N.W.2d 30 (Iowa 1991); Smith v. Deppish, 807 P.2d 144 (Kan. 1991); People v. Wesley, 589 N.Y.S.2d 197 (N.Y. App. Div. 1992); State v. Pierce, 597 N.E.2d 107 (Ohio 1992); Kelly v. State, 824 S.W.2d 568 (Tex. 1992); State v. Ford, 392 S.E.2d 781 (S.C. 1990); Rivera v. State, 840 P.2d 933 (Wyo. 1992); Jakobetz, 955 F.2d 786.

151. Interview with George W. Clarke, Deputy District Attorney, Assistant Chief, Training Division, Office of the District Attorney, San Diego County, California, in San Diego, Cal. (June 15, 1993).

152. *See supra* note 149.

153. Genetic Witness, *supra* note 19, at 7-8.

154. *Id.* at 8.

155. DNA Technology, *supra* note 15, at 144-145.

courts.[156]   Specifically, whether the methods for calculating DNA population frequency data are reliable continues to be debated.[157]   Before the
release of the NRC report the admissibility of population statistics was widely
supported.[158]   Prior to 1991, only a handful of cases excluded DNA evidence
because the statistics were challenged.[159]   However, with the release of the
Science articles in 1991 and the NRC report in 1992, more and more courts
began to question the admissibility of DNA population frequency data.[160]

1. Federal Courts

On the federal district court level, only two cases were heard prior to the
NRC report.[161]   Although one case used a relevancy standard and the other
case used a *Frye* related standard for admissibility, both cases admitted the
DNA population frequency data.   In the first federal opinion attacking the
use of population frequency data, the court in *United States v. Jakobetz*
admitted the DNA evidence under the relevancy standard.[162]   Upholding
the reliability of the FBI's techniques, the court concluded that the lower
court's findings "would satisfy not only the *Frye* standard, but the *Two Bulls*
and *Castro* standard as well."[163]   The second federal court to consider
DNA admissibility was heard by the magistrate in *United States v. Yee.*[164]
Under the requirements of the *Frye*-test, the magistrate recommended that the
FBI's DNA evidence be admitted.[165]   Affirming his recommendation, the

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156. *See, e.g.,* B.S. Weir, *DNA Fingerprinting Report* (Letter), 260 SCIENCE 473 (1993)
(citing State v. Guevara, No. K9-92-1873 (D. Minn. Jan. 26, 1993)).

157. *See* Atoigue, 1992 WL 245628, at *4; Commonwealth v. Lanigan, 596 N.E.2d 311,
316 (Mass. 1992); State v. Vandebogart, 616 A.2d 483, 493-94 (N.H. 1992); State v. Cauthron
846 P.2d 502, 514-517 (Wash. 1993); State v. Bible, 858 P.2d 1152, 1188-89 (Ariz. 1993).

158. *See e.g.,* Snowden v. State, 574 So. 2d 960 (Ala. Crim. App. 1990); Andrews v.
State, 533 So. 2d 841 (Fla. Dist. Ct. App. 1988); Martinez v. State, 549 So. 2d 694 (Fla. Dist.
Ct. App. 1989); People v. Lipscomb, 574 N.E.2d 1345 (Ill. App. 1991); People v. Miles, 577
N.E.2d 477 (Ill. App. 1991); Hopkins v. State, 579 N.E.2d 1297 (Ind. 1991); Davidson v.
State, 580 N.E.2d 238 (Ind. 1991); State v. Brown, 470 N.W.2d 30 (Iowa 1991); Smith v.
Deppish, 807 P.2d 144 (Kan. 1991); State v. Davis, 814 S.W.2d 593 (Mo. 1991); State v.
Pennington, 393 S.E.2d 847 (N.C. 1990); State v. Ford, 392 S.E.2d 781 (S.C. 1990); Glover
v. State, 787 S.W.2d 544 (Tex. App. 1990); Kelly v. State, 824 S.W.2d 568 (Tex. Crim. App.
1990); Mandujano v. State, 799 S.W.2d 318 (Tex. App. 1990); Bethune v. State, 821 S.W.2d
222 (Tex. Ct. App. 1991); Trimboli v. State, 817 S.W.2d 785 (Tex. App. 1991); Spencer v.
Commonwealth, 385 S.E.2d 850 (Va. 1989); *Jakobetz,* 955 F.2d 786 (8th Cir. 1992).

159. Thompson & Ford, *supra* note 5, at 58.

160. *See, e.g.,* Caldwell v. State, 393 S.E.2d 436, 443 (Ga. 1990); People v. Mohit, 579
N.Y.S.2d 990, 998 (N.Y.S. 1992); State v. Houser, 490 N.W.2d 168, 183-84 (Neb. 1992).

161. *See Jakobetz,* 955 F.2d 786; United States v. Yee, 134 F.R.D. 161 (N.D. Ohio 1991);
but see United States v. Two Bulls, 918 F.2d 56, 61 (8th Cir. 1990) (although the decision was
later vacated, the *Two Bulls* court rejected the DNA evidence under the *Castro* rational).

162. *Jakobetz,* 955 F.2d at 796-97, 800. *Jakobetz* was also the first federal appellate court
to consider the admissibility of DNA evidence.

163. *Id.* at 799.

164. 134 F.R.D. 161.

165. *Id.* at 202.

Yee court held that general acceptance existed for the FBI's data frequency calculations.[166]

Only one federal case regarding DNA admissibility has been published since the release of the NRC report.[167] In September 1993, the Eighth Circuit in *United States v. Martinez*,[168] decided whether DNA profiling evidence was admissible under the relevancy approached adopted in *Daubert*.[169] The appellate court found, under *Daubert*'s reliability requirement, that the techniques employed in the particular case to be reliable and admitted the evidence of a DNA "match."[170] The *Martinez* court was not provided with the opportunity, however, to decide upon the admissibility of DNA population frequency data since the trial court had excluded the statistical data in response to appellant's request.[171]

2. State Courts

a. Relevancy Jurisdictions. The impact of the NRC report on states employing a relevancy standard for admitting scientific evidence has been marginal compared to jurisdictions using a *Frye* related test. For example, in Ohio prior to the NRC report, the court in *State v. Blair*[172] found DNA statistical evidence admissible.[173] Five months after the NRC report, the Ohio Supreme Court in *State v. Pierce*[174] found, under the relevancy and reliability test used in *Jakobetz*, that the population frequency data was again admissible and that questions of reliability go to the weight of the evidence.[175] The court acknowledged the subpopulation debate in both the *Science* articles and the NRC report and concluded that "'[t]he court must allow the jury to discharge its duties of weighing the evidence, making

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166. *Id.* at 166.

