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DNA STATISTICAL EVIDENCE AND THE "CEILING PRINCIPLE:" SCIENCE OR SCIENCE FICTION?

A Thesis

Presented to

The Judge Advocate General's School, United States Army

The opinions and conclusions expressed herein are those of the author and do not necessarily represent the views of either The Judge Advocate General's School, the United States Army, or any other governmental agency.

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March 1994

DNA STATISTICAL EVIDENCE AND THE "CEILING PRINCIPLE:" SCIENCE OR SCIENCE FICTION?

by Captain Douglas A. Dribben

ABSTRACT: This thesis examines the scientific foundation behind the National Research Council's "ceiling principle" method of calculating Deoxyribonucleic acid (DNA) statistical evidence. Use of DNA evidence is becoming widespread in criminal cases. DNA evidence has generally been admitted by state and federal courts under the test for "novel scientific evidence." However, the defense bar, citing several scientists, has attempted to thwart the acceptance of DNA statistical evidence under the *Frye* test. To resolve the issue, the National Research Council developed a compromise, known as the "ceiling principle." This method replaces the actual numbers used in calculating the DNA statistics with more conservative numbers based upon an assumption that the ethnic make-up of the defendant affects the statistics. This thesis finds that the scientific research overwhelmingly refutes the assumption underlying the "ceiling principle," making its use unnecessary and unwise. It concludes that the "ceiling principle" does not pass muster under the Federal Rules of Evidence, which the Supreme Court recently ruled control admission of all scientific evidence in federal courts; accordingly, evidence derived via the "ceiling principle" is inadmissible in federal courts and courts-martial.

DNA STATISTICAL EVIDENCE AND THE "CEILING PRINCIPLE:" SCIENCE OR SCIENCE FICTION?

Douglas A. Dribben
Captain, U.S. Army

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In law, the man of the future is the man of statistics.
Oliver Wendell Holmes, Jr. (1897)

I. Introduction

Since 1986, prosecutors and defense attorneys have had a powerful weapon to aid them in settling the issue of identity of the perpetrator of a crime.[1] The forensic use of Deoxyribonucleic Acid (DNA) permits absolute exclusion of a defendant from the group of possible perpetrators, thus preventing the innocent from conviction and possible imprisonment. DNA can, alternatively, provide powerful circumstantial evidence that the defendant and the perpetrator are one and the same and help ensure that the guilty are brought to justice.

DNA evidence is comprised of two elements: the presence or absence of a "match" between the suspect's DNA and the evidentiary sample found at the crime scene, and the relevance of such a match. The admission of this evidence can thus take three forms: exclusion of all the DNA evidence, admission of the issue of a match alone, or admission of both the match and its relevance.

DNA evidence has been admitted in one form or another in most state and Federal courts. With the demise of the *Frye*[2] and *Frye*-based[3] standards of admissibility, there remains little or

no challenge to admitting evidence of a match between the evidentiary sample and the defendant's DNA in all Federal (including military) and most state courts.[4] This evidence can, and has, passed muster under the Federal Rules of Evidence (FRE).

A controversy over the scientific basis recently arose regarding admitting evidence demonstrating the relevance of a match between the DNA of the suspect and the evidentiary sample. This evidence is usually presented as a statistic -- the probability of such a match occurring at random by someone other than the perpetrator.[5] This probability is usually extraordinarily small, often as low as one in a million or less. Such evidence is damning in the eyes of the jury, and defense attorneys and their experts try hard to prevent its admissibility.

A new method of calculating this statistical evidence has arisen in response to this controversy. This method, called the "ceiling principle," is unduly conservative and operates to greatly increase the probabilities calculated by most U.S. DNA laboratories. Under the guise of science and the cloak of respectability provided by its sponsor, the National Academy of Sciences, this method is finding its way into many of the court decisions rendered in the past year.

Seemingly based on science, it enters the courtroom under the auspices of the rules of evidence governing admissibility of scientific evidence. Yet the method completely lacks any basis in science, and its admission contradicts the principles underlying the rules of evidence. The results of this new method of

calculating DNA statistical evidence may in and of themselves create a reasonable doubt as to the identity of the perpetrator.[6] At least, it greatly reduces the effectiveness of DNA evidence and creates a strong probability of confusing the finder of fact.

This paper's thesis is that statistical evidence calculated using the "ceiling principle" is not based on any scientific theory or body of knowledge, that it grossly overstates the probability of a random DNA match, and that its introduction into evidence along side or in place of the statistical evidence calculated using the "product rule"[7] has strong potential to confuse or mislead the finder of fact and may create doubt where it would not otherwise exist. Part II of this paper details the process of DNA analysis. Part III surveys the history of DNA evidence in American courts. Part IV addresses the controversy surrounding admission of DNA evidence. Part V examines the history behind the "ceiling principle" and its scientific underpinnings, if any. Part VI examines the relationship between the "ceiling principle" and the rules of evidence. Part VII contains the conclusion and recommendations.

II. DNA Analysis.

Organisms reproduce by transmitting genetic information from generation to generation. This is accomplished by the DNA molecule, which contains the genetic codes that determine inherited characteristics.[8] In humans, DNA is contained in

forty-six chromosomes: one pair of sex chromosomes and twenty-two pairs of autosomes.[9] Sperm cells contain half of these chromosomes; ova contain the other half.[10] During reproduction, half of an individual's DNA is provided by the father's sperm and half by the mother's ovum.[11]

Advances in science allow geneticists to isolate human genes. Most of these genes are involved in determining the structure and function of cells. Some, however, have no apparent function.[12] These apparently functionless genes exhibit wide variations among individuals and serve as the basis behind DNA analysis.[13]

A. *The Composition of DNA.*

Deoxyribonucleic acid (DNA) is the basic building block of all living cells. Found primarily in the chromosomes within the nucleus of all human body cells (except red blood cells),[14] DNA contains a genetic code which provides the basis for proteins necessary to create and sustain life.[15] The DNA molecule itself is composed of two strands intertwined in a spiral or double-helix formation (which resembles a zipper fastener).[16]

Each strand is composed of four different nucleotides, or bases, repeated hundreds of thousands of times. These bases are deoxyadenosine monophosphate (A), thymidine monophosphate (T), deoxycytidine monophosphate (C), and deoxyguanosine monophosphate (G). The bases associate with each other in only certain ways:

T on one strand of DNA will only bond with A on another strand; likewise, C will only bond with G. However, there are no limits to association between the bases on the *same* strand of DNA. Each association between two bases is known as a base pair. Thus, a sequence of a DNA molecule may look like:

```
A T G C C G A T G C A T A        G T C A C G T A G C T
| | | | | | | | | | | | |   or   | | | | | | | | | |
T A C G G C T A C G T A T        C A G T G C A T C G A
```

Because of these associational properties, if the sequence of one strand of DNA is known, the sequence of the other strand can be easily determined.[17]

There are over three billion base pairs in each strand of human DNA contained in each of approximately ten trillion cells in the human body.[18] The sequences of the base pairs in these strands determine the function of the cell and are responsible for creating limbs, blood, and bone cells. Most of a person's DNA encodes this type of information, although some has no currently known function.

DNA molecules within the chromosomes form genes. These genes help determine such things as whether an individual has blue or green eyes. Alternate forms of genes, such as the "blue-eye" gene and the "green-eye" gene are called alleles. Each human allele contains from one to 2,000 kilobase pairs, or Kb.

Most of the DNA in humans is the same from one person to another. An individual's DNA varies, however, at approximately three million sites, or loci.[19] These differences, called

"polymorphisms," occur at discrete loci within the genes along the DNA strand and exhibit a high degree of variation among individuals.[20] Geneticists have discovered that fragments of DNA are repeated many times at these sites, with the variation occurring in the number of times the sequences are repeated. For example, in the sequence:

A-C-T-G-A-T-G-A-T-G-A-T-G-A-T-C-G-A-A-T-G-A-T-G-A-T

the series G-A-T is repeated four times at one location and twice at another. The variations in number of the base series repeats are referred to as "variable number of tandem repeats," or VNTRs.[21]

Scientists have succeeded in mapping many human chromosomes and assigning specific loci for the alleles on these chromosomes.[22] An individual has at most two alleles at any one locus -- one inherited from the father and one inherited from the mother (although it is possible for both parents to pass on the same gene to their offspring). However, some of these loci have up to one hundred different alleles.[23] These polymorphic loci form the basis of DNA identification. When extracted from the person's DNA strand and examined, the variations are readily visible and provide the basis for differentiation between individuals.[24]

B. *The Theory of DNA.*

The DNA within a person's cells is identical regardless of the type of cell.[25] However, no two people have exactly the same DNA except identical twins.[26] These two precepts form the basis of DNA analysis. Because of them, DNA from a suspect's blood may be compared to a semen sample from the crime scene to determine the identity of the perpetrator.

Comparison of DNA samples is much like comparisons of a partial fingerprint. The human DNA is much too large to compare in its entirety.[27] Therefore, only a small portion is analyzed for forensic purposes.

If one strand is known, the other can be readily determined due to its complementary bonding properties. This is the heart of the DNA analysis. DNA comparison is per-formed by separating the helical molecule into its two component strands and breaking the strands down into smaller fragments. Then, a fragment from a strand of the DNA from one source may be compared to a fragment from a strand of the DNA from another source. If the DNA is identical, the complementary fragments will bond; if not, no bonding will occur. Since the fragments bond only with their counterpart fragments, bonding indicates that the two samples themselves match at the points compared.

No match provides conclusive proof that the suspect is not the criminal (if they were the same person, their samples should match everywhere, including the portion under examination). A

DNA match provides powerful, although not conclusive, evidence that the suspect (or his identical twin, if one exists), provided the evidentiary sample. Although the area under examination matches, other areas may not. A DNA inclusion is thus circumstantial, rather than direct evidence of identity.[28]

C. *Process of DNA Analysis.*

The most common form of DNA analysis is known as Restriction Fragment Length Polymorphism Analysis (RFLP analysis).[29] RFLP breaks down the DNA into different-sized fragments by application of a restriction enzyme at each of the VNTR loci. The resulting fragments are sequences of VNTRs taken from the polymorphic loci along the DNA molecule. Because of the difference in size of these fragments (determined by the number of tandem repeats), the DNA can be used to identify one individual from another.

In order for the genetic polymorphisms to be examined and compared, they must first be extracted from the DNA strand on which they are located.[30] Each polymorphic locus is extracted as an allele. Not every polymorphism is extracted, however; the laboratories currently extract and examine only a small portion of a person's polymorphic DNA. Because of the wide variation in these polymorphic loci, this is all that is required to obtain probabilities that can exclude all other living people as the donor of the sample.[31]

RFLP analysis requires at least 100 nanograms of relatively pure DNA. Some forensic DNA samples contain a lesser quantity or quality and cannot be analyzed by existing RFLP techniques. Another technique, called Polymerase Chain Reaction (PCR) is used to amplify the amount of DNA present in these samples.[32] PCR essentially synthesizes up to a million or more copies of the sample's DNA.[33] Once present in sufficient quantity, the test to detect the DNA's variation is performed fundamentally the same as in RFLP analysis.[34] Because RFLP analysis is used as the primary means of DNA analysis today, this paper will discuss only RFLP analysis.[35]

1. *Sample Collection*.

DNA identification lends itself best to violent crimes and sexual assaults, because these crimes are more likely to have samples of DNA left by the assailant. In violent crimes, the assailant is often cut by the victim in a defensive struggle or has traces of the victim's blood on his clothing, possessions, or weapon. In sexual assaults, the assailant usually leaves behind a semen sample as well as blood from a struggle with the victim. DNA can be obtained from samples of blood (containing white blood cells), semen (containing sperm cells), saliva (containing epithelial cells), and even roots of hair and body tissue.[36] The process of sample collection varies according to the type of sample and the medium on which it is deposited, but results in

the separation of the sample from the clothing or medium and preservation in an uncontaminated location, such as a laboratory test tube or evidence bag.

The sample is then delivered to the laboratory, where the DNA is extracted from the sample and purified. The DNA must be free of contaminants that will interfere with the extraction procedure and be of sufficient molecular weight and quantity to be tested.[37] These qualities depend upon the type and source of sample tested.[38] Each of the commercial laboratories (and the FBI) in the United States performing DNA analysis has its own protocol for performing these tasks. Accordingly, this paper will omit discussion of particular techniques and concentrate on the process in general.[39]

2. *Extracting Polymorphic Sections.*

The DNA strands in the sample's cells are over a million base pairs in length and contain both poly- and mono-morphic loci.[40] Thus, it is necessary to extract from the DNA strands the particular polymorphic loci to be examined. This is accomplished by severing the DNA molecule at the ends of the variable number of tandem repeat loci.

Restriction endonucleoses (REs) are enzymes which cleave the DNA strand wherever a certain sequence of bases occurs.[41] Each RE recognizes and cuts (or digests) a specific sequence of bases.[42] For example, the RE known as Hae III (used by the FBI)

severs the DNA strand between bases G and C wherever the sequence "G-G-C-C" appears.[43] Thus, for a sample VNTR DNA strand:

A-T-G-G-C-C-A-T-C-A-T-C-A-T-C-A-T-C-A-T-G-G-C-C-A-T-G-G-C-C-A-G

application of the RE Hae III results in four DNA fragments:

A-T-G-G, C-C-A-T-C-A-T-C-A-T-C-A-T-C-A-T-G-G,
C-C-A-T-G-G, and C-C-A-G

Of course, for samples examined in the laboratory, many thousands of fragments, each of varying length (depending upon the number of bases between the points of separation) result from the RE digestion process.[44]

3. *Electrophoresis.*

Now that the DNA polymorphic loci have been severed, it is necessary to physically separate them so they can be observed and measured. At this point, all of the DNA fragments are mixed together in a laboratory test tube. They are separated according to length by a process called electrophoresis.[45]

The laboratory uses a semi-solid matrix, or gel, somewhat the consistency of Jell-O®, as a sieve.[46] The gel contains a series of tiny pores which decrease in size from one end of the gel to the other.[47] An electric field is set up in the gel and the DNA fragments (which possess a negative charge) are attracted

to the positive anode.[48] The fragments migrate through the gel holes towards the positive anode. The smaller the fragment, the easier it is to move through the gel; thus, the larger fragments will move a lesser distance during the same period of time than the smaller fragments.[49] After a set period of time, the electric field is removed and the DNA fragments no longer move through the gel. At this point, the gel contains thousands of individual pieces of DNA separated by size. The fragments are too small to be seen by the naked eye. Even if visible, the fragments would appear as a continuum from one end of the gel to the other.[50]

4. *Separation of DNA Strands.*

The base pairs in the strands along the DNA molecule are held together by relatively weak hydrogen bonds. These bonds can be broken by the application of heat or high pH. However, the chemical bonds between bases along the *same* strand of DNA are much stronger. Therefore, when heat is applied or, more commonly, the DNA fragments are placed in a solution of sodium hydroxide,[51] the two strands of the helical DNA molecule are split apart, while the strands themselves retain their structural integrity. The result is a solution containing the separated DNA strands. This process is known as denaturation.[52] The process is also reversible; the reverse process is known as hybridization.[53]

5. *Southern Blotting.*

Southern blotting, named for Dr. Edwin M. Southern, who developed the basic procedure, transfers the DNA fragments from the gel to a more useable substance. In this procedure, a nylon membrane is placed in contact with the gel.[54] A transfer solution, often sodium hydroxide, is used in conjunction with blotting pads to wick the DNA from the gel onto the membrane in the same positions as in the gel. The membrane is then washed to remove any residual gel material and baked to fix the DNA in place.[55]

6. *Probe Hybridization.*

The DNA on the membrane is now composed of separated strands of different lengths, all too small to be visible to the naked eye. Now that the DNA molecule has been "unzipped," complementary DNA sequences (called probes) can be introduced and the DNA hybridized with these probes. The probes used in RFLP analysis recognize and bond with DNA from specific loci.[56] Each probe is identified by the VNTR it targets.[57]

These probes are radioactive to allow them to expose x-ray film and become visible. The probes are placed in a hybridization solution with the nylon membrane for several hours, gently agitated, and then washed with another solution to remove any excess probe.[58] The membrane now contains two types of DNA

fragments: those which have bonded with the radioactive probe and the remaining unbonded DNA.

7. *Autoradiography.*

The membrane is then placed in a plastic wrap and sandwiched between two sheets of X-ray film. The film and membrane are refrigerated for a period of days to allow the radiation from the probes on the membrane to expose the film. The film is removed from the membrane after exposure and developed as ordinary X-ray film.[59] The membrane is washed with a solution that removes all of the probe and then is analyzed again using a different probe.

The end result of the RFLP analysis is the X-ray film, known as an autoradiogram (commonly referred to as an autorad). The film is a copy of the nylon membrane, but the DNA fragments which bonded with the radioactive probe are now visible as dark bands on the autorad. The dark bands form a pattern much like a bar-code used in commercial practice. An autorad is made for each probe (and, in some circumstances, for all four probes together on the membrane).[60]

8. ***Matching.***

The DNA samples are not the only samples loaded in the gel when the RFLP process is performed. Each gel has several control lanes containing either DNA of known lengths or known human DNA

fragments. In addition, depending upon the laboratory protocol, several different evidentiary samples can be run on the same gel, since the DNA fragments migrate in straight lines through the gel. In fact, most quality control protocols require the suspect's sample and the evidentiary sample to be run in the same gel to eliminate any effect that different gels or solutions may have on the results.[61] The laboratory will discard the autorad unless all of the quality control measures are satisfied.

Now that the samples' DNA is visible on the autorad, they can be compared to determine whether or not the DNA from the suspect matches the DNA from the evidence. Each laboratory has its own criteria for declaring a match and its own procedures for automated analysis of the autorad. In general, the laboratory will declare a match if the DNA bands are within ± 2.5% to 5% molecular weight of each other.[62]

The first step is to view the DNA bands with the naked eye. If they do not align, the samples do not match;[63] the suspect thus could not have contributed the evidentiary sample. This result is called an exclusion.[64] If they are aligned, the samples are further compared using an automated analytical procedure. An automated method is necessary because closely-spaced bands may appear on the autorad that prevent the eye from accurately determining a match or non-match and to provide an objective method of measuring fragment size.[65]

Basically, the automated analysis consists of digitizing the autorad. The computer locates the area of maximum density within

each band on the autorad and compares it to that of the control lanes containing known-sized DNA fragments on the autorad. The computer interpolates the size of the evidentiary samples from the size of the control samples.[66] The result is a size (in Kb) for each band present in the evidentiary samples on the autorad. These sizes are then compared using the laboratory's matching criteria to determine whether or not a match exists.[67]

D. *DNA Statistics.*

The existence of a match alone is not conclusive. There exists the possibility that other parts of the DNA differ because only part of the individual's DNA is compared. A match means one of two things: either the suspect contributed the DNA found in the evidentiary sample, or someone else did and this person matches the suspect's DNA at the points examined by coincidence. This latter possibility can be calculated using standard statistical principles.

1. *Statistical Evidence.*

Statistical evidence is, by definition, circumstantial evidence.[68] Statistics can never be used to definitively prove an assertion; rather, they can be used only to demonstrate the frequency of an event's occurrence. The fact finder can then determine the relevance of, and weight to be given to, evidence

that the occurrence of an event (such as the defendant having an identifying characteristic that matches the evidentiary sample) is relatively rare.

Statistical evidence has generally fared well in American courts. Most courts, confronted with the issue, have permitted scientists to "present reasonable estimates of population frequencies and to articulate the mathematical calculations needed to arrive at the figure."[69] This type of statistical evidence is often admitted in criminal cases involving ABO blood types and paternity cases.[70]

The science of statistics is "concerned with the systematic and efficient collection and accurate analysis of data.... The analysis of data is the attempt to extract useful information from a set of data."[71] This analysis applied to DNA cases results in an inference that the suspect and the defendant are the same individual based upon the relative frequency of a match occurring between their DNA samples at random.[72]

2. *Databases.*

Each laboratory analyzing DNA has collected databases of DNA samples.[73] Laboratories use databases representative of the population to calculate the likelihood of the match occurring at random since it is not possible to test everyone in the United States. Although much debate occurred during the advent of forensic DNA analysis, the scientific community generally agrees

that a database consisting of as few as 150 individuals will suffice, so long as the individuals are unrelated.[74] Most of the major laboratories have databases of 300 individuals or more.[75]

Once the database has been collected, the laboratory analyzes all of the database samples using RFLP analysis and the resulting DNA sizes listed. Eight bands are present in a normal forensic test of four single-locus probes and two alleles per locus. Then, the laboratory compares the sizes of the fragments in the DNA match under investigation to those in the database to determine the relative frequency of each individual fragment.

