North Dakota Law Review

Volume 72 | Number 3 Article 6

1996

How Should North Dakota Approach the Admissibility of DNA: A Comprehensive Analysis of How Other Courts Approach the Admissibility of DNA

Michael A. Riley

HOW SHOULD NORTH DAKOTA APPROACH THE ADMISSIBILITY OF DNA: A COMPREHENSIVE ANALYSIS OF HOW OTHER COURTS APPROACH THE ADMISSIBILITY OF DNA

MICHAEL A. RILEY*

I. INTRODUCTION

The state of North Dakota has taken its first step towards the future of deoxyribonucleic acid (DNA) in their courts. On April 3, 1995, the Legislature passed Chapter 31-13, which allows for DNA testing of criminals convicted of sexual offenses and establishes a database to store the results of those DNA tests.[1] As a result, North Dakota will be confronted with DNA evidence in the near future. This paper will analyze the basic concepts behind DNA, the admissibility of scientific evidence, and the decisions of other courts that have ruled on the admissibility of DNA. This analysis will hopefully assist the development of this complicated legal issue in North Dakota.

---

* B.A., 1991, Saint Mary's College of Minnesota; M.S., 1994, University of North Dakota School of Medicine; J.D., 1995, University of North Dakota School of Law.

1. N.D. CENT. CODE ch. 31-13 (Supp. 1995). The definitions section provides that "'Department' means the department of corrections and rehabilitation. . . . 'Division' means the forensic science division of the department of health. . . . [and] 'DNA' means deoxyribonucleic acid." *Id.* § 31-13-01. Section 31-13-02, regarding admissibility of DNA testing as evidence, provides:

> In any court proceeding, DNA testing is deemed to be a reliable scientific technique, and the evidence of a DNA profile comparison must be admitted as prima facie evidence to prove or disprove the identity of any person. This section does not otherwise limit the introduction of any relevant evidence bearing upon any question at issue before the court. The court, regardless of the results of the DNA analysis, if any, shall consider other relevant evidence of the identity of the person as is admissible in evidence.

Section 31-13-03, regarding persons to be tested and costs, provides:

> The court shall order any person convicted on or after August 1, 1995, of any sexual offense or attempted sexual offense in violation of sections 12.1-20-03, 12.1-20-04, 12.1-20-05, 12.1-20-06, subdivision e or f of subsection 1 of section 12.1-20-07, or section 12.1-20-11 or any other offense when the court finds at sentencing that the person engaged in a nonconsensual sexual act or sexual contact with another person during, in the course of, or as a result of, the offense and any person who is in the custody of the department on or after August 1, 1995, as a result of a conviction of one of these offenses to have a sample of blood and other body fluids taken by the department for DNA law enforcement identification purposes and inclusion in law enforcement identification data bases. Notwithstanding any other provision of law, if the sentencing court has not previously ordered a sample of blood and other body fluids to be taken, the court retains jurisdiction and authority to enter an order that the convicted person provide a sample of blood and other body fluids as required by this section. Any person convicted on or after August 1, 1995, who is not sentenced to a term of confinement shall provide a sample of blood and other body fluids as a condition of the sentence or probation at a time and place specified by the sentencing court. The cost of the procedure must be assessed to the person being tested.

II. THEORY AND PROCEDURE BEHIND DNA ANALYSIS

A. TECHNICAL CONSIDERATIONS

The human body consists of trillions of cells.[2] Each of those cells, except red blood cells, contains a nucleus.[3] In each nucleus, there is an identical copy of each person's DNA.[4] This DNA is stored in 46 different units called chromosomes.[5] Each of these chromosomes has a partner, thus there are 23 different pairs of chromosomes.[6] These 46 chromosomes contain the universal code of life.[7] The code is very large and is responsible for transferring all of the genetic traits from one generation to the next.

The voluminous DNA code is able to accomplish this daunting task with only four different characters, called nucleotides.[8] These nucleotides are adenine (A), cytosine (C), guanine (G), and thymine (T).[9] The configuration of each chromosome consists of two continuous complimentary strands of these four nucleotides.[10] The two complimentary strands of DNA are bound together by bonds between the nucleotides and a phosphate backbone.[11] This is accomplished because the nucleotides can only be combined together in one particular way; adenine and thymine bind together and cytosine and guanine bind together.[12] When a pair of bases on two DNA strands match up with each other, they are called complimentary.[13] When bases are bound together, they are called a base pair.[14] This long molecule is known as the double helix or double stranded DNA.[15] The backbone of the double helix is made of alternating sugars and negatively charged phosphate groups.[16] This

---

2. SIMON EASTEAL ET. AL., DNA PROFILING: PRINCIPLES, PITFALLS AND POTENTIAL 8 (1991).
3. *Id.*
4. *Id.*
5. *Id.* at 9.
6. *Id.*
7. COMMITTEE ON DNA TECHNOLOGY IN FORENSIC SCIENCE ET AL., DNA TECHNOLOGY IN FORENSIC SCIENCE 2 (1992) [hereinafter DNA TECHNOLOGY].
8. *Id.*
9. *Id.*
10. EASTEAL, *supra* note 2, at 12.
11. BENJAMIN LEWIN, GENES IV 65 (1990). The As from the first strand will bind with the Ts from the second strand and the Gs with the Cs. *Id.* at 64. As and Gs are called purines and Cs and Ts are called pyrimidines. *Id.* at 65. The purines are the same size and the pyrimidines are the same size, because there is always one purine and one pyrimidine in every base pair, the double helix strand maintains a constant width. EASTEAL, *supra* note 2, at 14.
12. LEWIN, *supra* note 11, at 64.
13. *Id.*
14. EASTEAL, *supra* note 2, at 12.
15. *Id.* at 12.
16. *Id.* at 13. *See infra* notes 45-9 and accompanying text (discussing the importance of the negative charge to the separation of DNA fragments).

continuous double stranded DNA molecule is coiled tightly within the chromosome in order to fit all 46 chromosomes into the nucleus of each cell.[17]

The long DNA molecules are organized into genes.[18] Genes are the regions of the long DNA molecule that code for specific proteins.[19] Of the over 6 billion base pairs found in the 46 chromosomes, only about fifteen percent of the DNA is essential genetic information.[20] The other eighty-five percent, or non-coding regions, contain regions that consist of variable sized sequences of repeating DNA that occur one after another.[21] The regions of long-repeating sequences of DNA are called variable number tandem repeats (VNTR).[22] These tandem repeats allow DNA to be used as a tool for identification.[23] This is because the number of times a sequence of DNA repeats in any VNTR region varies between different individuals, this variation even occurs between a pair of chromosomes found in the same nucleus. Thus, DNA profiling is an excellent tool for the identification and exclusion of individuals.[24] It is the uniqueness in the length of the VNTR regions that allows for identification.[25]

One more aspect of DNA needs to be understood before we begin a discussion on profiling. There is a class of enzymes which is able to cut double stranded DNA molecules at specific sites.[26] These enzymes are called restriction endonucleases, but are more commonly referred to as restriction enzymes.[27] Restriction enzymes will recognize only a specific sequence of DNA and make a cut anywhere on the DNA molecule where that specific sequence of base pairs is present.[28]

This basic understanding of DNA and restriction enzymes will assist in our analysis of the processes used and the statistics behind DNA profiling.

---

17. EASTEAL, *supra* note 2, at 12. It is important that the DNA be packaged very tightly. *Id.* If the molecules were lined up end to end, the total length of the DNA in each nucleus would be about two meters in length. *Id.*

18. DNA TECHNOLOGY, *supra* note 7, at 2.

19. EASTEAL, *supra* note 2, at 194.

20. *Id.* at 23.

21. *Id.* For example, the sequence TAGGAT could be repeated millions of times. These small repeating segments are usually around 15-30 base pairs in length. *Id.*

22. *Id.* at 24. VNTR regions have many tandem repeats. *Id.*

23. *Id.* at 25.

24. EASTEAL, *supra* note 2, at 25.

25. *Id.* at 43.

26. *Id.* at 19.