167. *See e.g.*, United States v. Martinez, 3 F.3d 1191 (8th Cir. 1993). *Martinez* was also only the second federal appellate court to consider DNA admissibility. Note, however, that two weeks after *Martinez* was decided, the Fourth Circuit in *Spencer v. Murray*, denied petitioner's federal habeas corpus claim and affirmed the state court's finding that DNA evidence was admissible. Spencer v. Murray, No. 92-4006, 1993 WL 355844, *4 (4th Cir. Va. Sept. 16, 1993).

168. 3 F.3d 1191.

169. Although the trial court in *Martinez* applied the three prong test announced in *People v. Castro*, the appellate court found *Castro*'s test to be "at least as stringent as the test mandated in *Daubert.*" *Id.* at 1198.

170. *Id.* at 1197.

171. *Id.* at 1199. Appellant had made the suggestion that the district court exclude the statistical data. Yet, on appeal, appellant claimed that the exclusion of the statistical data prejudiced him because the jury would conclude that he was the only possible source of the DNA. *Id.* The court concluded that appellant was barred from raising this argument, however, under the doctrine of invited error. *Id.*

172. 592 N.E.2d 854 (Ohio Ct. App. 1993).

173. *Id.* at 866-67.

174. 597 N.E.2d 107 (Ohio 1992).

175. *Id.* at 115.

credibility determinations, and ultimately deciding the facts.'"[176] The jury was thus free to reject the DNA evidence if it believed it to be false or misleading.[177] In a pre-NRC report decision, the Texas Court of Criminal Appeals in *Kelly v. State*[178] held DNA population frequency data admissible under a relevancy and reliability standard.[179] The *Kelly* court's holding has remained intact despite several challenges to DNA evidence in 1992.[180] Florida has been similarly supportive of DNA statistical evidence under the relevancy test both before and after the NRC report.[181] In a post-NRC report case, the Florida Court of Appeals in *Toranzo v. State*[182] had no problem following pre-NRC case law admitting DNA population frequency data.[183]

In Wyoming, the supreme court in *Springfield v. State*[184] stated that the *Daubert* relevancy standard was paralleled under their state's version of the relevancy test.[185] The court noted the problems *Frye* jurisdictions had with the NRC report and the debate over population subgroups.[186] Yet, the *Springfield* court did not concern itself with the acceptability of the NRC's approach since, in its view, population substructure affected the weight of the evidence, and in addition, the jury was free to disregard or disbelieve the expert testimony.[187] The court therefore admitted the DNA statistical data since it would assist the jury and because the conservative statistical calculations of the NRC report had been used.[188]

b. *Frye* Jurisdictions. States employing a *Frye* related test have had more difficulty with the admission of DNA statistical data. Prior to the NRC report in a non-DNA case, the Massachusetts court in *Commonwealth v.*

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176. *Id.* (quoting United States v. Jakobetz, 955 F.2d 786, 796-97 (2d Cir. 1992).

177. *Id.*

178. 824 S.W.2d 568 (Tex. Crim. App. 1992).

179. *Id.* at 573-74.

180. *See* Glover v. State 825 S.W.2d 127, 128 (Tex. Crim. App. 1992); Trimboli v. State, 826 S.W.2d 953, 954 (Tex. Crim. App. 1992); Fuller v. State, 827 S.W.2d 919, 930 (Tex. Crim. App. 1992); Bethune v. State, 821 S.W.2d 222, 225 (Tex. Ct. App. 1992); Barnes v. State, 839 S.W.2d 118, 124 (Tex. Ct. App. 1992).

181. *See* Robinson v. State, 610 So. 2d 1288, 1291 (Fla. 1992); Martinez v. State, 549 So. 2d 694, 697 (Fla. 1989); Andrews v. State, 533 So. 2d 841, 849-51 (Fla. 1988).

182. 608 So. 2d 83 (Fla. 1992).

183. *Id.* at 84.

184. No. 92-162, 1993 WL 362357 (Wyo. Sept. 21, 1993).

185. *Id.* at *9.

186. *Id.* at *15.

187. *Id.* at *14-*15.

188. *Id.* at *15. In another example, the Delaware Supreme Court in *Nelson v. State* employed a relevancy standard almost identical to that used in *Daubert*. However, while the *Nelson* court deferred on deciding the admissibility of DNA statistical data, it nevertheless rejected the prosecution's claim that statistics go to the weight of the evidence, not the admissibility of the DNA matching evidence. Nelson v. State, 628 A.2d 69, 74 n.7, 76 n.9 (Del. 1993).

Gomes[189] admitted under a *Frye* related test statistical data obtained pursuant to the multiplication rule.[190]   In another pre-NRC case, the Massachusetts court in *Commonwealth v. Curnin*[191] used *Frye* again, this time to determine the admissibility of DNA evidence.[192]   Although the court found general acceptance for the theory underlying DNA technology, the court could not find general acceptance for statistical methods employed therein.[193]   The court noted that questions about subpopulations created uncertainty in the scientific community regarding the use of the multiplication rule.[194]   Finding a lack of general acceptance for the population statistics, the court held the DNA evidence inadmissible.[195]

Following the release of the NRC report, in *Commonwealth v. Lanigan*,[196] the Massachusetts court again considered the admissibility of DNA evidence. The court noted that although the magistrate in *United States v. Yee* had admitted population frequency data, the debate over population substructure had increased since then with the release of the NRC report and its specific concern over subpopulations.[197]   Finding a "lively, and still very current, dispute" in the scientific community regarding the existence of "population substructuring" possibly affecting the reliability of frequency estimates, the court affirmed the trial court's order denying DNA evidence.[198]

In another one of the few cases to challenge DNA frequency data before the release of the *Science* articles and the NRC Report, the Minnesota court in *State v. Schwartz*, rejected the use of population frequency data for DNA evidence under the Minnesota version of *Frye*.[199]   However, the court refused the statistical evidence not because of a lack of general acceptance in the scientific community, but because case law in existence prior to DNA analysis had traditionally rejected population frequency data in conventional,

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189. 526 N.E.2d 1270 (Mass. 1988) (using probability data for genetic markers found in a bloodstain).