Most laboratories have collected databases for three or more major populations.[76] This is necessary to counter "assortative mating," whereby people of one race, religion, or ethnicity tend to marry others with a common background. It is likely that the major population groups will exhibit some degree of variance as a group in their genetic makeup[77] even while not marrying for specific genes.[78]

3. *The Product Rule.*

Scientists make two major assumptions in statistical analysis. First, geneticists assume that the alleles at each locus are randomly selected; that is, no particular allele is associated with a particular locus. This assumption is somewhat restricted by mutation rate, natural selection, and other factors, but most scientists agree that these factors have not

been reliably shown to cause detectable deviations.[79] The independence within loci (such that the allele inherited from one parent is not governed by the allele inherited from the other parent) is known as Hardy-Weinberg Equilibrium (HWE).[80]

Second, scientists assume allele independence across loci. This assumption means that the presence of an allele at one loci is unrelated to the presence or absence of another allele at another loci. Although in general blond hair and blue eyes are often associated, people are unaware of the particular alleles they possess and do not select their mates based upon genetic composition. Random mating is the rule, not the exception, for humans. Additionally, RFLP analysis uses loci on separate chromosomes to help ensure independence.[81] Accordingly, scientists have found that sufficient independence exists at the VNTR loci for the statistical analysis to succeed.[82] This independence is called linkage equilibrium (LE).

Human geneticists use the product rule to calculate the probability of several individual events occurring simultaneously. The probability of each event occurring is multiplied by the probabilities of the other events. For example, the probability of obtaining three heads when a coin is flipped three times is calculated using the product rule, as the result of each flip is independent of the others. Since the probability of flipping a head on any particular flip of a coin is ½, the probability of having three heads in a row result on three flips is ½ x ½ x ½, or ⅛.

DNA analysis can use several forms of the product rule. The "pure" product rule multiplies all of the individual frequencies together without any conservative measures added.[83] The frequency for a heterozygous (meaning that the individual received different alleles from the mother and father) locus would be 2pq, where p is the frequency of the first allele and q is the frequency of the second allele. The frequency for a homozygous (the individual received the same allele from both parents) would be p^2 for the first allele and q^2 for the second allele. Thus, for an eight-loci sample with two homozygous (one of each allele) and six heterozygous loci, the "pure" product rule results in a frequency of $p^2 \times q^2 \times 12pq$.

The modified product rule used by the commercial testing laboratories and the FBI[84] adds a conservative measure to account for apparent, rather than actual, homozygotes. The appearance of a single band for a particular probe can be the result of several things; either the individual is a true homozygote; the "missing" band was small enough to migrate completely through the gel;[85] the DNA sample was degraded[86] or had too few repeats and the probe was unable to bind with the "missing" band;[87] the "missing" band did not migrate completely through the gel but did move past the control limits of the gel and thus was ignored by the laboratory protocol;[88] the "missing" band is actually present but close enough in size to the other allelic band as to be indistinguishable;[89] or, in cases of mingled samples, the band was not unique to the suspect.[90]

The laboratory cannot determine which of the above circumstances caused the apparent homozygosity. A homozygous locus is always rarer than a heterozygous locus.[91] The modified product rule replaces p^2 and q^2 with 2p or 2q.[92] Thus, the modified product rule is conservative in that it increases the frequency for apparent homozygous loci.

Forensic DNA laboratories use a further conservative measure in calculating the frequencies for the modified product rule. The laboratories create bins, or windows surrounding the DNA sample.[93] These bins match the size of the laboratories' match criteria; thus, if a laboratory declares a match for samples if they are within 2.5% of each other in size, the bin used on the database to calculate the allele frequency will include all database samples that are within 2.5% of the evidentiary sample. The frequency used will thus be greater than or equal to the actual frequency of the individual band within the database, because the frequency of all bands within the bin will be added to arrive at the bin frequency.

The product rule reveals the power of RFLP analysis. Many of the VNTR loci have probabilities under ten percent. If eight bands are used in the analysis, the probability is less than 0.1^8 or one in 100 million. This statistic is valid even though it is gained from a database containing samples from only 300-500 individuals. It is this power to identify an individual as the source of the evidentiary sample (as compared to probabilities of around one in one hundred for conventional genetic markers)[94]

that has caused some defense attorneys and experts to create an apparent controversy in the judicial acceptance of DNA analysis.[95]

III. DNA as Evidence.

DNA evidence was initially considered "novel" and thus had to pass certain hurdles[96] before being admitted into court. However, more experts began to testify regarding the techniques as more courts were presented with the evidence. As these experts pointed out, the techniques used in RFLP analysis were hardly novel; in fact, they had been used clinically for years. "The complete process -- DNA digestion, electrophoresis, membrane transfer, and hybridization ... [is] routinely used in molecular biology, biochemistry, genetics, and clinical DNA diagnosis; there is no difference in their forensic application."[97] Most DNA evidence is no longer treated as novel scientific evidence; however, this does not hold true for DNA statistical evidence.

The evidence was generally admitted with little or no objection by the defense in the first DNA cases.[98] Some of the judges themselves apparently understood little of the science behind the evidence but were content to let the evidence be presented to the jury.[99] However, the evidence (especially the statistical probability of a DNA match occurring at random between the defendant and the evidentiary sample) began to undergo significant challenge in 1989.[100]

A. *Evidentiary Rules for Admission of Scientific Evidence.*

The admissibility of scientific evidence has been determined by several different rules in United States courts. The Federal system began with case law, which was followed in several circuit courts of appeal (until *Daubert*).[101] Other circuits found the case law inconsistent with the enactment of the Federal Rules of Evidence in 1975.[102] Still others created a combination of the two standards, or modified their application of the single standard which they adopted.[103] The U.S. Supreme Court resolved the issue this year by deciding that the case law was inconsistent with, "absent from and incompatible with the Federal Rules of Evidence [and] should not be applied in federal trials."[104]

A discussion of the case law is still relevant because the Supreme Court adopted its "general acceptance" inquiry as part of the test under FRE 702. In addition, much of the determina-tion of general acceptance is made by examining decisions of other courts; as state courts have been presented with DNA evidence more often than federal courts, state court precedent is often persuasive. The recent Supreme Court decision is not binding in the state courts. Although some states' evidence codes are based on the Federal Rules of Evidence (and thus will probably incorporate the *Daubert* holding),[105] many states' codes are not and they will probably continue to require general acceptance as the deciding issue, rather than as merely a factor in deciding admissibility.

1. *The General Acceptance Test.*

Federal courts have employed a "general acceptance" test to determine whether novel scientific evidence may be admitted since 1923. This test was first enunciated in Frye v. United States:[106]

> Just when a scientific principle or discovery crosses the line between the experimental and demonstrable stages is difficult to define. Somewhere in this twilight zone the evidential force of the principle must be recognized, and while courts will go a long way in admitting expert testimony deduced from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs.[107]

The test was adopted by most Federal courts (at least until the adoption of the Federal Rules of Evidence) and over thirty state courts (although with some modification).[108]

The advantage of *Frye* is, of course, that some degree of support by other scientists in the relevant field of expertise is assured. It is presumed that the members of the relevant scientific community will examine the theory being propounded and subject it to testing to determine its validity before it is admitted into evidence. In other words, the scientists will act as a pseudo-jury prior to the court admitting the evidence.[109]

Of course, what *Frye* presumes is that scientists will subject the procedure and techniques to rigorous scrutiny and will attempt to reproduce the test and its claimed results per the scientific method. "It is certainly reasonable to expect science to withhold judgment on a new theory until it has been

well tested in the crucible of controlled experimentation and study. Such a procedure would require replication of original experiments, and scrutiny of the results in various scientific journals."[110] Indeed:

> [i]n order to prevent deception or mistake and to allow the possibility of effective response, there must be a demonstrable, objective procedure for reaching the opinion and qualified persons who can either duplicate the result or criticize the means by which it was reached, drawing their own conclusions from the underlying facts.[111]

It is this replication of results that is the heart of science.[112]

However, the assumption that general acceptance equates to validity is not always correct. History is replete with discoveries of "scientific principles" that are at first widely accepted, yet later proven false. For example, testimony by Christopher Columbus that the world was round would not be admissible under *Frye* in 1491 because the opposite was generally accepted, even though untrue. Today, most courts reject the "paraffin" test designed to determine whether an individual had residue from a gunshot on his person, although the test was continuously admitted as sound, generally accepted scientific evidence without any real challenge for over 25 years.[113]

The *Frye* court left much to be desired in creating this test. First, the court failed to provide any working definition of "general acceptance." In its aftermath, *Frye* has created heated discussion over who and how many must accept the principle before the courts may admit it into evidence.

For example, *Frye*'s requirement of "general acceptance in the particular field in which it belongs"[114] poses the question of establishing the field. Since the evidence in question is novel, determining which particular scientific field it falls under is often a tough question. The relevant fields for DNA evidence could be composed of molecular biologists,[115] human geneticists,[116] biologists,[117] statisticians,[118] forensic scientists,[119] chemists,[120] serologists,[121] pathologists,[122] and technicians,[123] among others. Indeed, the selection of the relevant field may turn out to be case-dispositive.[124]

In addition, the court gave no definition of general acceptance. Thus, some courts have looked for evidence that the principle's acceptance among the relevant field(s) is "widespread," "prevalent," and "extensive though not universal,"[125] while another has suggested that the test requires agreement by a "substantial section of the scientific community."[126] Some have even raised this standard to require a "clear majority" of scientists,[127] although all agree that unanimity or consensus is not required.[128] In addition, most agree that one scientist, no matter how impressive his credentials, is insufficient to find general acceptance. "[Courts] cannot accept a technique simply because a Nobel Prize winner takes the stand and testifies, 'I have verified this theory to my satisfaction, and I stake my professional credentials on the theory.'"[129]

Although the opinion was addressed to the scientific principle, *Frye* has been expanded to include the technique (and

sometimes the particular laboratory's process)[130] in the requirement of general acceptance. However, general acceptance of the specific procedures should not be enough to exclude relevant and reliable evidence. Because there may be many procedures to accomplish the same result and witnesses from commercial laboratories may have a financial or proprietal bias towards their method, it may be that no specific method has obtained "sufficient" general acceptance, yet the theory itself and one or more procedures are valid. On the other hand, failure to follow accepted procedures may make otherwise admissible evidence inadmissible.[131]

Instead, *Frye* poses a danger that, once one court finds the evidence admissible, the court's decision will carry so much precedential value that the *Frye* test becomes general acceptance within the *legal*, not *scientific*, field. Indeed, some legal commentators have said that a "beneficial consequence of the *Frye* test is that it may well promote a degree of uniformity of decision" and that:

> once a trial court has admitted evidence based upon a new scientific technique, and that decision is affirmed on appeal by a published appellate decision, the precedent so established may control subsequent trials, at least until new evidence is presented reflecting a change in the attitude of the scientific community.[132]

Until such time as a novel scientific theory or procedure loses its novelty and becomes judicially noticed (such as fingerprinting)[133], *Frye* mandates that science, not the courts, control.

Another problem with *Frye* is that it abdicates the judicial role in determining admissibility of evidence. As courts have

pointed out, the sole inquiry under *Frye* is not the reliability of the technique, but only whether or not the relevant scientific field has generally accepted the principle (and/or the technique).[134] Because of this, many courts have modified *Frye* so that the test becomes general acceptance of the reliability of the scientific principle or technique.[135] This test abdicates the judge's role in determining the admissibility of evidence and reduces him, in effect, to "counting heads."[136]

Frye also brings with it a certain degree of judicial evasiveness. When faced with such a hard and fast rule, courts have been required to create several methods of avoiding the application of the rule when its outcome would be unsatisfactory. Courts have found many ways to define "novel scientific evidence" such that the evidence in question is not subject to *Frye*,[137] defined *Frye* such that it applies only to "pseudoscience,"[138] or equated general acceptance with reliability.[139] *Frye* is also misused to exclude relevant evidence that on its face meets the test.[140]

2. *The Relevancy Test*.

Because of the problems involved in interpreting and applying *Frye*, many jurisdictions fashioned a "relevancy" test (with reliability one prong of relevance). They did so because, as stated above, the *Frye* inquiry went not to reliability, but only to general acceptance. With the adoption of the Federal

Rules of Evidence,[141] FRE 702[142] focussed the controversy over the standard for admitting scientific evidence.

FRE 702 omitted any mention of *Frye*, either in the text or in the analysis.[143] This omission (and its significance) divided the Federal courts into two camps: those which held the Rule superseded *Frye*,[144] and those which held that *Frye* was "part and parcel"[145] of FRE 702.[146] The controversy was finally settled by *Daubert*.

The same did not hold true in the military judicial system. The drafters of Military Rule of Evidence (MRE) 702 specifically stated that the rule "may be broader and *may* supersede *Frye v. United States*. . . . The Rule's sole explicit test is whether the evidence in question 'will assist the trier of fact. . . .'"[147] The military courts took the position that *Frye* was effectively superseded.[148]

Those courts and commentators in the relevancy camp believe that the admissibility of scientific evidence is to be determined like that of all other expert evidence. So long as the proffered evidence is relevant, reliable, helpful to the fact-finder, and not overly prejudicial, the evidence should be admissible. These are the requirements of FREs 401-403 and 702.

The Third Circuit championed the relevancy test in *United States v. Downing*.[149] In *Downing*, the court expressly rejected *Frye*, adopting instead a general relevancy test. The court concluded that the Federal Rules of Evidence "neither incorporate nor repudiate"[150] *Frye*. Instead, "a particular degree of

acceptance ... within the scientific community is neither a necessary nor a sufficient condition for admissibility; it is, however, one factor that a ... court normally should consider...."[151]

Downing defined "novel scientific evidence" as "evidence whose scientific fundaments are not suitable candidates for judicial notice...."[152] For such evidence, the court must inquire as to the soundness of the scientific process or technique; its possibility of overwhelming, confusing, or misleading the jury; and its connection to the particular disputed issue on which it is offered.[153] According to the *Downing* court, once "a technique has found favor with a significant number of other courts, a ... court may exercise its discretion to admit the evidence through judicial notice."[154]

Where the technique has not been the subject of extensive litigation, the court suggested examining several factors enumerated by Judge Weinstein and Professor Berger. These factors include the "novelty" of the technique, the existence of a body of specialized literature, the non-judicial uses of the technique, the frequency and type(s) of errors, and the credentials of the expert witnesses.[155] The court then balances the degree of assistance the evidence will offer against the dangers of confusing or misleading the fact-finder. Finally, the court must ensure the probative value is not substantially out-weighed by prejudice to the accused.[156]

Under *Downing*, the trial court properly assumes the role of deciding on the admissibility of scientific evidence rather than the scientists in the field.[157] The court hears evidence (usually on a motion *in limine*) and decides the question of admissibility based on a preponderance of the evidence under FRE 104(a). Although the court denied it, *Downing* essentially defined FRE 702 as requiring helpfulness, which it defined as a combination of FREs 401-403.[158] This is the identical procedure used for all types of evidence.

3. *The Military Experience*.

The military courts, like most Federal courts, initially adopted the *Frye* test as the controlling standard of admissibility for novel scientific evidence.[159] *Frye* remained as the standard for over thirty years. However, most of the courts of review expressed some concern or discontent with this standard.

The Navy-Marine Corps Court of Military Review first mentioned MRE 702 as a different standard from *Frye*. In *United States v. Jefferson*,[160] the court took note that MRE 702 was a lesser standard than *Frye*. However, the court did not have to apply the new standard because it found that the challenged evidence was generally accepted by the relevant scientific community.[161]

The Army Court of Military Review was next to comment in *United States v. Bothwell*.[162] *Bothwell* involved the admissibil-

ity of psychological stress evaluation (PSE) evidence, by which changes in a person's voice modulation were said to indicate deception. The court was apparently applying a precursor of the relevancy test, although it stated that *Frye* was the controlling standard and had been so for almost thirty years. The court stated that evidence must be relevant to be admissible, and "relevance is, in part, a function of the reliability of the underlying technique."[163] This was a departure from the strict "general acceptance" test of *Frye*. The court noted that PSE's reliability was in question because it was still in the "'experimental' rather than 'demonstrable' stage."[164] The court stated that the trial court's refusal to admit the PSE evidence was error, but held the error harmless.[165]

The Court of Military Appeals (COMA) also departed from *Frye* in *United States v. Mustafa*.[166] There, the court faced the question of admissibility of blood-spatter analysis evidence. The court found that "[t]here is a body of specialized knowledge which would permit a properly trained person to draw conclusions as to the source of the blood,"[167] eliminating the need to determine whether such evidence was or was not generally accepted (as the defense objection claimed). The court stated that, "[t]o be admitted, expert testimony need only be helpful, i.e., relevant."[168] Nowhere did the court require general acceptance of such an admittedly novel technique.[169] Indeed, in light of the debate in Federal courts regarding *Frye*/FRE 702, COMA's emphasis

on "helpful" and "relevant" was a strong step towards abandoning *Frye*.

The Army and Air Force Courts were the next to signal the impending demise of *Frye* in the military. In *United States v. Carter*, the Army Court stated:

> The test for admissibility under MRE 702 is whether the expert's testimony is helpful to the trier of fact. There is no requirement that the expert's testimony is absolutely necessary or that the testimony be based on scientific principles that are generally accepted in the scientific community. We have some doubts, therefore, of the continued applicability of the Frye test as concerns this issue.[170]

In *United States v. Gillette*,[171] the Air Force Court was faced with the issue of "faceprint" evidence (similar to fingerprints). The court held that a witness would be able to testify about a "faceprint" found on a plastic bag because his "specialized knowledge in criminal investigation techniques would be of assistance to the factfinders."[172] Interestingly, the court did not "decide if a 'faceprint' has sufficient scientific acceptance to be admissible in the same manner as finger and palm prints or as handwriting or voice analysis which are admitted as conclusive proof of identity."[173] The court departed from *Frye*, apparently on the basis that, since a "faceprint" would not provide conclusive evidence, it need not meet the requirement of general acceptance. The court apparently read MRE 702 as applying to less than conclusive evidence, while the *Frye* standard was reserved for what the courts considered "conclusive evidence."