27. *Id.* There are many types of restriction enzymes that recognize many different sequences of DNA. *Id.*

28. *Id.* For example, if there is a restriction enzyme that recognizes the sequence AAGGAA, every time the restriction enzyme comes across this sequence in the DNA, it will bind to that sequence and cut the DNA at that specific site. *See id.*

B. PROFILING WITH RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS

As we have seen in the previous section, there are certain properties of DNA that make it an excellent tool for identification: (1) the DNA molecule has sequences in the non-coding regions which have VNTRs;[29] (2) the DNA molecule can be cut at specific, selected sites;[30] and (3) the length of the restriction fragments can be measured for identification.[31] Simply stated, cutting the DNA molecule with a specific restriction enzyme leaves different sized restriction fragments. These restriction fragments will have different sizes depending on an individual's DNA make up. Because of this variance in the restriction fragments between individuals, scientists are able to determine if a sample came from a specific individual. The combination of these properties allows the manipulation of the DNA molecule in a way that allows for identification. This process is known as restriction fragment length polymorphism (RFLP).[32]

There are approximately ten steps in the RFLP process.[33] These steps transform the DNA found in a given sample into a form that can be used for identification purposes.

The first of ten procedures involved in the RFLP method of DNA profiling is the collection of tissue from the crime scene, the victims, and the suspects.[34] Samples are compared with one another to see if there is a match. The matched samples are compared to databases in order to determine what the calculated frequency of a specific allelic pattern would be in the population. The result of which is the probability that someone other than the defendant left the tissue at the scene of a crime. Furthermore, it is also possible to take samples from a crime scene, run them through a database of past sex offenders, and determine if the tissue is from an individual who has previously committed a sex crime.[35]

The DNA is then extracted from all of the tissue samples.[36] There are three steps used to extract the DNA from these samples.[37] In the first

---

29. *See supra* notes 21-25 and accompanying text (discussing VNTRs and their usefulness in identification).

30. *See supra* note 26 and accompanying text.

31. *See supra* note 25 and accompanying text.

32. EASTEAL, *supra* note 2, at 20-21. This process measures and compares the lengths of the VNTR regions between two samples. *Id.*

33. *Id.* at 64.

34. *Id.*

35. *See supra* note 1 and accompanying text (discussing North Dakota Century Code section 31-13-03).

36. EASTEAL, *supra* note 2, at 64.

37. *Id.* at 51-52.

step, the cell membrane is broken up and the cellular proteins are inhibited to prevent destruction of the DNA.[38] The second step involves the removal of the cellular membrane and the cellular proteins.[39] The last step involves the precipitation of the DNA.[40] Once precipitated, the sample is then ready to be quantified to determine the amount of DNA.[41]

The DNA molecule is then digested with a restriction enzyme.[42] Recall from above that these restriction enzymes cut the DNA at specific sites.[43] This process cuts the DNA molecule at many known, specific sites, leaving many restriction fragments, each several hundred to several thousand base pairs in length.[44]

Next, the fragments from the digestion step need to be separated by size.[45] To accomplish this, the restriction fragments are moved through an agarose gel by creating an electric field across the gel.[46] This separation technique is called electrophoresis.[47] Because the phosphate backbone of the DNA molecule is negatively charged, the restriction fragments will migrate through the agarose gel.[48] The pores in the gel allow small molecules to move faster through the gel than larger molecules, creating the separation needed for identification.[49]

The next step is to denature the separated restriction fragments.[50] Denature, in this context, means to turn the double stranded DNA molecules into single stranded molecules; separating the base pairs from each other forms two single stranded restriction fragments.[51]

Once the DNA is denatured, it is then transferred to a specially treated nylon membrane.[52] The DNA is fixed to the nylon membrane by heat or ultraviolet light, depending on the type of nylon membrane

---

38. Michael A. Riley, Characterization of the Chromatin Structure of the SV40 Promoter Region by Deletional Analysis 33 (1994) (unpublished M. Sci. thesis, University of North Dakota); *see also* EASTEAL, *supra* note 2, at 51-52.

39. Riley, *supra* note 38, at 33; *see also* EASTEAL, *supra* note 2, at 52.

40. Riley, *supra* note 38, at 33. The purified DNA is then precipitated (taken out of solution) with 20% potassium acetate and 2.5 volumes of ice cold 100% ethanol. *Id.* This mixture is stored at -20 degrees Celsius for at least 4 hours. *Id*; *see also* EASTEAL, *supra* note 2, at 52.

41. Riley, *supra* note 38, at 33; *see also* EASTEAL, *supra* note 2, at 52.

42. EASTEAL, *supra* note 2, at 64.

43. *Id.* at 19.

44. DNA TECHNOLOGY, *supra* note 7, at 36.

45. EASTEAL, *supra* note 2, at 64.

46. *Id.* at 46.

47. *Id.*

48. *Id.* at 46-47.

49. DNA TECHNOLOGY, *supra* note 7, at 37.

50. EASTEAL, *supra* note 2, at 55.

51. *Id.* This is done by soaking the gel in a basic solution such as sodium hydroxide (NaOH).

52. *Id.* at 56. This membrane does not bind double stranded DNA molecules as well as it binds single stranded molecules. *Id.* at 55. This is to facilitate the binding of the radiolabled probe. *Id.* at 58.

used.[53] This is done to prevent the restriction fragments from becoming dissociated from the membrane during the rest of the procedure.[54] A radiolabled probe, which is designed to bind to a specific sequence of DNA, is washed over the nylon membrane.[55] The probes will bind to the restriction fragments because both are single stranded and under normal body pH and temperature conditions, DNA has an affinity for being double stranded.[56] By making the probe complimentary to the target DNA,[57] the radiolabled probe will bind only to the target restriction fragments it was designed for,[58] allowing only the desired restriction fragments to be observed during the identification stage.[59] This process is necessary because, if all of the restriction fragments were visible, they would appear as a smear on the x-ray film due to the fact that there are millions of restriction fragments bound to the nylon membrane.[60]

The next step is to expose the radiolabled restriction fragments to an X-ray film.[61] After a predetermined amount of time, the x-ray film is developed to reveal a banding pattern which represents the desired fragments called alleles.[62] It is these alleles that are used in the identification process. Because these alleles are so variable in size, their position on the x-ray film establishes identification.[63]

The final step involves an analysis of the allelic patterns to determine identification.[64] When the known sample is electrophoresed[65] alongside an unknown sample, it is easy to determine if there is a match because the position of the alleles will be the same for both the suspect and the sample taken from the victim or crime scene.[66] This would be called a match. Once there is a match, the allele size is determined and

---

53. *Id.* at 58.

54. *Id.*

55. EASTEAL, *supra* note 2, at 58. The nylon membrane will only bind the single stranded DNA. This is important because the radiolabled probe is also single stranded and complimentary to the target DNA. *Id.* at 59-60. Thus, when the two complimentary strands come together they will bind. *Id.* This allows us to identify the restriction fragments because the radiolabled probes are easily detected. *Id.* at 60.

56. *Id.* at 59.

57. *See supra* notes 9-14 and accompanying text (discussing base pairing on complimentary strands).

58. EASTEAL, *supra* note 2, at 59-60.

59. *Id.* at 60.

60. *Id.* at 62.

61. *Id.* This is called auto radiography and it is done in a light tight box by placing the x-ray film in direct contact with the nylon membrane. *Id.*

62. *Id.*

63. EASTEAL, *supra* note 2, at 63.

64. *Id.*

65. Electrophoreses is a process of separation where electrical current is applied across a medium causing charged molecules to move through the medium. *Id.* at 54. In this case the charged molecules are the DNA sample.

66. *Id.* at 87-90.

then compared with known databases to calculate population frequencies for that particular pattern.[67] It is these population frequencies which will indicate the probability that a random individual from the general population could have left the tissue sample containing the DNA.[68]

The above was a brief description of the RFLP process which is the first of two major steps in the preparation of DNA for use in the courts. The next section will deal with the statistics behind the use of DNA.

C. STATISTICAL BASIS FOR INTERPRETATION

When an allelic pattern is analyzed, there are three categories they can fall into: exclusion, inconclusive, and inclusion.[69] If a banding pattern is an exclusion, there is proof that the two samples did not come from the same source.[70] If the allelic pattern does not show banding, then the results are inconclusive and further investigation and experimentation needs to be done.[71] If the allelic pattern matches, it is an inclusion.[72] When there is an inclusion, the samples may have come from the same source, but the frequency of that pattern in the general population must also be determined.[73] This will give the probability that someone, other than the suspect, could have left the tissue sample at the crime scene. The strength of these calculations depends on the number of alleles tested and the frequency of those alleles in the general population.