190. *Id.* at 1276-77, 1279-80.

191. 565 N.E.2d 440 (Mass. 1991).

192. *Id.* at 443.

193. *Id.* at 441-42. Since *Frye* itself was not satisfied, the court did not inquire into whether the procedures were applied properly. *Id.* at 442.

194. *Id.* at 443-44.

195. *Id.* at 445. "We need not resolve the propriety of the forensic DNA testing conducted in this case because we conclude that there is no demonstrated general acceptance or inherent rationality of the process by which Cellmark arrived at its conclusion that one Caucasian in 59,000,000 would have the DNA components disclosed by the test that showed an identity between the defendant's DNA and that found on the nightgown." *Id.* at 442.

196. 596 N.E.2d 311 (Mass. 1992).

197. *Id.* at 315-16.

198. *Id.* at 316.

199. State v. Schwartz, 447 N.W.2d 422, 424, 428-29 (Minn. 1989).

non-DNA serology.[200]   Finding the probability data "integral to DNA typing," the court refused to admit the evidence altogether.[201]   In case decided two months after the NRC report's release, the Minnesota court in *State v. Jobe*[202] held that the FBI protocol established an appropriate set of standards and guidelines for admitting DNA evidence.[203]   Although the court did not address the issue of population statistics since it was not raised on appeal, the supreme court reviewed the entire NRC report and found nothing in it inconsistent with the court's holding.[204]   The court further concluded that the basic DNA testing procedures went to the weight of the evidence, but whether the procedures were actually complied with were subject to admissibility under the state's version of *Frye*.[205]

In May 1992, the Minnesota district court in *State v. Alt*[206] acknowledged the release of the NRC report and its concern over population substructure, and subsequently issued an order limiting the use of DNA test results.[207]   In light of the debate over population subgroups, the district court held that the FBI statistical calculations were not generally accepted under *Frye* and therefore could not admitted.[208]   Upon review, however, the appellate court reversed the district court's decision even though the appellate court found the scientific debate to affect the application of the multiplication rule.[209]   The appellate court concluded that the NRC's adoption of the modified ceiling principle created general acceptance within

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200. *Id.* at 428-29. Minnesota, in a unique trilogy of case law, has limited admission of population frequency data to the frequencies of individual loci and prohibited the use of the multiplication rule (i.e., the multiplying of the individual locus frequencies). *See* State v. Joon Kyu Kim, 398 N.W.2d 544, 547 (Minn. 1987) (limiting the use of population frequency data for fear the jury would interpret such statistical evidence as a measure of the defendant's guilt); State v. Jobe, 486 N.W.2d 407 (Minn. 1992); State v. Johnson, 498 N.W.2d 10 (Minn. 1993). *See also* State v. Alt, 504 N.W.2d 38, 42 n.6 (Minn. Ct. App. 1993) ("locus frequencies . . . are the strongest probability evidence admissible under *Joon Kyu Kim* and *Johnson*.").

201. *Id.* at 428. Curiously, the Minnesota court expressly withheld comment on a newly enacted state statute which provided admissibility for population data frequencies and subsequent DNA test results. *Id.* at 429 n.6. *See* Minn. Stat. § 634.25-26, (Supp. 1989). Note, however, that the Minnesota Supreme Court has recently questioned the validity of this statute. *State v. Alt*, 504 N.W.2d 38, 41 n.2 (Minn. 1993) (citing State v. Nielsen, 467 N.W.2d 615, 620 (Minn. 1991)).

202. 486 N.W.2d 407 (Minn. 1992).

203. *Id.* at 419-20.

204. *Id.* at 420 n.4.

205. *Id.* at 420.

206. 504 N.W.2d 38 (Minn. Ct. App. 1993).

207. *Id.* at 41.

208. *Id.* at 41. In June 1992, the prosecution filed a motion to reconsider claiming the FBI calculations were consistent with the NRC report. *Id.* In August 1992, the prosecution again offered the population frequency data consistent with the state's case law regarding the presentation of statistical evidence. *Id.* at 41-42. The district court, however, in December 1992, denied all motions relating to the admission of DNA evidence and confirmed its May 1992 order. *Id.* at 42.

209. *Id.* at 49-51. Although the product of the multiplication rule is not disclosed to the jury in Minnesota, the court found the scientific debate to affect even the probability calculations on individual loci. *Id.* at 49-50.

the scientific community.[210]   It therefore allowed the statistical evidence to be admitted if calculated according to the NRC's approach and remanded the case.[211]

In contrast to Minnesota, the Arizona Supreme Court in August 1993, refused to admit DNA population statistics altogether.[212]   In *State v. Bible*, the supreme court applied basically a straight forward *Frye* test "subject to a foundational showing."[213]   Noting the significant controversy over the last two years concerning population subgroups, including the science articles as well as case law in other states, the court found the probability calculations to be flawed and not generally accepted within the scientific community.[214]   In another *Frye* jurisdiction, the Colorado court in *Fishback v. People*[215] found that the trial court in October 1989, had properly concluded that population frequency calculations were generally accepted at the time.[216]   However, the reviewing court conceded "that considerable debate has emerged in the three years since the trial in this case concerning the acceptability of the statistical frequencies . . ."[217]   The court then left the question open as to whether or not the method for calculating the frequency data was generally accepted in light of the new events.[218]

3. California Case Law

a. Interpretation of *Kelly-Frye*.   Perhaps the best example of the impact of the *Science* articles and the NRC report is demonstrated in California.[219] In California, the admissibility standards for scientific evidence are controlled by a modified *Frye* test.   In *People v. Kelly*,[220] the California Supreme Court required that "correct scientific procedures" be shown to have been

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210. *Id.* at 51.   *Similarly see* Vandebogart, 616 A.2d at 493-95 (reversing trial court's decision to admit DNA statistical data, yet citing and giving praise to the NRC's approach).

211. *Id.* at 51, 53.   In accordance with the state's case law, the statistical evidence was limited to frequencies of individual loci. *Id.*

212. *See* State v. Bible, 858 P.2d 1152, 1190 (Ariz. 1993).