The Court of Military Appeals resolved the issue a year later. In *United States v. Gipson*,[174] the court was faced with the question of admissibility of polygraph evidence. Both the prosecution and defense wished to introduce polygraphs. The trial judge denied the defense (and the prosecution) the opportunity to lay a foundation of general acceptance of polygraphy under *Frye*. The judge excluded both sides' proffered evidence, citing a lack of general acceptance and concern that polygraphic evidence may deprive the fact-finder of its duty of determining witness credibility.[175]

COMA essentially adopted *Downing* for the military, citing the case no less than nine times and quoting extensively from it.[176] COMA looked to previous cases in which it had interpreted the MREs as relaxing the standard of admissibility of expert testimony in general and found the rejection of *Frye* to be "in line with that policy."[177] COMA found that MREs 401-403 and 702 are the applicable standard for admissibility of expert testimony regarding scientific evidence which could not be judicially noticed and that the military rules creating such a standard were properly within the authority of the President to promulgate.[178]

Like *Downing*, COMA did not dispense entirely with *Frye*'s requirement for general acceptance. COMA held that general acceptance is but one of the indicia of scientific reliability of the proffered evidence required under MRE 702, rather than making such acceptance disposatory. COMA stated that the absence of

general acceptance may be outweighed by other factors (similar to those in *Downing*).[179]

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

The United States Supreme Court finally resolved the split among the various Circuit courts (and the military) in *Daubert v. Merrell Dow Pharmaceuticals, Inc.*[180] The parents of Jason Daubert and Eric Schuller sued Merrell Dow, alleging that the children's birth defects were caused by Bendectin, a drug made by the defendant. At trial, Merrell Dow introduced an affidavit from an expert who had reviewed more than thirty published studies of the drug and found no evidence linking Bendectin to birth defects. He concluded that the drug posed no risk to fetuses. Plaintiffs countered with testimony from other experts who had recalculated data from the same studies as Merrell Dow's expert and claimed a causal link between Bendectin and the childrens' deformities. The trial court termed the plaintiffs' studies unpublished and non-peer-reviewed recalculations of previously published and reviewed studies, held them inadmissible under *Frye*, and granted summary judgment for Merrell Dow.[181] The Ninth Circuit Court of Appeals affirmed.[182] The Supreme Court granted *certiorari* with the express purpose of resolving whether *Frye* or the Federal Rules of Evidence controlled admissibility of scientific evidence.[183]

The Court noted that the Federal Rules were legislatively-created and thus interpreted them as it would a normal statute. First, the Court found no requirement of general acceptance in the plain language of FRE 702. Neither did the legislative history mention *Frye* or its standard. Instead, the history of the Federal Rules of Evidence evinced a "liberal thrust" and a "'general approach of relaxing the traditional barriers to 'opinion' standard.'"[184] Thus, the Court held that the general acceptance standard was "austere" and "absent from and incompatible with the Federal Rules of Evidence."[185]

The Court reiterated that the trial judge has a "gate-keeping" function, by which he is to ensure that evidence admitted under FRE 702 has a basis in science.[186] Before admitting proffered scientific expert testimony, the court must find that the testimony constitutes scientific knowledge that will assist the trier of fact to understand or determine a fact in issue. This finding is a preliminary question to be resolved pursuant to FRE 104(a).[187]

The Court stressed that the evidence be scientifically sound: "In 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. . . . In short, the requirement that an expert's testimony pertain to 'scientific knowledge' establishes a standard of evidentiary reliability."[188] The Court explained that its use of the term

"reliability" encompassed both validity of the principle and reliability of its results.[189]

The Court went on to list the factors to be considered in determining whether the evidence was sufficiently grounded in science.[190] Trial judges should look to whether the principle can be tested and the results replicated. In addition, peer review and publication are important considerations, as are the error rate of the procedure. Finally, general acceptance is important, although this determination does not require identification of a particular scientific community.[191] Most importantly, the Court noted that "[t]he focus, of course, must be solely on principles and methodology, not on the conclusions that they generate."[192]

The Court concluded by reminding trial judges that they must balance the scientific evidence against the danger of misleading the jury, unfair prejudice, or confusing the issues. The judge must perform the FRE 403 balancing test, just as is necessary for non-expert testimony. However, because "[e]xpert evidence can be both powerful and quite misleading .... the judge exercises more control over experts than over lay witnesses."[193]

Thus, the Court held that scientific evidence is no different from any other under the Federal Rules of Evidence. So long as an examination of the technique reveals a reliable basis in science and the witness meets the minimum qualifications as an expert, the witness may testify if his testimony would be helpful and relevant to a contested issue and is not misleading, overly confusing, or substantially more prejudicial than probative.

This is the standard to be applied in Federal cases regarding DNA, at least until DNA evidence is judicially noticed.[194] If the NRC Committee's recommendations (discussed infra) are followed, trial courts may and should take judicial notice of all of the DNA evidence but the statistical evidence.

B. *DNA's Acceptance in the Courts.*

DNA has fared well under all of the standards (*Frye*, *Downing*, and their hybrids). As of March 2, 1992, DNA evidence has been conducted in over 14,700 criminal investigations and admitted in over 610 criminal trials, while being rejected in only twelve cases.[195] Since then, the great majority of federal and state decisions have admitted the evidence.[196] DNA has not yet played a significant factor in courts-martial.[197]

Where the evidence has been excluded, more often than not it is the statistical probability of a random match between the DNA of defendant and the evidentiary sample that has caused the courts' concern.[198] Although statistical evidence regarding the frequency of genetic characteristics in connection with serological tests generally faces little opposition,[199] the DNA statistical evidence has been excluded on numerous bases. Some states have statutes which discourage or prohibit the introduction of all statistical evidence.[200] Others found that, although the theoretical basis for DNA was generally accepted, the method by which the statistics were calculated was not.[201]

One court excluded the statistics because of due process concerns.[202] Of those courts that excluded the statistical evidence, many held that evidence of a DNA match was irrelevant or overly prejudicial without some method of informing the jury what a match meant.[203]

IV. The Controversy.

Until 1989-90, DNA evidence was generally non-controversial. DNA evidence, although novel (and thus subjected to the evidentiary tests described above), was found to be generally accepted by an overwhelming majority of courts. There were some early attacks regarding the possibility of band shifting, lack of national standards, differing criteria for declaring a match, and questionable laboratory techniques (use of ethidium bromide gels, loading mass, etc.) but these attacks were generally short-lived and unsuccessful.[204] It was not until *United States v. Yee*[205] that DNA was assailed in force.

A. *United States v. Yee.*

In ***Yee***, three members of the Hell's Angels motorcycle gang executed an individual in Ohio, mistaking him for a member of a rival gang whom the three believed responsible for shooting a member of their gang. John Bonds, Mark Verdi, and Wayne Yee were charged with the shooting. At trial, the government offered

evidence that DNA found in blood on the seat of Yee's car matched Bonds' DNA. The defendants objected, and a federal magistrate held a six-week *Frye* hearing in which twelve expert witnesses testified and over 200 exhibits were introduced regarding DNA RFLP analysis.[206]

At the conclusion of the hearing, the magistrate found[207] that the pertinent scientific community was composed of molecular biologists and population geneticists.[208] The magistrate rejected the defense's contention that a consensus was required, and listed several factors that could aid the fact-finder in determining general acceptance. The magistrate stated:

> In summary, I have not encountered, and the parties have not cited, a case applying the *Frye* standard rejecting the admissibility of evidence where a set of experts, such as in this case, have testified that the procedure was generally accepted. Where such experts have testified, the evidence has been admitted despite firmly held countervailing views of the opponent's experts. [209]

The magistrate found that the relevant scientific community had generally accepted the RFLP technique; thus, the DNA evidence, including the statistical probability of a match occurring at random, was admissible. The defendants were subsequently convicted, and their convictions upheld on appeal.

The magistrate heard from various defense witnesses challenging all aspects of the FBI's laboratory protocol, including the use of ethidium bromide in the electrophoresis gel, the possibility of bacterial contamination, and the amount of restriction endonuclease. The prosecution witnesses testified that the protocol was proper and provided correct conservative

results. The magistrate also considered the Report by the Congressional Office of Technology Assessment, which stated that forensic DNA testing was "reliable and valid." The report also found that "[q]uestions about the validity of DNA typing -- either the knowledge base supporting technologies that detect genetic differences or the underlying principles of applying the techniques *per se* -- are red herrings that do the courts and the public a disservice."[210] The magistrate found that these challenges were insufficient to require that the evidence be excluded.

At the magistrate's hearing, the prosecution called four witnesses relative to the issue of population genetics and statistical evidence: Dr. Patrick Conneally of the Indiana University School of Medicine, Dr. Stephen P. Daiger of the University of Texas Health Science Center, Dr. C. Thomas Caskey of the Baylor College of Medicine, and Dr. Kenneth K. Kidd of Yale University School of Medicine. The defense called Dr. Richard C. Lewontin of Harvard University, and Dr. Daniel L. Hartl of the Washington University School of Medicine. The court called Dr. Eric S. Lander of the Massachusetts Institute of Technology. These witnesses' testimony and reports prepared by Drs. Lewontin and Hartl[211] formed the basis of the defense attack on DNA at *Yee* and have been submitted to and relied upon in almost every case that has excluded DNA evidence since *Yee*.[212]

B. *The Problem: Population Subgrouping.*

Drs. Lewontin and Hartl testified (and their reports echoed their testimony) that the statistical evidence of the probability that Bond's DNA and the DNA found in the blood in the back seat of Yee's car matched randomly should not be admitted into evidence because they claimed that the method by which the probability was calculated had not been generally accepted by the relevant scientific community.[213] The FBI calculated the probability as one in 35,000.[214]

Dr. Lewontin testified that he believed that, because the frequency of blood types varies among European nationalities, there may be a similar variation in the genes analyzed by RFLP analysis in Americans who, according to Dr. Lewontin, are generally descended from "relatively recent[ly] arriv[ed]" immigrants. He believed that this variation has not been sufficiently diluted because of a "lack of interethnic group mating."[215] Drs. Lander and Hartl agreed with Dr. Lewontin.

Population subgrouping would be a problem in DNA analysis because the probabilities calculated from a general database could be based on under- or over-represented subgroups. If, for example, a database was composed of Caucasians in general, but the database had an overrepresentation of "Reds" (a fictional subgrouping of individuals who have red hair), the probability calculated using that database of an individual selected at random having the gene which causes red hair would be greater

than the actual probability of the population as a whole. On the other hand, if "Reds" were absent from the database but present in the population, the probability calculated from the database would be smaller than the actual probability from the population.

This is the crux of the DNA opponents' argument. They believe that 1) it is possible that population subgrouping exists within the databases used by DNA laboratories; 2) this population subgrouping causes some subgroups to be either over- or underrepresented in the databases; 3) that because of this over- or underrepresentation, any probability of a random match occurring calculated by use of the databases would be skewed; 4) the degree of effect (if any) of population substructure on the statistics cannot be determined;[216] and 5) there is no conservative step or method known to Drs. Lewontin and Hartl that could compensate for the effects of population subgrouping.[217]

Although the magistrate ruled against the defense experts in *Yee* and allowed the DNA statistics into evidence, Drs. Lewontin, Hartl, and Lander continued to testify and author reports, letters, and articles which suggested that the statistical evidence was not grounded in science.[218] Using this theory, the defense was successful in excluding the DNA statistics in several cases.[219] Because of these results and the claim by the defense that the statistics were not generally accepted under *Frye*, the National Academy of Science's National Research Council undertook a study of the science surrounding DNA evidence in general and the statistics involved in DNA identification.[220]

C. *The National Research Council.*

The National Research Council (NRC) is an agency of the National Academy of Sciences (NAS), a "private, non-profit, self-perpetuating society of distinguished scholars engaged in scientific and engineering research, dedicated to the furtherance of science and technology and to their use for the general welfare." Congress granted the NAS a charter mandating it to "advise the federal government on scientific and technical matters."[221] Based upon requests by the FBI, lawyers, and scientists, the NRC began in January, 1990 a study of the forensic aspects of DNA technology. The study was funded by the FBI and the National Institute of Justice, among others.

The NRC established a committee to conduct the study. The Committee was composed of individuals with diverse backgrounds, including, among others, two of the witnesses in *Yee*, Drs. Eric S. Lander[222] and C. Thomas Caskey.[223] The Committee met several times over a two-year period, and heard testimony from various individuals in April 1990. The Committee issued its report on April 14, 1992.[224]

1. ***The NRC Report.***

The NRC report generally validated the utility and reliability of DNA evidence. The report's major conclusion "confirm[ed] the general reliability of using DNA typing evidence

in criminal cases." The report stated that "DNA samples are capable of providing 'strong evidence' for pointing to the perpetrator of a crime or clearing an innocent suspect."[225] The report recommended that courts confronted with DNA evidence should judicially notice the underlying theory of identification by DNA RFLP analysis.[226] The report recommended that courts constrain their inquiries under both *Frye* and *Daubert* to whether the laboratory procedure in the instant case was correctly followed and whether the statistics offered were "appropriately conservative."[227]

However, the major impact of the report involves the use of DNA statistical evidence. The Committee devoted an entire chapter to the statistical basis of DNA analysis.[228] Their underlying assumptions and recommendations regarding the use and validity of statistical evidence form the basis of the controversy surrounding the NRC's report.

2. *Chapter Three of the NRC Report.*

In Chapter Three, the NRC first states that "say[ing] that two patterns match, without providing any scientifically valid estimate (or, at least, an upper bound) of the frequency with which such matches might occur by chance, is meaningless."[229] This statement appears, at first glance, to make sense; however, a closer examination reveals that it does not. Clearly, the fact that the suspect has a characteristic which matches that of the

perpetrator is both legally and logically relevant to the issue of identity unless the characteristic is universal. Since, in our judicial system, the suspect is presumed innocent on a plea of not guilty, it is relevant and helpful to the finder of fact to know that the accused shares a common trait with the perpetrator. Of course, the weight of the match depends upon its rarity.

However, the report is most controversial in its discussion of the problem of population substructure. The Committee first notes the existence of what it determines to be "[s]ubstantial controversy ... concerning the methods of estimating the population frequencies of specific DNA typing patterns." The NRC then cites to works by Dr. Lander, Lewontin, and Hartl and responses to them, the non-peer reviewed invited editorial of Dr. Lander, responses to it, and the Lewontin/Hartl and Chakraborty/Kidd articles in SCIENCE.[230] The report then goes on to state that this controversy goes not to the weight of the evidence, but rather to its admissibility since it calls into question the scientific validity of the particular method used.

This paragraph of the report is extremely important. By describing the efforts of Lander, Lewontin, and Hartl as a "substantial controversy," the NRC rejected the characterization of their efforts by the judiciary (as in *Yee*) and, in jurisdictions governed by *Frye*, foreclosed the admissibility of the statistical evidence by ensuring that general acceptance cannot be found.[231] Interestingly, SCIENCE magazine, in which two of the

major articles appeared,[232] introduced the articles as "Richard Lewontin and Dan Hartl hav[ing] taken on *the forensic science establishment*."[233] It also noted that the magazine's editor found errors in the paper's data and conclusions.[234]

The report echoes its theme a few pages later.[235] Its discussion of population substructure recites the same articles and letters by Lewontin, Hartl, and Lander as "considerable debate" about the possibility of significant substructure. The report then repeats their criticisms in detail, while affording only a sentence to the views of the DNA supporters.[236]

The NRC report stated that:

> [r]ecent empirical studies concerning VNTR loci detected *no deviation from independence within or across loci*. Moreover, pairwise comparisons of all five-locus DNA profiles in the FBI database showed no exact matches; the closest match was a single three-locus match among 7.6 million pairwise comparisons. These studies are interpreted as indicating that multiplication of gene frequencies across loci does not lead to major inaccuracies in the calculation of genotype frequency--at least not for the specific polymorphic loci examined.[237]

These statements clearly refute the position of Lewontin, Lander, and Hartl. The NRC failed to cite a single study showing no independence of VNTRs within or across loci; rather, they cited studies which show the alleles are independent. Indeed, the Committee stated that "no evidence of population substructure is demonstrable with the markers tested so far...."[238] This independence validates the use of the product rule in calculating the possibility of a random DNA match.

Amazingly, the NRC chose to reject this information and rely on an outdated and incorrect study by Dr. Lewontin.[239] The Committee *assumed* the existence of population substructure and developed a recommended method to account for any effect it may have in calculating probability estimates. This is the aspect of the NRC report which has had the greatest impact on admissibility of DNA statistical evidence.

The Committee report stated that it "has chosen to *assume for the sake of discussion* that population may exist...."[240] The Committee rationalizes first that it is possible and appropriate to use conservative numbers because, according to the Committee, "the statistical power lost this way can often be recovered through typing of additional loci."[241] This excuse is circular; the Committee wishes to lessen the numbers arrived at by the use of DNA analysis, but can correct this by using additional probes, whose statistical power must *also* be diluted. In addition, this recommendation fails to address the issue of an evidentiary sample that, due to degradation or sample size, will not respond to four or more probes.[242]

Rather than arrive at the correct number, the number calculated by this means will actually be even further reduced for each additional probe used. Evidently, though, the number will approach the maximum with which the Committee can be comfortable. Left unanswered by the report is the final number of probes required before this limit is reached.

Next, the report states that its recommendations are based on the necessity of applying to present and future forms of DNA analysis and different loci. The Committee again mentions that, for loci currently tested, empirical studies show independence between and across loci.[243] However, the Committee's concern over possible future methodologies and its determination to address an issue not properly before it was unnecessary and its unstated assumption that future loci used may not be independent is unsupported. Regardless, the suggested solution should be reserved for any future loci which demonstrate population substructure, not for those loci used currently and for which there is no evidence of population substructure.[244]

The report states that the only way to determine the effect, if any, of population substructuring is to measure it empirically (evidently discounting the studies that the report itself references earlier in the chapter). The NRC claims that population subgrouping cannot be readily detected by conventional means or theoretical considerations.[245] The Committee uses an admittedly extreme and hypothetical example to show that the ability of the test for Hardy-Weinberg equilibrium is relatively weak in detecting substructure.[246] Nor can the differences between racial groups be used as an upper bound for the allele frequencies because, according to a study by Dr. Lewontin in 1972, "the genetic diversity between subgroups within races is greater than the genetic variation between races."[247]

Unlike Drs. Lander and Lewontin, the NRC believes that it "is feasible and important to estimate the degree of variability among populations to evaluate the impact of population substructure on genotype frequencies estimated with the multiplication rule."[248] The report recommends direct sampling of allele frequencies in multiple ethnic subgroups.[249] This sampling, according to the Committee, is the only way to detect population subgrouping.

The Committee fails, however, to define which subgroups to sample or how these subgroups are to be defined (other than by stating, "e.g., ethnic subgroups"[250] and "genetically relatively homogeneous").[251] Ultimately, the Committee chose to leave the "selection, collection, and analysis of such samples [to be] overseen by" yet another committee which the NRC recommends be created.[252]

Interestingly, the NRC recommends that some of the sample populations include "English, Germans, Italians, Russians, Navahos, Puerto Ricans, Chinese, Japanese, Vietnamese, and West Africans."[253] The Committee did not state how it determined these groups to be representative of population groups in the United States. In addition, there is no evidence that these groups are themselves homogenous and are not comprised of subgroups.

After collection, the samples will be measured to determine the frequency for each allele found. The Committee believes that 200 alleles (two from each of 100 individuals drawn at random from the population) is a sufficiently large database to

determine whether some allelic frequencies are significantly greater than in the general population.[254] If such a significant deviation is found, it becomes the "ceiling" frequency for that allele for all defendants. If the examiners find no significant deviation, the greater of the largest frequency found or five percent becomes the "ceiling" frequency.[255]

The Committee selected five percent because it felt that "allele frequency estimates that were substantially lower would not provide sufficiently reliable predictors for other, unsampled subgroups."[256] The Committee believed that "[e]ven if one sees allele frequencies of one percent in several ethnic populations, it is not safe to conclude that the frequency might not be five-fold higher in some subgroups."[257] Once again, there is no data provided to support this assumption.

The report recommends two methods of presenting to the court the probability of a match between the suspect's and the sample DNA occurring at random: direct sampling of a database and a method it terms the "ceiling principle."[258] The "ceiling principle" is nothing more than the product method using the "ceiling" frequencies calculated above.[259] However, until the collection and analysis of population subgroups recommended above occurs, the Committee recommends using a modification of the "ceiling principle" instead.[260]

Direct sampling occurs when the testing laboratory examines its database to determine whether or not any samples within the database match the multilocus genotype of the suspect/evidentiary

sample. The jury would be told that the sample did not match any of the samples in the database.[261] The jury would also be told the number of samples contained in the database, denoting its rarity.[262]

However, with few databases consisting of over 1000 samples,[263] this method would provide a maximum rarity of 1/1000. Another way of stating this is to say that "it is 99% likely that the true frequency is less than one in 218."[264] This figure is deceptively misleading when one realizes that, "if everyone in the world had the same two parents, who were heterozygous for different alleles at four independent loci, the frequency of any particular four-locus profile would be one in 256."[265] The Committee admits that "such estimates do not take advantage of the full potential of the genetic approach."[266]

Even using the NRC's modified ceiling principle (discussed below), the maximum rarity would be one in 6.25 million.[267] And, if population substructure did exist within the database and did cause an effect on the frequencies of the individual loci, then the database would not be truly representative of the relevant population and thus may result in the same problems as Lander and Lewontin claim are caused by the product rule. Thus, the direct sampling method adds slight evidence to the question of identity.

Then, the expert should inform the jury of the probability of someone else randomly matching the suspect's and evidentiary DNA sample calculated via a form of the "ceiling principle." During the pendency of the sampling of fifteen to twenty genetic-

ally relatively homogeneous populations, the expert should calculate the probability using the "modified ceiling principle."[268] The "ceiling principle" is the recommended method to use after completion of the above studies, provided no evidence of any significant population subgrouping appears.[269]

At this point, a discussion of the term "ceiling principle" is necessary. "Ceiling" is an improper description of the method, as the word implies a maximum value. In fact, the method requires use of a *minimum* value (the greater of the frequency calculated empirically or five percent).