The ceiling principle, as recommended by the Committee on DNA Technology in Forensic Science, otherwise known as the National Research Council (NRC),[74] is the most common method for determining population frequencies for a specific allelic pattern accepted by courts.[75] The acceptance of the ceiling principle is due to the conservative nature of the resulting probabilities.[76]

---

67. *Id.* at 90-91.

68. EASTEAL, *supra* note 2, at 90-91.

69. An individual's specific allelic pattern is called their genotype. *Id.* at 194. A genotype is the specific DNA make up of an individual. *Id.* Genotype is an individual's allelic pattern as observed on the exposed x-ray film.

70. DNA TECHNOLOGY, *supra* note 7, at 75.

71. *Id.*

72. *Id.*

73. *Id.*

74. This is the committee that authored DNA TECHNOLOGY IN FORENSIC SCIENCE (1992). *See supra* note 7.

75. This is the trend that I have discovered throughout the research that I did for this paper. The committee report is the most conservative way to calculate population frequencies which is why courts struggling with this issue usually adopt this method to afford the accused this benefit. *See* PAUL C. GIANNELLI & EDWARD J. IMWINKELRIED, SCIENTIFIC EVIDENCE § 17-8(E) (Supp. 1994) (listing court decisions directing DNA admissibility when the NRC recommendations are followed).

76. DNA TECHNOLOGY, *supra* note 7. The results of the ceiling principle approach, as recommended by the NRC report, are conservative because of the way in which they are calculated. This

There are three main steps for calculating population frequencies using the ceiling principle.[77] The first step is to determine the ceiling frequencies for the alleles found in similar bins.[78] This is accomplished by grouping all of the alleles into bins.[79] A bin is a range where alleles of different sizes can no longer be reliably distinguished from one another.[80] Once the bins are determined, the frequency of each bin is calculated.[81] The assumption is that the frequency calculated for a particular bin in the database, is a projection of the frequency of the general population.[82] Once the bin frequencies are determined, a ceiling is incorporated into the calculated frequencies.[83] The ceiling principle involves using several databases until a database of at least three of the major races; Caucasians, Blacks, Hispanics, Asians, and Native Americans can be studied.[84] Until the databases from the different race groups can be analyzed, the committee report suggests using a ten percent floor on the frequency.[85] The calculation for the frequency of each bin in the databases begins by determining which of the databases has the highest frequency for each of the bins.[86] This frequency will then be subjected to the ninety-five percent upper confidence limit (UCL) calculation.[87] If

approach does not use the suspect's observed genotypes to calculate the population frequency but rather it uses the higher of 10% or the highest observed genotype in the databases used. This means that the lowest possible value that can be used in calculating the frequency of one of the suspects observed genotypes will be 10%. Thus, if one of his observed genotypes is lower than 10%, the method of calculation recommended by the NRC will bring the value to at least 10%. This will substantially increase the chances that a random individual has the same overall observed genotype.

77. *Id.*

78. *Id.*

79. *Id.*

80. Bins can be either fixed or floating. David H. Kaye, *DNA Evidence: Probability, Population Genetics, and the Courts*, HARV. J. L. & TECH. 101, 102 (Fall 1993). The floating bin uses the suspects allele as the mark and then includes all alleles in the data base that fall within plus or minus a calculated number from the suspect allele. *Id.* at 122 n.95. The fixed bin uses a fixed length which is established by using a sizing ladder to determine what bin the suspect's DNA falls into. *Id.* at 122 n.96.

81. *Id.*

82. DNA TECHNOLOGY, *supra* note 7, at 85-86. It should be noted here that it is a good argument to claim that the database used was not in Hardy-Weinberg equilibrium, thus the calculated population frequencies will not be representative of the general population. Kaye, *supra* note 80, at 125 (citing several cases).

83. DNA TECHNOLOGY, *supra* note 7, at 86.

84. *Id.* at 91.

85. *Id.* at 92. Ten percent floor means that if a database has an observed allelic frequency where less than 10% of the database has that allele, then the lowest number the NRC would suggest would be 10%. *Id.* Thus, if only 5% of the alleles in the database have that genotype, the minimum number that should be allowed into the calculation should be 10% rather than the observed 5%. *Id.*

86. *Id.*

87. *Id.* The upper confidence limit is calculated by adding the 95% upper confidence limit (UCL) to the data base with the highest bin frequency. *Id.* The formula for calculating the 95% (UCL) is: $95\%\ UCL = p + 1.96\ \sqrt{[p(1-p) / N]}$, where p is the observed frequency in the data base with the highest bin frequency at the suspect's allele, and N is the number of chromosomes in the data base, or the number of individuals in the data base times two. *Id.* Basically, this means that there is a calculation done to the data to make it more reliable. This has the effect of making the calculation more favorable to a possible suspect.

this calculated allelic frequency is not greater than 0.10 (ten percent), then a default of 0.10 will be used.[88] Thus, if the highest bin frequency plus its calculated ninety-five percent UCL is below 0.10, such as 0.078, the calculated frequency defaults to 0.100.[89]

Once the ninety-five percent UCLs are calculated, we can compare the suspect's allelic pattern, or genotype, with the ceiling frequencies found in the databases.[90] This will reveal the frequency for the suspect's alleles in the databases.[91] Each person's paired chromosomes will give rise to two alleles, one at each of the VNTR regions on each chromosome.[92] The suspect's alleles are then compared with the other databases to determine their approximate frequency in the databases.[93]

The second step in implementing the ceiling principle is to calculate the frequency of each of the suspect's observed pair of alleles.[94] This formula will give the frequency of one observed pair of alleles.[95] This procedure is then done on each of the tested alleles to determine the frequency for each pair of the suspect's alleles.[96]

After frequencies have been determined for each pair of alleles, the third step of the ceiling principle involves calculating the frequency of the overall genotype.[97] This is accomplished by using the multiplication rule.[98] The multiplication rule will give the calculated frequency of the suspect's overall genotype in the general population.[99] This is accomplished by multiplying together each of the individual alleles that were calculated in the second step.[100] To obtain the number in the form that

---

88. DNA TECHNOLOGY, *supra* note 7, at 92.

89. *Id.* If one had three databases where the allele in question had UCL frequencies of 0.098, 0.087, and 0.219, one would select 0.219 because that is the highest frequency for the allele. *See id.* If the three databases had the following observed UCL frequencies 0.099, 0.023, and 0.009, one would take 0.100 as the observed frequency because none of the observed UCL frequencies were above the floor of 0.100. *Id.*

90. *Id.* at 81.

91. Kaye, *supra* note 80, at 124.

92. *Id.* The reason that you might not get two alleles is because an individual could be homozygous. *Id.* at 124, n.101. This means that both chromosomes have the same allelic form, or will migrate to the same place on the gel. EASTEAL, *supra* note 2, at 195.

93. Kaye, *supra* note 80, at 124. Remember, the frequencies in the databases are the projection for the general population.

94. *Id.* This is accomplished by using the formula [2(frequency of allele 1)(frequency of allele 2)]. DNA TECHNOLOGY, *supra* note 7, at 78. The factor of two in the formula is necessary to take into account the frequency that allele 1 comes from the father (P1) and allele 2 from the mother (P2) and then vise versa. *Id.*

95. DNA TECHNOLOGY, *supra* note 7, at 78.

96. *Id.*

97. *Id.*

98. *Id.* at 83. The multiplication rule is simply taking the calculated frequencies for each of the individuals allelic positions tested and multiply them by each other. *Id.*

99. Kaye, *supra* note 80, at 127. This is assuming that the databases are in Hardy-Weinberg equilibrium and that the different genotypes are not linked in any way. DNA TECHNOLOGY, *supra* note 7, at 78.

100. DNA TECHNOLOGY, *supra* note 7, at 83.

most people are accustomed to seeing, divide the resulting number into 1. This final number is the probability of selecting a random individual from the general population who has the same genotype as the suspect.