213. *Id.* at 1183 (citing State ex rel. Collins v. Superior Court, 644 P.2d 1266, 1282 (Ariz. 1982).   This foundational showing relates the expert's qualifications, proper application of testing techniques, and accurate recording of test results. *Id.* at 1184.

214. *Id.* at 1188-89.   The court found the calculations to be flawed for three reasons: "(1) they are impermissibly based on the disputed assumptions of linkage equilibrium; (2) the database relied on is of disputed statistical validity; and (3) the database relied on is not in Hardy-Weinberg equilibrium." *Id.*

215. 851 P.2d 884 (Colo. 1993).

216. *Id.* at 894.

217. *Id.*

218. *Id.* at 895.

219. State v. Bible, 858 P.2d 1152, 1188 ("impact of articles is best demonstrated by California cases").

220. 549 P.2d 1240 (Cal. 1976).

used in testing in addition to *Frye*'s requirements.[221]   Recent California Supreme Court decisions have interpreted this additional third prong of the *"Kelly-Frye"* rule to test the scientific technique and not the competency with which it is applied, i.e., "correct" procedures, not procedures applied "correctly."[222]   Accordingly, deficiencies in testing affect only the weight of the evidence, not its admissibility.[223]   The California Supreme Court in *People v. Cooper*,[224] supported this interpretation of the *Kelly-Frye* rule and reaffirmed the fact that the manner in which testing is conducted does not bear on admissibility.[225]

b. Application of *Kelly-Frye* to DNA Evidence.   In spite of the state Supreme Court's guidance, some disagreement still exists as to whether the *Kelly* requirement mandates that "correct" procedures be utilized or that such procedures merely be used "correctly."   In the state's first case on DNA identification evidence, the court of appeals in *People v. Axell*[226] questioned the scope of the third prong of *Kelly-Frye* with respect to DNA evidence.[227] The court determined that the supreme court had not intended to overrule the "third prong" of *Kelly* and that the trial court had erred in not subjecting the 'procedures used' to the *Kelly-Frye* test.[228]   The *Axell* court, however,

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221. *Id.* at 1244. In addition to *Frye*'s "general acceptance," *Kelly* requires the proponent to satisfy a second and third inquiry: the reliability of the scientific method—usually through the opinion testimony of a qualified expert on the subject and that correct scientific procedures were used in the particular case. *Id.*

222. *See e.g.*, People v. Farmer, 765 P.2d 940, 965 (Cal. 1989) ("Careless testing affects the weight of the evidence and not its admissibility, and must be attacked on cross-examination or by other expert testimony."); *see id.* (citing People v. Coleman, 46 Cal.3d 749, 775 (1988) ("[T]he *Kelly-Frye* rule tests the fundamental validity of a new scientific methodology, not the degree of professionalism with which it is applied.")). One California appellate court has also supported this interpretation. *See* People v. Smith, 215 Cal. App. 3d 19, 28 (1989) (finding appellant's argument—alleging careless testing procedures—to be in error).

223. *Farmer*, 765 P.2d at 965.

224. 809 P.2d 865 (Cal. 1991).

225. *Id.* at 814. In *Cooper*, the court rejected the defendant's challenge that a blood and saliva protein analysis was inadmissible due to an alleged defect in the testing process—and held that the *Farmer-Smith* interpretation of *Kelly-Frye* was correct. *Id.* Furthermore, the Supreme Court in *People v. Shirley* determined that any hearing conducted pursuant to the *Frye* rule is not to determine whether or not a technique is in fact reliable. People v. Shirley, 31 Cal. 3d 18, 55 (1982). Rather, the inquiry is merely to determine whether or not that method is "generally accepted" as reliable by the scientific community. *Id.*

226. 235 Cal. App. 3d 836 (1991).

227. *Id.* at 862.

228. *Id.* The appellate court also cited the district court's opinion in *U.S. v. Jakobetz* for similar reasoning. *Id.* The reference to the federal district court is interesting. In the district court's decision, the court found that flaws that may exist in the application of DNA profiling in the particular case are issues of admissibility rather than issues of weight for the jury to decide. United States v. Jakobetz, 747 F. Supp. 250, 257 n.16 (D. Vt. 1990). However, upon review (and after the *Axell* case), the federal appellate court stated, "The district court should focus on whether accepted protocol was adequately followed in a specific case, but the court, in exercising its discretion, should be mindful that this issue should go more to the weight than to the admissibility of the evidence." Jakobetz, 955 F.2d 786, 800. (2d Cir. 1992). *See* People v. Barney, 8 Cal. App. 4th 798, 823-25 (1992).

demonstrated its confusion as to "correct" versus "correctly" by citing *People v. Kaurish*[229] to allege that the California Supreme Court, before its *Cooper* decision, applied *Kelly-Frye* to procedures used "correctly."[230] In *Kaurish*, the court was concerned with the reliability of the electrophoresis test;[231] it was not concerned with whether it was used "correctly" as the *Axell* court had inferred.[232] Moreover, the supreme court in *Cooper*, as noted above, specifically dismissed any argument that errors in the testing process were subject to *Kelly-Frye*.[233] As such, it appears that until the California Supreme Court grants review on a DNA case, the California Court of Appeals will remain at odds with the California Supreme Court's interpretation of the third prong of the *Kelly-Frye* test in regards to DNA evidence.[234]

c. *Kelly-Frye* and Population Frequency Data. In non-DNA cases, the California Supreme Court has traditionally admitted population frequency data without a *Kelly-Frye* inquiry.[235] After a review of these cases, however, the Court of Appeals in *People v. Axell* refused to admit DNA population frequency statistics without a *Kelly-Frye* inquiry.[236] Although the *Axell* court conducted a *Kelly-Frye* inquiry, which found the statistical procedures used to be generally accepted, and admitted the DNA evidence, it curiously dismissed settled California supreme and appellate court case law which held methods for calculating population frequency data to be sufficient

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229. 802 P.2d. 278 (Cal. 1990).

230. *Axell*, 235 Cal. App. 3d at 862 ("[T]he [California Supreme] court still listed this third requirement as a subject of the hearing on admissibility in *People v. Kaurish*, even though it stated that *careless* testing affects the weight of the evidence and not its admissibility in *People v. Cooper*.") (emphasis added) (citations omitted).