The word "principle" has a specific meaning in science. A "principle" is a "scientific law that explains a natural action."[270] Since, as discussed below, there is no scientific basis for replacing the empirically-derived frequency with either five or ten percent, the NRC's recommended method hardly qualifies as a principle.[271]

The "ceiling principle" is designed to correct for the assumed existence (and substantial effect, which must also be assumed) of population substructure. The NRC was concerned not only with population substructure in existing databases but also that the particular suspect may belong to a population not covered by these databases.[272] Thus, the Committee recommends essentially the creation of a "super frequency," which is the greatest frequency with which the particular allele appears across *all* populations and subgroups. The end result may be that, for loci one through eight, the greatest frequency may

appear in the English, German, Western African, Navajo, Chinese, Puerto Rican, Italian, and Japanese populations, respectively.[273] The "ceiling principle" uses these frequencies, rather than the frequencies from any single population. Of course, should any of them be less than five percent, the figure of five percent is substituted for the actual figure.

Finally, until the studies of these "relatively homogeneous" populations are completed, the "ceiling principle" is modified to raise the threshold frequency from a minimum of five percent to a minimum of ten percent.[274] Ten percent is, according to the Committee, a "pragmatic approach to recognize the uncertainties in current population sampling."[275] This figure is "designed to address a remaining concern that populations might be substructured in unknown ways with unknown effect and ... reflects the greater uncertainty in using allele frequency estimates as predictors for unsampled subpopulations."[276] The product rule is applied to the frequencies determined empirically from the existing databases for Blacks, Caucasians, and Hispanics, substituting ten percent for those individual frequencies found to be less than ten percent. This calculation gives the resulting frequency to be reported to the court.

3. *The Remainder of the NRC Report.*

Chapter Six, entitled "Use of DNA Information in the Legal Systems," discusses the *Frye* standard for admissibility[277] and

lists assumptions whose validity is questioned when the evidence is offered:

> 1) [E]xcept for identical twins, each person's DNA is unique;
>
> 2) the technique used allows one to determine whether two DNA samples show the same patterns at particular loci;
>
> 3) the statistical methods used and the available population databanks allow one to assess the probability that two DNA samples from different persons would by chance have the same patterns at the loci studied...; and,
>
> 4) ...the laboratory's procedures and analyses in the case in question were performed in accordance with accepted standards and provide reliable estimates of the probability of a match.[278]

The Committee notes that the first assumption is so firmly established in human genetics that courts may judicially notice it.[279] The Committee makes the same recommendation regarding Restriction Fragment Length Polymorphism analysis using the Southern blotting procedure.[280] The third assumption is also reliable enough to allow the analysis into evidence so long as it is "appropriately conservative."[281] The Committee stresses that the solution is "not to bar DNA evidence, but to ensure" that only conservative figures are used.[282] The fourth assumption is a case-by-case issue.[283]

The remainder of Chapter Six is a recitation of the court decisions, both Federal and state, which have addressed the admissibility of DNA evidence.[284] There is a discussion of the growing trend among states to legislate the admission of DNA evidence, effectively removing the question from the courts.[285]

The rest of the NRC Report concerns itself with a discussion of standards for laboratories conducting DNA analysis;[286] DNA databanks and privacy interests;[287] and the social, economic, and moral/ethical implications of DNA.[288]

V. The "Science" Underlying the "Ceiling Principle."

The NRC issued its report in an attempt to resolve the apparent controversy over the scientific reliability of the DNA evidence (primarily statistical evidence) being offered in courts by both the prosecution and the defense.[289] However, the report has accomplished just the opposite; there is now more of a controversy over the report and its significance than there was over the evidence.[290] As the Sixth United States Circuit Court of Appeals stated in *Bonds*, "[t]here is no dispute that the NRC Report exists, but there is considerable dispute over the significance of its contents."[291]

This controversy has caused some courts to exclude all DNA evidence.[292] Eric Fisher, director of the NRC's board on biology in Washington, D.C., stated, "[c]learly there is continuing controversy in the area, in fact, a growing controversy." But, he added, the NRC never intended for its report to become the back-drop to a court opinion ruling DNA inadmissible. "I think you could safely say that what happened in [*People v. Barney*] was not an intended effect because the Committee very pointedly said

that DNA was an important forensic tool and should continue to be used," he said.[293]

No one seriously argues with the proposition that some degree of population substructure is present in humans.[294] All human population categories are composed of subgroups; there are no truly homogeneous populations. However, merely because some population substructure is present does not mean that it has such an effect as to alter the forensic reliability of DNA frequency statistical evidence.

The "ceiling principle," clearly the most controversial part of the NRC Report,[295] was designed to correct for the assumed presence and effects of population substructure in determining the statistical probability that the match between the suspect's DNA and the evidentiary DNA occurred at random. Once calculated, this probability should then be introduced into evidence to demonstrate that, due to the rarity of the DNA pattern, it is likely that the accused left the evidentiary sample.[296] This calculation[297] is to be offered as scientific evidence under FRE 702.

A. *The Committee's Justification.*

The problem with the "ceiling principle" is that there is no scientific basis underlying it. The NRC Report offered only an *assumption* both that population substructure exists *and*, albeit implicitly,[298] that its effect is so substantial as to render the

use of the product rule unscientific and unworthy of admission into evidence. The Committee made this assumption in the face of strong evidence to the opposite.[299]

In order to qualify as scientific evidence, the proffered information must have a basis in science.[300] "Scientific methodology today is based on generating hypotheses and testing them to see if they can be falsified; indeed, this methodology is what distinguishes science from other fields of human inquiry."[301] The Supreme Court called the ability to reproduce the results of the experimentation as "a key question" in determining admissibility of scientific evidence in Federal courts.[302]

The Committee generated a hypothesis when it assumed that population substructure does have significant effects on use of the product rule in forensic DNA analysis. However, the Committee failed to test its hypothesis prior to adoption and publication of its "ceiling principle." While calling for someone[303] to sample fifteen to twenty allegedly genetically homogeneous populations, the Committee could not cite a single study in support of its assumption. Instead, the Committee cited only the work of Drs. Bruce Weir, Neil Risch, and Bernard Devlin disproving the assumption.[304] This procedure is not in accordance with accepted scientific method.

The only support given by the Committee for its assumption was a paper written by Dr. Richard Lewontin over twenty years ago.[305] In that article, Lewontin stated that "[c]ontrary to common belief based on difference in skin color and hair form,

studies have shown that the genetic diversity between subgroups within races is greater than the genetic variation between races."[306] The weight of the evidence gathered since Lewontin's report was published argues against Lewontin's (and the Committee's) assertion regarding differences in genetic diversity between and among races.[307] Lewontin himself has abandoned that position since the publication of the NRC Report. He and Dr. Hartl now "*reiterate* the conclusion that there is *approximately as much* genetic variation among ethnic groups within major races as there is among the races."[308]

In fact, this "controversy" about population substructure is "qualitatively the same issue that has confronted the forensic serologist for years."[309] Yet courts have routinely accepted testimony regarding probability estimates of protein combinations in serology using databases drawn only on racial lines (like the DNA databases).[310] Dr. Hartl even admitted in *Yee* that the issues were the same, but, in his opinion, the quantitative difference in estimates justify differential treatment in court.[311] The Supreme Court holds otherwise: "[D]ifferences among experts [that are] quantitative, not qualitative.... go to the weight of the evidence and not the admissibility of such testimony...."[312]

B. *The Subsequent Research.*

Scientific research published subsequent to the NRC Report continues to disprove the Committee's assumption.[313] Dr. Ranajit

Chakraborty conducted a study in which he determined that the DNA databases do not show evidence of significant population substructuring.[314] Many defense experts assert that the presence of a large number of homozygotic samples within forensic databases is caused by population substructure.[315] Dr. Chakraborty's study reveals that the number of apparent homozygotes is too great to be caused by population substructure and explains that they are the result of imperfections in the RFLP methodology.[316] He also demonstrated that, should such substructure be present within the American population, the RFLP procedures currently used by the commercial and FBI forensic laboratories already have conservative measures built in to negate any possible effect from population substructure.[317]

Dr. George Herrin reexamined in 1993 the study by Drs. Devlin and Rich cited by the Committee. His study confirmed that multi-locus matches in forensic databases were extremely rare.[318] More importantly, he showed that "the frequency of such matches does not significantly exceed the number that would be expected if the alleles are statistically independent...."[319] This last result is an important indicator of the absence of substructure among the databases.

Finally, the Federal Bureau of Investigation undertook a study of several population groups worldwide[320] and recently published a four-volume set of reference data.[321] This data does not support the Committee's assumption of significant population substructure. The study concluded instead that, "[b]ased on the

data contained in this compendium, differences in allele frequencies at a particular locus do *not* have forensically significant effects on VNTR profile frequency estimates when subgroup reference databases from within a major population group are compared."[322] The U.S. District Court for the Virgin Islands recently relied upon this report in admitting DNA statistics into evidence.[323]

C. *The "Ceiling Principle" At Work.*

Applying the "ceiling principle" to a hypothetical case illustrates the lack of scientific basis. Assume a rape occurred in an average American large town or city (population 100,000 to 250,000). The suspect, a resident of the town, is Caucasian. Under the "ceiling principle," the eight alleles of the suspect's DNA pattern are found most often in the reference databases as follows:

Locus 1: Eskimo - 4.6%	Locus 2: Japanese - 11.2%
Locus 3: Oglala Sioux - 13.8%	Locus 4: !Kung Bushmen - 7%
Locus 5: Puerto Rican - 9.7%	Locus 6: Korean - 12.8%
Locus 7: Italian - 12.2%	Locus 8: Maori - 15.5%

According to the "ceiling principle," these are the allelic frequencies to be multiplied, regardless of the fact that the suspect belongs to none of the reference databases.[324] Moreover, those frequencies less than ten percent (Eskimo, !Kung Bushmen, and Puerto Rican) must be replaced by ten percent prior to multiplication.[325] Science provides no basis for using allele

frequencies within databases of individuals whose connection to the crime scene is nonexistent.

In addition, science strives to progress and learn more through the scientific method. However, regardless of the outcome of the search for the effect of population substructure, the science of forensic DNA analysis will be "frozen" at the minimum levels established by the NRC.[326] And, should some small population be found with extremely high frequencies for particular alleles, those frequencies will become the minimum used in the "ceiling principle" regardless of the isolation or minimal size of that population.[327] This "freezing" is contrary to science.[328]

D. *The Scientists Speak.*

Perhaps the lack of scientific basis behind the "ceiling principle" is best stated by the scientists themselves. The major complaint of the "critics from all perspectives is that the 'ceiling principle' is not a principle of science."[329] Professor Elizabeth Thompson, the University of Washington's Chair of Department of Statistics, described the "ceiling principle" as a "data-driven, interest-ridden, voodoo, pseudo-statistical, *ad hoc* methodology to which no statistician (or scientist) should be a party."[330] Dr. Richard Lewontin has also stated that "[i]n my view, the 'modified ceiling principle' has *no rational basis* and has been chosen by *entirely arbitrary means*."[331] Lewontin has

also said, "It's just totally irrational [the way that the Committee selected ten percent] out of the air [as the minimum frequency used in the] 'modified ceiling principle'".[332]

Population geneticist Newton Morton says that the Committee "ignore[s] any attempt to describe the substructuring and tr[ies] to alter the gene frequencies in a way that many of us regard as illogical."[333] He calls the result "absurdly conservative."[334] A discussion at the Second International Symposium on the Forensic Aspects of DNA Analysis[335] which included Dr. Oscar Zaborsky (the Committee's Study Director for the DNA Technology in Forensic Science project), made clear that "the ceiling principle has no basis in science."[336]

Another Committee member, Richard Lempert, calls it a "'second best' solution;"[337] one that "does not provide a good scientific estimate of the probability...."[338] In fact, Lempert states that the product rule's calculations are "closer by several orders of magnitude ... than ... the number ... which the ceiling principle generates."[339] Lempert also admits that recent studies disprove the NRC's assumption of substantial population substructure, and agrees that "the concern the ceiling principle most directly addresses, the possibility that the frequency of a defendant's alleles in the defendant's ethnic group narrowly defined is substantially higher than it is in a general population data base, is most often irrelevant."

Lempert admits that the "ceiling principle" is based in great part on a "value" judgment of the Committee members that

probabilities offered should be conservative. Lempert states that there is "no scientific basis for this value ...."[340] "Science alone," Lempert states, "cannot provide a yardstick with which to measure the Committee's recommendations."[341] Finally, Dr. Neil Risch summed up the feeling of most of the scientific community: "If I were asked if there is any scientific justification to the ceiling principle, I'd have to say no."[342]

Throughout the debate, the scientific underpinnings of DNA statistical evidence have rarely been in serious dispute. Instead, it is a judgment dispute, which is properly decided by courts, not scientists. As Lempert admits, the "ceiling principle" is based on values, rather than science. SCIENCE magazine characterized the debate as "not about right and wrong but about different standards of proof...." and quoted one geneticist as saying that it is "a religious argument."[343]

The final word may yet belong to the National Research Council. The Council has agreed to conduct another study of the issue of population substructure and the "ceiling principle."[344] The study will be conducted by an "entirely new committee."[345] However, the committee has yet to be named or completely funded, and probably will not be.[346]

VI. DNA Under *Daubert*.

Federal (and Military) Rules of Evidence 702 and 401-403 are the bases for admitting expert testimony on DNA as scientific

evidence. These rules have displaced *Frye* as the relevant admissibility standard in Federal courts (to include courts-martial.) How will the NRC's recommended "ceiling principle" fare under these rules?

A. *Federal Rules of Evidence 401/402 - Relevance.*

Evidence must be relevant to a fact in issue in order to be admissible. FRE 401 defines relevancy as having "*any* tend-ency" to make the existence of a material fact more probable or less probable than it would be without the evidence."[347] The "ceiling principle" must somehow relate to a fact at issue in order to meet Rule 401's requirement. Rule 402 declares that evidence "which is not relevant is not admissible."[348]

There has been some debate over the question to which DNA evidence relates at a trial.[349] Critics have stated that the issue is the likelihood that someone of the same ethnicity and race as the suspect would match the sample.[350] One court has even excluded DNA evidence entirely because the defendant "belongs to an ethnic group whose genotype frequencies may occur more frequently than the FBI's estimate."[351]

This assertion is misleading. In American criminal jurisprudence, a defendant who pleads not guilty is presumed to be innocent, and that presumption is valid until proven otherwise beyond a reasonable doubt.[352] Thus, the population of *possible suspects*, not the defendant, is the relevant population. Unless

there is some information defining the suspect as a particular ethnic group or subpopulation, the current Black, Caucasian, and Hispanic, and Asian databases are the legally relevant databases.

The NRC Committee recognized this when it stated that "[s]ome legal commentators have pointed out that frequencies should be based on the population of possible perpetrators, rather than on the population to which a particular suspect belongs. Although this argument is formally correct, practicalities often preclude use of that approach."[353] The Committee failed to list these practicalities.[354]

However, "the ethnicity of the class of people who are potential contributors can rarely be defined...."[355] When some identification of the suspect is made, forensic scientists agree that "it is usually possible only to classify an individual into one of the major racial groups, at best."[356] Thus, unless there is other evidence which places the class of suspects *only* in a precise ethnic, as opposed to racial, group *and* the defendant is a part of that group, the defendant's particular ethnic background is irrelevant.[357]

Likewise, the probabilities calculated by the "ceiling principle" are completely irrelevant. The "ceiling principle" uses the highest frequency from among several subpopulations (and then may substitute an artificial frequency of five or ten percent).[358] Thus, the "ceiling principle's" suspect may be Black for one allele, Caucasian for another, Hispanic for a third, Japanese for a fourth, and Kiowa Indian for another! Obviously,

such figures have *no* relevance to the issue of whether the defendant in a particular case contributed the evidentiary sample (unless the defendant is part Black, Caucasian, Hispanic, Japanese, and Kiowa Indian.) Thus, calculations using the "ceiling principle" fail to meet the requirements of Rule 401 and should be excluded under Rule 402.

B. *Federal Rule of Evidence 702 - Scientific Basis.*

The Supreme Court focused on the reliability of proffered scientific expertise.[359] *Daubert* holds that a trial judge:

> [f]aced with a proffer of expert scientific testimony ... must determine at the outset, pursuant to [FRE] 104(a), whether the expert is proposing to testify to (1) scientific knowledge that (2) will assist the trier of fact to understand or determine a fact in issue. This entails a preliminary assessment of whether the reasoning or methodology underlying the testimony is scientifically valid and of whether that reasoning or methodology properly can be applied to the facts in issue.[360]

Unlike some commentators desired,[361] the Court did not limit the application of this preliminary assessment to evidence offered by the government. Instead, the Court's holding applies equally to evidence offered by the defense. Thus, the "ceiling principle" must be subjected to this test.[362]

The Court stated that, "in order to qualify as 'scientific knowledge,' an inference or assertion must be derived by the scientific method."[363] Obviously, then, the NRC Committee's *assumption*, contradicted by voluminous evidence,[364] fails to qualify under the *Daubert* definition of scientific knowledge and

should be excluded from evidence. However, the remainder of this section will "assume for the sake of discussion"[365] that the "ceiling principle" is not excluded by this requirement.

C. *Federal Rule of Evidence 702 - Reliability.*

The Court cited several factors to use in determining the reliability of scientific evidence. The key question, the Court felt, was whether or not the theory or technique had been tested and was capable of replication.[366] The considerable body of research performed after publication of the NRC Report proves the report's assumption of any significant effect of population substructure on allele frequency calculations is false.[367] No study to date has validated the "ceiling principle" through tests.[368]

The next factor cited by the Court is the degree to which the theory has been subjected to peer review and publication. "Submission to the scrutiny of the scientific community is a component of 'good science.'"[369] Again, the peer reviewed literature strongly criticizes the "ceiling principle" for lack of scientific merit.[370]

Another consideration is the known or potential error rate and, presumably, the types of errors caused. There have been studies of the "ceiling principle" which demonstrate the possibility of error. Dr. Joel Cohen, a long-time opponent of DNA evidence, has demonstrated that the presence of linkage

disequilibrium and Hardy Weinberg disequilibrium (two of the indicators of population substructure, the assumption upon which the "ceiling principle" is based) can cause the "ceiling principle" to *underestimate* a profile frequency.[371]

However, Cohen himself felt that this study considered an "unrealistic theoretical population ... with perfect linkage between loci."[372] Accordingly, he undertook another study to determine whether the "ceiling principle" was reliable on more realistic populations. His later study found that the "ceiling principle *can* fail to be conservative for an individual genotype."[373] Thus, the "ceiling principle" is subject to errors detrimental to the defendant, and these errors argue against its reliability under *Daubert*.

Finally, the Court looks to the general acceptance of the technique or theory. As the controversy which sparked the NRC's report demonstrates, there is a large body of scientists who deny that population substructuring has a significant effect on allele frequencies. Greater controversy over the NRC Committee's assumption has resulted since the NRC's report was published.[374] Clearly, the hoped-for general acceptance of the "ceiling principle"[375] has failed to materialize and cannot support its admissibility into evidence.

D. *Rule 403 - Prejudicial, Misleading, Confusing, and Cumulative Evidence.*

Rule 403 is designed to exclude some otherwise relevant evidence whose "probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury, or by considerations of undue delay, waste of time, or needless presentation of cumulative evidence."[376] Although there is a presumption of admissibility created by the word "substantially," it is slight.[377] Finally, Rule 403 does not provide the judge any discretion where the evidence is barred by another evidentiary rule, such as FREs 401 and 702. Rule 403 only permits judges to exclude *otherwise admissible* evidence.[378]

Evidence derived from the "ceiling principle" is prejudicial to the defendant when it results in allele frequencies that make the defendant's DNA profile seem rarer than it really is. This type of error is possible.[379] The judge may find that this possibility of error, unless shown to be nonexistent in the particular case, is sufficiently prejudicial to bar admission of the "ceiling principle." However, since the "ceiling principle" calculations are usually offered by the defense (who believes them to be more conservative than the modified product rule figures),[380] the judge will probably not exclude the evidence based on undue prejudice.