It is claimed that the ceiling principle approach reduces the chances of the data being undermined by population substructure.[101] Population substructure results from one race group having a specific set of alleles which does not have the same frequency as the rest of the population.[102] For example, if a certain ethnic group had an ordinarily low frequency at a specific allele, and this allele was compared to the general population, the probability of another person having that same allele would be extremely low. This would unfairly prejudice a suspect belonging to that ethnic group because the probability that someone else could have the same genotype would be lower than if compared to the general population, which would not have a low frequency for that specific allele. Thus, the ceiling principle allows for a method of calculating population frequencies which is independent of the race because frequencies automatically default to 0.100.[103]

III. ADMISSIBILITY OF SCIENTIFIC EVIDENCE IN THE COURTS AND ITS APPLICATION TO DNA

There are several tests used by different jurisdictions to determine the admissibility of scientific evidence. This section will outline and discuss what these tests are and the steps used by the courts in implementing these tests.

A. THE *FRYE* TEST

Many courts determine the admissibility of scientific evidence under *Frye v. United States*.[104] Currently, there are over fifteen states which have decided the admissibility of DNA using the *Frye* test.[105]

---

101. *Id.* at 92.

102. *See id.* at 79-80 (discussing concerns about population substructure).

103. *Id.* If the ceiling principle calculation is done on four different alleles, the greatest probability achievable is 1 in 6.25 million; three alleles would be 1 in 125,000 and two alleles would be 1 in 2500. This further demonstrates that even with the conservative nature of the NRC method, if you need to obtain a higher frequency you need to test more alleles because the more alleles tested greatly reduces the chance of finding someone else with the same genotype.

104. Frye v. United States, 293 F. 1013 (D.C. Cir. 1923).

105. *Ex parte* Perry, 586 So. 2d 242, 250 (Ala. 1991); Harmon v. State, 908 P.2d 434, 439 (Alaska Ct. App. 1995); State v. Bible, 858 P.2d 1152, 1181 (Ariz. 1993); Fishback v. People, 851 P.2d 884, 890 (Colo. 1993); Hayes v. State, 660 So. 2d 257, 262 (Fla. 1995); Caldwell v. State, 393 S.E.2d 436, 441 (Ga. 1990); State v. Montalbo, 828 P.2d 1274, 1280 (Haw. 1992); Franson v. Micelli, 645 N.E.2d 404, 406 (Ill. App. Ct. 1994), *judgment vacated on other grounds*, 666 N.E.2d 1188 (Ill. 1996); State v. Colbert, 896 P.2d 1089, 1097 (Kan. 1995); Commonwealth v. Lanigan, 641 N.E.2d 1342, 1348 (Mass. 1994); State v. Schwartz, 447 N.W.2d 422, 424 (Minn. 1989); State v. Davis, 814 S.W.2d 593,

Under the *Frye* standard, "the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs."[106] Some states use the *Frye* test, but simply refer to it as the general acceptance test.[107] This test uses the scientific community as the reviewing body to determine if the proposed scientific evidence has met with enough general acceptance so as to be reliable for use in a court of law.[108]

When the *Frye* test is applied to DNA cases, most courts use a two-pronged analysis.[109] They require that both the theory and the technique implementing the theory be generally accepted.[110] One example of this test is the New Hampshire approach: (1) general acceptance in the relevant scientific community of the scientific theory or principle; and (2) general acceptance in the relevant scientific community of the techniques, experiments, or procedures applying that theory or principle.[111]

Courts using *Frye* have come to different conclusions concerning both DNA match evidence and DNA statistical evidence. Some states allow only the match evidence,[112] while some states allow both statistical and match evidence,[113] and some states allow neither.[114] Match evidence refers to the fact that the alleles of the suspect are similar to the alleles found in the samples collected at the crime screen.[115] Many courts looking at match evidence, using the *Frye* test, have found that the principles underlying DNA profiling are generally accepted in the

---

600 (Mo. 1991); State v. Carter, 524 N.W.2d 763, 778 (Neb. 1994); State v. Vandebogart, 652 A.2d 671, 677 (N.H. 1995); State v. Williams, 599 A.2d 960, 963 (N.J. Super. Ct. Law Div. 1991); People v. Wesley, 633 N.E.2d 451, 454 (N.Y. 1994); Commonwealth v. Crews, 640 A.2d 395, 399 (Pa. 1994); State v. Ford, 392 S.E.2d 781, 784 (S.C. 1990); State v. Buckner, 890 P.2d 460, 461 (Wash. 1995).

106. *Frye*, 293 F. at 1014.

107. *See Harmon*, 908 P.2d at 410 (discussing the techniques and procedures used to test the evidence as generally accepted in the scientific community).

108. *Frye*, 293 F. at 1014.

109. State v. Vandebogart, 616 A.2d 483, 490 (N.H. 1992), *aff'd on reh'g in banc*, 652 A.2d 671 (N.H. 1995) (finding admission of population frequency was harmless error).

110. *Id.* at 490.

111. *Id.*

112. *See, e.g.*, State v. Bible, 858 P.2d 1152, 1193 (Ariz. 1993) (concluding random match probability calculations are not accepted in the scientific community and therefore not admissible).

113. *See, e.g.*, State v. Bloom, 516 N.W.2d 159, 167 (Minn. 1994) (concluding that match evidence as well as statistical evidence is admissible).

114. *See, e.g., State v. Carter*, 524 N.W.2d 763, 783 (Neb. 1994) (holding that match evidence will not be admissible if not accompanied by statistical probability evidence resulting from a generally accepted method of calculation).

115. DNA TECHNOLOGY, *supra* note 7.

relevant scientific communities.[116] There appear to be no jurisdictions holding that the underlying principles behind DNA profiling are not generally accepted in the relevant scientific communities. Thus, match evidence is generally admissible under *Frye*.

However, simply because a jurisdiction finds that the underlying principles behind DNA profiling are generally accepted, does not mean that statistical evidence will be admitted. There has been a great deal of debate over whether or not there is general acceptance in the relevant scientific communities concerning the calculation of population frequencies.[117] The debate in the *Frye* courts has been slowly coming to an end with most courts accepting population frequency evidence.[118] Of these courts, most accept population frequencies when calculated using the ceiling principle.[119] There are still a few courts that do not allow DNA statistical evidence,[120] however, the trend is towards allowing population frequencies into evidence under the *Frye* standard.[121] Of the courts which did not allow population frequencies into evidence, two have alluded to the fact that if the calculations were done using the ceiling principle, they might have been allowed into evidence.[122]

---

116. *See Ex parte* Perry, 586 So. 2d 242, 250-51 (Ala. 1991); State v. Bible, 858 P.2d 1152, 1185 (Ariz. 1993); Fishback v. People, 851 P.2d 884, 892 (Colo. 1993); Hayes v. State, 660 So. 2d 257, 264 (Fla. 1995); State v. Colbert, 896 P.2d 1089, 1097 (Kan. 1995); Harris v. Commonwealth, 846 S.W.2d 678, 681 (Ky. 1992); State v. Bloom, 516 N.W.2d 159, 167 (Minn. 1994); Polk v. State, 612 So. 2d 381, 388-90 (Miss. 1992); State v. Davis, 814 S.W.2d 593, 600-02 (Mo. 1991); People v. Wesley, 633 N.E.2d 451, 455 (N.Y. 1994); Commonwealth v. Crews, 640 A.2d 395, 402 (Pa. 1994); State v. Ford, 392 S.E.2d 781, 784 (S.C. 1990); State v. Buckner, 890 P.2d 460, 461 (Wash. 1995). DNA profiling means the science underlying DNA manipulation.

117. C.G.G. Aitken, *Evaluating DNA Evidence For Identification*, 4 S. CAL. INTERDISCIPLINARY L. J. 49, 61 (Fall 1995); Sarah E. Snyder, *Experimental or Demonstrable: Has DNA Testing Truly Emerged From the Twilight Zone? An Assessment of Washington's Response to DNA Identification*, 31 WILLAMETTE L. REV. 201, 218-19 (Winter 1995).

118. *See Hayes*, 660 So. 2d at 264-65; *Colbert*, 896 P.2d at 1097; *Harris*, 846 S.W.2d at 681; Commonwealth v. Lanigan, 641 N.E.2d 1342, 1345 (Mass. 1994); State v. Schwartz, 447 N.W.2d 422, 428-29 (Minn. 1989); *Davis*, 814 S.W.2d at 602-03; *Wesley*, 633 N.E.2d at 455; *Ford*, 392 S.E.2d at 784.

119. *See Lanigan*, 641 N.E.2d at 1349; State v. Vandebogart, 652 A.2d 671, 675 (N.H. 1995).