231. A process where cellular components withdrawn from biological evidence are separated.

232. *Kaurish*, 802 P.2d 278, 318 (Cal. 1990); *see* Axell, 235 Cal. App. 3d at 862.

233. People v. Cooper, 809 P.2d 865, 908 (Cal. 1991) ("[T]he *Kelly/Frye* rule tests the fundamental validity of a new scientific methodology, not the degree of professionalism with which it is applied. Careless testing affects the weight of the evidence and not its admissibility. . . .") (citation omitted) (citing *Farmer*, 765 P.2d at 965)).

234. There are only four published opinions in California (all on the appellate level) which rule on the admissibility of DNA identification evidence. *See* Axell, 235 Cal. App. 3d 836; Barney, 8 Cal. App. 4th 798 (1992); *Pizarro*, 10 Cal. App. 4th 57; People v. Wallace, 14 Cal. App. 4th 651 (1993). However, it is important to note that the California Supreme Court refused to certify for publication the appellate court's discussion of DNA testing in *People v. Littleton*. People v. Littleton, 9 Cal. Rptr. 2d 288, 288 n.* (1992).

235. *See* People v. Brown, 709 P.2d 440, 464 n.6 (Cal. 1985) (statistical use of blood/semen stain-typing evidence); People v. Coleman, 459 P.2d 1160, 1289-90 n.23 (Cal. 1988), *cert. denied*, Coleman v. California, 489 U.S. 1100 (1989) (statistical use of ABO blood typing evidence).

236. *Axell*, 235 Cal. App. 3d at 866-67. "[T]he calculation of statistical probability is an integral part of the process and the *underlying method* of arriving at that calculation must muster pass under *Kelly-Frye*." *Id.* (emphasis added). It is important to note that the *Axell* court found the "underlying method" utilized (by Cellmark Diagnostics) in this case to be "generally accepted" under the *Kelly-Frye* test. *Id.* at 868.

without a *Kelly-Frye* hearing.[237] In fact, the California Supreme Court in *People v. Brown*,[238] a case cited in *Axell*, specifically noted that population frequency data was traditionally admitted in both California and other jurisdictions.[239]

Furthermore, in a post-*Axell*, non-DNA decision, the California Supreme Court in *People v. Fierro* specifically dismissed a defendant's claim that population frequency data was inadmissible without a *Kelly-Frye* hearing.[240] The court noted that "[b]oth California and the majority of other jurisdictions have traditionally admitted statistical blood-group evidence."[241]

Even with the guidance of the supreme court in these non-DNA cases, Justice Chin of the California Court of Appeals in *People v. Barney*, nevertheless agreed with *People v. Axell* and concluded that population frequency data calculations must be subject to a *Kelly-Frye* hearing.[242] With *Axell*'s apparently misplaced interpretation of *Kelly-Frye* in the context of population frequency data, the *Barney* court was ripe to find controversy in the wake of the NRC report. With citations to both the NRC report and the *Science* articles, the court found "disagreement between two groups, each significant in both number and expertise."[243] Accordingly, the appellate court found a lack of general acceptance regarding the frequency calculation method and held the DNA evidence inadmissible.[244] Remarkably, the court went beyond whether the admissibility of population frequency data should be subject to the *Kelly-Frye* standard. The court determined that the issue

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237. *Id.* at 866-67. *See, e.g.*, People v. Brown, 709 P.2d 440 (Cal. 1985) (statistical evidence not applicable under the general acceptance test of *Kelly* or *Frye*); People v. Gallego, 802 P.2d 169 (Cal. 1990); People v. Yorba, 257 Cal. Rptr. 641 (1989); People v. Coleman, 759 P.2d 1260 (Cal. 1988); People v. Poggi, 753 P.2d 1082 (Cal. 1988). *See also* People v. Collins, 438 P.2d 33, 36 (Cal. 1968) (statistical evidence must be "critically examined" considering the possible unfairness to a defendant which might result from presenting erroneous methods to a jury).

238. 709 P.2d 440.

239. *Id.* at 536 n.6.

240. People v. Fierro, 821 P.2d 1302, 1344 (Cal. 1991).

241. *Id.* (citing People v. Brown, 40 Cal. 3d at 536 n.6). Many other jurisdictions admit population frequency data without a *Frye* related hearing. *See, e.g.*, Prater v. State, 820 S.W.2d 429, 439 (Ark. 1991); Martinez v. State, 549 So. 2d 694, 696-97 (Fla. 1989); Caldwell v. State, 393 S.E.2d 436, 444 (Ga. 1990); State v. Montalbo, 828 P.2d 1274, 1282 (Haw. 1992); People v. Miles, 577 N.E.2d 477, 485 (Ill. 1991); People v. Lipscomb, 574 N.E.2d 1345, 1359-1360 (Ill. App. Ct. 1991); State v. Brown, 470 N.W.2d 30, 33 (Iowa 1991); Smith v. Deppish, 807 P.2d 144, 159 (Kan. 1991); Cobey v. State, 559 A.2d 391, 398 (Ma. Ct. Spec. App. 1989); People v. Adams, 489 N.W.2d 192, 197-98 (Mich. 1992); People v. Wesley, 589 N.Y.S.2d 197, 201 (N.Y. App. Div. 1992); State v. Pierce, 597 N.E.2d 107, 114-115 (Ohio 1992); Commonwealth v. Rogers, 605 A.2d 1228, 1236 n.10 (Pa. Super. Ct. 1992); Kelly v. State, 824 S.W.2d 568, 574 (Tex. Crim. App. 1992); Satcher v. Commonwealth, 421 S.E.2d 821, 833-34 (Va. 1992); United States v. Jakobetz, 955 F.2d 786, 799 (2d Cir. 1992).

242. People v. Barney, 8 Cal. App. 4th 798, 823 (1992); *see also Pizarro*, 10 Cal. App. 4th 57 (questioning whether the statistical significance of a DNA match has been generally accepted).

243. *Barney*, 8 Cal. App. 4th at 819; Clarke, *supra* note 9, at 10.