The "ceiling principle" evidence is confusing and may mislead the jury. "Courts and commentators have traditionally

viewed mathematical probability estimates with extreme caution because of its need for foundational support and its need for sufficient explanation to the factfinder."[381] The foundational support for the "ceiling principle" is lacking, as discussed above. Evidence derived from the "ceiling principle" requires the jury understand why two very different statistics are being offered, and forces jurors to confront the underlying complex population genetics issues in great detail. Some courts have excluded DNA statistics on this basis.[382]

The evidence also may be a waste of time because it is irrelevant. Since the allele frequencies used may come from populations to which neither the defendant nor the pool of possible suspects belong, it has no relevance to the issue of identity. Replacing the DNA evidence with other evidence illustrates this point. For example, in *Yee*,[383] an eyewitness stated that the assailant had black hair. Black hair is most prevalent in Chinese. Using the ceiling principle, the jury must attempt to weigh the significance of black hair to the issue of identity with only the knowledge that almost all Chinese have black hair, rather than the likelihood of encountering a black-haired person in the population at random.

Finally, the "ceiling principle" is cumulative evidence of identity. Regardless of the method used to calculate the frequency of a match, a multi-locus match is extremely rare.[384] The "ceiling principle" does not greatly increase the frequency in many cases.[385] And, where it does, the frequencies are still

extremely low. Thus, its admission does not often provide significant new information.[386]

VII. Conclusion.

The National Research Council's "ceiling principle" is an unnecessary and unsound method of calculating the frequency of a DNA profile in a population. The NRC ignored scientific studies which demonstrated that there was no significant effect on the allele frequencies due to population substructure. Further studies have shown that the NRC's assumption to the contrary was unwise and untenable. Because of its lack of scientific basis, there is no general acceptance of the "ceiling principle" by the relevant scientific community.

The Supreme Court interpreted Federal Rule of Evidence 702 as rejecting the *Frye* test of general acceptance.[387] Instead, the Court held that reliability is the key to admissibility of scientific evidence. The "ceiling principle" is not reliable as it devolves from an unsupported and incorrect assumption. Therefore, it is inadmissible under FRE 702.

The "ceiling principle" is also irrelevant to the issue of identity in the case. The "ceiling principle" requires use of several databases regardless of their connection to the facts of the case. As the hypothetical case discussed above[388] demonstrates, the "ceiling principle" may require use of populations who have no connection to the crime scene, the

suspect, or the defendant. Unless the proponent of the evidence demonstrates a connection, however tenuous, between the databases actually used and the facts of the case, the "ceiling principle" is irrelevant and should be excluded under FRE 401.

Finally, the "ceiling principle" may be prejudicial to the defendant by not producing a conservative number and may confuse the jury with its debate over population substructure. It is also cumulative evidence. Therefore, it fails the FRE 403 balancing test and should be excluded.

The "ceiling principle" was a well-intentioned, but ill-fated attempt to circumvent *Frye's* requirement of scientific basis by drastically reducing the empirically-derived statistical evidence and substituting instead a "standard of practice 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."[389] However, what is generally accepted is that the evidence is conservative, *not* that it is scientifically valid. This concern is a value judgment for the courts, not the scientists, to make.

There is almost general acceptance that the "ceiling principle" is scientifically *invalid*. Thus, the "ceiling principle" should not be admissible in jurisdictions that follow *Frye*. And, since it fails to meet the requirements of the Federal and Military Rules of Evidence, the "ceiling principle" should be held inadmissible in Federal trial courts and military courts-martial.

ENDNOTES

1. DNA was first used by criminal investigators in England in the celebrated case of Colin Pitchfork in 1985, which was detailed in JOSEPH WAMBAUGH, THE BLOODING (1989). Commercial laboratories in the United States first used DNA analysis in 1986. OFFICE OF TECHNOLOGY ASSESSMENT, U.S. CONGRESS, GENETIC WITNESS: FORENSIC USES OF DNA TESTS (1990) [hereinafter GENETIC WITNESS]. The first reported criminal case was Andrews v. State, 533 So. 2d 841 (Fla. Dist. Ct. App. 1988).

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

3. *See, e.g.*, People v. Castro, 545 N.Y.S.2d 985 (Sup. Ct. 1989) (Bronx County) (adding a requirement that the laboratory comply with proper procedures in conducting DNA test before the evidence is admissible).

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

5. Because the current DNA techniques permit analysis of only a small part of a person's DNA, it is possible that two individuals have identical DNA at the sites, or loci, examined, yet differ at other loci. Thus, to prevent the jury from believing that a DNA match is conclusive, it is necessary to explain the possibility (and likelihood) that the defendant and the evidentiary sample match at the loci examined but have different DNA at unexamined

loci and that someone other than the defendant also matches the evidentiary sample at the loci examined. *See also infra* § II.D.

6. This is often referred to as the "defense attorney's fallacy." This is the jury's tendency to disregard evidence that is unlikely if the defendant is innocent when many others may share the same characteristic. Richard Lempert, *DNA, Science and the Law: Two Cheers for the Ceiling Principle*, 34 JURIMETRICS J. 41, 54 (1993). This fallacy exists, for example, when the jury is told that there is a one in 50,000 chance that the defendant's DNA and the evidentiary DNA match at random. If the local population was 250,000, the defense may attempt to claim five people are incriminated by the evidence.

7. The product rule is simply the multiplication of the frequencies of independent events to determine the frequency of their simultaneous occurrence. *See infra* § II.D.3.

8. GENETIC WITNESS, *supra* note 1, at 3.

9. *Id.* at 41.

10. F. Samuel Baechtel, *A Primer on the Methods Used in the Typing of DNA*, 15 CRIME LABORATORY DIG. 3 (1988).

11. *Id.*

12. GENETIC WITNESS, *supra* note 1, at 41.

13. *Id.* at 42-43.

14. However, DNA is found in white blood cells, so blood stains found at the crime scene and samples taken from suspects may be compared. *Id.* at 4.

15. Baechtel, *supra* note 10, at 3.

16. Figure 1 is a diagram of the DNA molecule. *See infra* Appendix at A-1.

17. Baechtel, *supra* note 10, at 3.

18. Because of the large number of base pairs in each allele, DNA sample sizes are commonly referred to in Kilobases (Kb), or one thousand base pairs.

19. *Castro*, 545 N.Y.S.2d at 988.

20. It has been estimated that at least one base per thousand varies between individuals. D.N. Cooper et al., *An Estimate of Unique DNA Sequence Heterozygosity in the Human Genome*, 69 HUM. GENETICS 201, 205 (1985).

21. Alec J. Jeffreys et al., *Individual-Specific "Fingerprints" of Human DNA*, 316 NATURE 76 (1985). An excellent metaphor that explains VNTRs occurs in Virgin Islands v. Penn: "[E]ach VNTRs is like a word in the genetic code that is common to everyone.... Thus, if each VNTRs is like a word, then the genetic code stutters when it speaks that word. In other words, each person's

DNA code is different in how many times it 'stutters' that word." 838 F. Supp. 1054, 1058 (D.V.I. 1993).

22. For example, the locus responsible for cystic fibrosis is on chromosome 7. GENETIC WITNESS, *supra* note 1, at 42.

23. GENETIC WITNESS, *supra* note 1, at 42.

24. *Castro*, 545 N.Y.S.2d at 988.

25. Except for sperm cells and ova, which each contain exactly half the DNA found in the other cells, the differences between DNA in differing types of cells can only be detected through specific and detailed laboratory testing. These minor differences are not detectable using the DNA analysis methods discussed in this paper. GENETIC WITNESS, *supra* note 1, at 42.

26. COMMITTEE ON DNA TECHNOLOGY IN FORENSIC SCIENCE, NATIONAL RESEARCH COUNCIL, DNA TECHNOLOGY IN FORENSIC SCIENCE 3 (1992) [hereinafter NRC REPORT].

27. Indeed, the length of the DNA in the chromosomes of a single cell is approximately 1.5 meters and is comprised of almost twelve billion bases. Roger Kahn, *DNA Chemistry and Genome Organization: An Introduction for the Forensic Scientist*, *in* PROC. INT'L SYMP. ON FORENSIC ASPECTS DNA ANALYSIS 11 (1989).

28. Brief of Amicus Curiae, People v. Britton, No. A058925 (Cal. Ct. App. 1993).

29. Kenneth R. Kreiling, Comment, *DNA Technology in Forensic Science*, 33 JURIMETRICS J. 449, 451 (1993).

30. An examination of each base pair of an individual's DNA would be unduly expensive, highly impractical, and unwarranted, as most of the DNA is identical in all humans. C. Thomas Caskey et al., *DNA: The History and Future Use of Forensic Analysis, in* PROC. INT'L SYMP. ON FORENSIC ASPECTS DNA ANALYSIS 3,4 (1989).

31. The world population in 1991 is estimated at 5,423,000,000, or less than six billion. MARK S. HOFFMAN, THE WORLD ALMANAC 817 (1993). Probabilities in DNA evidence have ranged as low as one in 739 billion, which clearly excludes all other people on earth. NRC REPORT, *supra* note 26, at 75.

32. Dr. Edward Blake was the first scientist to perform a forensic DNA analysis using the PCR DQ-alpha system in 1986. Edward Blake et al., *Polymerase Chain Reaction (PCR) Amplification and Human Leukocyte Antigen (HLA) DQ-α* Oligonucleotide Typing on Biological Evidence Samples: Casework Experience, 37 J. FORENSIC SCI. 700 (1992).

33. Catherine T. Comey, *The Use of DNA Amplification in the Analysis of Forensic Evidence*, 15 CRIME LABORATORY DIG. 99 (1988); NRC REPORT, *supra* note 26, at 40-42.

34. NRC REPORT, *supra* note 26, at 42. However, PCR testing is slightly different. The FBI laboratory uses a specific region

in one of the major histocompatibility complex genes known as DQ-α, which contains four different alleles. A 242 base-pair sample is taken, amplified, and applied to a nylon membrane using the dot-blot procedure. In this procedure, the samples are hybridized with different probes that detect each of the four alleles (and the four subtypes of allele 1). Then, the samples are matched if they contain the same alleles and allele subtypes. Comey, *supra* note 33, at 99-101.

35. A third technique is known as direct sequencing. In this method, polymerase chain reaction (PCR) technology is used to synthesize complementary strands of DNA taken from mitochondria (a part of the cell outside of the nucleus). Then, the synthesized fragments (the mitochondrial DNA is cleaved by the introduction of derivative bases rather than restrictive enzymes) are separated by electrophoresis. Unlike RFLP analysis, their length is determined by a scanning device which scans a certain portion of the agarose gel. Once all fragments have been scanned, the exact base sequence of the strand is known. However, this method is much more costly and requires more time to perform. Baechtel, *supra* note 10, at 8-9.

36. John S. Waye et al., *A Simple and Sensitive Method for Quantifying Human Genomic DNA in Forensic Specimen Extracts*, 7 BIOTECHNIQUES 852 (1989).

37. Bruce Budowle et al., *Fragment-Length Polymorphisms for Forensic Science Applications*, in METHODS IN NUCLEIC ACIDS RESEARCH 186 (1991). However, DNA has proven to be extremely hardy under conditions which might arise at a typical crime scene. *See, e.g.*, Dwight E. Adams et al., *Deoxyribonucleic Acid (DNA) Analysis by Restriction Fragment Length Polymorphisms of Blood and Other Body Fluid Stains Subjected to Contamination and Environmental Insults*, 36 J. FORENSIC SCI. 1284 (1991); Bruce Budowle et al., *Validation with Regard to Environmental Insults of the RFLP Procedure for Forensic Purposes, in* FORENSIC DNA TECHNOLOGY 83 (M.A. Farley & J.J. Harrington, eds. 1991); Ted R. Schwartz et al., *Characterization of Deoxyribonucleic Acid (DNA) Obtained from Teeth Subjected to Various Environmental Conditions*, 36 J. FORENSIC SCI. 979 (1991); Walter Bär et al., *Postmortem Stability of DNA*, 39 FORENSIC SCI. INT'L 59 (1988).

38. For example, semen, containing nucleated sperm, has a higher volume of DNA than a comparable amount of blood, which contains anucleated red blood cells. NRC REPORT, *supra* note 26, at 28 (Table 1.1).

39. In addition, none of the techniques used in forensic DNA analysis are new. They have been used in laboratories conducting blood and DNA testing for clinical, diagnostic, and experimental use for many years. *Castro*, 545 N.Y.S.2d at 989-90; NRC REPORT, *supra* note 26, at 27.

40. GENETIC WITNESS, *supra* note 1, at 3-4.

41. *Id.* at 46.

42. *Id.*

43. Bruce Budowle et al., *Hae III - A Suitable Restriction Endonuclease for Restriction Fragment Length Polymorphism Analysis of Biological Evidence Samples*, 35 J. FORENSIC SCI. 530, 531 (1990).

44. GENETIC WITNESS, *supra* note 1, at 46.

45. *Id.*

46. *Id.* The gel is normally made of agarose, but may also be made of acrylamide.

47. *Id.*

48. *Id.*

49. *Id.*

50. Bruce Budowle et al., *An Introduction to the Methods of DNA Analysis Under Investigation in the FBI Laboratory*, 15 CRIME LABORATORY DIG. 8, 12 (1988) [hereinafter *Introduction*]; Baechtel, *supra* note 10, at 5.

51. Bruce Budowle & F. Samuel Baechtel, *Modifications to Improve*

the Effectiveness of Restriction Fragment Length Polymorphism Typing, in APPLIED AND THEORETICAL ELECTROPHORESIS 182 (1990).

52. *Introduction, supra* note 50, at 8.

53. Kahn, *supra* note 27, at 14.

54. GENETIC WITNESS, *supra* note 1, at 46.

55. Budowle & Baechtel, *supra* note 51, at 182.

56. Single-locus probes recognize fragments from only one locus on a specific chromosome, while multi-locus probes recognize fragments from loci on many chromosomes. Single-locus probes are preferred for RFLP analysis due to their high degree of sensitivity. Most forensic laboratories in the U.S. use three to five single-locus probes in DNA analysis. Single locus probes produce one or two bands for analysis, depending upon whether the individual inherited the same or different alleles from the mother and father. *DNA Identification: Hearings Before the Subcomm. on the Constitution of the Senate Comm. on the Judiciary*, 101st Cong., 1st Sess. 92 (1989) (CELLMARK DIAGNOSTICS, DNA FINGERPRINTING™ MANUAL) [hereinafter *DNA Identification Hearings*].

57. For example, the FBI laboratory uses a probe called D4S139. The "D" is an abbreviation for "DNA;" the "4" represents the fourth chromosome; the "S" is an abbreviation for "segment;" and

"139" represents the 139th segment of DNA on the chromosome. *Penn*, 838 F. Supp. at 1061.

58. Budowle & Baechtel, *supra* note 51, at 182.

59. *Id.* at 182-83.

60. Figure 2 is a schematic of the DNA analysis process using Southern blotting. *See infra* Appendix at A-2.

61. BUREAU OF JUSTICE STATISTICS, U.S. DEP'T OF JUSTICE, FORENSIC DNA ANALYSIS: ISSUES 5 n.10 (1991) [hereinafter FORENSIC DNA ANALYSIS].

62. *Statement of the Working Group on Statistical Standards for DNA Analysis*, 17 CRIME LABORATORY DIG. 53, 56 (1990) [hereinafter *Working Group on Statistical Standards*]. This is to compensate for the variation of up to ± 2.5% in size measurement of DNA fragments from the same source. Bruce Budowle et al., *Data for Forensic Matching Criteria for VNTR Profiles, in* PROC. INT'L SYMP. ON HUMAN IDENTIFICATION 104 (1989). However, most matches in the FBI system occur within ± 1.5% of each other because, in part, samples beyond that are discarded by the technician in the visual examination of the autoradiogram prior to the automated analysis. Interview with Dr. Bruce Budowle, FBI Forensic Science Research and Training Center, Quantico, VA (Feb. 3, 1994).

63. Unless the phenomenon of band shifting occurs. Band shifting is where the same size DNA fragments in different lanes migrate a different distance through the agarose gel due to

inconsistencies in the gel's composition. *See, e.g.*, Eric S. Lander, *Invited Editorial: Research on DNA Typing Catching Up with Courtroom Application*, 48 AM. J. HUM. GENETICS 819, 820 (1991). Band shifting's recognition and correction are beyond the scope of this paper and will not be further addressed.

64. This type of result recently freed Kirk Bloodworth from Maryland's death row after being twice convicted in 1985 and 1987 of raping a young girl. In a 1992 test using polymerase chain reaction (PCR) techniques, Bloodworth's DNA did not match DNA amplified from semen stains on the victim's underwear. At the time of his trials, PCR techniques were not available. Paul W. Valentine, *Man Cleared by DNA Gets Pardon*, WASHINGTON POST, Dec. 23, 1993, at A8.

65. Keith L. Monson & Bruce Budowle, *A System for Semi-Automated Analysis of DNA Autoradiograms*, *in* PROC. INT'L SYMP. ON FORENSIC ASPECTS DNA ANALYSIS 127 (1989).

66. Figure 3 is an autoradiogram analyzed by an automated system. *See infra* Appendix at A-3.

67. *Id.* at 129-30.

68. *See, e.g.*, Castaneda v. Partida, 430 U.S. 482, 513-14 (1977) (Powell, J., dissenting).

69. EDWARD W. CLEARY ET AL., EVIDENCE: CASES AND MATERIALS 309 n.1 (4th ed. 1988).

70. *E.g.*, United States v. Gwaltney, 790 F.2d 1378 (9th Cir. 1986).

71. PANEL ON STATISTICAL ASSESSMENTS AS EVIDENCE IN THE COURTS, NATIONAL RESEARCH COUNCIL, THE EVOLVING ROLE OF STATISTICAL ASSESSMENTS AS EVIDENCE IN THE COURTS 3 (Stephen E. Fienberg, ed. 1989).

72. This inference comes about because, as discussed *supra* at § II.D.3., a match between DNA samples is not conclusive of identity. An exclusion, however, *is* conclusive that the suspect and the defendant are *not* the same individual.

73. Because each laboratory uses different restriction enzymes (The FBI uses Hae III, while Cellmark uses Hinf) and different probes which recognize and cut separate portions of DNA, the laboratories cannot combine their databases. Interview with Dr. Bruce Budowle, FBI Forensic Science Research & Training Center, in Quantico, VA (Feb. 3, 1994).

74. The number refers to individuals, not alleles. Each individual is expected to provide two alleles per locus. Ranajit Chakraborty, *Sample Size Requirements for Addressing the Population Genetic Issues of Forensic Use of DNA Typing*, 64 HUM. BIOLOGY 141, 157 (1992).

75. Interview with Dr. Bruce Budowle, FBI Forensic Science Research and Training Center, Quantico, VA (Feb 3, 1994); United States v. Brooks, No. 92-112-COL (M.D. Ga. 1992).

76. The FBI uses Black, Caucasian, and Southwestern and Southeastern Hispanic databases; Cellmark uses Black, Caucasian, and Western Hispanic databases; others use an Asian database. Interview with Dr. Bruce Budowle, FBI Forensic Science Research & Training Center, in Quantico, VA (Feb. 3, 1994).

77. *Penn*, 838 F. Supp. at 1063.

78. Obviously, some genes *are* desired or avoided in marriages, but these genes are the ones that determine the physicalities that make the individuals part of a common group. The DNA sought by RFLP analysis, on the other hand, has no known function, is highly polymorphic regardless of assortative mating, and thus would not violate Hardy-Weinberg equilibrium (see *supra* text at note 31.)

79. Neil J. Risch & Bernard Devlin, *On the Probability of Matching DNA Fingerprints*, 255 SCIENCE 717, 718 (1992). *See also* Bruce Budowle & Keith L. Monson, *A Statistical Approach for VNTR Analysis, in* PROC. INT'L SYMP. ON FORENSIC ASPECTS DNA ANALYSIS 121, 124 (1989).

80. G.H. Hardy, *Mendelian Proportions in a Mixed Population*, 28 SCIENCE 49, 50 (1908).

81. NRC REPORT, *supra* note 26, at 48.

82. *Id.* at 80 ("Recent empirical studies concerning VNTR loci

detected no deviation from independence within or across loci.") (citation omitted).

83. *See* Brief of Amicus Curiae at 62, People v. Britton, No. A058925 (Cal. Ct. App. 1993).