120. *See Bible*, 858 P.2d at 1193 (concluding that there is no general acceptance of random match probability calculations and they are therefore inadmissible); *Crews*, 640 A.2d at 402 (stating that statistical information has not achieved widespread acceptance in scientific community and therefore trial court's refusal to entertain the information was proper); State v. Carter, 524 N.W.2d 763, 783 (Neb. 1994) (finding no general acceptance of statistical probability calculations and therefore trial court's admission of such evidence was error).

121. *Developments in the Law–Confronting the New Challenges of Scientific Evidence*, 108 HARV. L. REV. 1481, 1557-58 (1995).

122. *See* State v. Buckner, 890 P.2d 460, 462 (Wash. 1995) (stating that "the expert should be permitted to describe the test results to the jury using the Committee's 'ceiling principle' or another statistical model proven to be accepted in the scientific community"). The expert in this case testified that Buckner's DNA is a 1 in 19.25 billion "match" to the forensic sample. But this figure is nearly four times the current population of the earth. The jury was told that the match was "unique in the population," in violation of dictates of a previous Washington case. *Id.* (citing State v. Cauthron, 846 P.2d 502, 516 (Wash. 1993)). *See also Vandebogart*, 652 A.2d at 678-79 (holding that the ceiling principle is a conservative means by which to carry DNA evidence across the threshold of admissibility).

There are some *Frye* jurisdictions that will not uncouple the population frequencies from the match evidence even though they find that the underlying science behind the match evidence is generally accepted. These courts generally have found that if the statistics are not admissible, then the match evidence has no meaning and should not be admitted into evidence either.[123] These courts have based their conclusion on the NRC report which states that without frequencies, the match is meaningless.[124] The court in *United States v. Yee*[125] stated that "[w]ithout 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 patterns are as common as pictures with two eyes, or as unique as the Mona Lisa."[126]

Courts using the *Frye* test to determine the admissibility of DNA evidence lean towards admitting both match and statistical evidence, if calculated with the ceiling principle.[127] This means that if a party is trying to get DNA evidence in front of the jury, their best chance would be to use the ceiling principle. This does not mean that *Frye* jurisdictions will not admit population frequencies calculated through other methods, but that parties should keep in mind that under the *Frye* test, it is more likely that both match and population frequency evidence will be admissible using the ceiling principle.

To conclude, it is clear, based on the analysis of courts using the *Frye* test, that the trend in such jurisdictions is to admit DNA evidence.[128] Most courts using the *Frye* test, now find that the principles underlying DNA profiling are generally accepted in the relevant scientific communi-

---

123. *See Carter*, 524 N.W.2d at 783 (holding that DNA match evidence is not admissible if not accompanied by statistical evidence calculated from a generally accepted method); State v. Cauthron, 846 P.2d 502, 516 (Wash. 1993) (stating that DNA match testimony, without statistical information based on a generally accepted scientific theory, is not helpful to the trier of fact).

124. DNA TECHNOLOGY, *supra* note 7. "Therefore, we hold that evidence of a DNA match will not be admissible if it has not been accompanied by statistical probability evidence that has been calculated from a generally accepted method." *Carter*, 524 N.W.2d at 783.

125. 134 F.R.D. 161 (N.D. Ohio 1991).

126. United States v. Yee, 134 F.R.D. 161, 181 (N.D. Ohio 1991).

127. *See, e.g.*, State v. Bloom, 516 N.W.2d 159, 167 (Minn. 1994) (stating that a properly qualified expert may give an opinion as to match probability using the NRC's "ceiling principle" approach to computing the statistics).

128. This trend is also found in California which uses a test similar to that used in *Frye* in determining the admissibility of scientific issues. *See* People v. Kelly, 549 P.2d 1240, 1244 (Cal. 1976) (requiring, in addition to *Frye*, that the reliability of the method be established by a properly qualified expert on the subject). In *People v. Leahy*, California reaffirmed the *Kelly* test, stating that the court in *Kelly* set forth the general principles for admitting scientific evidence and that the decision in *Kelly* would not be reconsidered or modified. 882 P.2d 321, 323 (Cal. 1994). The *Kelly* test has three principle components: (1) is there general acceptance; (2) is the expert qualified expert; and (3) were correct scientific procedures followed. *Kelly*, 549 P.2d at 1244. Using the *Kelly* test, the court in *People v. Burks* found that population frequency data calculated using the ceiling principle was admissible. 43 Cal. Rptr. 2d 791, 793 (Cal. Ct. App.), *review granted*, 905 P.2d 418 (Cal. 1995). Even though the California Supreme Court has never addressed the issue of DNA admissibility, this fourth district case appears to be representative of California's position on DNA. *See id.*

ties.[129] The majority of courts admit both match and population frequency evidence,[130] with a minority of courts allowing only the match evidence,[131] and an even smaller minority allowing neither the population frequencies nor the match evidence when they are uncoupled.[132]

B. THE *DAUBERT* TEST

In *Daubert v. Merrell Dow Pharmaceuticals, Inc.*,[133] the Supreme Court held that the adoption of the Federal Rules of Evidence superseded the *Frye* test for determining the admissibility of scientific evidence in federal courts.[134] The federal rule of evidence that applies to scientific evidence is Rule 702.[135] Rule 702 states that "[i]f scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise."[136] The Court stated in *Daubert* that the word "scientific" implies that the testimony will be based in the sound theories, methods, and procedures of the particular discipline.[137] The Court further concluded that the word "knowledge" implies more than a subjective belief on the part of the witness.[138] In other words, scientific knowledge means that the assertion must be based on the scientific method, which by definition raises the assertion above a mere subjective belief.[139] The second part of Rule 702 stating that the "knowledge assist the trier of fact to understand the evidence or to determine a fact in issue," relates to the fit between the evidence and the

---

129. *See, e.g.*, State v. Colbert, 896 P.2d 1089, 1097 (Kan. 1995) (stating that DNA testing and the RFLP process are reliable, have gained general acceptance in the scientific community, involve scientifically and professionally established techniques and are therefore admissible under the *Frye* standards).

130. *See, e.g.*, *Bloom*, 516 N.W.2d at 167 (concluding that in addition to match evidence, a properly qualified expert should be allowed to testify as to statistical information regarding the match).

131. *See, e.g.*, Commonwealth v. Crews, 640 A.2d 395, 402 (Pa. 1994) (disagreeing with the Appellant's argument that the physical test results are meaningless without statistical conclusions).

132. *See, e.g.*, State v. Carter, 524 N.W.2d 763 (Neb. 1994) (holding that DNA match evidence is not admissible if not accompanied by statistical evidence).

133. 509 U. S. 579 (1993).

134. Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 589 (1993).

135. FED. R. EVID. 702.

136. *Id.*

137. *Daubert*, 509 U.S. at 590.

138. *Id.*

139. *Id.*

> [I]n order to qualify as "scientific knowledge," an inference or assertion must be derived by the scientific method. Proposed testimony must be supported by appropriate validation—i.e., "good grounds," based on what is known. In short, the requirement that an expert's testimony pertain to "scientific knowledge" establishes a standard of evidentiary reliability.

Id.

facts of the case.[140] Thus, any evidence that does not fit may not be admissible.[141] These two sections of Rule 702 form the basis for the *Daubert* test.

The criteria used for determining if scientific evidence is admissible under *Daubert* is whether: (1) the scientific knowledge can or has been tested; (2) the scientific knowledge has been subjected to peer review; (3) there is a known or potential rate of error; and (4) there is general acceptance in the scientific community.[142] These steps allow the trial judge to examine the reasoning and methodology behind the offered evidence and to ask whether the evidence fits with the facts of the case.[143] In *Daubert*, Justice Blackmun stated that the fit is important because it "is not always obvious, and scientific validity for one purpose is not necessarily scientific validity for other, unrelated purposes."[144] Justice Blackmun used an example of moon phasing to illustrate fit.[145] The study of the phase of the moon could be used to determine the amount of light on a given night, but could not be used to determine if an individual behaved irrationally on that night.[146] Thus, the inquiry under *Daubert* is a flexible one, the focus of which must be based on the underlying principles and methodology of the scientific technique.[147]

There is some criticism that *Daubert* is too lenient when compared to *Frye*.[148] It is argued that any type of junk science could be admissible using the *Daubert* criteria.[149] The Court in *Daubert* responded by stating 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."[150]

There are under ten states which have decided to adopt the less demanding *Daubert* test for determining the admissibility of DNA

---

140. *Id.* at 591. "An additional consideration under Rule 702—and another aspect of relevancy—is whether expert testimony proffered in the case is sufficiently tied to the facts of the case that it will aid the jury in resolving a factual dispute." United States v. Downing, 753 F.2d 1224, 1242 (3d Cir. 1985).