244. *Barney*, 8 Cal. App. 4th at 819. The California Supreme Court denied review on November 25, 1992.

was whether the NRC's frequency calculation method would eventually be generally accepted, and if so, then DNA analysis should be admissible in California.[245] More recently, on March 25, 1993, in another opinion by Justice Chin, the appellate court in *People v. Wallace* again subjected population frequency data calculations to a *Kelly-Frye* inquiry.[246] Justice Chin found that a "raging" debate still existed among population geneticists regarding population frequency calculations and held the evidence inadmissible.[247]

With such reasoning, the California Court of Appeals has seemingly reached a paradoxical conclusion. Although the *Barney* court felt that the significance of a DNA match was the "pivotal element of DNA analysis," to inform a jury of the probability of such a match was prohibited.[248] However, that conclusion was specifically refuted by the NRC report which noted that "even with today's technology, which used 3-5 loci, a match between two DNA patterns can be considered strong evidence that the two samples came from the same source."[249]

Thus, the California appellate courts have deviated from the state's supreme court case law as well as case law from many other states, which support the admission of population statistics under the multiplication rule without a *Kelly-Frye* or similarly related inquiry.[250] At least in DNA cases, the court of appeals has essentially subjected the methodology of the multiplication rule to *Kelly-Frye*.[251] Rather than allowing the statistical results of the multiplication rule to apply to the evidence's weight, as the California supreme court has done in blood-typing cases,[252] the appellate courts have chosen instead to make the multiplication rule in the DNA context an issue of admissibility.[253] This is most significant in that agreement over a particular probability is likely to be difficult in any complex scientific subject.[254]

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245. *Id.* at 822.

246. People v. Wallace, 14 Cal. App. 4th 651 (1993).

247. *Id.* at 659.

248. Barney, 8 Cal. App. 4th at 817, 825 (citing DNA Technology, *supra* note 15, at 74). The Court of Appeals in *Barney* held any evidence of inclusionary DNA test results must be banned from the jury. *Id.*

249. DNA Technology, *supra* note 15, at 74.

250. *See supra* note 249.

251. *See supra* text accompanying note 250.

252. *See supra* note 243.

253. The multiplication rule is not a new or novel technique, although its application to DNA typing is. Thompson & Ford, *supra* note 5, at 54; *see* DNA Technology, *supra* note 15, at 77.

254. *See* Daubert v. Merrell Dow Pharmaceuticals, Inc., 113 S. Ct. 2786, 2795 (1993) ("arguably, there are no certainties in science.").

IV. A FORWARD LOOK AT DNA STATISTICAL EVIDENCE

Due to the complexity and significant debate surrounding DNA evidence, particularly the statistical calculations, its basic value in the truth-seeking process of our judicial system has been overlooked. Rather than questioning the gap between the numbers of two opposing scientific groups, courts should realize that there exists some number that everyone can agree on. Furthermore, even beyond the obviousness of this concept, DNA critics Lewontin and Hartl have apparently reiterated their original opinion on population subgroups and inadvertently suffered a major breakdown in their original argument.[255]

A. A Conservative Consensus

Considering the support that the OTA, the NRC, and the vast case law have given to DNA evidence, there is little doubt that it is strong evidence.[256] The only real question, as the court in *U.S. v Porter*[257] stated, is "how strong?"[258] The *Porter* court, which could not find general acceptance among scientists for the probabilities put forth by the prosecution, noticed the absence of an inquiry as to whether a consensus existed for a more conservative number.[259] If the odds against a coincidental match are substantial, then the jury should know. Yet, the odds "do not have to be thirty million to one for evidence of the match to be admissible."[260] Even with the current questioning surrounding population frequency data, there remains room for a consensus among scientists with more conservative numbers.[261]

Using this line of reasoning and acknowledging the debate between the scientists over the effect of population subgroups on the multiplication rule, the court in *People v. Mohit*[262] asked, "[s]houldn't the jury know that there was a match and that the possibility of the perpetrator being someone other than the defendant is remote, even if it is difficult to say precisely how remote?"[263] If one side claimed that the odds of a match are one in one million and the other side claims that the odds are only one in 100,000, then, as stated by the *Mofit* court, "no credible segment of the scientific communi-

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255. *See infra* Part IV.b.

256. *See* DNA Technology, note 15, at 74 ("a match between two DNA patterns can be considered strong evidence that the two samples came from the same source.").

257. 618 A.2d 629 (D.C. 1992).

258. *Id.* at 641.

259. *Id.*

260. *Id.*

261. *See* State v. Vandebogart, 616 A.2d 483, 494 (N.H. 1992) (remanding the case to determine if a consensus could be reached on the NRC's technique).

262. 579 N.Y.S.2d 990 (N.Y. Sup. Ct. 1992.)

263. *Id.* at 993, 996-98.

ty would claim that the probability estimates . . . in this case or any other could be higher than one in 100,000."[264] As such, the *Mofit* court admitted the probability calculations based on more conservative numbers than the prosecution had proposed.[265] In *Caldwell v. State*, the prosecution's experts stated that the odds of a random match were one in 24 million while the defense experts claimed that the odds were only one in 250,000.[266] Finding agreement among all the scientists that the odds were at least in line with the "more conservative" figure of one in 250,000, the *Caldwell* court admitted the evidence.[267]

The reasoning of the *Mofit* and *Caldwell* courts directly applies to the current scientific debate which seems to center on whether to use calculations supported by the NRC report versus the calculations used by the FBI and other labs. There appears to be no reason not to admit at least the more conservative numbers espoused by the NRC since all those in the field accept the NRC's calculations—even if some scientist believe them to be too conservative. As long as some agreed upon number can be put forth which will help establish the fact in controversy, it should go to the jury to determine its reliability.[268]

Excluding DNA evidence entirely, because of disagreement over its strength, is contrary to our adversarial system of justice. "A criminal trial is not a game, but a quest for truth."[269] Only rarely, should a factual determination be excluded from jury consideration. With safeguards built in, the judicial system is designed for the jury to hear and weigh all the relevant evidence. A vigorous cross-examination, qualification of expert witnesses, careful instructions on the burden of proof, and contrary evidence from other experts are all means for DNA evidence to be attacked which allows the jury to make its own factual determination of reliability.[270] If scientific or specialized knowledge will assist the jury to understand the evidence or to determine a fact in issue, then an expert should testify.[271]

Unfortunately, the adversarial nature of the justice system has not always seemed so clear when a court is faced with the complexity of the science

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264. *Id.* at 999.