84. *See, e.g., Working Group on Statistical Standards, supra* note 62, at 54. Membership of the Working Group includes the Federal Bureau of Investigation, Lifecodes Corporation, Cellmark Diagnostics, and Dr. Eric S. Lander.

85. Bruce Devlin & Neil Risch, *A Note on Hardy-Weinberg Equilibrium of VNTR Data by Using the Federal Bureau of Investigation's Fixed-Bin Method*, 51 AM. J. HUM. GENETICS 549, 550 (1992) [hereinafter *A Note on Hardy-Weinberg Equilibrium*].

86. NRC REPORT, *supra* note 26, at 58.

87. *Id.*

88. Record at 305, *Brooks*, Cr. No. 92-112-COL(JRE), (M.D. Ga. 1992).

89. *A Note on Hardy-Weinberg Equilibrium, supra* note 85, at 550.

90. Record at 304, *Brooks*, Cr. No. 92-112-COL(JRE), (M.D. Ga. 1992).

91. Let p equal the probability of allele 1 and q equal the

probability of allele 2. Since p and q are both less than 1, ($p+q=1$, $p,q\neq0$) p^2 will always be less than pq.

92. Bruce Budowle & Keith L. Monson, *The Approach Used by the FBI for Calculating Ceiling Frequencies*, 19 CRIME LABORATORY DIG. 84, 86 (1992).

93. The FBI uses fixed bins, which do not depend on the particular sample. Bruce Budowle & Keith L. Monson, *Perspectives on the Fixed Bin Method and the Floor Approach/Ceiling Principle*, *in* PROC. 1992 INT'L SYMP. ON HUM. IDENTIFICATION 391, 392 (1992) [hereinafter *Floor Approach*]. Thus, a particular evidentiary sample may lie on the border between two bins. In this case, the FBI uses the larger of the two bins' frequencies. Bruce Budowle et al., *Fixed-Bin Analysis for Statistical Evaluation of Continuous Distributions of Allelic Data from VNTR Loci*, 48 AM. J. HUM. GENETICS 841, 846 (1991). Cellmark and Lifecodes use floating bins that center themselves on the evidentiary sample to avoid this possible issue. Brief of Amicus Curiae at 63, People v. Britton, No. A058925 (Cal. Ct. App. 1993).

94. NRC REPORT, *supra* note 26, at 77.

95. *Id.* at 76. *See also* William C. Thompson, *Evaluating the Admissibility of New Genetic Identifica-tion Tests: Lessons from the "DNA War,"* 84 J. CRIM. L. 22, 84 & n.287 (1993).

96. *See infra* §§ III.A.1 and III.A.2.

97. NRC REPORT, *supra* note 26, at 38. Southern blotting has been around since 1975. Edwin M. Southern, *Detection of Specific Sequences Among DNA Fragments Separated by Gel Electrophoresis*, 98 J. MOLECULAR BIOLOGY 503 (1975). *See also DNA Identification Hearings*, *supra* note 56, at 13 (testimony of Prof. James E. Starrs) ("All of this is familiar turf to biologists since the same Mendelian principles and the same establishment of population frequencies occurs in the every day genetic markers known as ABO blood grouping.").

98. Andre A. Moenssens, *Novel Scientific Evidence in Criminal Cases: Some Words of Caution*, 84 J. CRIM. L. 1 (1993); Michael N. Schmitt & Laura H. Crocker, *DNA Typing: Novel Scientific Evidence in the Military Courts*, 32 A.F. L. REV. 227, 269 (1990) ("*Castro* ... represents the first full-fledged attack on DNA identification.").

99. *See, e.g., DNA Identification Hearings, supra* note 56, at 10-12 (testimony of Prof. James E. Starrs); Lander, *supra* note 62, at 819; ANDRE A. MOENSSENS ET AL., SCIENTIFIC EVIDENCE IN CRIMINAL CASES § 1.03 (3d ed. 1986).

100. *See, e.g.*, United States v. Martinez, 3 F.3d 1191, 1194 (8th Cir. 1993); *Yee*, 134 F.R.D. at 161; *Castro*, 545 N.Y.S.2d at 985. *See also* Kreiling, *supra* note 29, at 457.

101. David G. Ego, *Supreme Court Knocks Out Frye Admissibility*

Test for Scientific Evidence in Federal Arena, 20 CRIME LABORATORY DIG. 41 (1993).

102. *Id.*

103. *See, e.g., Castro*, 545 N.Y.S.2d at 985; People v. Kelly, 549 P.2d 1240 (Cal. 1976).

104. *Daubert*, 113 S. Ct. at 2794.

105. New Mexico's Supreme Court noted that its evidence rules are identical to the Federal rules, and thus abandoned *Frye* in the wake of *Daubert*. State v. Alberico, 1993 WL 387950 (N.M. 1993).

106. 293 F. 1013 (D.C. Cir. 1923).

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

108. GENETIC WITNESS, *supra* note 1, at 91.

109. As one court stated, the scientists will "form a kind of technical jury, which must first pass on the scientific status of a procedure before the lay jury utilizes it in making its findings of fact." People v. Barbara, 255 N.W.2d 171, 194 (Mich. 1977).

110. People v. Collins, 405 N.Y.S.2d 365, 369 (Sup. Ct. 1978).

111. United States v. Baller, 519 F.2d 463, 466 (4th Cir.), *cert. denied*, 423 U.S. 1019 (1975).

112. Observation and experimentation are used to find shortcomings, to determine how to make improvements, and "to discover how to eliminate known artificialities, distortions, oversimplifications, and errors in the descriptions, explanations, and predictions of reality that the theory affords." Only after a theory has survived a period of this kind of testing, review and refinement can it be used without significant questions, and even then, it remains open to renewed doubt. One philosopher has written that this process not only reflects the scientific method, but that "it *is* the scientific method."

Bert Black, *A Unified Theory of Scientific Evidence*, 56 FORDHAM L. REV. 595, 623 (1988), (citing F. Suppe, *Afterword* to THE STRUCTURE OF SCIENTIFIC THEORIES 706 (F. Suppe ed. 2d ed. 1977); Ziman, *What is Science*, in INTRODUCTORY READINGS IN THE PHILOSOPHY OF SCIENCE 35, 40 (E.D. Klemke et al. eds. 1980); and K. POPPER, THE LOGIC OF SCIENTIFIC DISCOVERY 47 (2d ed. 1968)).

113. *Daubert*, 113 S. Ct. at 1236 n.14.

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

115. *E.g.*, Dr. David E. Housman in *Andrews*, 533 So. 2d at 849.

116. *E.g.*, Dr. Daniel L. Hartl in United States v. Yee, 134 F.R.D. 161 (N.D. Ohio 1991); Dr. Kenneth K. Kidd in People v. Wesley, 533 N.Y.S.2d 643 (Albany County Ct. 1988).

117. *E.g.*, Dr. Richard Borowsky in *Wesley*, 533 N.Y.S.2d at 731.

118. *E.g.*, Drs. Ted Emigh and Bruce S. Weir in State v. Futrell, 436 S.E.2d 884 (N.C. Ct. App. 1993).

119. *E.g.*, Dr. Allen Giusti in *Andrews*, 533 So. 2d at 849.

120. *E.g.*, Dr. F. Samuel Baechtel in State v. Jobe, 486 N.W.2d 407 (Minn. 1992).

121. *E.g.*, Dr. Edward Blake in People v. Mack, 15 Cal. Rptr. 2d 193 (Dist. Ct. App. 1992).

122. *E.g.*, Dr. Brian Hjelle in People v. Barney, 10 Cal. Rptr. 2d 731 (Ct. App. 1992).

123. *E.g.*, Ms. Paula Yates of Cellmark in *Brooks*, No. 92-112-COL(JRE) (M.D. Ga. 1992).

124. *E.g.*, United States v. Williams, 583 F.2d 1194, 1198 (2d Cir. 1978), *cert. denied*, 439 U.S. 1117 (1979); People v. Williams, 331 P.2d 251 (Cal. App. Dep't Super. Ct. 1958).

125. United States v. Zeiger, 350 F. Supp. 685, 688 (D.D.C.), *rev'd*, 475 F.2d 1280 (D.C. Cir. 1972).

126. United States v. Williams, 443 F. Supp. 269, 273 (S.D.N.Y. 1977), *aff'd*, 583 F.2d 1194 (2d Cir. 1978), *cert. denied*, 493 U.S. 1117 (1979).

127. People v. Guerra, 690 P.2d 635, 656 (Cal. 1984).

128. *Yee*, 134 F.R.D. at 165, citing United States v. Kozminski, 821 F.2d 1186 (6th Cir. 1987) (*en banc*).

129. Edward J. Imwinkelried, *The Standard for Admitting Scientific Evidence: A Critique from the Perspective of Juror Psychology*, 100 MIL. L. REV. 99, 104 (1983).

130. *E.g.*, *Castro*, 545 N.Y.S.2d at 987.

131. *See id.* at 999.

132. CLEARY, *supra* note 69, at 290.

133. *See* MOENSSENS ET AL., *supra* note 99, at 439.

134. *Yee*, 134 F.R.D. at 196; People v. Shirley, 31 Cal. 3d 18, 55 (1982) ("Our duty is not to decide whether [the scientific evidence] is reliable as a matter of fact, but simply whether it is generally accepted.").

135. Black, *supra* note 112, at 595. Judge Guy of the Sixth Circuit stated that "[t]he . . . inquiry is, of course, the crucial one here; that is, whether the testimony is in 'conformity with a generally accepted explanatory theory.'" *Kozminski*, 821 F.2d at 1215 (Guy, J. dissenting) (citations omitted).

> Implicit in the language is the predicate that the theory be firmly anchored in sound, reliable, and sufficiently accurate scientific principles, and sufficiently established to the point of having achieved general acceptance within the particular field to which it belongs. Stated differently, the scientific explanatory theory must have (a) received at least some exposure within the scientific peerage to which it belongs; (b) received peer evaluation to determine its scientific validity and reliability; and

(c) achieved general acceptance within the scientific community to which it belongs.

Kozminski, 821 F.2d at 1201 (Krupansky, J. concurring).

136. *E.g.*, Harper v. State, 292 S.E.2d 389, 395 (Ga. 1982).

137. *E.g.*, United States v. Hadley, 918 F.2d 848, 853 (9th Cir. 1990).

138. United States v. Valdez, 722 F.2d 1196, 1201 n.19 (5th Cir. 1984).

139. "We deem general acceptance as being nearly synonymous with reliability." United States v. Franks, 511 F.2d 25, 33 n.12 (6th Cir.), *cert. denied*, 422 U.S. 1042 (1975).

140. *E.g.*, People v. Davis, 72 N.W.2d 269 (Mich. 1955) (The court admitted polygraph has proven value but noted possibility of error of ten to twenty-five percent. The evidence established a relationship between lies and blood pressure, respiration, and galvanic skin response. The court found polygraphy an acceptable method, but was dismayed by the possibility of the jury according great weight to the evidence. The court refused to admit the evidence, citing *Frye*.).

141. Pub. L. No. 93-595, 88 Stat. 1926-48 (1975).

142. FED. R. EVID. 702. "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified

as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise." Military Rule of Evidence 702 is identical. MANUAL FOR COURTS-MARTIAL, United States, MIL. R. EVID. 702 (1984) [hereinafter MCM].

143. FED. R. EVID. 702 (Analysis).

144. *See, e.g.*, J. WEINSTEIN & M. BERGER, WEINSTEIN'S EVIDENCE 702-16 (omission of mention of *Frye* was "tantamount to an abandonment of the general acceptance standard.").

145. Schmitt & Crocker, *supra* note 98, at 231.

146.

> It is not clear whether Rules 702 and 703 are intended to codify something like the *Frye* test or whether they establish a less demanding standard for scientific evidence.... It would be odd if the Advisory Committee and the Congress intended to overrule the vast majority of cases excluding such evidence as lie detectors without explicitly stating so.

STEPHEN A. SALTZBURG & KENNETH R. REDDEN, FEDERAL RULES OF EVIDENCE MANUAL 633 (4th ed. 1986).

147. MCM, *supra* note 142, Mil. R. Evid. 702 (analysis).

148. *See infra* text accompanying notes 173-74.

149. 753 F.2d 1224 (3d Cir. 1985).

150. *Id.* at 1235.

151. *Downing*, 753 F.2d at 1237.

152. *Id.* at 1237.

153. *Id.*

154. *Id.* at 1241.

155. *Id.* at 1239, (citing WEINSTEIN & BERGER, *supra* note 144, at 702-19 nn.10, 11).

156. "[E]ven if the proffered evidence satisfies Rule 702, the ... court may nonetheless invoke Rule 403 to exclude the evidence if the court finds its probative value to be substantially outweighed by other dangers, e.g., confusion of the issue or waste of time." *Downing,* 753 F.2d at 1242-43.

157. *Id.* at 1240 n.21. *See also* United States v. Gipson, 24 M.J. 246, 251 (C.M.A. 1987) ("'Ordinarily ... the answer must lie in the judge's own experience, his general knowledge, and his understanding of human conduct and motivation.' In other words, the judge has considerable room to exercise 'judgment.'") (citation omitted).

158. Of course, *Downing* retreated from this slightly by defining "helpfulness" as requiring scientific reliability "beyond that required to meet a standard of bare logical relevance." *Downing,* 753 F.2d at 1235.

159. United States v. Ford, 16 C.M.R. 185, 187 (C.M.A. 1954).

160. 17 M.J. 728 (N.M.C.M.R. 1983).

161. *Id.* at 731.

162. 17 M.J. 684 (A.C.M.R. 1983).

163. *Id.* at 686.

164. *Id.* at 688.

165. *Id.* at 687-88.

166. 22 M.J. 165 (C.M.A.), *cert. denied*, 479 U.S. 953 (1986). Interestingly, *Mustafa* could have resolved the issue seven years before *Daubert*, as Justices White and Brennan would have granted *certiorari* to resolve the issue of whether the military and Federal rules of evidence superseded *Frye*. 479 U.S. at 953.

167. *Id.* at 168.

168. *Id.*

169. In fact, in *Mustafa*, the court was not faced with a typical "duel of experts" regarding the evidence. The witness, a CID agent, had no degrees in the field, had not written any papers, but had merely undergone a five-day training course and participated in other unspecified training. The court could have held that, although the science itself was generally accepted, the witness was not qualified. However, under the liberal construction of MRE 702, the court upheld the trial judge's finding that the witness was competent and allowed the evidence. *Id.* at 167-68.

170. 22 M.J. 771, 774 (A.C.M.R. 1986), *aff'd*, 26 M.J. 428 (C.M.A. 1988) (citations omitted).

171. 22 M.J. 840 (A.F.C.M.R. 1986), *aff'd*, 25 M.J. 243 (C.M.A. 1987), *cert. denied*, 484 U.S. 1011 (1988).

172. 22 M.J. at 842.

173. *Id.*

174. 24 M.J. 246 (C.M.A. 1987).

175. *Id.* at 247.

176. *E.g.*, *id.* at 249-52.

177. *Id.* at 251 (citing *Mustafa*, 22 M.J. at 167-68, and United States v. Snipes, 18 M.J. 172, 178 (C.M.A. 1984)).

178. *Id.*, 24 M.J. at 251.

179. *Id.* at 252 (citing the factors enumerated in *Downing*, 753 F.2d at 1238-39).

180. 113 S. Ct. 2786 (1993).

181. 727 F. Supp. 570, 575 (S.D. Cal. 1989).

182. 951 F.2d 1128 (9th Cir. 1991).

183. 113 S. Ct. 320 (1992).

184. 113 S. Ct. at 2794 (quoting Beech Aircraft Corp. v. Rainey, 488 U.S. 153, 169 (1988)).

185. *Id.*

186. *Id.* at 2795 n.7.

187. FRE 104(a) states: "Preliminary questions concerning the qualification of a person to be a witness, the existence of a privilege, or the admissibility of evidence shall be determined by the court...." Under FRE 104(a), the rules of evidence are not applicable except with respect to privileges. The proponent of the evidence has the burden of establishing its admissibility by a preponderance of the evidence. *See* Bourjaily v. United States, 483 U.S. 171, 175-76 (1987).

188. *Daubert*, 113 S. Ct. at 2795.

189. *Id.* at 2795 n.9.

190. *Id.* at 2796-97.

191. *Id.* Since the Court's list is not exclusive, presumably the *Downing* factors of the witness' credentials, novelty of the technique, and its non-judicial uses are also valid criteria.

192. *Id.* at 2797.

193. *Id.* at 2798 (quoting WEINSTEIN, RULE 702 OF THE FEDERAL RULES OF

EVIDENCE IS SOUND; IT SHOULD NOT BE AMENDED, 138 F.R.D 631, 632 (1991)).

194. This rule will also apply in courts-martial. It is important to note that, to date, two Circuits have judicially noted the RFLP technique: the Second Circuit, in United States v. Jakobetz, 955 F.2d 786, 799-800 (2d Cir.), *cert. denied*, 113 S. Ct. 104 (1992) (before *Daubert*); and the Eighth Circuit in United States v. Martinez, 3 F.3d 1191, 1197 (8th Cir. 1993) (after *Daubert)*.

195. John T. Sylvester, *Recent Developments in DNA Admissibility, in* PROC. THIRD INT'L SYMP. ON HUMAN IDENTIFICATION 61, 67 (1992).

196. *Martinez*, 3 F.3d at 1195. Since mid-1992, Arizona (State v. Bible, 858 P.2d 1152 (Ariz. 1993)); Arkansas (Swanson v. State, 823 S.W.2d 812 (Ark. 1992)); Colorado (People v. Lindsey, 1993 WL 2650 (Colo. Ct. App. 1993)); Hawaii (State v. Montalbo, 828 P.2d 1274 (Haw. 1992)); Illinois (People v. Mehlberg, 618 N.E.2d 1168 (Ill. App. Ct. 1993)); Kentucky (Harris v. Commonwealth, 846 S.W.2d 678 (Ky. 1993)); Louisiana (State v. Quatrevingt, 617 So. 2d 484 (La. Ct. App. 1992)); Maryland (Jackson v. State, 608 A.2d 782 (Md. Ct. Spec. App.), *cert. denied*, 614 A.2d 84 (Md. 1992)); Michigan (People v. Adams, 489 N.W.2d 192 (Mich. Ct. App. 1992)); Oregon (State v. Futch, 860 P.2d 264 (Or. 1993)); Tennessee (State v. Harris, 1992 WL 127441

(Tenn. Crim. App. 1992)); Texas (Kelly v. State, 824 S.W.2d 568 (Tex. Crim. App. 1992)); Washington, (State v. Kalakosky, 852 P.2d 1064 (Wash. 1993)); and Wyoming (Springfield v. State, 860 P.2d 435 (Wyo. 1993)) have all upheld admission of DNA evidence.

197. DNA evidence was to be offered in United States v. Scott, 24 M.J. 186 (C.M.A. 1987). COMA remanded the case due to a claim of ineffective assistance of counsel. The prosecution sent samples of vaginal swabbings to Cellmark Laboratories for testing, but the tests were inconclusive due to the age of the samples. Cetus Corporation then tested the samples using PCR. Initial results indicated that DNA from semen in the swabbings was consistent with that of the accused, but the accused was acquitted prior to further testing. Long, *The DNA "Fingerprint": A Guide to Admissibility*, ARMY LAW., OCT. 1988, at 36, 44. In United States v. Lake, CM 8800570 (A.C.M.R. 1989), the defense stipulated to DNA evidence from Cellmark. Thus, the issue was not appealed. Long, ARMY LAW., at 44. DNA was also admitted in United States v. Johnson, 1993 CMR LEXIS 313 (A.F.C.M.R.), United States v. Hayes, 37 M.J. 769 (A.C.M.R. 1993), and United States v. Zaccheus, 31 M.J. 766 (A.C.M.R. 1990), but was not an issue on appeal in any of these cases. DNA was used to prove paternity in United States v. Williams, 1989 CMR LEXIS 727 (A.F.C.M.R.), and likewise was not an issue on appeal. No military court of appeal has had to rule on the admissibility of DNA as of February 21, 1994.

198. *See, e.g.*, State v. Alt, 504 N.W.2d 38 (Minn. 1993) (modified statistics admissible); United States v. Porter, 618 A.2d 629 (D.C. 1992) (remand to trial court to determine admissibility of modified statistics under *Frye*); State v. Vandebogart, 616 A.2d 483 (N.H. 1992) (statistical evidence not admissible under *Frye*); Caldwell v. State, 393 S.E.2d 436 (Ga. 1990) (modified statistics admissible).