141. *Daubert*, 509 U.S. at 591-92.

142. *Id.* at 593-94.

143. *Id.* at 592-93.

144. *Id.* at 591.

145. *Id.*

146. *Daubert*, 509 U.S. at 591.

147. *Id.* at 594-95.

148. *Id.* at 595-96. *See supra* text accompanying note 104 (discussing the application of the *Frye* test).

149. *Daubert*, 509 U.S. at 595-96. "Respondent expresses apprehension that abandonment of 'general acceptance' as the exclusive requirement for admission will result in a 'free-for-all' in which befuddled juries are confounded by absurd and irrational pseudoscientific assertions." *Id.*

150. *Id.* at 596.

evidence.[151] Some states have acknowledged the existence of *Daubert* in their DNA cases, and have chosen not to decide the applicability of *Daubert* in cases where the court is determining the admissibility of DNA evidence.[152]

Federal courts are bound by the *Daubert* decision. Thus, a brief discussion concerning the application of *Daubert* by the Circuit Courts of Appeals, regarding the admissibility of DNA evidence, is necessary. The Second Circuit examined the general theory underlying DNA profiling as well as the specific techniques employed by the Federal Bureau of Investigation (FBI) to calculate population frequencies and concluded that in the future, courts could take judicial notice of their reliability.[153] In 1993, the Eighth Circuit concluded that, in the future, courts can take judicial notice of the reliability of the general theory and techniques of DNA profiling, which includes both match and population frequencies.[154] Two other circuits that have found that DNA is admissible under *Daubert* are the Ninth Circuit in *United States v. Chischilly*,[155] and the Tenth Circuit in *United States v. Davis*.[156] Both found match and population frequency evidence to be admissible. Of these four circuits that have addressed the DNA issue, all four have admitted DNA evidence based on the FBI's method for calculating population frequencies. This approach is different from the state court approach, where the preference is to use the NRC's ceiling method for calculating population frequencies.[157]

Of the states using *Daubert*, only one state has rejected the admissibility of statistical evidence concerning population frequencies.[158] In *State v. Streich*,[159] the Vermont Supreme Court concluded that, even

---

151. Moore v. State, 915 S.W.2d 284, 294 (Ark. 1996); Nelson v. State, 628 A.2d 69, 73-74 (Del. 1993); Mitchell v. Commonwealth, 908 S.W.2d 100, 101-02 (Ky. 1995); State v. Quatrevingt, 670 So. 2d 197, 204 (La. 1996); State v. Weeks, 891 P.2d 477, 489 (Mont. 1995); State v. Schweitzer, 533 N.W.2d 156, 159 (S.D. 1995); State v. Streich, 658 A.2d 38, 46 (Vt. 1995).

152. *See* State v. Bible, 858 P.2d 1152, 1183 (Ariz. 1993) (concluding that this was not the case to determine whether Arizona should adopt *Daubert*). "In application, *Daubert* leaves many questions unanswered." *Id.* at 1183 (citing United States v. Daubert, 509 U.S. 579, 600 (1993) (Rehnquist, C.J., concurring in part and dissenting in part)).

153. United States v. Jakobetz, 955 F.2d 786, 799-800 (2d Cir. 1992).

154. *See* United States v. Martinez, 3 F.3d 1191, 1197 (8th Cir. 1993) (noting the Second Circuit's conclusions as to reliability of DNA profiling and holding that in the future courts may take judicial notice of such), *cert. denied*, 114 S. Ct. 734 (1994)).

155. *See* United States v. Chischilly, 30 F.3d 1144, 1156 (9th Cir. 1994) (concluding that under *Daubert*, the three main components of DNA profiling "pass muster" under Rule 702 of the Federal Rules of Evidence).

156. *See* United States v. Davis, 40 F.3d 1069, 1074-75 (10th Cir. 1994) (discussing *Daubert* and holding that the district court fulfilled the requirements of *Daubert*).

157. I have found that state courts find security in the conservative nature of the NRC report. DNA TECHNOLOGY, *supra* note 7.

158. *See* State v. Streich, 658 A.2d 38, 48 (Vt. 1995).

159. 658 A.2d 38 (Vt. 1995).

under the more relaxed *Daubert* test, they were unwilling to admit the FBI's unmodified product rule.[160] In *Streich*, the state used the FBI's fixed bin method for calculating the population frequencies.[161] The court stated that, had the ceiling principle been used, the statistical evidence may have been admissible.[162] The court stated that the use of a more conservative approach for the calculation of the population frequencies minimizes the risk of error.[163] The court did not address the question of whether the admissibility of the match was contingent on finding the population frequencies admissible.[164]

There is one state which used the *Daubert* test to find that match evidence, by itself, was not admissible.[165] In *Nelson v. State*,[166] the Delaware Supreme Court concluded that match evidence does meet all the criteria of *Daubert*, except when the statistical basis behind the population frequency does not meet *Daubert*, neither methods are admissible.[167] The court stated that without population frequencies, the jury would not be able to give any meaning to the match evidence.[168] However, the court did suggest that in subsequent DNA cases that trial courts should look to the NRC report's ceiling principle rather than other methods.[169] This could be interpreted to mean that this court did not care for the FBI's method of calculating the population frequencies, but would be receptive to the NRC's ceiling principle.

The majority of states using *Daubert* have found that both match and statistical evidence are admissible.[170] These cases admitted a range of different approaches for the calculation of population frequencies, including the FBI's bin approach.[171] Some states have concluded that the use of the FBI's bin method to calculate population frequencies renders the statistics inadmissible.[172] Even though those states rejected

---

160. State v. Streich, 658 A.2d 38, 48 (Vt. 1995). The unmodified product rule as used by the FBI does not employ any of the NRC report's conservative methods for the statistical calculation of the population frequencies. *Id.*

161. *Id.* at 45.

162. *Id.* at 48-49.

163. *Id.* at 49.

164. *See Streich*, 658 A.2d at 38.

165. *See* Nelson v. State, 628 A.2d 69, 76 (Del. 1993) (holding that DNA evidence is admissible only when there is both match evidence and statistical evidence to support the match).

166. 628 A.2d 69 (Del. 1993).

167. Nelson v. State, 628 A.2d 69, 76 (Del. 1993).

168. *Id.*

169. *Id.* at 76-77.

170. *See* State v. Weeks, 891 P.2d 477, 491 (Mont. 1995); State v. Schweitzer, 533 N.W.2d 156, 158 (S.D. 1995). The South Dakota Supreme Court did, however, state in *Schweitzer* that if the statistical evidence had not been admissible, they would not have allowed the match into evidence. *Id.* at 160.

171. Mitchell v. Commonwealth, 908 S.W.2d 100, 101-02 (Ky. 1995) (allowing both statistics and match evidence using the FBI method for calculating the statistics).

172. *See, e.g.*, State v. Streich, 658 A.2d 38, 49 (Vt. 1995) (concluding that the DNA population

population frequency evidence, the courts strongly suggested that the use of the ceiling principle may have alleviated some of their concerns and suggested that in the future, the ceiling principle should be consulted.[173]

Thus, two things are clear from the holdings of the courts utilizing *Daubert*. First, it is easier to get DNA evidence admitted under *Daubert* than with *Frye*, because under *Frye* there needs to be more "general acceptance" of the evidence. Secondly, even though it is easier to get population frequencies admitted under *Daubert*, there still is a preference in the state courts for the ceiling principle, because it appears that those courts prefer the conservative nature of the ceiling principle.[174] Therefore, the test a jurisdiction uses will be a major factor in whether DNA evidence will be admissible.