265. *Id.*

266. Caldwell v. State, 393 S.E.2d 436, 443-44 (Ga. 1990).

267. *Id.*; *see* People v. Wesley, 589 N.Y.S.2d 197, 259 (N.Y. App. Div. 1992) (holding the more conservative frequency calculations admissible). *But see also* United States v. Porter, 618 A.2d 629 (D.C. Ct. App. 1992) (court follows the reasoning from *Mofit*, but was unable to find a consensus).

268. *Porter*, 618 A.2d at 641. For other DNA cases admitting population statistics *see* Smith v. Deppish, 807 P.2d 144, 157-59 (Kan. 1991); Martinez v. State, 549 So. 2d 694, 696-97 (Fla. Dist. Ct. App. 1989).

269. *Porter*, 618 A.2d at 640 (quoting Womack v. United States, 350 A.2d 381, 383 (D.C. 1976)).

270. United States v. Jakobetz, 955 F.2d 786, 800 (2d Cir. 1992); *similarly see supra* text accompanying note 147.

271. Daubert v. Merrell Dow Pharmaceuticals, Inc., 113 S. Ct. 2786, 2795 (1993).

behind DNA evidence. In *People v. Barney,* the California Court of Appeal's leeriness of juror capability was clear:

> [W]e cannot reasonably ask the average juror to decide such arcane questions as whether genetic substructuring and linkage disequilibrium preclude use of the Hardy-Weinberg equation and the product rule, when we ourselves have struggled to grasp these concepts. The result would be predictable. The jury would simply skip to the bottom line—the only aspect of the process that is readily understood—and look at the ultimate expression of match probability, without competently assessing the reliability of the process by which the laboratory got to the bottom line.[272]

American jurors, however, are routinely asked to resolve complex issues involving scientific evidence. Appraisal methodologies in eminent domain actions, actuarial estimates in wrongful death suits, expert opinions regarding surgical care in malpractice suits, and expert opinions concerning the proper functioning of breath alcohol instruments in driving under the influence cases are some of the many examples where jurors decide questions based on difficult questions in esoteric fields.[273] Moreover, in *United States v. Jakobetz,* the Second Circuit stated, "we do not think that a jury will be so dazzled or swayed as to ignore evidence suggesting that an experiment was improperly conducted or that testing procedures have not been established."[274]

B. Lewontin's & Hartl's Reiteration:

As stated earlier, much of the current debate over which statistical method most accurately reflects the odds of a DNA match stems from a series of articles in the journal *Science.*[275] Recently, in the April 23, 1993 issue of *Science,* Dr. Hartl and Dr. Lewontin responded to attacks on their article and the NRC report.[276] In their response, Hartl and Lewontin revised their earlier opinion regarding population substructuring.[277] In their original article of December 20, 1991, they concluded that the use of the multiplication rule was unjustified since the existence of subpopulations marred the results.[278] Hartl and Lewontin had supported this hypothesis with test results that led them to state that there is on average one-third more

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272. People v. Barney, 8 Cal. App. 4th 798, 817 (1992).

273. *See supra* note 152.

274. *Jakobetz,* 955 F.2d at 797.

275. *See supra* text accompanying notes 61-64.

276. Daniel L. Hartl & Richard C. Lewontin, *DNA Fingerprinting Report* (Letter), 260 SCIENCE 473, 474 (1993).

277. *Id.; see supra* text accompanying note 72.

278. Lewontin & Hartl, *supra* note 58, at 1748-49.

genetic variation among ethnic groups than there is between races.[279] While still using the same data, they now conclude "that there is approximately as much genetic variation among ethnic groups within major races as there is among the races."[280] Curiously, their new opinion suggests that there is approximately one-third more variation among races than among ethnic groups within major races.[281] This reversal of opinion, according to Dr. Chakraborty, "should be sufficient to illustrate that the effect of population substructuring has little impact on the significance attached to DNA profile match found in forensic case analyses."[282]

Additionally, Hartl and Lewontin argue that their new analysis demonstrates that current methods of statistical calculations are prejudiced against the defendant, and "no amount of argument will make them conservative."[283] However, in response to the Lewontin & Hartl letter, scientists from Yale University pointed out that Lewontin and Hartl were apparently misled by their inadequate data.[284] Specifically, they found Hartl's conclusion that using a cognate database[285] will induce a large upward bias in the estimated probability to be in error.[286] Hartl's data, they noted, used such small samples that an individual's profile within the cognate database artificially increased the estimated probability.[287] The small sample size created large correlations among the allele probabilities which yielded a higher probability in the cognate database than in the noncognate database[288] Thus, the Yale scientists state that Hartl and Lewontin "again imbue a statistical artifact with a population genetic meaning . . ."[289]

The impact of these recent letters in *Science* goes to the heart of the DNA population frequency debate. It was the force behind Lewontin's and Hartl's original articles and studies back in 1991 that brought attention to the possible effect of population substructuring on the multiplication rule.[290] Their hypothesis alleged that subgroups share differing genetic structure from

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279. *Id.* at 1747.

280. Hartl & Lewontin, *supra* note 276, at 474.

281. *Id.*

282. Ranajit Chakraborty, *NCR Report on DNA Typing* (Letter), 260 SCIENCE 1059 (1993).

283. Hartl & Lewontin, *supra* note 276, at 474.

284. B. Devlin et al., *NRC Report On DNA Typing* (Letter), 260 SCIENCE 1057, 1058 (1993). Devlin *et al.*, chose not to belabor Hartl and Lewontin's first hypothesis since Chakraborty and Kidd had previously shown Hartl and Lewontin's results to be "artifacts of using inappropriate data." *Id.*

285. A "cognate database" matches the DNA type with a database of the same ethnic group, i.e., an Italian DNA profile would use a database made up of Italians.