199. *E.g.*, Commonwealth v. Gomes, 526 N.E.2d 1270 (Mass. 1988).

200. State v. Jobe, 486 N.W.2d 407 (Minn. 1992) (rejected statistics based upon prior, non-DNA precedent which held statistical evidence too prejudicial to be admissible).

201. *See* State v. Cauthron, 846 P.2d 502 (Wash. 1993).

202. Nelson v. State, 628 A.2d 62 (Del. 1993) (statistics excluded because indigent defendant had no expert to counter the evidence at trial).

203. *See* Commonwealth v. Curnin, 565 N.E.2d 440, 443 (Mass. 1991) (DNA match inadmissible "without telling the jury anything about the likelihood of that match occurring.").

204. FORENSIC DNA ANALYSIS, *supra* note 61, at 21 ("With few exceptions, critics cite concerns about only one issue that goes to the underlying science of DNA testing....").

205. 134 F.R.D. 161 (N.D. Ohio 1991), *aff'd sub nom.* United States v. Bonds, 12 F.3d 540 (6th Cir. 1993).

206. *Yee*, 134 F.R.D. at 164; *Bonds*, 1993 WL 515452 at * 6.

207. The district court adopted the magistrate's findings.

208. *Yee*, 134 F.R.D. at 164-65.

209. *Id.* at 165.

210. GENETIC WITNESS, *supra* note 1, at 8.

211. Richard C. Lewontin, *Population Genetic Problems in the Forensic Use of DNA Profiles* (1990) [hereinafter Lewontin, *Yee* Report]; Daniel L. Hartl, *Expert Report* (1990) [hereinafter Hartl, *Yee* Report]. Both of these reports are non-peer reviewed and were not presented to the government until the day the author testified. Brief of Amicus Curiae in Support of Respondent, People v. Britton, No. A058925 (Cal. Ct. App. 1993).

However, the reports are now peer reviewed. Dr. Bruce Budowle and John Stafford have written and published responses to Hartl and Lewontin critical of the reports. Bruce Budowle & John Stafford, *Response to Expert Report by D.L. Hartl, Submitted in the Case of United States v. Yee*, 18 CRIME LABORATORY DIG. 101 (1991); Bruce Budowle & John Stafford, *Response to "Population Genetic Problems in the Forensic Use of DNA Profiles" by R.C. Lewontin, Submitted in the Case of United States v. Yee*, 18 CRIME LABORATORY DIG. 109 (1991).

212. *See* People v. Pizarro, 12 Cal. Rptr. 2d 436 (Cal. App. 1992); State v. Despain, No. 15589 (Ariz. Cir. Ct. 1991); United States v. Porter, 618 A.2d 629 (D.C. 1992).

213. *Yee*, 134 F.R.D. at 181-82.

214. Interestingly, at trial an FBI serologist testified *without objection* that the probability of someone randomly matching the blood using standard ABO blood analysis and the *product rule using general population databases* was less than 1 in 100. Brief for Appellee at 40, United States v. Bonds, 12 F.3d 540 (6th Cir. 1993).

215. *Yee*, 134 F.R.D. at 181.

216. "One cannot compensate for a bias without knowing how large it is." Lander, *supra* note 63, at 821. Interestingly, Lewontin and Hartl state that the probabilities calculated using the product rule can be off by as much as two or more orders of magnitude (or a power of 100). Richard Lewontin & Daniel Hartl, *Population Genetics in Forensic DNA Typing*, 254 SCIENCE 1745, 1749 (1991). How they arrived at this figure is confusing, however, for in the same article they state that "the magnitude and direction of the error depends upon the particular VNTR locus, the bands observed, and the reference database." *Id.* at 1746. Also, from what is the probability off by a power of 100? Since the authors never examined the VNTR data which was made available to them, how do they determine the "accurate" number? Brief of

Amicus Curiae, People v. Britton, No. A058925 (Cal. Ct. App. 1993).

217. *Yee*, 134 F.R.D. at 182-83. However, both Drs. Lewontin and Hartl have now accepted use of some form of the product rule as proper and scientifically accepted. Krane et al., *Genetic Differences at Four DNA Typing Loci in Finnish, Italian, and Mixed Caucasian Populations, in* 89 PROC. NAT'L ACAD. SCI. U.S.A. 10583 (Nov. 1992)(Hartl); Daniel L. Hartl & Richard C. Lewontin, *Letter to the Editor*, 260 SCIENCE 473-74 (1993).

218. *See* Lewontin & Hartl, *supra* note 216.

219. *E.g.*, Commonwealth v. Curnin, 565 N.E.2d 440 (Mass. 1991) (court found, based on testimony by a defense expert, that, due in part to the possibility of population subgrouping, there was no general acceptance of the method of calculating the statistical probability of a random match between the defendant's DNA and the DNA of a semen stain found at the crime scene.).

220. Kreiling, *supra* note 29, at 450.

221. NRC REPORT, *supra* note 26, at vi.

222. Although the magistrate in *Yee* accepted Dr. Lander as an expert (the only areas of expertise the magistrate found relevant were molecular biology and population genetics, *Yee*, 134 F.R.D. at 164-65), Lander's training is *not* in population genetics, but rather in mathematics. NRC REPORT, *supra* note 26, at 175.

Indeed, the Committee has come under fire for its composition by Dr. Neil Risch ("The major problem is that there was no population geneticist on that panel"). And, Dr. Victor McKusick, chairman of the Committee, admits "[w]e probably could have done with more representation in that respect." Peter Aldhous, *Geneticists Attack NRC Report as Scientifically Flawed*, 259 SCIENCE 755 (1993).

223. Dr. Caskey resigned from the Committee on December 21, 1991, prior to the adoption of any conclusions and the publication of its report. NRC REPORT, *supra* note 26, at iii.

224. The report was to be issued at a later date. However, the New York Times obtained a pre-publication copy of the report and printed an article about the report on April 14, 1992. The Times article (which was reprinted in the Baltimore Sun), misstated the major conclusions of the report, forcing the NRC to schedule an impromptu briefing that morning by Dr. McKusick, the Committee chairman, Dr. Haig Kazazian, and Paul Ferrara and Dr. Eric Lander by telephone. *Id.* at x.

225. National Research Council, National Academy of Sciences, Press Release (Apr. 14, 1992).

226. NRC REPORT, *supra* note 26, at 133.

227. *Id.* at 134.

228. *Id.*, ch. 3 ("DNA Typing: Statistical Basis for Interpretation).

229. *Id.* at 74.

230. *Id.* This is essentially the same "substantial" controversy referred to in most cases rejecting DNA statistical evidence.

231. This has proven true. *See, e.g., Porter*, 618 A.2d at 629; People v. Barney, 10 Cal. Rptr. 2d 731 (1992).

232. Lewontin & Hartl, *supra* note 216, and Ranajit Chakraborty & Kenneth Kidd, *The Utility of DNA Typing in Forensic Work*, 254 SCIENCE 1735 (1991).

233. Leslie Roberts, *Was SCIENCE Fair to its Authors?*, 254 SCIENCE 1722 (1991).

234. When SCIENCE editor Dan Koshland reviewed the article, he found that the data did not support the authors' conclusions. He telephoned Dr. Lewontin to ask him to revise the paper. Lewontin's response was that "if there was any attempt to hold up the paper or withdraw it, 'it would be met with the biggest stink he had ever heard.'" *Id.*

235. NRC REPORT, *supra* note 26, at 79.

236. *Id.* at 80.

237. *Id.* (emphasis added).

238. *Id.* at 13-14.

239. Richard C. Lewontin, *The Apportionment of Human Diversity*, 6 EVOLUTIONARY BIOLOGY 381-98 (1972) [hereinafter *Apportionment*].

240. NRC REPORT, *supra* note 26, at 80.

241. *Id.*

242. Interview with Dr. Bruce Budowle, FBI Forensic Science Research and Training Center, Quantico, VA (Feb 3, 1994).

243. NRC REPORT, *supra* note 26, at 81-82.

244. *Id.* at 13-14.

245. *Id.* at 81.

246. *Id.*

247. *Id.* at 82 (citing *Apportionment*, *supra* note 239). Lewontin repeated this contention in Lewontin & Hartl, *supra* note 216, at 1747.

248. NRC REPORT, *supra* note 26, at 90.

249. *Id.* at 81.

250. *Id.* at 82.

251. *Id.* at 90.

252. *Id.*

253. *Id.* at 84.

254. *Id.* However, others, such as the American Association of Blood Banks, take the position that 200 individuals are required to generate a valid statistical analysis of the group's frequencies. Note, *DNA Fingerprinting and the Need for a National Data Base*, 17 FORDHAM URB. L.J. 323, 331, 349 (1989). In addition, Drs. Devlin and Risch use data from studies by Drs. Lewontin and Hartl to demonstrate that the "sample sizes [suggested by the NRC] are inadequate for population genetic inference from VNTRS...." B. Devlin & Neil Risch, *NRC Report on DNA Typing*, 260 SCIENCE 1057, 1058 (1993). In fact, they term the sample size "[t]he *critical flaw* in the study design...." B. Devlin et al., *Statistical Evaluation of DNA Fingerprinting: A Critique of the NRC's Report*, 259 SCIENCE 748, 749 (1993) (emphasis added).

255. NRC REPORT, *supra* note 26, at 83. The NRC actually recommends either a flat percentage or the 95% upper confidence limit for the allele frequency. The 95% upper confidence limit is calculated by the formula:

$$p+1.96\sqrt{p(1-p)/n}$$

where p is the allele frequency and N is the number of samples in the database. This article will use the term "allele frequency" to represent the greater of the actual allele frequency or the

95% upper confidence limit when discussing the "ceiling principle."

256. *Id.* at 84.

257. *Id.*

258. This is clearly the influence of Drs. Lander and Lewontin, who recommended the use of a "ceiling principle." These "ceilings" would be the highest frequency observed within the subpopulation databases of the relevant major racial groups similar to that collected by the Centre d'Etude du Polymorphisme Humain (to which the NRC cites (NRC REPORT, *supra* note 26, at 91)). The product rule could then be used to calculate a maximum probability, which would be valid even if the defendant's own ethnic composition is not represented in the databases. Eric S. Lander, *Letter to the Editor*, AM. J. HUM. GENETICS 899, 902 (1991); *see also* Lewontin & Hartl, *supra* note 216, at 1749.

259. NRC REPORT, *supra* note 26, at 82.

260. *Id.* at 91.

261. *Id.*

262. *Id.*

263. *See supra* text at § II.D.2.

264. Bruce S. Weir, *Population Genetics in the Forensic DNA Debate*, *in* PROC. NAT'L ACAD. SCI. U.S. 11654, 11655 (1992) [hereinafter *Population Genetics*].

265. *Id.* The chance of any one allele occurring would be ½. The probability for eight such loci would be $\frac{1}{2}^8$, or 1 in 256.

266. NRC REPORT, *supra* note 26, at 76.

267. Sylvester, *supra* note 195, at 69.

268. NRC REPORT, *supra* note 26, at 91-92.

269. *Id.* at 92.

270. WEBSTER'S NEW WORLD DICTIONARY 1130 (2d. C. ed. 1978).

271. "Floor Approach" is a more accurate description. *Floor Approach*, *supra* note 93, at 398.

272. NRC REPORT, *supra* note 26, at 92.

273. These are the NRC's recommended populations. *See supra* note 245.

274. NRC REPORT, *supra* note 26, at 92

275. *Id.*

276. *Id.*

277. *See supra* § III.A.1.

278. NRC REPORT, *supra* note 26, at 133.

279. *Id.*

280. *Id.* at 133-34.

281. *Id.* at 134.

282. *Id.*

283. *Id.*

284. *Id.* at 135-41.

285. *Id.* at 141-42.

286. *Id.*, ch. 4.

287. *Id.*, ch. 5.

288. *Id.*, ch. 7.

289. Victor A. McKusick, Statement at the National Research Council Press Conference (Apr. 14, 1992).

290. "It 'appears that the level of debate has only increased as a result of the NRC Report'". Thompson, *supra* note 95, at 64 (citing LAURENCE MUELLER, THE USE OF DNA TYPING IN FORENSIC SCIENCE, in ACCOUNTABILITY RESEARCH 2 (1993)).

291. United States v. Bonds, 1993 WL 515452 at *8 (6th Cir. 1993).

292. Commonwealth v. Daggett, 622 N.E.2d 272 (Mass. 1993); People v. Barney, 10 Cal. Rptr. 2d 731 (Ct. App. 1992). In *Daggett*, the prosecution offered no numerical data; instead, Cellmark's expert testified only that a match was "highly unlikely." The Massachusetts Supreme Court not only would have excluded statistical evidence, but found admission of the non-numerical testimony error because of controversy over population substructure. *Daggett*, 622 N.E.2d at 275.

293. Richard Barbieri, *Jury Still Out on DNA Evidence; Scientists' Ongoing Debate Over Genetic Evidence Has Left Courts at Odds on its Admissibility*, THE RECORDER, Nov. 29, 1993, at 1.

294. "It is universally accepted that substructure exists within major population groups." Bruce Budowle & Keith L. Monson, *The Forensic Significance of Various Reference Population Databases for Estimating the Rarity of Variable Number of Tandem Repeat (VNTR) Loci Profiles*, in DNA FINGERPRINTING: STATE OF THE SCIENCE 177, 178 (S.D.J. Pena et al., eds. 1993).

295. *See* Aldhous, *supra* note 222, at 755.

296. DNA thus far has almost always been corroborative of evidence of blood type, eye-witness identification, or other evidence on the issue of identity. For example, in People v. Barney, 10 Cal. Rptr. 2d 731 (Ct. App. 1992), the victim found the defendant's wallet that he had left at the scene, which contained a photograph and the defendant's name. In People v.

Howard, 10 Cal. Rptr. 2d 731 (Ct. App. 1992), the companion case to *Barney*, the defendant's blood type was extremely rare, found in only 1.2 of 1,000 Blacks and non-existent in Caucasians. Rockne P. Harmon, *Legal Criticisms of DNA Typing: Where's the Beef?*, 84 J. CRIM. L. 176, 178 (1993) [hereinafter *Where's the Beef?*]. In *Brooks*, Cr. No. 92-112-COL(JRE) (M.D. Ga. 1992), the defendant's blood type was found in only 7 out of 1,000 Blacks.

297. Another problem with the "ceiling principle" is that it fails to specify any one calculation. The Committee was unclear on which populations were to be sampled, whether the calculation eliminated the need for binning, and whether the "ceiling principle" calculation was to complement or replace calculations derived from the modified product rule currently in use. Kreiling, *supra* note 29, at 481-82; *see also* Thompson, *supra* note 95, at 80-81. This uncertainty has dramatic results. In State v. Anderson, 853 P.2d 135 (N.M. Ct. App.), *cert. granted*, 848 P.2d 531 (N.M. 1993), the FBI, using the "ceiling principle," found the probability of a random match to range from one in 1.26 million (using floating bins and four probes) to one in 877 (using fixed bins and three probes). Dr. Laurence Mueller, a defense expert, found the probability to be one in eighty-four. Thompson, *supra* note 95, at 81 n.275.

298. The Committee only assumed explicitly that population substructure existed, not that it had any effect on the statistics. NRC REPORT, *supra* note 26, at 80 ("Although mindful

of the controversy, the committee has chosen to assume for the sake of discussion that population substructure may exist and provide a method for estimating population frequencies in a matter that adequately accounts for it.").

299. *Id.*

300. *Daubert*, 113 S. Ct. at 2796. *See also* MOENSSENS, *supra* note 99, at 7-8.

301. *Daubert*, 113 S.Ct. at 2796.

302. *Id.*

303. The Committee desired that an organization to be known as the National Committee on Forensic DNA Typing be created to oversee such analysis. NRC REPORT, supra note 26, at 90. No such committee presently exists; nor are there plans to create it. *Population Genetics*, *supra* note 264, at 11657.

304. NRC REPORT, *supra* note 26, at 80 (citing Bruce Weir, *Independence of VNTR Alleles Defined as Fixed Bins*, 130 GENETICS 873 (1992)); Risch & Devlin, *supra* note 79, at 717.

305. NRC REPORT, *supra* note 26, at 82 (citing *Apportionment*, *supra* note 239, at 381).

306. *Id.* Lewontin claims that variation between individuals within populations is responsible for 85.4% of the genetic variation, with 8.3% attributable to variations between

populations and 6.3% attributable to variations between ethnic groups. B. Devlin & Neil Risch, *Ethnic Differentiation at VNTR Loci, with Special Reference to Forensic Applications*, 51 AM. J. HUM. GENETICS 534, 546 (1992) [hereinafter *Ethnic Differentiation*].

307. Aldhous, *supra* note 222, at 755. Using the restriction enzyme Hae III, Devlin and Risch analyzed the data and determined that, if the Hispanic group was broken up into Southeastern and Southwestern databases, as most forensic laboratories do, there is very little variation between populations -- 2.6% for locus D17S79 and 2.9% for D2S44, calling Lewontin's conclusions into question. *Ethnic Differentiation*, *supra* note 306, at 546.

308. Hartl & Lewontin, *supra* note 216, at 474 (emphasis added). Interestingly, a close examination of what they actually say is revealing. Lewontin stated in *Yee* that "there is one-third more genetic variation on the average for these ... genes among [ethnic groups within races] than there is on the average between [races]." Lewontin, *Yee* Report, *supra* note 211. Lewontin and Hartl restated this observation in their SCIENCE article. Lewontin & Hartl, *supra* note 216, at 1747. When confronted with the volume of data demonstrating more variation between major population groups than among subgroups, Hartl and Lewontin calculated the ratio to be one-third more racial than ethnic, *the opposite direction* from their previous pronouncements. Bruce Budowle & Keith L. Monson, A Perspective on the Polemic on DNA Statistical Inferences in Forensics 8-9, Publication No. 93-13,

Laboratory Division, FBI (1993). For them, the same degree of variation that, in 1990 was strong evidence for concern, is in 1993 reduced to "approximately as much" when it failed to support their argument. Daniel L. Hartl & Richard C. Lewontin, *Response to Devlin et al.*, 260 SCIENCE 473 (1993). Drs. Roychoudhury and Nei analyzed population data from industrialized societies (Lewontin's study consisted of small, isolated populations not representative of the United States) found that differences among races were twenty times as great as differences among ethnic groups. Budowle & Monson, A Perspective on the Polemic on DNA Statistical Inferences in Forensics, *supra* at 9.

309. Appellee's Brief at 45, United States v. Bonds, 1993 WL 515452 (6th Cir. 1993).

310. *Id.* Indeed, in Commonwealth v. Gomes, 526 N.E.2d 1270 (Mass. 1990), one defense expert testified that:

> gene frequencies may vary among locations and ethnic or racial groups.... [S]imply multiplying the gene frequencies failed to take into account certain variable factors, such as the possibility that some traits *may not be independently inherited*, possible differences in gene frequencies due to differing socioeconomic status, and the *lack of genetic purity* in American racial groups.

Id. at 1280 (emphasis added). The evidence was admitted.

311. Appellee's Brief at 45, United States v. Bonds, 1993 WL 515452 (6th Cir. 1993) (citing Record at 259-61 in *Yee*, 134 F.R.D. at 161).

312. Barefoot v. Estelle, 463 U.S. 880, 902 (1983).

313. Bruce Budowle et al., *The Assessment of Frequency Estimates of Hae III-Generated VNTR Profiles in Various Reference Databases,* J. FORENSIC SCI. 15 (forthcoming 1994). *See also* John Brookfield, *Law and Probabilities,* 355 NATURE 207 (1992). There have been *no* peer reviewed articles since publication of the NRC Report which demonstrate any significant effect of population substructure on the statistical calculations. Brief of Amicus Curiae in Support of Respondent at 54, People v. Britton, No. A058925 (Cal. Ct. App. 1993).

314. Ranajit Chakraborty et al., *Effects of Population Subdivision and Allele Frequency Differences on Interpretation of DNA Typing Data for Human Identification, in* PROC. 1992 INT'L SYMP. ON HUM. IDENTIFICATION 205 (1992).

315. *Id.* at 209.

316. *Id.* at 209-10.