C. THE RELEVANCY STANDARD

The majority of the remaining states use a relevancy standard for determining whether or not to admit scientific evidence.[175] The relevancy standard is essentially the same as the *Daubert* test for determining the admissibility of scientific evidence.[176] The relevancy test normally has a variation of three basic questions: (1) is it relevant; (2) is the witness a qualified expert; and (3) will the evidence assist the trier of fact.[177]

The states that use the relevancy test for determining the admissibility of scientific evidence are primarily concerned with whether or not the person testifying is an expert.[178] In *State v. Peters*,[179] the Wisconsin Court of Appeals stated that "the fundamental determination of

---

frequency statistics using the FBI's "bin method" were improperly admitted).

173. *Id.* at 49.

174. *See Vandebogart*, 652 A.2d at 678-79 (holding that the ceiling principle is a conservative means by which to carry DNA evidence across the threshold of admissibility).

175. *See* State v. Pierce 597 N.E.2d 107, 112 (Ohio 1992) (stating that the standard for admissibility of scientific evidence in Ohio is whether the evidence is relevant); State v. Peters, 534 N.W.2d 867, 872 (Wis. 1995) (stating that the Wisconsin Supreme Court has rejected *Frye* in favor of the relevancy test).

176. The relevancy standard and *Daubert* are basically the same because they are both based on the Federal Rules of Evidence. Further, due to the difficulty in distinguishing relevancy from *Daubert*, only those states that did not expressly state that *Daubert* was their test for the admissibility of scientific evidence are discussed here.

177. *Peters*, 534 N.W.2d at 872.

178. *See* Steve v. Anderson, 881 P.2d 29, 36 (N.M. 1994) (requiring that the expert be qualified); *Pierce* 597 N.E.2d at 111-12 (quoting Federal Rule of Evidence 702 in stating that if scientific knowledge will assist the trier of fact, a witness qualified as an expert may testify thereto); State v. Futrell, 436 S.E.2d 884, 887 (N.C. Ct. App. 1993) (stating that when a properly qualified expert offers evidence, the testimony is relevant); *Peters*, 534 N.W.2d at 872 (noting that scientific evidence is admissible if it is relevant, the witness is qualified as an expert, and the evidence will assist the trier of fact in the determination of a fact).

179. 534 N.W.2d 867 (Wis. Ct. App. 1995).

admissibility comes at the time the witness is qualified as an expert."[180] Wisconsin and other states like it, hold that vigorous cross-examination allows the underlying theory to be attacked.[181] In *People v. Vann*,[182] the Appellate Division of the Supreme Court of New York stated that the defendant's challenge to the methodology behind the FBI's statistical calculations goes only to the weight and not to the admissibility of the evidence.[183] Thus, where the qualified witness's testimony is admissible, any controversy or problems in the underlying theory will be exposed through vigorous cross-examination.[184]

There are approximately ten states that use the relevancy test for determining the admissibility of scientific evidence.[185] Of these states only one does not allow DNA population frequencies into evidence.[186] In *Rivera v. State*,[187] the Wyoming Supreme Court held that when introducing DNA evidence, the best policy would be to avoid using population frequencies.[188] The court based their decision on a Minnesota case in which that court stated that statistics, such as population frequencies, would exaggerate the impact of DNA testing in the eyes of the jury.[189] Following the Wyoming decision, the Minnesota Supreme Court in *State v. Bloom*,[190] made an exception to their rule against using statistics in criminal cases.[191] In *Bloom*, the court carved out an exception for statistical evidence based on the NRC report's method for calculating conservative population frequencies using the ceiling principle.[192] It is not certain if the Wyoming courts will follow the Minnesota courts on this issue. If they do, most of the courts using the relevancy test would allow into evidence properly calculated population frequen-

---

180. State v. Peters, 534 N.W.2d 867, 872 (Wis. Ct. App. 1995) (quoting State v. Walstad, 351 N.W.2d 469, 487 (Wis. 1984)).

181. *Id.* It is then through this adversarial system that the truth will come out.

182. 627 N.Y.S.2d 473 (Sup. Ct. App. Div. 1995).

183. People v. Vann, 627 N.Y.S.2d 473, 476 (Sup. Ct. App. Div. 1995).

184. *See Peters*, 534 N.W.2d at 872 (stating that theories can be attacked through cross examination).

185. Prater v. State, 820 S.W.2d 429, 431 (Ark. 1991); State v. Brown, 470 N.W.2d 30, 32 (Iowa 1991); State v. Anderson, 881 P.2d 29, 35 (N.M. 1994); State v. Daughtry, 459 S.E.2d 747, 759 (N.C. 1995); State v. Pierce, 597 N.E.2d 107, 112 (Ohio 1992); State v. Futch, 860 P.2d 264, 268 (Or. Ct. App. 1993); Flores v. State, 871 S.W.2d 714, 722 (Tex. Crim. App. 1993); State v. Woodall, 385 S.E.2d 253, 259-60 (W. Va. 1989); State v. Peters, 534 N.W.2d 867, 872 (Wis. Ct. App. 1995); Rivera v. State, 840 P.2d 933, 941 (Wyo. 1992).

186. *Rivera*, 840 P.2d at 942.

187. 840 P.2d 933 (Wyo. 1992).

188. Rivera v. State, 840 P.2d 933, 942 (Wyo. 1992).

189. *Id.* (citing State v. Schwartz, 447 N.W.2d 422, 428 (Minn. 1989)).

190. 516 N.W.2d 159 (Minn. 1994).

191. State v. Bloom, 516 N.W.2d 159, 167 (Minn. 1994).

192. *Id.* The Minnesota Court now allows DNA based statistical evidence in criminal cases after the Minnesota legislature passed a statute mandating the use of population statistics in criminal trials.

cies using the ceiling principle.[193] Furthermore, because these states rely on the use of vigorous cross-examination to demonstrate the faults of a given method, they are also more willing to allow other methods than states using the *Daubert* or *Frye* test for the calculation of population frequencies.[194]

IV. THE ADMISSIBILITY OF DNA IN NORTH DAKOTA

The North Dakota Supreme Court has not addressed the issue of the admissibility of DNA evidence. This may soon change, as North Dakota will have to tackle the evidentiary problems surrounding DNA, because of a new North Dakota statute which makes DNA evidence admissible and mandates the collection of DNA samples from sex offenders.[195] This new statute should help North Dakota catch up with the rest of the states in the use of DNA evidence, because North Dakota now has the legal tools to initiate a sex offenders database and to establish a stronger forensic science division capable of handling DNA.[196] These advances in the law will enable the courts to start utilizing DNA evidence, because the statute also makes DNA evidence admissible in court.[197] However, the legislature did not specify whether the statute meant that match evidence and statistical evidence are admissible or simply that match evidence is admissible.[198] The language of the statute states that "evidence of a DNA profile comparison must be admitted as prima facie evidence to prove or disprove the identity of any person."[199] The question is whether "DNA profile" covers just the match evidence or both the match and the statistical evidence. This important issue will have to be addressed by the North Dakota Supreme Court because there is nothing in the legislative history indicating that the legislature considered the distinction between these two types of evidence.[200] Based on the

193. Prater v. State, 820 S.W.2d 429, 433 (Ark. 1991); State v. Brown, 470 N.W.2d 30, 32 (Iowa 1991); State v. Anderson, 881 P.2d 29, 47 (N.M. 1994); State v. Daughtry, 459 S.E.2d 747, 758 (N.C. 1995); State v. Pierce, 597 N.E.2d 107, 115 (Ohio 1992); State v. Futch, 860 P.2d 264, 272-73 (Or. Ct. App. 1993); State v. Peters, 534 N.W.2d 867, 873-74 (Wis. Ct. App. 1995).

194. *See, e.g., Peters*, 534 N.W.2d at 873-74 (allowing ceiling principle). *See also Anderson*, 881 P.2d at 47 (allowing the FBI method).

195. N.D. CENT. CODE ch. 31-13 (Supp. 1995). *See supra* note 1 (providing text of statute).

196. *See id.* § 31-13-05 (providing for the establishment of a centralized data base of DNA records for convicted sexual offenders).

197. *Id.* § 31-13-02.

198. *See id.* (providing no express exclusion of statistical evidence).