286. *Id.*

287. *Id.*

288. *Id.*

289. *Id.* The scientists went on to state the NRC's proposed study of population substructure, using small sample sizes, would be inadequate for the same reasons. *Id.*

290. *See* Lewontin & Hartl, *supra* note 58; DNA Technology, *supra* note 13, at 80 & n.10; *see also* People v. Barney, 8 Cal. App. 4th 798, 818-20 (1992).

the rest of the population which, if not considered, invalidates the results of the multiplication rule. From such a hypothesis, they vigorously opposed current DNA identification methods which has led courts now to question and even reject DNA evidence. The importance of Lewontin and Hartl's article is evidenced by the judicial reliance on it.[291] In *People v. Barney,* the court reviewed Lewontin's and Hartl's hypothesis and its criticism by Chakraborty and Kidd and subsequently stated that the debate "changes the scientific landscape considerably, and demonstrates indisputably that there is no general acceptance of the current process."[292] The *Barney* court found that the studies and opinion by Lewontin and Hartl had "eclipsed" the court's finding in *Axell*[293] that there was general acceptance for the population frequency calculations. In *U.S. v. Porter,* the trial court held the DNA evidence inadmissible noting the "substantial controversy among distinguished scientists as to the soundness of certain assumptions on which [the frequency] calculation was predicated."[294]

Lewontin's and Hartl's recent reversal of opinion represents a major breakdown in their population substructuring theory. By saying that there is at least as much genetic variation among ethnic groups as there is among major races, Lewontin and Hartl have abandoned the idea that subgroups affect the multiplication rule. Essentially, their data yields the same conclusion that Chakraborty, Kidd and the NRC committee found—any effect of population substructure on the multiplication rule's reliability is negligible.[295] The judicial impact of Lewontin's and Hartl's revised opinion has yet to be felt. Over the last two years, the debate, which has led courts to find a lack of general acceptance, has centered around their original contention that subpopulations vary more than major races. Their reversal will likely impact the future debate regarding population substructure and DNA evidence.

Furthermore, Dr. Chakraborty responded with new data in the May 21, 1993 issue of *Science* to Hartl and Lewontin's letter of April 23.[296] Chakraborty cited new studies which examined the regional differences within racial groups more closely in regard to DNA markers. These new studies support the earlier opinion, with which Hartl and Lewontin now agree, that genetic differentiation among subgroups has a negligible effect on

291. *See, e.g., Barney,* 8 Cal. App. 4th at 818-20.

292. *Id.*

293. *Id.* at 820-21.

294. United States v. Porter, 618 A.2d 629, 636 (D.C. App. Ct. 1992). For other decisions excluding DNA evidence due to the controversy behind the Lewontin and Hartl article *see* Commonwealth v. Lanigan, 596 N.E.2d 311, 315-16 (Mass. 1992); State v. Vandebogart, 616 A.2d 483, 493-94 (N.H. 1992); State v. Houser, 490 N.W.2d 168, 182-85 (Neb. 1992).

295. *See* DNA Technology, *supra* note 15, at 80. *See also* Chakraborty & Kidd, *supra* note 43, at 1738.

296. Chakraborty, *supra,* note 282, at 1059.

the multiplication rule.[297] Such data, Chakraborty states, "appears to provide adequate justification for the current forensic practice in relation to legal applications of DNA typing."[298] In addition, initial data from these studies indicates that variation between individual DNA profiles is so large that it "dwarfs" any differences between populations.[299] This conclusion supports the independency of allele frequencies needed for the multiplication rule. In fact, based on this data, Chakraborty concluded that the rarity of each multilocus DNA sequence "virtually eliminates the possibility of miscarriage of justice when a match is observed over three or more loci."[300]

CONCLUSION

Since DNA evidence was first used in the American court system in 1986, critics have questioned its reliability. Initially, the soundness and the theory behind DNA technology was challenged. Disproved, and DNA theory intact, critics have tried in recent years to attack the probabilities associated with a DNA match. Finding a group of well-qualified genetic scientists with a small amount of preliminary data indicating that DNA probability matches may not be as extreme as thought, critics have propelled these scientists and their opinions to the forefront of DNA admissibility.

At the forefront, judges must decide whether to admit the DNA evidence or to subject it to an admissibility standard, such as the *Frye* standard. Although several courts have admitted DNA evidence and its frequency data without such an inquiry, many other courts have considered the frequency data an integral part of DNA evidence and subjected it to a *Frye*-like inquiry. In spite of this, these same courts will admit, without a *Frye* hearing, the expert testimony and test results in non-DNA cases, such as, a blood alcohol test where the margin of error can vary greatly from person to person. The court will then admit the results and leave the probability of error to the weight of the evidence. Why should the result be any different with DNA evidence?

Although DNA evidence may be complex, and even questionable to many people, that does not justify its inadmissibility. The justice system was designed for juries to be able to hear relevant, but possibly questionable scientific evidence. The qualification of experts, an extensive cross-examination, presentation of contrary evidence, and careful instructions on the burden of proof are all means to attack DNA evidence and its probabilities. Withholding DNA evidence altogether, because expert opinions may

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297. *Id.*
298. *Id.*
299. *Id.*
300. *Id.*

differ on the odds of match, is contrary to the fact-finding function of the jury and the truth seeking nature of the justice system.

In addition, it should not be overlooked, that the NRC report, which has received so much judicial deference, could not upon its own inquiry find any appreciable effect of subpopulations on the multiplication rule. Moreover, scientists such as Lewontin and Hartl, who helped create most of the current debate on population frequencies, have suffered a major breakdown in their original hypothesis. Upon closer study of their original data, they have reiterated what their opponents, such as Chakraborty and Kidd have been saying all along: that subpopulations vary genetically as much as the larger populations thus having a negligible effect on DNA population frequencies.

Finally, no one is disputing that some number should be admitted. As far as a reasonable doubt is concerned, there is really very little difference between one in a million and one in 100 million, or one in a million and one in a 100,000. Furthermore, when experts disagree on a number, why not allow the jury to see the more conservative number. This is only common sense. For example, if prosecution experts were to testify that the chance of a duplicate DNA match was one in two million, but defense experts testified that the odds of a match are closer to one in 200,000, certainly the prosecution experts would agree that the chance of a match is *at least* as small as a one in 200,000. Either way, the statistical evidence assists with the strength of the evidence and should go to the jury. There is no requirement that the odds of a coincidental DNA match need to be 50 million to one for it to be admissible. Such a view stigmatizes DNA evidence as the magic bullet—which it is not. What it is, and remains, is "a highly discriminating, very reliable piece of evidence."[301]

*R. Stephen Kramer**

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301. Sherman, *supra*, note 6, at 30 (Statement of John Hicks, Director of the F.B.I. Crime Laboratory).