317. These measures include the use of bins, taking the larger frequency of the two bins when a sample falls on the border of two bins, collapsing fixed bins so that each bin contains at least five alleles, and the use of the value 2p rather than p^2 in the product rule. *Id.* at 210.

318. George Herrin, *Probability of Matching RFLP Patterns from Unrelated Individuals,* 52 AM. J. HUM. GENETICS 491 (1993). Herrin

study used databases from eight different laboratories in the Southeastern United States.

319. Thompson, *supra* note 95, at 75-76.

320. The data is not new; rather, it is a collection of data already available to geneticists, the Committee, and Drs. Lander, Hartl, and Lewontin. Copies have been provided to all former members of the Committee. Letter from Rockne P. Harmon, Senior Deputy District Attorney, Alameda County, California District Attorney's Office, to the Honorable Justices of the California Court of Appeal, First Appellate District, Division Three 6-7 (Apr. 9, 1993) [hereinafter Harmon Letter]. The data compilation was completed by February, 1992, two months prior to the release of the NRC Report. The NRC failed to consider the data in its recommendations. Interview with Dr. Bruce Budowle, FBI Forensic Science Research and Training Center, Quantico, VA (Feb. 3, 1994).

321. FEDERAL BUREAU OF INVESTIGATION, VNTR POPULATION DATA: A WORLDWIDE STUDY 1993 [hereinafter WORLDWIDE STUDY].

322. *Id.* at 6. Indeed, even "[u]sing a Norwegian database in place of, for example, a Spanish database will not likely result in forensically significant differences in the estimates of DNA profile frequencies." *Id.* This study effectively strips the NRC's "ceiling principle" of whatever scientific basis, if any, it had.

323. Virgin Islands v. Penn, 1993 WL 388146 at *18 (D.V.I. 1993).

324. "The ceiling principle yields the same frequency for a genotype, regardless of the suspect's ethnic background, because the reported frequency represents a maximum for *any* possible ethnic heritage. Accordingly, the ethnic background of an individual suspect should be ignored in estimating the likelihood of a random match." NRC REPORT, *supra* note 26, at 85 (emphasis added).

325. *Id.* at 92.

326. For example, for a particular allele, the minimum frequency used will be either five or ten percent, depending upon whether the modified or unmodified "ceiling principle" is used. Or, if a population is found which has a greater frequency, that frequency will become the minimum used. Thus, in the hypothetical discussed *supra*, the frequency used for allele 8 will always be at least 15.5 percent, as that is the frequency found in the Maori population.

327. ***Floor Approach***, ***supra*** **note 93, at 399.**

328. *Id.*

329. Thompson, *supra* note 95, at 80.

330. *Id.* at 88 n.272 (citing State v. DeFroe, No. 92-1-03699-8 (Wash. Super. Ct. 1993)).

331. *Id.* at 88 n.272.

332. Aldhous, *supra* note 222, at 755.

333. *Id.*

334. Newton Morton, *Genetic Structure of Forensic Populations*, *in* 89 PROC. NAT'L ACAD. SCI. U.S. 2556 (1992).

335. This symposium was open to invitees from around the world. Approximately 300 attended. The FBI, its host, sent invitations to all members of the Committee on DNA Technology in Forensic Science. Drs. Lander, Hartl, and Lewontin all declined to participate. Harmon Letter, *supra* note 320, at 6.

336. *Id.* at 7.

337. Lempert, *supra* note 6, at 51.

338. *Id.* at 45.

339. *Id.*

340. *Id.* at 47.

341. *Id.*

342. *Id.*

343. Roberts, *supra* note 233, at 1721.

344. Peter J. Neufeld, *Have You No Sense of Decency?*, 84 J. CRIM. L. 189, 197 (1993).

345. *Id.*

346. Interview with Dr. Bruce Budowle, FBI Forensic Science Research and Training Center, Quantico, VA (Feb. 3, 1994).

347. SALTZBURG & REDDEN, *supra* note 146, at 109.

348. FED. R. EVID. 402.

349. *See, e.g.*, Bruce S. Weir, *Forensic Population Genetics and the National Research Council (NRC)*, 52 AM. J. HUM. GENETICS 437 (1993) [hereinafter *Forensic Population Genetics*]; Bernard Robinson & Tony Vignaux, *Why the NRC Report on DNA is Wrong*, NEW L.J., Nov. 20, 1992, at 1619; NRC REPORT, *supra* note 26, at 85; Ian W. Evett & Bruce S. Weir, *Flawed Reasoning in Court*, 4 CHANCE: NEW DIRECTIONS FOR STAT. & COMPUTING 19 (1991).

350. *E.g.*, Richard C. Lewontin, *The Dream of the Human Genome*, N.Y. REV., May 28, 1992, at 38 ("The identity of that reference group depends in complex ways on the circumstances of the case."). Dr. Hartl apparently has some problem focusing on the question. In *Yee*, Hartl said that the laboratory should state the likelihood of someone of the defendant's ethnic group and not of the general population, matching the evidentiary sample.

Record at 283-84, *Yee*, 134 F.R.D. at 161. In December, 1991, he and Lewontin went so far as to advocate that "each particular individual may require a different reference group...." *Population Genetics*, *supra* note 261, at 1748. Hartl later stated, however, "We are talking about the chance that there is *someone else in the world* who matches." Tim Beardsley, *Pointing Fingers: DNA Identification is Called Into Question*, SCI. AM., Mar. 1992, at 26, 27.

351. State v. Passino, No. 185-1-90 (Vt. Dist. Ct. 1991). The defendant was part Italian, part French, and part Abenaki Indian, and the FBI could not produce a comparable database. The crime occurred near a state highway in a county with some Abenaki population, and Dr. Lewontin admitted that an argument could be made that "the entire population of western Vermont and eastern New York is the appropriate reference groups." Richard C. Lewontin, *Which Population?*, 52 AM. J. HUM. GENETICS 205 (1993).

352. Estelle v. Williams, 425 U.S. 501, 503 (1976).

353. NRC REPORT, *supra* note 26, at 85. The point has not been confined solely to legal commentators; scientists have also raised the issue. *See* J. Buckleton et al., *Who is "Random Man?"* 31 J. FORENSIC SCI. SOC'Y 463 (1991); THE USE OF STATISTICS IN FORENSIC SCIENCE (C. G. Aitkin & D. A. Stoney, eds., 1991).

354. However, "practicalities" argue in *favor* of the current general population database approach. How is the prosecutor to

learn of the defendant's particular ethnic makeup when the defendant invokes his right to silence? Where are the forensic laboratories to find individuals with "pure" ethnic backgrounds to form subpopulation databases? In the case of a murder victim's DNA analyzed from bloodstains found on the defendant's property, how is the prosecutor to determine the deceased victim's ethnic heritage? All of these practicalities favor use of the existing general databases.

355. *Floor Approach*, *supra* note 93, at 391.

356. B. Devlin et al., *Technical Comments*, 253 SCIENCE 1039 (1991).

357. Even Lewontin has concluded that:

> It is clear that our perception of relatively large differences between human races and subgroups, as compared to the variation within these groups, is indeed a biased perception and that, based on randonly [sic] chosen genetic differences, human races and populations are remarkably similar to each other, with the largest part by far of human variation being accounted for by the differences between individuals. Human racial classification is of no social value and is positively destructive of social and human relations. *Since such racial classification is now seen to be of virtually no genetic or taxonomic significance either, no justification can be offered for its continuance.*

Lewontin, ***supra*** note 242, at 397. This quote argues not only against subgroup databases, but conceivably against racial databases as well.

358. *See supra* text at notes 273-74.

359. *Daubert*, 113 S. Ct. at 2795.

360. *Id.* at 2796.

361. Professor Giannelli would set the burden of proof that a scientific principle is valid at the preponderance of the evidence for criminal defendants and beyond a reasonable doubt for the prosecution. Paul Giannelli, *The Admissibility of Novel Scientific Evidence: Frye v. United States, A Half Century Later*, 80 COLUM. L. REV. 1197, 1249-50 (1980).

362. This is true because, in the usual case, the prosection offers expert testimony of the probability of a random match calculated using the product rule. The defense, if unable to exclude all DNA statistical evidence, counters with its own calculations using the "ceiling principle." *See, e.g., Brooks*, Cr. No. 92-112-COL(JRE) (M.D. Ga. 1992).

363. 113 S. Ct. at 2795.

364. See *supra* § V.B.

365. As did the NRC Committee. NRC REPORT, *supra* note 26, at 80.

366. *Daubert*, 113 S. Ct. at 2796.

367. Specifically, the FBI's worldwide study, *supra* note 321. *See also supra* § V.B.

368. *See, e.g.* Lempert, *supra* note 6, at 45-46; WORLDWIDE STUDY, *supra* note 321.

369. 113 S. Ct. at 2797.

370. *See* Aldhous, *supra* note 222, at 755.

371. *Forensic Population Genetics*, *supra* note 349, at 439, (citing Joel E. Cohen, *The Ceiling Principle is Not Always Conservative in Assigning Genotype Frequencies for Forensic DNA Testing*, 51 AM. J. HUM. GENETICS 1165 (1992)).

372. Jennifer R. Slimowitz & Joel E. Cohen, *Violations of the Ceiling Principle: Exact Conditions and Statistical Evidence*, 53 AM. J. HUM. GENETICS 314, 316 (1993).

373. *Id.* at 317.

374. *See supra* text at notes 290-91.

375. Dr. Eric Lander stated, "I only worry that renewed controversy about wanting higher odds will confuse the courts into doubting that there is general acceptance that the ceiling principle provides a conservative estimate." Aldhous, *supra* note 222, at 756.

376. FED. R. EVID. 403.

377. SALTZBURG & REDDEN, *supra* note 146, at 138.

378. *Id.* at 141.

379. Slimowitz & Cohen, *supra* note 372, at 316.

380. Obviously, the defendant would like all evidence of a DNA inclusion to be suppressed. The defense often attempts to offer statistics calculated using the "ceiling principle" to rebut the government's use of statistics calculated by the modified product rule. *See Bonds*, 1993 WL 515452 at *7 (1 in 35,000 by modified product rule, 1 in 17 by "ceiling principle"); Record at 112, *Brooks*, Cr. No. 92-112-COL(JRE) (M.D. Ga. 1992) (1 in 734,000 by modified product rule, 1 in 12,000 by "ceiling principle").

381. Davis v. State, 476 N.E.2d 127, 134 (Ind. Ct. App. 1985).

382. State v. Wheeler, No. C89-0901 (Or. Super. Ct. 1990).

383. 134 F.R.D. at 161.

384. *Population Genetics, supra* note 264, at 11656; *Ethnic Differentiation, supra* note 306, at 546; *A Note on Hardy-Weinberg Equilibrium, supra* note 85, at 549.

385. In *Barney*, 10 Cal. Rptr. 2d at 731, for example, the frequency calculated using the modified product rule was one in seven million. Using the "ceiling principle," the result was one in six million. *Where's the Beef?, supra* note 296, at 181 n.47.

386. At first glance, the assertion that the "ceiling principle" is both misleading and cumulative seems contradictory. A closer examination reveals that it is the *basis* of calculating the

"ceiling principle" (that allele frequencies from several different and unrelated databases or the minimum five or ten percent are used) that is misleading, while the *result* (that a match between the defendant's DNA and the evidentiary sample is rare) is merely cumulative.

387. Aldhous, *supra* note 222, at 755 (Committee members interviewed "generally defended the ceiling principle on the grounds that it was designed to reduce the controversy over the admissibility of DNA evidence in court....")

388. *Supra* text at note 324.

389. Thompson, *supra* note 95, at 80.

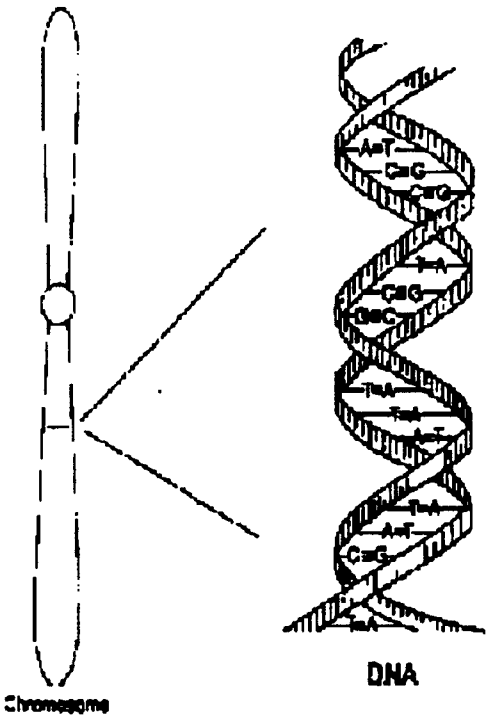

Figure 1 Representation of the double-helical DNA molecule (expanded from a chromosome).

Source: DNA TECHNOLOGY IN FORENSIC SCIENCE (1992). Reprinted with permission from the National Research Council, National Academy of Sciences.

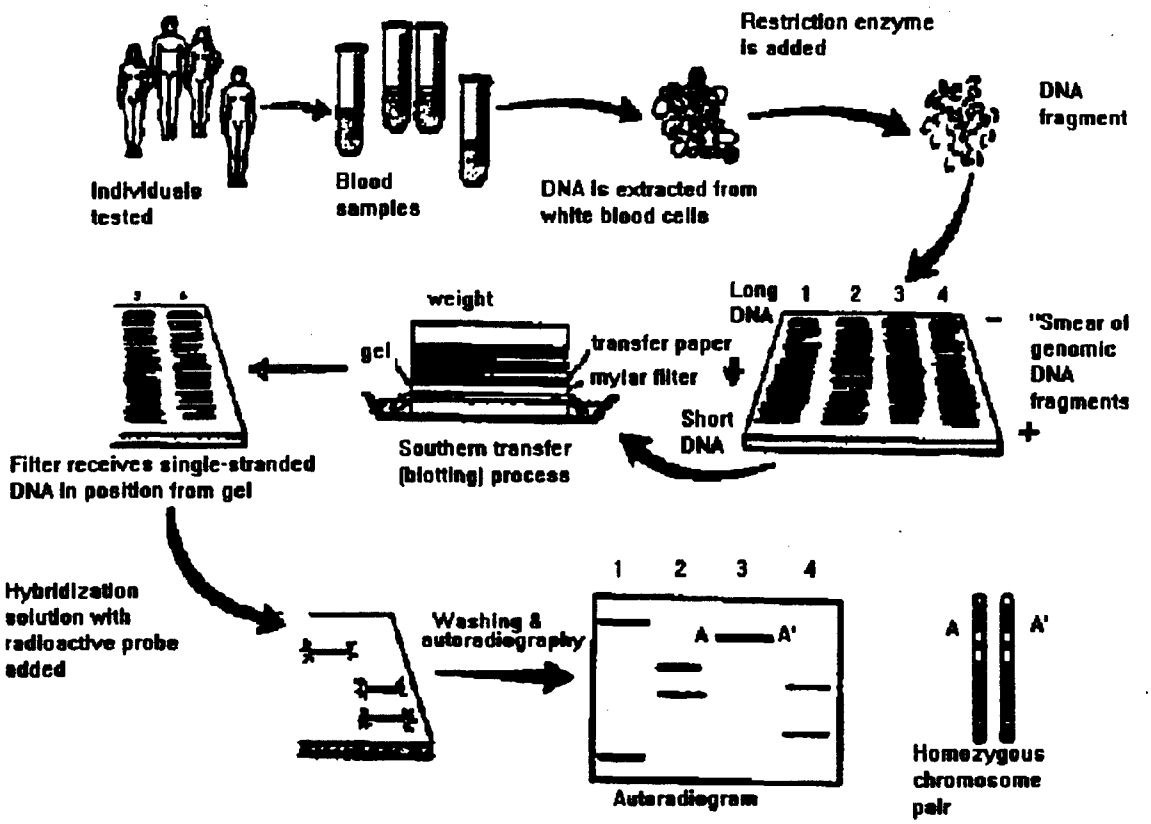

Figure 2 Schematic of DNA analysis using Southern Blotting. The autorad reveals a single-locus, multi-allelic analysis of four samples. Sample 3 is homozygous (A-A').

Source: DNA TECHNOLOGY IN FORENSIC SCIENCE (1992). Reprinted with permission from the National Research Council, National Academy of Science.
Source

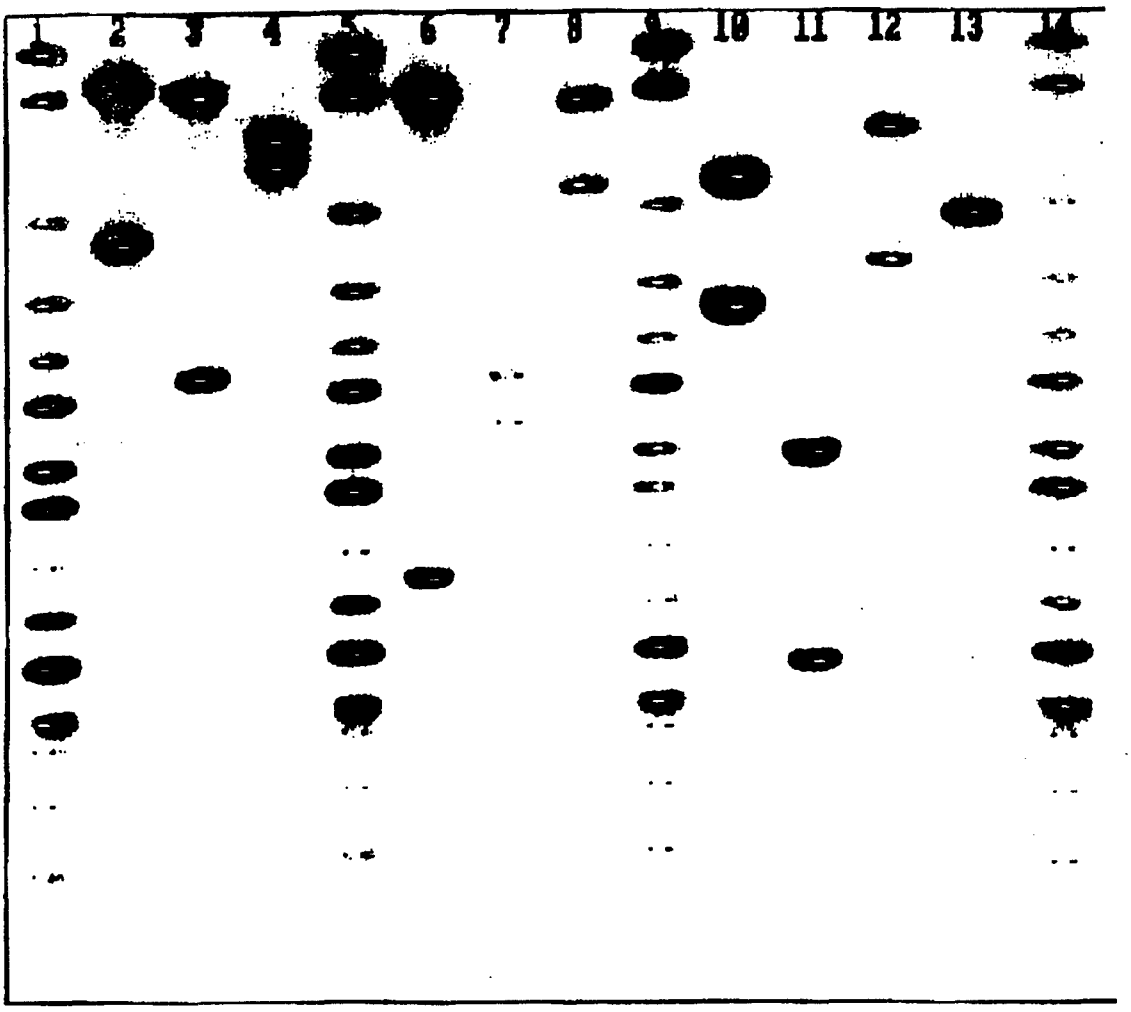

Figure 3 DNA Autoradiogram using automated analysis. The dark spots are DNA samples bound with radioactive probe; the light bands are the center of mass as determined by the computer.

Source: OFFICE OF TECHNOLOGY ASSESSMENT, U.S. CONGRESS, GENETIC WITNESS: FORENSIC USES OF DNA TESTS (1990).