199. *Id.*

200. There is no way of knowing whether the North Dakota Legislature considered the difference between the two types of evidence and then chose to intentionally exclude statistical evidence. In Minnesota, the issue was resolved by the legislature. Kathleen W. Berdan, Comment, *The Admissibility of DNA Evidence: Minnesota No Longer Stands Alone*, 20 WM. MITCHELL L. REV. 1063, 1064 (1994) (citing MINN. STAT. §§ 634.25, 634.26 (1992)) After Minnesota enacted a statute making DNA admissible, the Minnesota Supreme Court in *State v. Schwartz* stated that there would be a limitation on

wording of the statute, the lack of legislative history, and Minnesota's struggle, it would not be surprising if the North Dakota Supreme Court concludes that the statute covers only match evidence.

A. ANALYSIS OF NORTH DAKOTA'S CASE LAW CONCERNING THE ADMISSIBILITY OF SCIENTIFIC EVIDENCE

It is unclear exactly what test North Dakota courts use for determining the admissibility of scientific evidence. North Dakota has never expressly adopted the *Frye* or the *Daubert* test for determining admissibility of scientific evidence.[201] Nevertheless, in *City of Fargo v. McLaughlin*,[202] the North Dakota Supreme Court based their acceptance of the horizontal gaze nystagmus test during a DUI investigation on the widely accepted principles that alcohol will affect the outcome of this test.[203] The language the court used is similar to the general acceptance language found in opinions from courts that use the *Frye* test.[204] However, this is insufficient evidence to demonstrate that the North Dakota Supreme Court uses the *Frye* test. The court further noted that *Daubert* has superseded the *Frye* test in federal courts for determining the admissibility of scientific evidence, but did not rely on either test in reaching its conclusion that the gaze test was admissible.[205] However, a recent law review article points out that even though the North Dakota Supreme Court may not choose to apply *Daubert*, "the court has generally found that federal court decisions are persuasive authority when interpreting similarly worded rules in North Dakota."[206] Based on this reliance, North Dakota courts may choose to implement *Daubert* for determining the admissibility of scientific evidence.

---

the use of population frequency statistics. 447 N.W.2d 422, 428 (Minn. 1989). The exclusion of statistical evidence by the courts, despite the statute, prompted the legislature to amend the statute to specifically allow statistical evidence concerning DNA. *Id.* The legislature also introduced a number of bills proposing to amend the state's constitution to allow statistical evidence. *Id.* at 1065. The Minnesota Supreme Court then overruled its previous *Schwartz* decision in *State v. Bloom*. *Id.* (citing State v. Bloom, 516 N.S.2d 159 (Minn. 1994)). In *Bloom*, the Minnesota Supreme Court justified the use of population frequencies based on the recent adoption of the NRC reports conservative ceiling method for the calculation of these population frequencies. 516 N.W.2d at 167.

201. *See* State v. Swanson, 225 N.W.2d 283, 285 (N.D. 1974) (stating that the court may be required to re-examine its previous decision in which it refused adoption of Frye, but this was not the case to do it in); City of Fargo v. McLaughlin, 512 N.W.2d 700, 707 (N.D. 1994) (concluding that evidence of the horizontal gaze nystagmus test was admissible, but not referring to any particular test of admissibility).

202. 512 N.W.2d 700 (N.D. 1994).

203. City of Fargo v. McLaughlin, 512 N.W.2d 700, 706 (N.D. 1994).

204. *See supra* note 108 and accompanying text.

205. *McLaughlin*, 512 N.W.2d at 705.

206. Charles R. Honts & Bruce D. Quick, *The Polygraph in 1995: Progress in Science and the Law*, 71 N.D. L. REV. 987, 1014 (1995) (citing State v. Farzaneh, 468 N.W.2d 638, 641 (N.D. 1991) (following federal precedent because North Dakota's rule was so similar to the corresponding Federal Rule of Evidence, even though it was based upon the Uniform Rules of Evidence)).

In *State v. Brown*,[207] the North Dakota Supreme Court admitted hypnotic testimony in a criminal trial, even though some jurisdictions precluded the testimony based on *Frye*.[208] The court stated that:

> Should our decision result in exposing the jury in each case to the testimony of expert witnesses as to the reliability and uses of hypnosis as an investigative tool, so be it. We believe this alternative is preferable to the potential exclusion of relevant testimonial evidence and the end of hypnosis as an investigative tool in this jurisdiction. Expert scientific and medical testimony is hardly a new phenomenon in a criminal trial setting . . . We are firmly of the belief that jurors are "quite capable of seeing through flaky testimony" and pseudo-scientific "claptrap".[209]

Even though *Brown* deals with hypnosis, it does demonstrate the court's willingness to admit questionable evidence.[210] The court feels that vigorous cross-examination will enlighten the jury about pseudo-scientific information, allowing them to make an educated decision.[211] Thus, it can be argued that the court will admit DNA evidence through a qualified expert and allow the jury to determine the credibility of the evidence.

Because it is unclear how the Supreme Court of North Dakota will determine the admissibility of scientific evidence, attorneys must be aware of the issues that may arise under any of the predominant theories concerning the admissibility of scientific evidence. The admissibility theories discussed in this paper should enable attorneys to argue their side of a DNA admissibility issue.

Regardless of which admissibility test North Dakota decides to follow, it appears that most states are moving towards admitting both match and population frequencies into evidence. There was a period in the 1990s when courts found too much controversy among scientists concerning the calculations behind population frequencies. This stemmed from an argument between two leading groups of scientists.[212] A heated debate over population substructure continued until 1993 when

---

207. 337 N.W.2d 138 (N.D. 1983).

208. State v. Brown, 337 N.W.2d 138, 151 (N.D. 1983).

209. *Id.* at 151-52 (quoting People v. Williams, 183 Cal. Rptr. 498, 502 (Cal. Ct. App. 1982) (Gardner, J., concurring)).

210. *See id.* at 151 (stating that the court would rather admit the evidence rather than exclude it resulting in the "end of hypnosis as an investigative tool").

211. *Id.*

212. *Compare* Ranajit Chakraborty & Kenneth K. Kidd, *The Utility of DNA Typing in Forensic Work*, Vol. 2 SCIENCE 1735 (Dec. 1991) *with* R.C. Lewontin & Daniel L. Hartl, *Population Genetics in Forensic DNA Typing*, Vol. 2 SCIENCE 1745 (Dec. 1991).

one of the groups modified their position after the NRC report because of the conservative nature of the resulting probabilities.[213] Although, they still stand firm in their conclusion that there is a need for further study to determine the amount of population substructure because ethnic groups often have significant differences in a allele frequency distributions.[214] They claim that only continued research will determine the amount of conservativism used in the ceiling principle.[215] Since then, courts have been more willing to admit population frequencies, the majority of which approved the conservative ceiling principle as discussed in the NRC report.[216] While it is still easier to get the ceiling principle into evidence, some courts are also allowing the FBI's bin method into evidence.[217] Thus, whatever test the North Dakota Supreme Court decides to use for determining the admissibility of DNA evidence, the strong trend throughout the United States indicates that they may find DNA evidence admissible.

V. CONCLUSION

We have seen that the trend in both federal and state courts has been to admit DNA evidence. Courts seem more willing to accept the NRC's conservative ceiling method for calculating the population frequency, but this does not mean that this is the only method for calculating population frequencies, it simply means that, at this time, most state courts are more comfortable using the ceiling principle as defined in the NRC report. It is my opinion that the science behind DNA is valid and generally accepted by the relevant scientific community. Even though the science behind the DNA evidence is accepted by the relevant scientific community, a problem arises because the various methods for calculating population frequencies raises legitimate questions as to validity. If the statistical calculations are faulty, there is the possibility of serious error at the expense of the accused. Therefore, when analyzing how to approach the admissibility of DNA evidence, North Dakota courts should consider all of the theories concerning the admissibility of DNA.

---

213. Daniel L. Hartl & R.C. Lewontin, *Letters*, Vol. 260 SCIENCE 473 (Apr. 1993).

214. *Id.* at 474.

215. *Id.* at 474. It is through this continuing research that scientists will be able to determine if the arbitrary 10% lower bound, as used in the ceiling principle, is too conservative. *Id.*

216. *See* PAUL C. GIANNELLI & EDWARD J. IMWINKELRIED, SCIENTIFIC EVIDENCE (Supp. 1994) (listing court decisions directing DNA admissibility when National Academy of Sciences recommendations are followed).

217. *See* United States v. Chischilly, 30 F.3d 1144, 1154 (9th Cir. 1994) (stating that the existence of scientific institutions that may interpret data more conservatively does not indicate a "lack of general acceptance" under *Daubert*).